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'DNA' AND LANGUAGE
THE NATURE OF THE SYMBOLIC-REPRESENTATIONAL SYSTEM IN CELLULAR PROTEIN SYNTHESIS AND HUMAN LANGUAGE COMPREHENSION

A DISSERTATION SUBMITTED TO
THE FACULTY OF THE DIVISION OF HUMANITIES
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COMMITTEE ON THE CONCEPTUAL FOUNDATIONS OF SCIENCE

BY
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ABSTRACT

A unique cellular "symbolic-representational" system first arose from a prebiotic substrate at the origin of life, permitting Darwinian evolution to occur. Although the subsequent history of life witnessed incredible increases in complexity and diversity, and the development of new levels of organization, a similar system did not reemerge on any intermediate level until the origin of thought and language in Pleistocene hominids. My main tasks are to establish the analogy and then to make some use of it. The analogy leads to a novel and interesting model of language processing in the human brain, and has a number of philosophical and scientific implications for the origin and nature of symbolic-representational systems.

Chapter I discusses the use of analogy and critically reviews previous attempts to compare biology and language. Chapter II reviews some existing general treatments of symbolic systems and introduces a new framework for the present investigation. Chapters III, IV, and V develop the three main parts of the analogy and Chapter VI summarizes progress toward the stated goals.

CHAPTER I

INTRODUCTION

There have been numerous published comparisons of the genetic code and language in the years since the discovery of the structure of DNA in the 1950's, and its relation to protein structure in the early 1960's; in fact, the topic has become somewhat hackneyed. Beginning with molecular biologists who described a "central dogma" (Crick, 1958) in essentially linguistic terms, biologists and linguists have continually felt the urge to draw parallels. DNA has variously been labeled an alphabet (Beadle, 1963), a book (Platt, 1962), a Morse code (Berlinski, 1972), a phonemic system (Jakobson, 1970), the "deep structure" of a transformational grammar (Masters, 1970), a set of hypotheses (Goodwin, 1972), and a "pure language of commands" (Ratner, 1974). Jakobson (1970) equated bacterial operons with "syntactic units", Zwick (1978) compared proteins to sentences, while Hofstader (1979) drew parallels between the genetic code and Godel numbering. The linguist Lees (1980) communicates a sweeping vision:

> the analogy between these two levels is unmistakable. On at least two separate occasions in the history of our corner of the universe, a new kind of complex control system of interacting elements arose spontaneously to generate a self-contained, homeostatic, evolving organism. The first, the biological world of life arose in a substrate of chemical interactions, and in time, it invented the genetic code. The second, the mental world of the intellect, arose on a substrate of nervous interactions in the brains of higher species, and in time it invented a linguistic code (p. 225).

The treatments of Pattee (1980, 1982) and Waters (1981a, 1981b) review the literature and draw interesting parallels at several levels, calling once again for a coherent theory of natural symbol systems. For all the enthusiasm, though, the endeavor has remained largely programmatic. Partly this is a result of a less than delicate treatment of the details of the relevant scientific fields in the rush to compile a parallel list. In other cases, though, it must be blamed on an over-cautious approach:

> The very complexity of natural symbol systems that makes them interesting creates traps for those who attempt to interpret the analogy too literally. Detailed isomorphisms, such as those equating codons and words or nucleic acids with phonemes offer no explanations, and the purpose of a theory is to explain, not to catalogue (Waters, 1981a, p. 3).

Just as a line of inquiry begins to call upon concrete details, there is an instinctive retreat:

> [The] transformation from linear, discrete, sequential, rate-independent symbol strings [DNA] to the three-dimensional, continuous, highly parallel, rate-dependent function [enzyme] should be carefully considered, at least as a conceptual basis for a theory of linguistic competence. There is no reason [however] to expect that at the level of the brain the structures executing this transformation are like synthetases and ribosomes (Pattee, 1980, p. 267).

The jaundiced eye sees on one hand, a multitude of explicit catalogs devoid of an explanatory theory, and on the other, no more than tantalizing fragments of such a theory through a haze of qualifications. As a result, most mainstream researchers have understandably come to regard the topic as a refuge for the loose-thinker, dillettante, or an otherwise productive colleague temporarily in the grip of holistic spasms.

I believe the idea deserves a less timid treatment. In this study, I will argue that a more specific, closely-reasoned analogy-- and consequently, a more constrained analogy --is the basis for important insights into the fundamental nature of a symbolic-representational system. I would like not only to motivate and explicate a structural and functional parallelism between cellular protein synthesis and human language perception, but also to make some conceptual use of the analogy as it develops, exploiting both comparisons and contrasts. The three interrelated goals of this project are-- 1) to specify the scale- or level-independent constraints in building a self-contained symbolic-representational system, 2) to suggest a way to construct a neurobiological processing model of language understanding, and, 3) to give a more specific definition of what is necessary to make a system capable of evolution. In the process I hope to promote a certain philosophical perspective on the origin and nature of meaning and reference. In the remainder of this introduction, I will discuss the use of analogy, previous work on this analogy, related analogies at different levels, and a rationale for why one would expect to find similarities in the two systems.

The Use of Analogy

There has been a long-lived interest in metaphor and analogy in philosophy, literary criticm, and linguistics (e.g., Richards, 1936; Black, 1962; Shibles, 1971; Ortony, 1979; Lackoff and Johnson, 1980). In philosophy of science by contrast, analogy and analogical reasoning have for a long time been viewed with ambivalence or suspicion (e.g., Suppe, 1977). Thus, Duhem (1914/1954) grants that after

> two categories of very distinct and dissimilar phenomena [have] been reduced by abstract theories, it may happen that the equations in which one of the theories is formulated are algebraically identical to the equations expressing the other (p. 96).

However, one should not confuse this "logical coordination of abstract theories", which is sometimes capable of providing insight, with the use of mere models, especially concrete ones, which can only lead the shallow mind to superficial or artificial connections. Duhem is metaphorically indignant-- the mechanically-minded modeler "seeing the dusty smoky smelly automobile, regard[s] it as the triumphal chariot of the human spirit" (p. 93). Analogy subsequently played a rather minimal role in logical empiricist philosophy of science (e.g., Hempel, 1965).

The recent regrowth of interest in scientific discovery (e.g., Nickles, 1980a, 1980b), however, has been accompanied by a renewed interest in complex explanatory analogy in both history and philosophy of science and cognitive psychology (Sellars, 1965; Hesse, 1966; Harre, 1970; North, 1980; Glucksberg et al., 1982; Darden, 1983; Gentner and Stevens, 1983). Analogy seems to be a fundamental tool, not only in learning about science, but also in generating it. A fluid-flow/current and potential/height analogy, for instance, has long been used to effectively guide students in reasoning about simple DC circuits (see Larkin, 1983, and Gentner and Gentner, 1983, for some experimental support). On the other hand, analogy often is intimately involved in scientific discovery. This is nicely illustrated by the recent construction of a complex-valued logic (Spencer-Brown, 1979) that turned out to have a number of applications ranging from digital-only counting circuits to a proof of the four-colour problem. The primary move involved constructing a simple recursive formula (2) parallel to the type used to define complex numbers (1):

(1) $-1/x = x$ solution is an imaginary number ($\sqrt{-1}=i$) used to define a complex component magnitude orthogonal to real positive and negative numbers

(2) $\sim a = a$ solution is a new "imaginary" truth value component, "orthogonal" to "real" (T,F) truth-values

Similar examples can be found in many scientific fields (see e.g., North, 1982; Darden, 1983).

Of course, Duhem's fear that the unconstrained mind can find a given thing a bit analogous to just about anything else was in part justified. And a main thrust of recent work on analogical reasoning has been to find sensible criteria (beyond Duhem's algebraic identity) for picking out productive alignments from a sea of 'virtual' analogies. A concurrent task has been to make a taxonomy of different types of models or analogies (e.g., Harre, 1970; Gentner, 1983). Although my main purpose is not to discuss analogy *per se*, a few comments about these issues are in order.

The present theoretical framework for explanatory analogy is relatively uncontroversial and has much in common with the discussions of Hesse (1966) and Gentner (1983). The two systems to be compared must first be broken down into parts. Hesse, for example, presents parallel lists of properties and implied within-list relations, while Gentner employs a more explicit "semantic network" (of the sort originally proposed by Collins and Quillian (1969)), made up of object-nodes containing object attributes and predicate links specifying relations between objects. Specifics aside, I would agree (using Gentner's solar system/atom example) that similar "relations" (e.g., the central object is more massive that the orbiting objects) are often more important in setting up the analogy than similar concrete "attributes" (e.g., the central object is hot and yellow). One problem with this approach is that sometimes it is difficult to determine whether something is a "relation" or an "attribute" (e.g., objects are accelerated by an immaterial field). Another is that it ignores context; as Wimsatt, (1976, 1980a) and Hooker (1975) have stressed, a number of contextual or ceteris paribus conditions must also be specified (e.g., most of the system consists of empty space; collisions are rare; the system is relatively isolated). Higher-order relations (systematic connections among lower-order relations) seem especially important in constraining analogy (Gentner, 1983). In physics, such simultaneous constraints are usually expressed mathematically (e.g., Newtonian law of universal gravitation); however, this is only one of several ways of expressing systematicity and it does not seem appropriate to the present task, at least to start with. To conclude, I would like to retain the explicit, visual, map-like presentation of the cognitive psychologist, but make use of a more heterogeneous ontology (see Chapter 2) than is suggested by a typical "semantic network" with uniform nodes and one-to-one links.

So far, an analogy has been drawn as if it were a static comparison between two equally decomposed, equally 'transparent' systems. Such an analogy might be used to introduce students to an already well developed theoretical framework in a domain. A more interesting situation from the standpoint of trying to construct new theories arises when certain parts of the 'exposed' structure of one system suggest the existence of similar objects and relations in a 'hidden' or as yet unknown part of the other system. Hesse (1966) gives predictions derived in this way the somewhat counter-intuitive label, the "neutral analogy", to indicate that the target system may or may not have an analogous entity or relation. Darden (1983), following Oppenheimer (1956), has also noted that a failed analogy (e.g., the expected medium of electromagnetic waves was not found) can be as productive as a successful one; although a new idea or theory so derived does not owe a 'structural' debt to the analogical process, that process was nevertheless indispensible in directing the search for new theory and evidence.[1]

In this light, the present study will first try to establish enough connections between the 'exposed' parts of the two systems to suggest that they are strongly analogous. Second, certain parts and relations of the more completely understood biochemical system will be used to model the parts and relations that are still 'hidden' from direct examination in human language understanding. In the process, I hope to bring some order to an extensive body of less direct observations. At each stage, I will try to show how alternate analyses using different levels, units, or correspondences in the two systems are not as effective or coherent. Finally, implications of the resulting model--and of disanalogies between the two systems --can be developed.

I implied above that previous attempts at the DNA/language analogy were superficial. In some cases what I think are crucial sets of information have only recently become available; in other cases, however, vague assessments of what fields and data the analogy is intended to apply to are responsible. It is a sobering excercise to consider the number of fields that a thorough analysis demands we consider. First, there are many relevant observations, often with subtle implications, buried inside the mountains of reports generated yearly in biophysics, biochemistry, molecular biology and cellular

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[1] It is interesting to compare the process of predictive analogical comparison sketched out with heuristics for predictive interlevel identification, as developed by Wimsatt (e.g., 1976, 1980a) and Darden (1974) and Darden and Maull (1977). These heuristics apply to the development of interlevel links between entities in two theories where the theories are about phenomena at different levels of organization in a system (e.g., macroscopic genetic _vs_. molecular genetic phenomena) There are a number of similarities with the strategy outlined above; the most obvious difference is that there is no requirement in analogy that the entities compared actually be identical, and in fact, except in special cases, they never are. This intriguing relationship needs to be investigated in more detail than is possible here.

biology. Second, the analogy is intimately involved with what is known about neuroanatomy, neurophysiology, and neuropsychology. Cognitive psychology and psycholinguistics constitute a third major area to be consulted. Finally, one must deal with linguistics, *per se*. It is obviously imperative in this light to steer a careful course between facile generalizations and unanalyzed detail. Since the subject and scope of the analogy forces a great reliance on the current scientific literature, it will be sometimes necessary to take sides in ongoing debates, or occasionally even invent things, particularly in considering suggestions about the nature of 'hidden' phenomena mediating language comprehension. However, as noted above, this is certainly one of the legitimate motivations for carrying out an analogical comparison. I hope the results convince the reader that a productive 'middle-ground' between pure philosophy and the anastomosing tunnels of contemporary scientific disciplines does actually exist.

Previous Work

In the opening paragraphs, I too hastily dismissed previous work as well-intentioned but flawed. Therefore, after briefly discussing some of the initial incarnations of the idea, I critically examine three recent, and by comparison, extended treatments of the analogy.

Early Molecular Biology

The reference to a recognizably linguistic analogy dates at least to Schrodinger (1944) who proposed a "hereditary codescript" embodied in an "aperiodic crystal". His book has often been cited as an inspiration to the molecular biologists who worked on the "coding problem" in the 1950's (Judson, 1979). Preliminary evidence that strings of DNA bases somehow coded for the strings of peptides in proteins already existed at the time the DNA structure was solved by Watson and Crick (1952). One of the first concrete proposals following that discovery was the coding scheme of the cosmologist Gamow (1954) in which peptides were polymerized directly off of a DNA template. The DNA sequence was to specify the peptide sequence by means of the different shaped cavities in the main groove of the double helix (each formed by two pairs of adjacent bases ten base pairs apart) that resulted from different base sequences. The scheme was clearly not very plausible stereochemically to someone with a structural chemistry background like Crick. However, it immediately inspired further work by Crick and others. Gamow notably used a linguistic metaphor:

> the hereditary properties of any given organism could be characterized by a long number written in a four-digital system [of DNA bases]. On the other hand, the enzymes... can be considered as long words based on a 20-letter alphabet [of amino acids]. Thus the question arises about the way in which four-digital numbers can be translated into such 'words'.

This metaphor was modified (incorrectly as we shall see) by Crick (1959) who claimed that it was

> possible, however, to consider the [coding] problem in an abstract way as that of translating from one language to another; that is, from the 4-letter language of the nucleic acids to the 20-letter language of the protein (p. 35).

Earlier Crick et al. (1957) had proposed an elegant but ultimately incorrect scheme they called a "comma-less" code. It allowed unambiguous decoding of triplets of bases in continuous DNA strands because it was set up to make "sense" in only one frame; The two alternate ways of "reading" the strand three bases at a time would result in "nonsense". Today, the metaphorical use of "language", "translation", "letters", "reading", and "sense" is hardly noticed; it seems casual and appropriate. In the late 1950's, however, such talk was not considered natural by many biologists, and in Crick's case, it was hardly a casual turn of the phrase-- it was rather a campaign to convince biochemists to think in a different way than many had grown accustomed to, about a problem that is, (quoting from Crick's paper on the central dogma, the sequence hypothesis, and the adaptor hypothesis)

> independent of the biochemical steps involved, and deals only with the transfer of information. This aspect of protein synthesis appeals mainly to those with a background in the more sophisticated sciences . Most biochemists in spite of being rather fascinated by the problem, dislike arguments of this kind (1958, p. 158).

Regardless of the validity of Crick's taxonomy of science, he was one of the first after Gamow, and the first biologist to give a clear voice to the feeling that there was something language-like happening in cells. This realization accompanied what Judson (1979) describes as the main transformation in ideas in the rise of molecular biology-- the notion of <u>biological specifity</u> in linear sequences, in 3-D structure, and in the connection between the two. It had seemed much less natural to speak of rules, codes, and grammars before the regular structure of DNA was known and at a time when proteins were conceived of as heterogeneous, dynamically interchanging populations or "species" (for a clear late statement of this view, see Haurowitz (1956)). As it turned out, the early metaphors stuck, and a few linguistic terms were permanently taken over into molecular biology-- e.g., protein synthesis is still called "translation".

Molecular biologists, however, had never been interested in developing the comparison into a productive analogy in the sense described in the previous section, and the parallels are haphazardly drawn. The "language" of the molecular biologists' analogy was no more taken to be like a linguist's natural language than was their "information" much like anything in information theory. The comparison of polypeptide assembly to language "translation" was particularly unfortunate as we shall see. The first quote from Crick also mixes levels. Thus, DNA bases are like "letters" that are grouped into "words" but then unexpectedly, each of these three letter words are "translated" into single amino acid "letters". It seems that the target system for the analogy was actually something more like a coding process that related two sets of uninterpreted symbols (see also Berlinski (1972)), than a true language. Interested linguists surprisingly have been for the most part satisfied with the biologists' informal parallels; Jakobson (1970), for example, equates phonemes with DNA bases, words with codons (i.e., triplets), and codon sequences with well-formed syntactic units, but then accepts without comment, a "translation" into a "peptidic language", for what should logically be--following the previous pairings --something more like the "meaning extraction" step or a semantic interpretation. The paper by the linguist Lees (1980) avoids this inconsistency-- "a word (in most cases) has a meaning, a triplet specifies a particular amino acid" --but this intriguing idea is carried no further.

Three recent attempts to develop the comparison more rigorously are Hofstader (1979, 1982), Waters (1981a, 1981b), and Pattee (1980, 1982). Each treatment in its own manner violates the maxims of good explanatory analogy. Nevertheless, the oversights are often subtle and help to emphasize how careful one must be, when dealing with such complex systems, to get the overall context of a comparison right before splashing around in the details.

Godel Numbering and the Genetic Code

Hofstader (1979) is particularly interested in examples of what he calls the "Strange Loop" phenomenon that

> occurs whenever, by moving upwards (or downwards) through the levels of some hierarchical system, we unexpectedly find ourselves back where we started (p. 10).

He then goes on the give examples from, and draw analogies between the musical compositions of Bach, the lithographs and engravings of Escher, number theory in the light of Godel's Incompleteness Theorem, paradoxes in the philosophy of language, high-fidelity record players, and cellular protein synthesis, among others. To see how the analogies with the genetic code go wrong, it is easiest to start with one that works--an analogy between Godel's first proof (Godel, 1931; Nagel and Newman, 1954) and a specially constructed version of the so-called Epimenides paradox, or the liar paradox (see e.g., Quine, 1966). Hofstader presents eight basic parallels in the development of an undecidable, self-referential sentence within the two systems (p. 449). Furthermore, the overall context of the paradoxes is similar; neither greatly affects the way most mathemeticians or language users, respectively, go about their business. Rather, the paradoxical sentences revealed simply that there are unavoidable "holes" in any possible axiomatic system; stated another way, one cannot have both a <u>complete</u> and a <u>consistent</u> axiomatization of a formal system. An important point is that neither Godel's theorems, nor Quine's version of the Epimenides paradox actually <u>explain</u> how number theory and the rest of mathematics on one hand, or first-order predicate logic and natural language on the other, actually work; instead, they point to special, albeit important, conditions where the systems break down.

It is easier now to see the lopsidedness of the mapping between the construction of Godel's sentence and protein translation (table on p. 533). A fundamental difference between the two is that the genetic code *does* actually explain how cells in the main work, not just how they malfunction in certain special circumstances. Equally important, the operation of the genetic code is key to every cell's continued survival; Godel numbering, thankfully, has no similar function for most working mathematicians deriving a proof. In essence, Hofstader has compared the whole guts of one system to a small part of another-- in particular, to a specialized apparatus by which an unexpected incompleteness of that system was demonstrated.[2] Now a contextual or global mismatch between the two systems does not automatically vitiate an analogy, especially is there is a good explanation or if there exist strong parallelisms elsewhere.

Turning to Hofstader's focal comparisons, however, we find many of them forced as well. For example, DNA strands are compared to *Principia*-like number theory strings but then the complementary RNA strand, which is equal in length to the DNA, is analogized with a string of the higher order constructs that might appear in a number theory proof; such a higher order string may be a great deal shorter than its *Principia Mathematica* equivalent. In one of Hofstader's earlier examples (p. 204, 212) he shows with some glee that "5 is prime" (an RNA-like string) can be decomposed rather opaquely into the more explicit, lower level language (a DNA-like string) as:

(3) $\forall d{:}\exists e{:}{\sim}\exists b{:}\exists c{:}(d+Se) = (SSb*SSc)$

---

[2] Of course, Godel's result made the axiomatic system of Whitehead and Russell's *Principia Mathematica* considerably less interesting given that the whole motivation for constructing the system had been to provide a consistent and complete foundation for logic, type theory, and number theory, and it was hoped, the rest of mathematics.

(where small letters are variables, S stands for successor, and * for multiplication). Clearly, (3) is not a one-to-one mapping from "5 is prime" in any obvious sense; the pair of number theory sentences in this case are remarkably different from their intended analogues at the cellular level. Some of Hofstader's mappings are of course less opaque, but without explanation, the analogy is too vague to be very productive.

The most important difficulties arise in the comparison between Godel numbering and the genetic code. At one point, Hofstader draws up a modified Godel numbering scheme to look like the genetic code (p. 535); it is made up of triplets (cf. codons) of four possible numbers (cf. RNA bases) standing for Principia-like symbols (+, S, etc.-- cf. amino acids). But in a previous table, the RNA => protein step is compared with "arithmetization". On the surface, "arithmetization" would seem to go exactly the opposite way-- that is, symbols => numbers. In fact, Hofstader is comparing de-arithmetization to protein synthesis. What happens is that certain "informal statements about number theory" (i.e., what he is comparing to RNA strands) in addition to being the "interpretation" of formal Principia-like statements (cf. DNA strands), can be partially reinterpreted by decoding the strings of numerals in them via the "Godel code" to get a different set of meta-mathematical statements (also Principia-like) about Principia-like statements. It is these meta-mathematical statements that are compared to the amino acid strands that constitute proteins. Thus, in contrast to the situation in molecular biology, we end up after de-arithmetization with the same sort of stuff that we started with. Each symbol by itself means the same thing as before; however, the de-arithmetization step has generated a new (but predictable) logical string from a string of numerals in one of the starting statements. Of course, this is exactly what Godel needed to produce an undecidable sentence meaning approximately "there is no formula that is the proof of the formula we are in now". But in protein synthesis, as previously noted, the decoded protein product is made of fundamentally different stuff than the initial DNA (or RNA) sequence. The two different types of units when isolated "mean" different things biochemically. After concatenation, the "meanings" of polypeptide chains are, in any biochemically sensible use of the word, orders of magnitude more diverse, and qualitatively different than the biochemical meanings of DNA strands; in addition, polypeptides play by entirely different "rules" (e.g., of backbone constrained self-assembly).

Finally, there is a major, and quite obvious disanalogy between the two systems in the way information is transmitted across levels. In the genetic code, one can find the same "piece" of information at all three levels (a DNA triplet, its complementary mRNA triplet, and the amino acid it codes for) and the order of these pieces (RNA splicing aside) is strictly preserved in mappings between levels. The lack of a one-to-one map between Hofstader's DNA and RNA analogues was already mentioned. But there is a similarly opaque mapping between his RNA and protein analogues implicit in the previous discussion. As was noted above, Godel demonstrated that one can construct a mapping that uniquely associates a single number (i.e., a string of numerals) with arbitrarily long symbol sequences, including, for example, Principia-like proofs. In the specially designed Godel-numbers that Hofstader uses, the mapping is one-to-one between triplets of digits in the numerical part of the RNA-like (metalanguage) starting string, and symbols in the de-arithmetized product. However, the important point here is that only a part of the putative RNA-analogue-- i.e., the numerical part --can be so decoded; this contrasts sharply with the molecular situation where all of the RNA can be decoded. A second disanalogy is that the putative protein analogue can include not only the whole starting DNA-like string, but also some other stuff; again, this is how one can get to Godel's undecidable sentence. Nevertheless, this last breakdown in the one-to-one mapping between levels never occurs in cells because because the decoded string is made out of different stuff than the string we start with. This is not to say that proteins cannot interact with or "refer to" DNA, or other proteins for that matter; but it is to say that proteins can never include the DNA strings that they are decoded from as a subset of their own strings because they contain no DNA. Differences in the two mapping schemes are summarized in Figure 1.

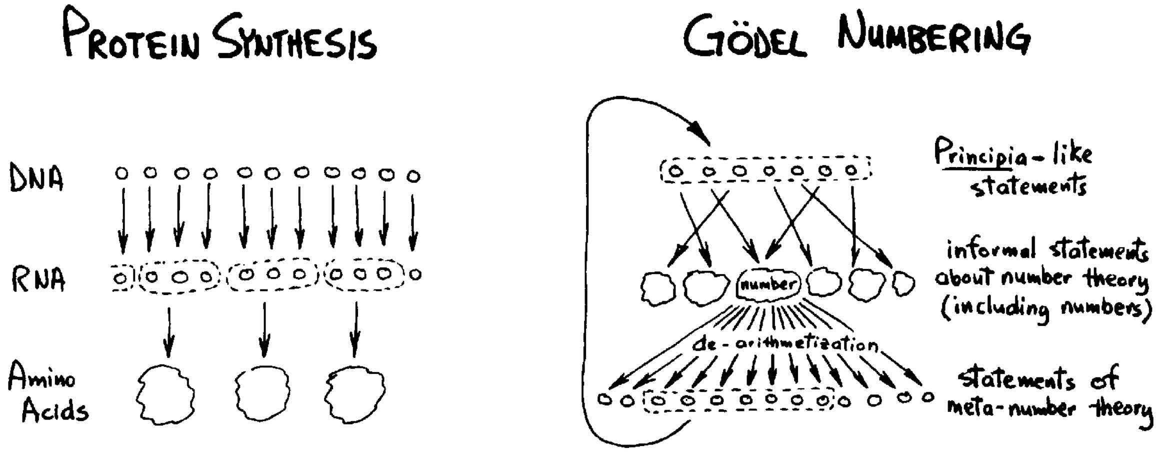

FIG. 1: Analogy Presented in Hofstader (1979)

One might object that I have treated Hofstader unfairly by insisting on overly concrete comparisons. But lacking specific suggestions as to where more abstract senses were intended, I feel unembarassed in sticking to the interpretations of entities and relations given by people actually working in the various scientific fields used in the analogy. The point is not to eliminate all but the strictest parallelisms, but rather, to get a very clear idea of what is supposed to be analogous and what is not. In the present case, it appears that Godel numbering and Godel sentences are not very similar to the structures involved in cellular genetics; the analogy is neither drawn carefully enough, nor is it very productive.

The Gene as Word

A second extended treatment of the analogy is that of Waters (1981a, 1981b). Following Pattee (see below), he wants to compare biological heredity and human language as examples of "natural symbol systems" (as opposed to "formal symbol systems" like mathematical logic or computer languages) to see if a set of underlying global principles can be derived. Compared with Hofstader, Waters is more on track in setting up the basic context of the comparison. But a failure to keep the organization of the two sets of entities parallel at a key point in his discussion leads to peculiar results. The anomalous match-ups are the result of concentrating too much on "attributes" at the expense of systematic "relations"-- a violation of one of the maxims outlined earlier.

As with most previous treatments, Waters points out that both DNA and sound streams take

> the form of strings on an alphabet, an alphabet of phonemes in the linguistic code and of nucleotide bases in the genetic code. Furthermore, these strings are structured hierarchically, through intermediate levels of organization, e.g., morphemes and codons. Each small alphabet element is meaningless unto itself, but can produce a potentially infinite set of meaningful strings. Finally, in each code, the string processing mechanism operates sequentially, reading or writing one alphabet element at a time (1981b, p. 2).

Clearly, phonemes and DNA bases are to be directly compared. But then Waters says that morphemes and codons are only "examples" of intermediate levels of organization, implying that perhaps, they are not parallel-- in spite of the fact that these are the first higher level units past the meaningless subunits of each string. As we shall see, he has ulterior motives for not comparing words to codons; unfortunately, this bias leads to an essentially incorrect characterization of the meaning extraction process. He correctly emphasizes the sequential nature of string processing but fails to note that aside from replication and transcription, it does not involve "reading one alphabet element at a time" as stated above. Instead, the "alphabet elements" are recognized in small groups--i.e., the three RNA bases in a codon and the two to ten or so sound segments per word. The parallel between codons and words is even recognized by many contemporary molecular biologists who use these terms interchangeably (see e.g., Watson, 1976) without quotes. Waters, by contrast, proposes to skip the codon level entirely and compare entire genes, consisting of hundreds or thousands of DNA bases to single linguistic words, which commonly contain four or five phonemic segments. The motivation for this is that when compared to single word meanings, Waters seems to think that amino acids have no "independent meaning". Aside from the fact that amino acids have intrinsic, independently definable attributes-- e.g., different hydrophobicities, different acidities, different van der Waals surfaces --that are directly responsible for the eventual structure and function of an enzyme composed of them, and that would seemingly qualify as component "meanings", this scheme requires such a mismatch in relations between the two systems (see fig. 2) that it is a little difficult to take the very specific parallels about a "generative grammar", later proposed by Waters, seriously. Between-system differences are not only possible but are to be expected; nevertheless, major structural mismatches without explanation can only cripple the project.

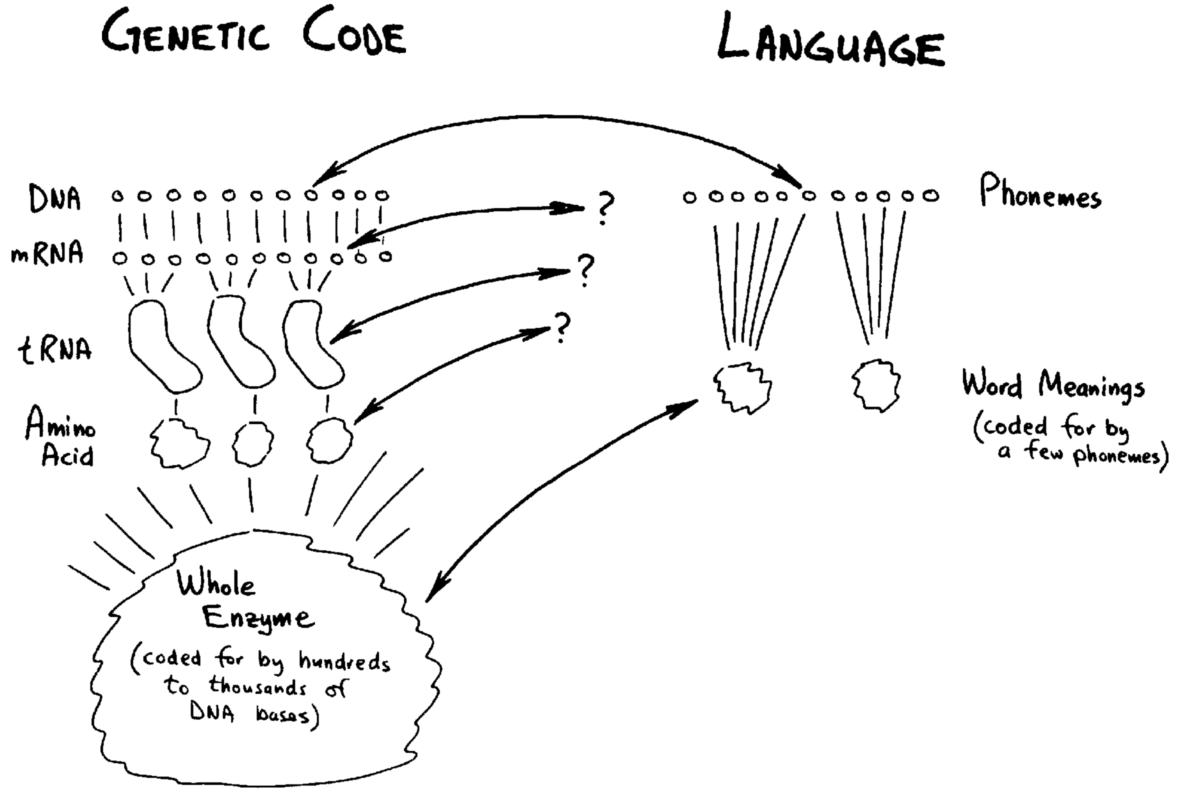

FIG. 2: Schematic Summary of Waters (1981a, 1981b)

The critical mismatch of words with whole genes leads to peculiar comparisons at higher levels. Thus, sentences are compared to DNA strings in prokaryotes (bacteria and blue-green algae) called operons. Operons consist of short control sequences (i.e. non-coding sequences) followed by one or more structural genes (i.e., genes coding for proteins). Regulatory proteins interact with the control sequence to allow the following structural genes to be "read"-- i.e. transcribed into mRNA and subsequently decoded into protein --if the specific substrate (i.e., target molecule) of these proteins is present. The regulatory protein detects the substrate by binding it specifically. Waters provides a small set of five DNA "phrase structure" rules that generate the slightly different sequences of control elements in negatively and positively controlled operons; these could actually be condensed to a single formula. As written, the rules unintentionally imply some unusual hierarchical relationships. For example, GENE => (GENE)+GENE implies a recursive relationship that seems inappropriate to describe nothing more than the occurrence of different numbers of genes in different operons. The major objection, however, is that the supposed "syntax" of operons serves an entirely different purpose than the syntax of sentences. Operons are basically switches, deciding whether or not a certain stretch of coded information gets interpreted. It is not unusual for a "grammatical" or "syntactically well-formed" operon to be in a switched-off state-- this is well within its normal range of functional behaviors. A "switched-off" sentence, by contrast, would be rather unusual-- in fact, this normally does not occur at the linguistic level; it might correspond to listening to a spoken sentence with one's ears plugged. Sentence modifiers come to mind, but again, it would be an unusual modifier that when understood, served to make the remainder of the sentence inaudible. Sentential syntax is usually thought of as having a closer association with "meaning extraction", even though syntax be thought of as distinct from meaning itself. All in all, the omission of the codon level has lead to forced comparisons at higher levels as well.

Protein Folding and Semantics

A third extended treatment of the comparison is by Pattee (1980, 1982). Pattee has long been interested in the idea of biological "constraints" in relation to the distinctive goal-directed behavior that first appeared on Earth three billion years ago in the form of temporal and spatial control of chemical reactions in single cells. More recently, he has explicitly invited psychologists to examine the "primitive embodiment of a symbol-matter system" in cells as "an excercise in mental hygiene", and as an alternative to the study of artificial symbol systems (e.g., artificial intelligence (AI) programs). Pattee state that

> if we expect to get anywhere with the mind-body problem at the brain level, then our concepts must at least be adequate in scope and precision to explain the symbol-matter relation in single cells... (1982, p. 325).

I agree. In its basic outlook and atmosphere, Pattee's approach is the closest to mine. My major complaint, already voiced, is that it is not concrete enough; if we are to get somewhere, we must not be embarassed to draw up an explicit analogy, if good reasons for doing it that way can be given. In the absence of models with clear parts, analogical comparison is much less productive.

Pattee is very clear about the biological level. He gives a compressed but insightful characterization of one aspect that is worth quoting at length:

> Artificial machines are not constructed so cleverly [as cellular genetic systems]. It is as if we could design any machine so that it could be assembled simply by hooking the parts together in a chain, and then have the chain spontaneously form itself into a functioning mechanism. In other words, the genetic symbols are <u>not</u> related to their referent action in any detailed or explicit form, but only through an implicit harnessing of natural laws and structures which needs no instructions. In fact, the amount of information in the genetic symbol string is only a very small fraction of the information that would be necessary for a

> completely formal and explicit specification of the structure of an enzyme. There are certainly no symbols in the gene for the 3-D coordinates of each amino acid residue, let alone for each atom in the enzyme. Life would hardly be possible if such symbolic detail were necessary, since the mass of each gene would far exceed the mass of the cell it could describe (1980, p. 266).

There are fundamental issues at stake here of great relevance to neurobiological, psychological, linguistic, and philosophical studies of language; Pattee, unfortunately, is not as incisive in crossing from biology to language. His analogy rests on two basic comparisons. The first is between the gene/enzyme relation on one hand, and the word-string/meaning relation on the other. Pattee calls the gene a "symbolic representation" of the enzyme, as presumably, a word is a "representation" of a meaning; going the other way, a gene "refers to" an enzyme just as a word-string (rather awkwardly) "refers to" a meaning. This is the "information processing" or "symbol processing" side of the analogy. The second comparison is between the enzyme/substrate relation and the meaning/object relation. The proper substrate is "recognized" by an enzyme in a manner presumably similar to which an object is "directly recognized" (without symbols) by a Gibsonian meaning "resonance" in a perceptual system. Another aspect of this relation is that the enzyme catalyzes a chemical reaction involving the substrate while the meaning presumably can act on, or initiate action upon objects (Pattee is not explicit). This is the ecological realism or "direct perception" side of the analogy. At the cellular level, the enzyme is common to both comparisons. At the level of language, Pattee circumnavigates. From the word side, a "meaning" is generated, or better, "self-assembles" by the rules of "meaning folding" (these rules are the "deep structure of the brain") but it is not clearly stated anywhere what actually results from, or mediates the direct perception of objects, or whether it is supposed to be the same thing as what gets generated by word strings. I have taken the liberty of making it the same thing in my schematic diagram (fig. 3) of Pattee's (1980, 1982) analogy. Finally, the two systems are said to exhibit "sematic closure", which means that the procedures and apparatus for generating meaning from the "symbolic representations" are themselves coded for in those symbols; Pattee, however, does not say what this implies for language (in cells, it means that tRNA, loading enzymes, and ribosomes, for example, are coded for in the DNA).

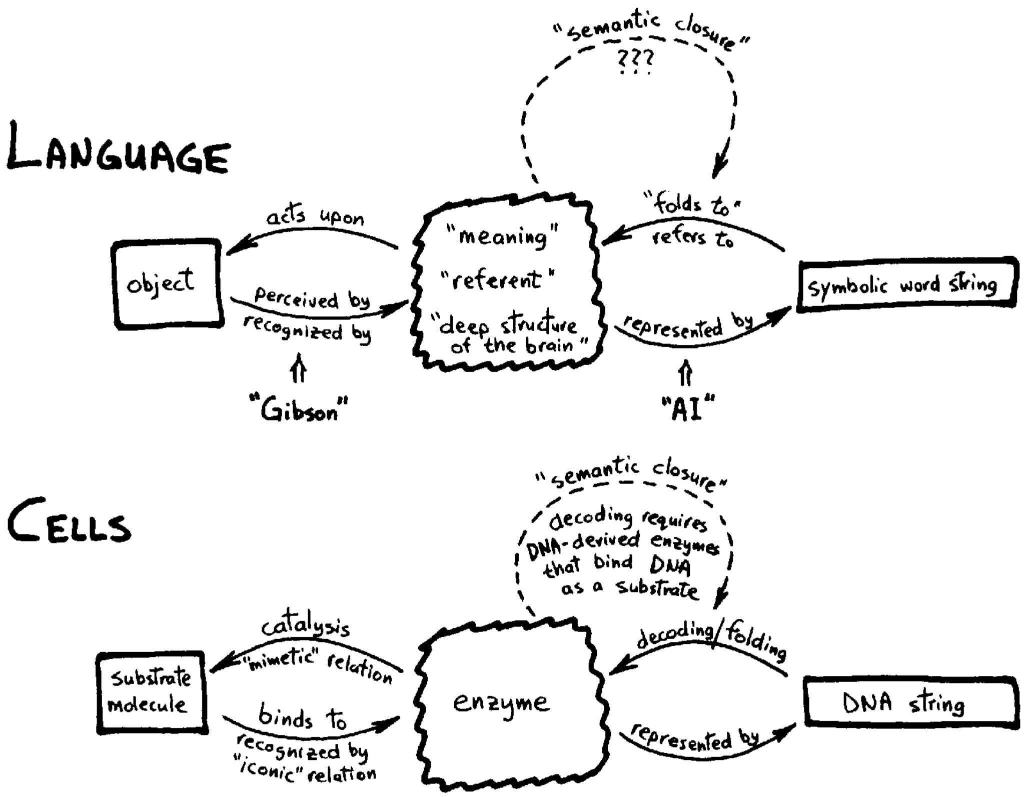

FIG. 3: Summary of Pattee (1980, 1982)

To begin with, it is a little unfair to divide cognitive psychology into just a "strong-AI" camp and an ecological "direct perception" camp;

these subfields provide convenient endpoints but many researchers "in between" (e.g., Hinton and Anderson, 1981; McClelland and Rumelhart, 1981; Marr, 1982; J.R. Anderson, 1983; most psycholinguists; most workers in visual perception) hold less incommensurable positions on perceptual and symbolic processing.

My key objection, however, is that it is often difficult to tell just what Pattee is referring to at the linguistic level. For example, in the case of "word" or "word string" in the first comparison, it is unclear whether this refers to actual sounds, marks on paper, words listened to, words read, words spoken, neural patterns underlying speech sound perception, motor system neurobiology, an activated word concept, or some combination of these. There are significant differences from both philosophical and experimental points of view among perception, production, and comprehension. Although he nowhere specifies it, the all important "folding" process seems to apply (correctly, I think) to perceived word sound strings. A similar criticism can be made with respect to the meaning/object relation. This could refer to lower level visual perception (e.g., what most Gibsonians have studied), sentence-like meanings constructed as a result of seeing actions and objects, sentence-like meanings constructed after hearing a sentence in relation to the perceptual processing of an object, motor patterns underlying behavior toward an object, and others. Again, there are more than terminological quibbles here.

The root of these problems is the stated intent of Pattee (1982) "not to model cognition or language at the brain level" (p. 325). Of course, this is not intrinsically objectionable. However, the context is an analogy set up so that brain states are just what it makes prediction about, as Pattee (1980) himself points out:

> We may compare the role of these... constraints [i.e., constraints on possible secondary and tertiary structures in proteins] to the postulated deep structures of the brain (p. 271).

To conclude, Pattee's work is inspirational; and I think the starting point is basically correct, in spite of the negative criticisms I have given.

Related Analogies at Different Levels

There have been a number of related attempts to draw an analogy between cultural or linguistic phenomena and biological processes, or to wholly or partially "reduce" one to the other. Three such projects are an evolutionary approach to language change, human sociobiology, and evolutionary epistemology. These pursuits have in fact generated a much larger and more visible literature than the work described above. There is not room here to take on the whole pack or to properly treat interfield or interlevel reduction (see e.g. Wimsatt, 1976, 1981; Darden and Maull, 1977)). But it will be helpful to discuss these approaches briefly to distinguish them clearly from the present project. Eventually, I will want to claim that the present analogy is in several respects the most basic; this does not make these other approaches less useful or interesting, but it will, I think, put them in a new perspective. As before, many of my criticisms turn on a lack of specificity in analogical comparison. The authors are obviously attracted to analogical comparison and want to draw very specific conclusions at certain points; but many seem unwilling or perhaps embarrassed to unambiguously state the terms and context of the comparison. This leads in several instances to shifting frameworks.

Language Evolution

Probably the most straightforward comparison is between the evolution of biological species and the evolution of languages. Historical and comparative linguistics (see Anttila (1972) and Bynon (1977) for recent summaries) in fact developed alongside evolutionary biology in the nineteenth century. One of the founders of Indo-European comparative grammar, Franz Bopp, explicitly compared a whole language to a living thing. His contemporary, August Schleicher, stated

> Languages are natural organisms which, outside the human will and subject to fixed laws, are born, grow, develop, age and die; thus they also illustrate the series of phenomena that are usually comprehended under the term life. Consequently, the science of language is a natural science (1863, quoted in Aarsleff (1982, p.16)).

These views were accompanied by obviously racist sentiments

> We can now see that certain nations, for instance, the Indian tribes of North America, already owing to their infinitely complicated languages truly luxuriating in forms, are not suited for a role in history and have therefore now decayed into regression and even extinction (1865, quoted in Aarsleff (1982, p. 295).

There was a reaction to this sort of thinking documented by Aarsleff (1982) that culminated by the turn of the century in the recognizeably modern work of Ferdinand de Saussure. A different form of the analogy, minus the racist overtones, has nevertheless persisted in historical linguistic investigations in this century, though often not explicitly (perhaps an understandable result of early excesses). It is the modern form of the analogy that we now consider.

Basically, one can quite sensibly line up a species rather than just one organism with a language. It is important to see that this alignment contrasts sharply, in terms of levels of organization, with the cell/person alignment implicit in the treatments described in the previous section (especially that of Pattee). These differences are diagrammed in Figure 4.

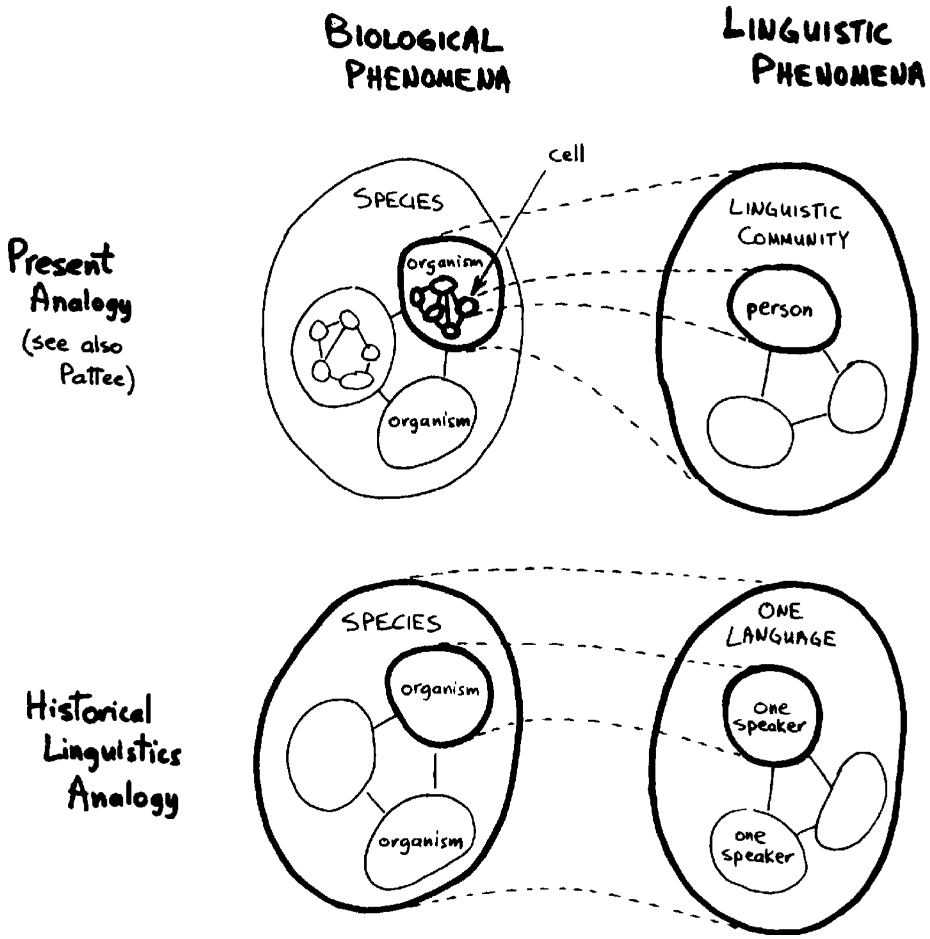

FIG. 4: Present Analogy and Historical Linguistics Analogy

A number of more specific comparisons can be drawn, starting with a species/language alignment. Thus, communities give cohesion to a language (cf. gene flow); language abilities develop in each speaker (cf. embryonic development); language must be transmitted directly to the offspring each generation (cf. heritability); languages gradually diverge, especially in spatially separated communities (cf. allopatric speciation); there is a low-level process of sound change-- driven by articulatory and perceptually-based interactions of nearby linguistic sound units --that continuously generates a significant part of the variation (cf. mutation). One of the tasks of the historical linguist has been to produce a "phylogeny" of languages. Another is to understand how the small-scale, short time-course processes (cf. microevolutionary processes) that generate geographical distributions of dialects (cf. subspecies, clines) give rise to wholesale rearrangements of phonology and syntax (cf. speciation, macroevolution). Sometimes new languages seem to have arisen without isolation and spatial discontinuity of speaking communities by means of sociolinguistic isolation (cf. sympatric speciation). The technique for adducing language relationships-- the "comparative method" (see e.g., Anttila, 1972, pp. 207-263) --shows remarkable resemblances to cladistic techniques in biological systematics. "Sets" of corresponding sounds (cf. homologous characters) between two or more languages are used to define a "proto-form" (cf. the cladists' primitive character state). Historical linguists attempt to construct branching diagrams that most parsimoniously fit the partially conflicting information about shared changes in sound/meaning correspondences (cf. the cladistic insistence on using shared derived characters (synapomorphies) and parsimony to get at the problem of parallelism and the character conflicts it leads to). I have here assembled more parallels that any one author, but without having distorted concepts by within-field standards or even having invented new terms.

Linguists themselves have pointed out several ways in which biological and linguistic evolution diverge. First, languages commonly incorporate ("borrow") words from neighboring languages, from the languages of an invader or colonizer, or from the invaded or colonized, with little regard for the phylogenetic distance of the source language.

Such a process seems much less common in biological evolution, although it must have occasionaly happened.[3] Second, languages would not seem to become more "adapted" or "fit" through time as a result of changing their system of sound/meaning correspondences. Third, this rarely happens by itself anyway (which is why comparative reconstruction is so difficult); it is usually accompanied by changes in the set of possible sounds (not just their arrangement) as well as in the meanings themselves. Fourth, linguists point out that languages are capable of expressing similar ranges of meaning, especially when given the freedom to paraphrase,[4] which seems to indicated that they have not really evolved that much overall. Once one or more of these differences are noted, the comparison is usually put aside without further explanation, often with the implication that it is something of an historical curiosity.[5]

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[3] For example, some bacteria will take up naked foreign DNA. In fact, this process (speeded greatly by $CaCl_2$ treatment) is an important step (called "transformation") in many recombinant DNA techniques. The incorporation of naked foreign DNA into the germ line of higher multicellular organisms, however, is apparently much rarer.

[4] It is not clear that intertranslatability applies in the same way between natural and scientific language, particularly in the case where a large, specialized vocabulary and a complex mathematical apparatus has been developed. The problem is most acute when the phenomena the scientific theory is about are at a markedly different level of organization than small human social groups (e.g., 'elementary' particles).

[5] The question of language evolution is inherently more controversial than questions of the evolution of the genetic code or of DNA sequences because of the social implications of language change. Linguists have long ago repudiated the notions of "correct speech" and "superior" natural languages. But when the "average person" hears, for example, in an English dialect, what a linguist would identify as a simple metathesis (see end of Chapter III)-- a sound change that has occurred repeatedly over thousands of years in thousands of languages --he or she usually unconsciously perceives it instead as a social cue-- e.g., as a sign of belonging to the same group if the metathesis appears in the hearer's speech. But is could easily be unconsciously perceived as a

Shifting to the perspective of the present investigation, there are interesting reasons why linguistic and biological evolution should be fundamentally different processes. What becomes clear with a cell/person alignment is that there is actually only <u>one</u> language at the biological level common to all cells and all organisms known on the Earth; aside from a minor difference in the genetic code in mitochondria, there is only one mapping from DNA triplets (cf. sounds) to amino acids (cf. meanings). In striking contrast to the rapid proliferation of human languages, often with radically different sound/meaning correspondences, there has been no detectable evolution of the genetic language since all existing lineages of organisms arose. Later, I will argue that this is probably due to several other differences between the systems (in particular, the presence of human language production and a larger set of basic word meanings). For now, it is sufficient to point out that the qualitative differences between the "evolution" of languages (in the sense of new sound/meaning correspondences) and organic evolution noted above arise because of the differing nature of what is changing in the two cases.

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sign of "sloppiness" or even "inferiority" by a hearer with more "correct" English. The issues are also tied up with the existence of a massive written literature, where the conflict between the natural tendency of spoken language to change and the tendency toward stasis exerted by the print is most clear. In the case of English, both "factions" have had their way over the years-- English is now pronounced differently than it used to be but spelled almost the same. The reason for mentioning these issues here is that I think they tend to run just under the surface in interdisciplinary interactions between linguists and biologists, especially with regard to comparisons between the two systems. Linguists feel, often with good reason, that when it comes to language, many biologists are like the "average person" and could stand a little enlightenment on the topic of language change, language evolution, "primitive" languages, and language "fitness". Some of the more outrageous posturings of sociobiologists have confirmed these suspicions, and have contributed to an over-hasty dismissal of more sober comparative investigations of linguistic and biological evolutionary mechanisms.

With human language change (putting aside for now the generation of previously non-existent sounds as well as word meanings) new sound/meaning mappings (decoding rules) appear, while in organic evolution, new coded DNA input sequences appear; in both cases, new "decoded" meanings result if everything else is held constant; we will call these meanings "outputs" for short in the following discussion.[6] Although some differences in coding efficiency or in resitance to noise in the input sequence do accompany different mappings (see e.g., Cullmann and Labouyges (1983) on noise immunity of the genetic code), <u>different mappings</u> (i.e., with input sequences held constant) do not allow nearly as wide (by many orders of magnitude) a range of possible outputs as do <u>different input sequences</u> (i.e., with mapping scheme held constant). In fact, in the biological case, most changes in the mapping would probably be lethal for an organism since multiple changes would be introduced in almost every protein sequence.[7]

The difference in the range of possible "outputs" can be seen from another perspective. Redundancy aside, given a particular one-to-one mapping scheme, it is possible to express any particular coded output sequence by fiddling with the coded input sequence; by contrast, given a particular coded input sequence, it can easily be shown that one cannot express most of the possible output sequences if one is restricted to fiddling with the mapping scheme. Another way of looking at this is

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[6] Of course, new input sequences appear in language as well-- almost every time one listens to speech or reads a passage (see Chpater II). But for now, we are considering just the analogy between organic evolution and sound/meaning "evolution".

[7] See Ninio (1983) and Chapter IV for a discussion of research on "nonsense suppressors" and "missense suppressors"-- <u>E</u>. <u>coli</u> mutants with tRNA's that recognize the wrong codon or that are inappropriately "loaded". In spite of the fact that the mapping is changed in these mutants, some of them do grow a little. It is not clear if such mutants can be viable in metazoans.

that the smallest change possible in the input sequence-- i.e., a single segment (base, sound) change --is very small (so small and localized that it might go unnoticed) allowing in principle, a complete sampling of the output space. By contrast, the smallest change possible in the mapping scheme-- i.e., changing the way one word is decoded (wherever it occurs) --is so large, that the space of possible outputs is very poorly sampled (so poorly, in fact, that it is difficult to arrive at an output that, in the molecular case, corresponds to a viable organism). This restricted range of possible outputs in the second case could roughly explain why phyletic language evolution (i.e., mapping-scheme evolution) does not seem to result in as much increased "fitness" or "adaptedness"; there is just much less potential variation to work with.

Thus, from the perspective of the present analogy, languages evolve in a way that biological organisms have not, although in principle, it is clear what the linguistic sort of evolution would look like at the biological level.[8] Conversely, it is natural to ask what the organic sort of evolutionary change would look like, or if it already exists, at the linguistic level. In fact, it does appear to exist (see the next section). To summarize, the most common analogy that has been used to match up language evolution with biological evolution starts with a species/language (or organism/person) comparison, in contrast to the cell/person comparison implicit in most of the previous section. Several striking disanalogies arise with species/language comparisons and they have been noticed by linguists and biologists on repeated occassions. If we move to the more fundamental cell/person alignment,

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[8] Another way that languages evolve that has no currently existing parallel in biological evolution is in the common changes in word meanings and in the set of sounds that are used, mentioned briefly above. This will be discussed further in Chapter III.

however, these disanalogies are more understandable in terms of different kinds of underlying processes in language evolution (in the comparative linguistics sense) and organic evolution.

Human Sociobiology

A second major area of inquiry where biological genetics and human linguistic phenomena have been explicitly or implicitly considered together is human sociobiology. The more vulgar forms prominent several years ago were not really analogical in nature but were driven by a "nothing more than" reductionism that has recurrently surfaced in the history of ideas especially in pronouncements about adjacent fields of science. A type-specimen of such a pre-emptive attack was the famous statement of the theoretical physicist Dirac (1929) dating to the time of early quantum mechanics:

> The underlying physical laws necessary for the mathematical theory of a larger part of physics and the whole of chemistry are thus completely known, and the difficulty is only that the application of these laws leads to equations much too complicated to be soluble.

Although insoluble equations were perhaps not a great solace to chemists, they could not fail to be impressed that physics, despite its present incompleteness, already explained all of chemistry (for current perspectives on this relationship see Bantz, 1980; Bogaard, 1981; Primas, 1981). In the past decade, many treatments of the relations between human culture and human genes had adapted a similarly pontifical tone (e.g., Wilson, 1975) as well as a mission to find proximate genetic causes for both wondrous and execrable human behaviors (e.g., language and warfare).

Recently, positions have moderated partly in light of rejoinders by philosophers, anthropologists, sociologists, and psychologists, and considerable effort has been expended in developing an analogy, interesting in the context of the present investigation, between genes and "culture" as parallel rather than mutually exclusive systems for transmitting information about phenotypes (see e.g., Pulliam and Dunford, 1980; Cavalli-Sforza and Feldman, 1981; Lumsden and Wilson, 1981; Boyd and Richerson, 1984). None of these authors have restricted the putative cultural analogues of genes and genotype to linguistic phenomena. Boyd and Richerson, for example, state

> the codification of culture via public symbol systems may have interesting effects on the human evolutionary process (see [their] Chapter VII) but to our minds these effects are less fundamental than the effect of social learning per se. It is possible that language and other symbolic capacities were late developments in human evolution... and that the apparently effective food foraging lifeways that characterized hominids until the late Pleistocene were transmitted by direct phenotypic copying unmediated by arbitrarily meaningful codes. It is even plausible that much of human behavior is still so acquired....

They define culture as "information capable of affecting the phenotype which individuals acquire from other conspecifics by teaching or imitation". But they also point to two basic differences between cultural and genetic transmission that make it unrealistic to treat the cultural system like "an extra genetic locus". First, it is not possible to represent cultural evolution as a process that transforms the distribution of genotypes at a locus in generation t into the distribution of genotypes in generation t+1 as is done in models of non-cultural populations.[9] Even the most stripped-down cultural evolution model requires that we take the distribution of starting phenotypes into account in order to predict the distribution of genotypes as well as expected phenotypes in generation t+1. Second, in

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[9] Actually, this approach is not even realistic for non-cultural evolution in any but the simplest case of one locus (see Wimsatt, 1981).

cultural transmission, genotype analogues are transmitted to an organism throughout its life rather than as one bolus at fertilization. The differences are summarized in the top two diagrams in Figure 5.

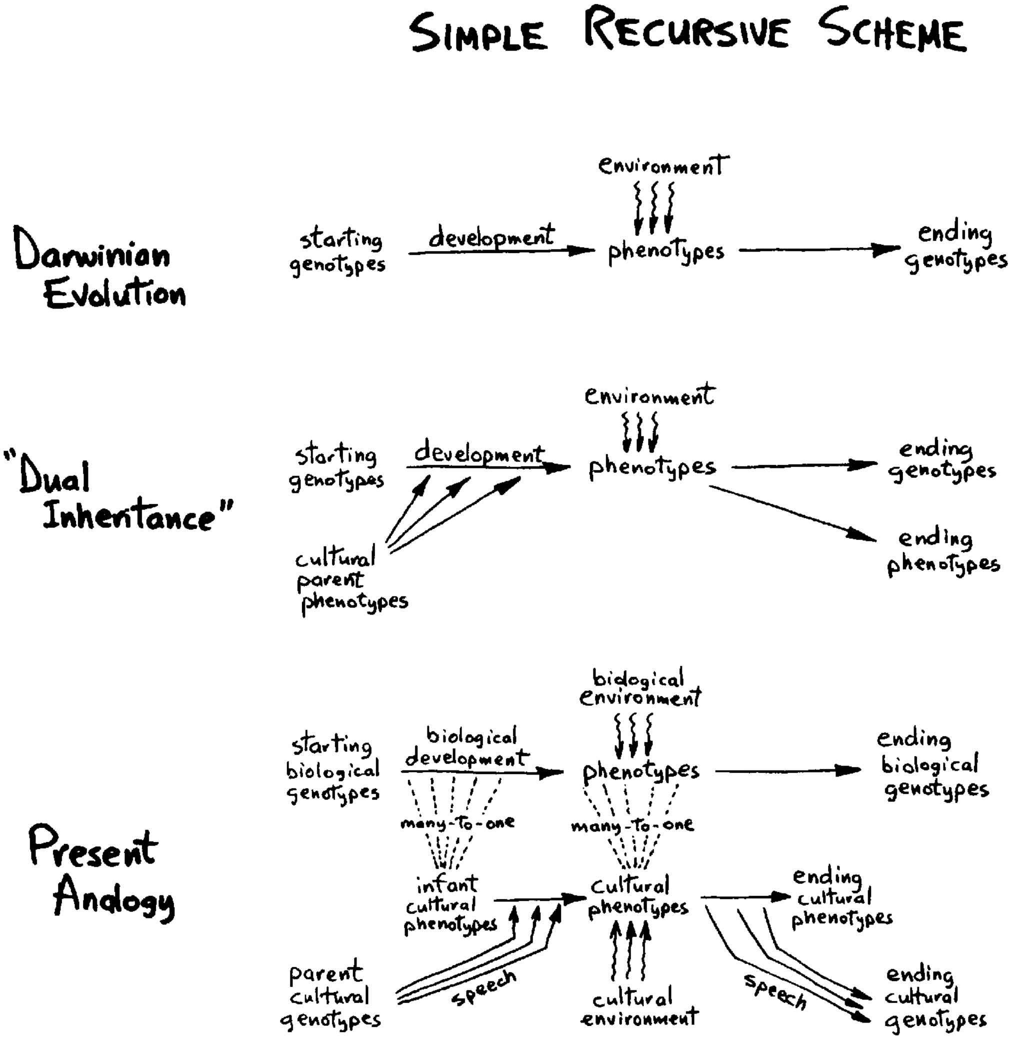

FIG. 5: Comparison of Three Recursive Schemes

Boyd and Richerson's so-called "dual inheritance" approach seems a sensible enough extension of neo-Darwinism and has been independently developed along broadly similar lines by several pairs of authors.

There are several substantial objections to it from the present prespective, nevertheless. The first stems from the definition of the phenotype. Boyd and Richerson draw an analogy between the "cultural genotype" and the ordinary genotype but then are unwilling to distinguish the structures that are generated; they <u>identify</u> the cultural phenotype with the biological phenotype rather than setting up an analogy between the two. Of course their stated intent is to study "gene/culture" interactions; and their approach sometimes results in what Lumsden and Wilson have characterized as a "struggle" between genes and culture for the preferred steady-state behavior of the population of behavioral phenotypes (p. 257). There seems to be little justification, however, for collapsing the products of these two entities in order to study an interaction between them. Such an identification gets by easier because, as Lumsden and Wilson have justly complained, the models "are almost wholly free of content from genetics, neurobiology, and psychology" (p. 264). This is not a new point and a number of authors have raised analogous critiques of non-cultural evolutionary theory with respect to the need to consider developmental mechanisms (Gould and Lewontin, 1979; Wimsatt, 1981; Kauffman, 1983). From the present perspective of an analogy at the cell/person level, the identification of the biological and cultural phenotypes in the individual is incorrect. The adult biological phenotype of a multicellular organism (such as a person) is generated from a zygote by ever increasing numbers of interacting cells, each of which contains a complete complement of genetic information as well as the decoding apparatus to derive a primary interpretation. Now, the advantage of identifying the cultural phenotype with the biological is that enculturated humans are clearly localizable units, like animals, for example. On the other hand, cultural information striking differs from genetic information in its distribution and interpretation. There is no reasonable sense in which cultural information could be thought of as existing in numerous duplicate copies in each of the cells or in any other repeated parts of an enculturated person. Likewise, cultural information is not initially interpreted piecemeal by each cell or other subunit; there is only one interpreting apparatus (sense organs and brain) per organism. These disanalogies go away if we take the cell/person alignment seriously and define the cultural phenotype as an interacting group of people. Each person in the group is capable of providing an independent initial interpretation of cultural information; and cultural information can be thought of as existing in many copies (e.g., mothers' speech to babies). Of course, the cell/person analogy does not deny that human cultural phenotypes actually "reside" in human biological phenotypes; the main point is that there is not a one-to-one relationship between the two.[10] The simplest recursive model of human cultural evolution that incorporates these distinctions is shown in the bottom diagram in Figure 5. There are disanalogies at this level as well-- for example, the copies of the cultural "genotype" for a cultural "organism" are less uniform; the information does not seem to start out "inside" a person as it does in cells; social groups are less distinct than are biological organisms; there appears to be no strict cultural analogue of a unitary zygote. In each case, I think interesting reasons can be provided for these differences (see Chapters II and III). The main point,

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[10] Such a framework, of course, is not new here. The idea of societal groups as organisms (though not persons as cells) has a long history in sociology (see e.g., Spencer's Principles of Psychology, the writings of Durkheim) and anthropology (see Jahoda (1982) for a review from a psychological perspective). The history of these concepts deserves a fuller treatment than is possible here.

nevertheless, is that the cell/person analogy better represents the overall architectures of information processing in the two systems.

Finally, returning to the question of the necessity of an arbitrary symbol interpreting system, it is interesting to note that at the biological level, at least, such a thing seems to be required in order for something to be "alive" and indeed to evolve. There is no explicit mention of symbols and coding systems in "Darwin's rules" (Lewontin, 1970)-- i.e., evolution requires heritable variations in fitness --but it is difficult to think of a counterexample lacking such a system or the resulting genotype/phenotype distinction (see the next section). Thus, one could at least countenance the possibility that a similar system is in fact necessary to support cultural "life" and evolution. That requirement might explain what Boyd and Richerson characterize as the "curious fact" that complex forms of cultural transmission seem genuinely rare in nature:

> The results of our model suggest that cultural transmission should be favored over genetic transmission under a fairly wide range of circumstances. The fact that cultural transmission is not common suggests that some additional explanation is required. One possibility is that some rare preadaptation is necessary in order for culture to evolve. Given that rudimentary forms of culture are common, this does not seem to likely. Another possibility is that there are other costs associated with cultural transmission that we have not considered so far.

Contra Boyd and Richerson, the "additional explanation" required probably did involve a rare and apparently unique "preadaptation"-- the origin of the human "linguistic code".

Lumsden and Wilson's (1981) book ranges breezily over numerous topics including developmental neurobiology, perception, cognitive psychology, and linguistics. There is no space here to mention the many issues raised. However, their juxtaposition of studies on genetically controlled neuronal cell migration and spreading activation in semantic networks throws into clearer relief the problem, inherent in most models of genes and "culture", of the nature of the interaction between the two. The authors do not discuss the nature of the interaction at length before proceeding; but this issue provides another perspective on what is wrong with identifying the biological phenotype with the cultural phenotype.

The main connection between cultural and genetic effects on the phenotype is the idea of a "biased" genotype-- i.e., one that predisposes the individual to acquire one rather than another cultural variant. Several arguments are marshalled to suggest that such a genotype (a single locus in their models) would be favored relative to an "unbiased" genotype in an environment in which the cultural variant selected by the bias is adaptive. Even assuming that "biased" genotypes for various cultural traits existed, it is not clear that these arguments are very robust. Thus, Maynard Smith and Warren (1982) and Boyd and Richerson (1983) have pointed out that the force favoring genetic differentiation is very weak under all but the specialized conditions Lumsden and Wilson choose. The intuitive explanation is simple-- genetically-caused differentiation requires reduced migration between habitats but such migration is just what is required to maintain enough cultural variability for the "biased" genotype to have an advantage (i.e., with only adapted cultural models, an unbiased genotype would do as well as a biased one). Since individuals with "biased" genotypes sometimes acquire the wrong cultural variant, the intensity of selection on genotypes is less than on cultural variants and the cultural choice genes will not be favored (Boyd and Richerson, 1983, p. 213). Thus, cultural transmission seems to slow genetic differentiation.

The criticisms are sound; for the present purpose, however, two other interrelated criticisms-- involving rates of change, and levels of organization --are more important. The first issue concerns the implicit assumption, common to both Lumsden and Wilson and their critics, that culturally and genetically based rates of change are similar enough that they can be modeled as if they directly interacted with one another (see also Boyd and Richerson, 1984, Chapter VI). General considerations suggest that culturally-based evolution is a great deal faster. It is difficult to compare the two directly but a difference of several orders of magnitude seems quite within reason (thousands of years of the archaeologist, anthropologist, or art historian compared to millions of years of the paleontologist). Cultural evolution happens so much faster on an absolute time scale than biological evolution that the latter seems stationary by comparison, at least since the Upper Paleolithic.[11] This does not deny that that there are interactions between the two; but the different rates of the processes make it unlikely that these interactions are very direct or specific from the point of view of trying to explain phenomena in a particular culture. Simon (1973) has discussed similar issues using examples from physical theory; the main idea is that phenomena occurring on very different time/energy scales (e.g., intranuclear *vs*. intramolecular interactions) are essentially decoupled from each other for many analytical purposes. There was at some point or period in human evolution, an all-important, *direct* evolutionary interaction between the biological and the cultural levels-- namely, the

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[11] See Butzer (1982) for a review that emphasizes the great cultural conservatism and the very slow rate of evolution (more nearly comparable to rates estimated from the animal fossil record) of the preceding stone tool cultures attributable to *Homo erectus*, *Homo habilis*, and *Australopithecus*.

incorporation into the human genome of the ability to develop a language. The very limited results obtained in other primates after extensive attempts at language teaching (see Chapter III) have emphasized the unique nature of the genetically-determined human predisposition to learn a language. Once language arose, however, cultural evolution developed a detached and incredibly complex life of its own. Of course, the genetic predisposition for language has been maintained, but it is unlikely that genetic mechanisms have had very much to say about the specifics of cultural evolution for several reasons, not the least of which is simply the lightning-fast <u>dynamics</u> of the process.[12] (especially since the Neolithic). These arguments are well-worn and not very controversial among many archaeologists, anthropologists, and sociologists. The topics involved, nevertheless, seem to perennially inspire, among interested biologists, ostensibly ingenuous oversights of the obvious differences in rate that seem to have largely decoupled cultural and genetic evolution and concomitantly, the genetic and cultural phenotypes.

A second interrelated issue raised by Lumsden and Wilson's treatment that is important in the context of the present project is the notion of evolution at different levels of organization.[13] Although the authors

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[12] Notice that is a rough sense, the underlying quantum chemical phenomena are much "faster" than the higher level genetic phenomena, and the same could be said for the lower level neural patterns underlying the higher level evolution of ideas; often "smaller" implies "faster" (see also Simon, 1973; Wimsatt, 1980b; Allen and Starr, 1982). It is interesting that the rate difference <u>between</u> these two pairs goes the opposite way-- "small" genetic evolution is <u>slower</u> than "large" cultural evolution. See Chapters II and VI for a discussion of why this should be so.

[13] I would like to distinguish "evolution at different levels of organization" from the macroevolution/microevolution debate (see Gould, 1980; Griesemer, 1983), and from the related questions surrounding the units of selection controversy (see Wimsatt, 1980a, 1981). In those discussions, there has never been an attempt to reestablish the

actually discuss developmental neurobiology and cognitive psychology one right after the other, they (and others) seem to gloss over a straightforward distinction between phenomena at different levels of organization. They would not be satisfied with a blurred distinction at the level of DNA, proteins, and cells, where it is clear that the quantum chemical description of the time evolution of DNA and other biomolecules plays a small role in mathematical models of genetic evolution of the type used by themselves, Boyd and Richerson, or Cavalli-Sforza and Feldman. Quantum chemistry will undoubtedly play a large role in understanding the detailed mechanism of DNA transcription or enzyme catalysis (see Chapter IV, V), but for the most part, it does not involve phenomena (e.g., charge distributions) at the "right level" to describe the effects of selection, sex linkage, many alleles at a locus, polygenic characters, and so forth on genetic evolution (see Wimsatt, 1976, 1981; Sober, 1981, for discussions). From the viewpoint of the present cell/person analogy, however, those very <u>genetic</u> phenomena appear as part of the "lower level" vehicle that underlies language language and culture. Models of genetic evolution might eventually explain how the neurons in human brains have evolved to be able to support the acquisition of a language after suitable exposure to one, but these mechanisms are not at the right level to explain very much about the evolution of the <u>content</u> of the cultural phenotype, which exists as a set of incredibly complex, learned patterns distributed throughout the brains of humans in a social "organism". Even when the cultural phenotype is defined as residing within one genetic phenotype, there is still a great difference in the scale of the basic level units

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genotype/phenotype distinction at a higher level of organization (see Wimsatt (1984) for a move in this direction).

of transmission in the two systems. Definitions of the cultural analogues of genes and proteins vary among authors and are quite vague (see e.g., Lumsden and Wilson's definition of a "culturgen"); however, it seems that several respectable candidates-- e.g., linguistic phenomena like sentences or cultural behaviors like a cooking procedure (gene analogues), neural patternings mediating sentence comprehension or the comprehension of a particular modeled behavior (protein analogues) --unavoidably refer to basic level units or entities that are on a higher level of organization than a gene or protein. This suggests that a very indirect relationship exists between genetic and cultural phenomena. At the very least, we can be sure that the simplest conceivable cognitive act involved in production of the cultural phenotype (a process corresponding to the initial extraction of meaning from a gene through protein translation) depends on complex interactions between very many gene products, including, for example, receptor cell proteins, proteins to direct the differentiation of many different neuronal cell types, and so on. In view of these relationships, it seems eminently as reasonable to distinguish biological and cultural phenotypes in these models as it is to distinguish their respective sources-- coded information in the genotype and in culture.

As an alternative to cutting the Gordian knot by simply inventing "biased" genes, the recent behavioral mutants in _Drosophila_ (see e.g., Hall, 1982; Quinn and Greenspan, 1984, for reviews) give one a more realistic flavor of what the interactions between cultural and genetic information might actually look like. Culturally transmitted behaviors are not prominent in flies. However, flies do exhibit rudimentary learning. A number of mutants with learning disabilities and metaphorical names (e.g., _dunce_, _cabbage_, _rutabaga_, _turnip_, _zucchini_) have been isolated. Several of these mutants were subsequently analyzed biochemically and they turned out to have defects at different points in their cyclic nucleotide metabolism. Cyclic nucleotides (e.g., cAMP) are known to have very general functions a "second messengers" in receptor-mediated signals carried by diffusible hormones and neurotransmitters, and a cAMP increase is thought to mediate short-term modification of synaptic efficacy in Aplysia. Clearly, there would be a rather indirect relationship between one of these genes and a given learned behavior. It is sobering to contrast the (probably representative) "distributed" interlevel mapping of these genes with the direct, "localized" mapping of Lumsden and Wilson's hypothetical cultural choice genes.

Evolutionary Epistemology

The third major area where biological and linguistic phenomena have been considered together in an analogical framework is evolutionary epistemology. The idea that conceptual evolution might profitably be compared to Darwinian organic evolution has been informally considered in many places and by many authors through the years. Here we shall mostly be concerned with the longer treatments of Campbell (1974, 1977), Toulmin (1972) and more recently, Hull (1982, 1983). Compared to the often Procrustean generalizations about human culture made by some human sociobiologists, the proclamations of evolutionary epistemologists have been muted, perhaps due to the closer attention paid to the "natural history" of culture, especially with regard to conceptual development in science. The difficulty of knowing and seeing more, however, is that it is harder to fit everthing into a tidy framework. In the analogies developed by evolutionary epistemologists, an appreciation of complexity has been accompanied by overly flexible models and, more damning from the view of the present project, shifting frameworks.

The main idea of evolutionary epistemology has been mentioned by many writers, mostly in passing. Campbell (1974) has exhumed many of the interesting and relevant passages. Thus, natural selection of variants in populations of organisms has been compared to "competing theoretical systems" in the history of science (Popper, 1934/1959), the natural selection of "behavior-patterns" in the life of a single organism (Ashby, 1952), aesthetic selection of subliminally-produced, unexpected, idea combinations (Poincare, 1913), selection by the "outer environment" of concepts and laws conceived or produced in undirected "flashes" by the "excessively unstable human brain" (James, 1880), the arrival at a "simple and solid combination" of ideas after having first gone through "numerous and unstable aggregates" (Souriau, 1881). Even these short quotes point to a variety of conceptions of how to draw an analogy between biological evolution and perceptual, linguistic, and thought processes in man (and animals). The recent regrowth of interest in evolutionary epistemology has raised many issues-- e.g., the question of how "blind" the variation is in conceptual or theoretical variants (see e.g., Richards (1977)) or of the locus of the selection process --that I cannot comment on directly here. Rather, I am more interested in the basic mapping scheme employed in these analogies-- something about which many of the disputants have been quite reticent. Some of the debates might be clarified, I think, if the differences in the implicit terms of the analogy were explicitly stated and compared. For the present purpose, such a statement will serve to distinguish evolutionary epistemology as a group of analogies at a different level that the present cell/person alignment.

A primary level of comparison in the evolutionary epistemology of Campbell and Toulmin is between an organism in an evolving species and a concept in the brain of a learner. A concept is usually thought of as word-sized or larger, but smaller than the entire conceptual content of the learner's brain. The goals of Campbell and Toulmin are broadly similar. Campbell would like to apply a selective retention paradigm to all "knowledge processes", in animals and plants (as well as in scientists). He even applies this perspective rather awkwardly to limb regeneration and appears to embrace Popper's bizarre extension of selection to crystal growth (Campbell, 1974, p. 420). But his main interest is surely in the evolution of nervous system function in animals and its relation to modes of individual and social knowing in humans, including especially, scientists. In his more recent William James lectures (1977), he concentrates at some length on the acquisition of word meanings ("concept learning") by children (lecture 3). Toulmin has expressed the goal of generalizing the "Darwinian mode of explanation" to encompass the evolution of scientific disciplines in his sprawling treatise (1972). He describes an "intellectual ecology"; rather complex organism-like concepts are thrust into the "environment" of the scientific forum, are selected and transmitted, they partially define each other's "niches", and so on. In many places, he explicitly compares organisms to concepts (e.g., p. 141) but in contrast to Campbell, his "concepts" are invariably "larger" and more complex than one word meaning. Toulmin does not want to get involved, however, with "specifically biological details" or get "drawn into discussions about genetics, predators, or water supply" (p. 139).

The organism/idea analogy interestingly constitutes a third way of mapping "biology" onto "language" (or knowledge), quite distinct from the cell/person analogy of the present project, and the species/language analogy of the historical linguist. In Figure 6, this third mapping has been appended to the two previous mappings from Figure 3. On the left are the biological entities, "species" and "organism", common to all forms of the analogy. On the right, the analogized entities are drawn approximately "to scale" (a scientist and his or her ideas is about the same size as an organism; disciplines and species are larger). When lined up this way, it is clear that evolutionary epistemology actually "goes the oposite way" from the present analogy; thus, the evolution of (large) organisms belonging to a species is compared with the evolution of a class of (small) things-- concepts --that can only reside within scientists. Although Campbell and Toulmin might not put up with concepts entirely "within the head", it is clear that both of them think that patterns in human neural networks, which undoubtedly <u>are</u> in the head, are involved in a big way with concepts.[14] By contrast, the analogy of the present treatment and of Pattee compares (small) cells with (large) humans. Since evolutionary epistemologists usually line up species with disciplines (thought of as "interbreeding" intellectual communities), it should be pointed out that there are no convenient biological entities left to analogize with a single person or scientist (see fig. 6, and below).

One result of starting with an organism/concept alignment is that the evolutionary epistemologist has had relatively little use for the genotype/phenotype or gene/protein distinction seen on the biological side. This lack of interest seems to have resulted because the

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[14] Notice that here, the "smaller" processes of concept change, concept learning, or "vicarious selection" (within one learner) are, as expected, faster than the "larger", presumably analogous processes of change in a lineage of organisms.

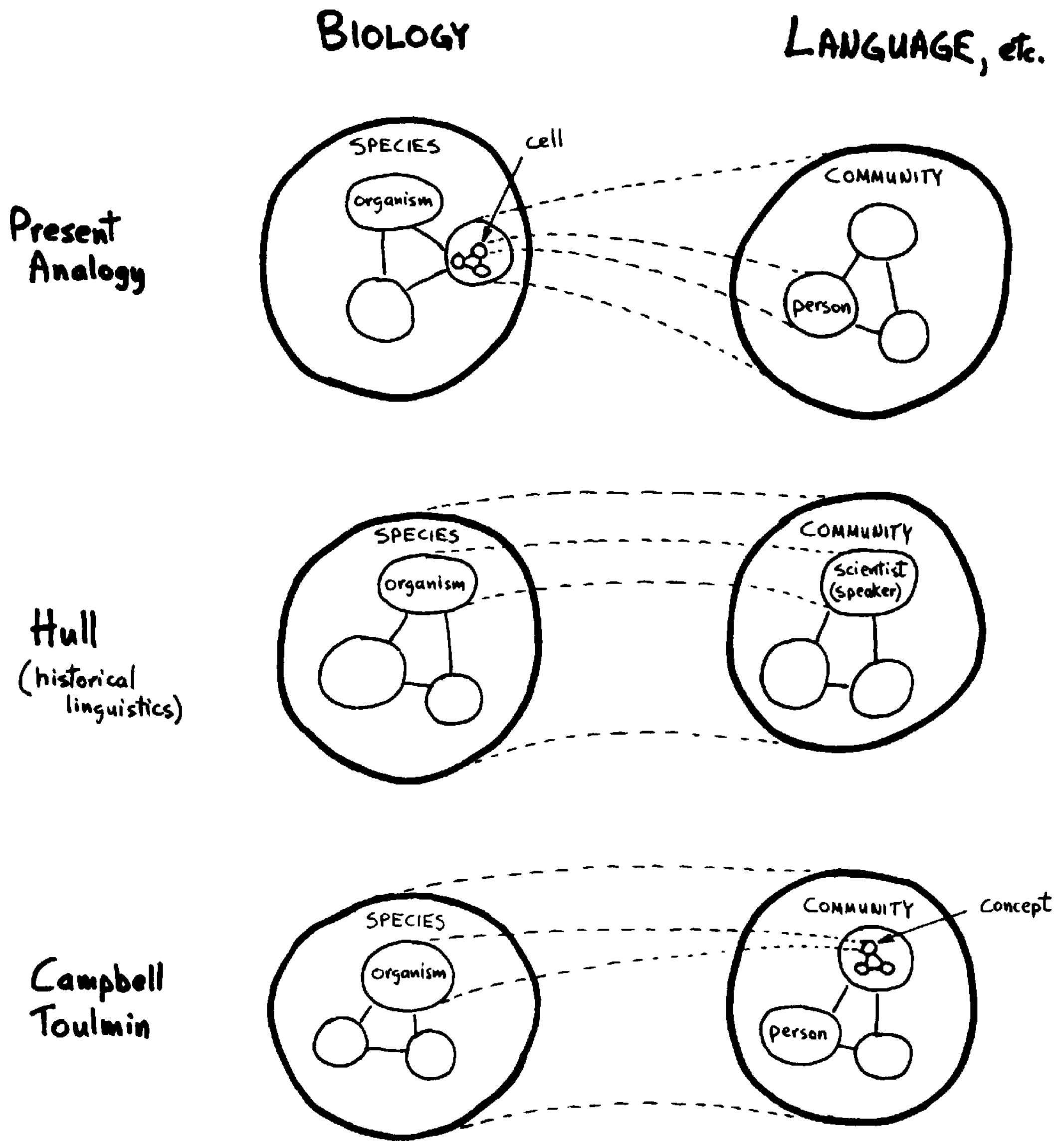

FIG. 6: Analogies at Different Levels

distinction would have to be analogized with something <u>within</u> a concept. Thus, Toulmin briefly mentions the distinction (p. 416) but it plays no part in the body of his narrative (perhaps also because it comes out as a "specifically biological detail"). Likewise, Campbell says little about the distinction. Kary (1982) recently criticized this aspect of evolutionary epistemology. Using somewhat different terms than her, I agree that a generalized theory of Darwinian evolution must include an analogue of the genotype/phenotype distinction as well as offspring discrete from parents. Otherwise, there is little to distinguish the theory from other deterministic theories of change-- e.g., the time "evolution" of a dynamical system in 6-dimensional momentum space, plate tectonic "evolution", the "evolution" of galaxies --that are clearly not "evolutionary" in the biological sense of the word. The function of an environmentally "insulated" generative entity (genotype) is taken over in Campbell's theory by the chance aggregations of ideas that are then selected, directly or vicariously. Notably, the "blind" nature of those generative events has been the point of much criticism. In view of the present schematization, these problems arise because two main properties of the genotype (as contrasted with the phenotype)-- its random mutability, and its decidedly non-random generative capacity --have been conflated in "blind variation". In addition, although many concepts exist together within one scientist's brain, none seem to have the relationship there of discrete parents and offspring; such a relationship is another probable requirement for Darwinian evolution as commonly understood to occur (see also the discussion of this in Kary (1982)). One way out is to draw an explicit genotype/phenotype distinction at the conceptual level.[15] This, however, does not solve the problem of discrete offspring. Another way is to redraw the analogy at

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[15] Recently, Wimsatt (1984, unpublished) has attempted to draw just such a distinction between generative, genotype-like groups of axioms and assumptions, and the generated, "environmentally sentient", phenotype-like scientific theory. In contrast to Campbell, and more like Toulmin, Wimsatt's organism analogue is much larger than a single word meaning.

a new (cell/person) level. The present thesis is an attempt to argue that the second strategy, which has only been hinted at previously, may be quite productive. As it turns out, the cell/person analogy does not "solve" the discreteness problem either, but is puts it in an intriguing new light.

Hull (1982, 1983) has recently given a critique of evolutionary epistemology incorporating his notion of species as spatiotemporal "individuals" in a network of lines of descent (instead of as classes or types with members). Hull's main point is that what counts in organic evolution are actual lines of descent; sorting by (morphological) classes may not divide up the historical geneological nexus at the right places. The same argument applies to conceptual evolution. Thus, as Olby (1979) quipped, Mendel was "no Mendelian" since in a real sense, his ideas "died" without issue; the so-called 'rediscoverers' of Mendel's laws-- deVries, Correns, and Tschermak --were the real 'Mendelians' since it was their work that was actually influential. In trying to develop this notion with respect to conceptual evolution, Hull sees that it won't do to have the nodes in the geneological network be concepts, grouped into similarity classes. Hull suggests that instead, we individuate scientific communities as taxonomists individuate species-- by using a "type specimen"; just as a particular organisim is used to mark a species, a particular <u>scientist</u> could be used to mark a conceptual community (1982, p. 297). Clearly this implies that the analogue of one biological node (i.e., one organism) is the entire conceptual system of a single scientist. Such a conceptual system is composed of what Hull calls, following Dawkins, "memes", which are gene analogues, near in size to unit concepts.

This organism/scientist alignment is quite different than the organism/concept alignment of "classical" evolutionary epistemology.[16] In terms of scale, it is closest to the mapping described above for the type of language evolution studied by the historical linguist and dialect geographer (i.e., organism/speaker; species/linguistic community). Hull's analogy also recalls the human sociobiologist's collapsing of the genetic and cultural phenotypes; he claims that memes only reproduce, but do not generate a phenotype (1982, p. 307) except in a "metaphorical sense" (p. 311); memes "literally" are taken only to modify the biological phenotype. The passages in question are difficult, but Hull seems to grant the gene-like memes themselves "literal" rather than just "metaphorical" status. The criticisms that were directed against similar positions taken by Boyd and Richerson (1984) and Lumsden and Wilson (1981) apply here as well. To conclude, While Hull's remap of the evolutionary epistemologist's analogy is more faithful to Mayr's "population thinking" as Hull has pointed out, it suffers as did its predecessors from an inadequate treatment of the analogue of the biological phenotype.

Rationale for Similarities

It should be clear from the previous section that there are several distinct ways to draw an analogy between biological evolution and linguistic, conceptual, or cultural evolution. Most has been written

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[16] Later, however, Hull (1982, p. 302) cites the work of Blute-- who compares organisms to acts, and adapted organisms to competent acts --in reference to individual and social learning, but without commenting on its apparent disharmony with an organism/scientist analogy. Blute's organism/act comparison is nearer to the "classical" organism/concept alignment. Apparently, Hull would have an analogy within an analogy-- i.e., a scientist's acts (involved in learning) are like biological organisms, but then on another level, the scientists whole conceptual system is like an organism, too.

about analogies set up so that the "sizes" of the phenomena being compared were roughly "congruent" (e.g., species compared to a language community; organism compared to a complex concept in a scientist's brain). By contrast, the "incongruent" between-level analogies presented earlier (e.g., cell compared to person) have received much less overt attention and the existing treatments have more often been febrile, poorly thought out, or too vague to be interesting. One might be tempted to conclude that the persistent disagreements that have arisen in trying to set up an approximately congruent analogy would only be multiplied with an <u>inter</u>level perspective. More concretely, if it is difficult to coherently compare organisms and ideas, comparing biomolecules and ideas could only be worse. In this last section I would like to sketch out a rationale for why, contrary to such expectations, one might expect to find deep similarities between the processes in cells and in linguistically competent human brains. In fact, the comparison at the cell/person level may be in several respects the most fundamental.

Defining the Common Problem

My motivating thesis is that a unique "symbolic-representational" system in cells first arose from a prebiotic chemical substrate at the origin of life, permitting Darwinian evolution to occur, and that although the subsequent history of life witnessed incredible increases in complexity and diversity, as well as the development of new levels of organization, a similar system did not reemerge on any intermediate level until the origin of thought and language in Pleistocene hominids. The detailed comparison begins in the next chapter; I would like here first to try to define the common "problem" that was, so to speak, "solved" by the origin of life and the origin of thought. Given the difficulty of comparing the systems as they currently exist, one might wonder how ideas about their origins could help.[17] Actually, I think the basic context of the comparison, which differs substantially from any of the treatments reviewed above, can best be seen from this angle.

Put crudely, the genetic code involved in cellular protein synthesis, and the neural patterns underlying human language perception are both mechanisms for escaping "determinism". This does not imply that these systems (which from now on will be called "symbolic-representational") create mysterious, irreducible, holistic forces. But it is a natural way of characterizing the "solution" to a surprizingly straightforward "problem" common to the pre-existing states. The pre-existing (pre-biotic, pre-linguistic) states can be described as complex, highly interactive, but deterministic, "soups" containing a number of different types of dynamically stable "units" (pre-biotic molecules, pre-linguistic neural firing-pattern-units in hominid brains). The "problem" is simply to represent, store, and reproduce information about how to make certain "reactions" (chemical reactions, alteration and recombination of neural firing-pattern-units) in this soup happen. The tricky part, is that the information, as well as all the interpreting apparatus has to be in the soup, and thus, subject to its deterministic buffettings. Many of the "reactions" can already happen a little by

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[17] The origin of language question, for instance, has long been the topic of feverish debate. Reflecting on this in the introduction to a well-attended conference on the origins of language (Harnad et al., 1976) Gordon Hewes ironically noted that the Linguistic Society of Paris, deluged with papers on "glottogenesis" had seen fit to prohibit all discussion of the topic in its 1886 bylaws. The origin of life question has weathered similar attempts to locate it beyond the 'scope of science' (see Farley (1977) for a historical review that covers early controversies over spontaneous generation up until Oparin's work in this century).

themselves without the system's help; the system, however, speeds many reactions, slows or prevents others, invents some new ones, and orders them-- in short, controls phenomena in the soup. Another way to describe the problem is that some way must be found to "camouflage" information from the dissipative attack of the soup, but it must not be hidden so well that it is inaccessible. In a sense, the resulting system is still locally "deterministic" since no new forces or rules of interaction have been added. But there is another clear sense in which the system escapes determinism; by storing information in a partially hidden, partially arbitrary form that the soup has trouble "seeing" and thus destroying, the system can evolve (in the Darwinian sense) very far away from its initial state into configurations that are exceedingly improbable from the soup's viewpoint.

The exposition so far is bound to have displeased the linguist more that the biochemist since "communication" has not been mentioned; what good, a linguist might ask, is language perception without language production. The surprising answer is that there seems to be no direct communication or language production at the cellular level-- only language "perception". In fact, I will want to claim that perhaps, the most fundamental function of a symbolic-representational system or "language" is to maintain a controlled network of "reactions", or what a biochemist would call a metabolic network. At the level of human language, this would be a "mental metabolism"-- that is, an operating system (in the functional, not literal sense) for controlling the network of "reactions" between the many varieties of neural firing-pattern-units in the human brain. From this perspective, the ability to communicate is an added bonus (with far-reaching consequences to be sure-- see Chapter II), but distinctly separable from a common core of similarities between the systems.

Three Parallel Constraints

So far, I have only suggested a similar <u>raison d'etre</u> for the two systems; what follows is a description of three, more specific contraints on constructing such a system, common to both levels of organization, that could account for extensive similarities in structure as well as function. The first constraint arises because so many distinct reactions must be controlled simultaneously. A large number of different types of units ("reactants") and special purpose devices to control each of the many reactions in the network must all coexist peacefully-- in close "proximity" to allow the network to function, but without interacting inappropriately with each other. Thus, one constraint is that the special purpose devices used by the system must have a great deal of <u>specificity</u> they must operate only on the intended unit in a highly interactive milieu.

A second constraint arises because the systems did not originate in a vaccuum, as was noted above, but from a "soup", containing a variety of classes of pre-existing "units". The structures in each system had to be built up partly out of these units. By itself, the necessity of "using what is at hand" would not be expected to yield parallelisms. However, for various reasons, only certain types of units, with certain types of pre-existing relations to entities in the "soup" can be used; thus, a second constraint leading to similarities is the nature of the pre-existing <u>units</u> that are assembled into the various "devices" needed to operate the system.

Finally, a third important constraint has to do with the assembly of units into special purpose "devices" that control "reactions". The devices are large and very complicated compared to the units; consequently, the reaction involved in assembling the units into "devices" is inherently more complex than most of the other reactions in the network, which result in smaller, simpler end products made up of one or a few units. The result is that the units must be assembled locally, one unit at a time; this breaks down what would be an impossibly complex reaction into a series of similar reactions, each of which is nearer in complexity to the numerous other controlled reactions in the "metabolic" network. This constraint suggests why the overall architectures of the two symbolic-representational systems are similar and why the devices built up from similar units have similar higher level structural constraints.

Stated baldly, the rationale for similarities given above is uncomfortably abstract and teleological, containing undeveloped premises and terms. The point of it, however, is not to construct a monadology, but to compactly introduce and motivate the analogy; supporting ideas and arguments will be filled in as the comparison between the two systems is considered in detail in the next chapters. In the case of the biochemically based system, the "units", "reactions", and the overall architecture are all quite "visible" and susceptible to rather direct experimentation (in contrast to monads, for example). This is less so for some parts of the human language system (e.g., neural firing patterns underlying language perception) where mostly indirect evidence (e.g., evoked potentials, language structure) exists. Using the analogy productively, however, leads to empirical predictions, some of which might soon conceivably be tested directly.

To conclude, the present project is not exactly like philosophy, science, or philosophy of science. Although one main thrust-- to define a rather abstract structure common to two ostensibly very different systems --is "philosophical", empirical scientific results play a much more important role than is common in philosophical investigation. On the other hand, the empirical predictions are less directly testable (at least today) and less local than those characteristic of scientific pursuits, especially in the physical and biological sciences. Finally, this project is unlike much contemporary philosophy of science, which has been concerned with trying to better understand why the process of "scientific investigation" works as well as it does, and with trying to point out some of the inherent biases in these successful strategies. Perhaps, the present analogical excercise could best be described as "philosophy using science". I hope to show that such a pursuit is not only possible but productive.

CHAPTER II

A FRAMEWORK FOR THE ANALOGY

Levels of Organization and Analogy

In the previous chapter, several different contexts and frameworks for an analogy between biological entities (species, organisms, cells, biomolecules) and 'cultural' entities (disciplines, languages, scientists, people, theories, words, neural firing patterns) were considered. Although, one might *a priori* have expected a well populated universe of such analogies, most previous treatments seem to have oscillated around three basic alignments-- that is, cell/person, organism/idea, and organism/speaker or organism/scientist. This seems to be due to the fact that, empirically, there are certain "levels of organization" at which entities are clearly distinguishable, and other "intermediate" levels where they are much less so. It is, thus, quite 'natural' to speak without preface about the biochemical, cellular, or organismal levels of structure in a vertebrate (as I did in the last chapter)-- these levels are defined by more clearly identifiable units than an infinite variety of theoretically possible intermediate 'levels' like "one-half the contents of a cell", or "the cells that make up two digits of the forelimb of a vertebrate". Levels are not restricted to living things; stars and galaxies define similarly salient levels in the large scale organization of matter. Wimsatt (1976), who has discussed these issues at length, described levels of organization as "maxima of predictability and regularity". And there is Aristotle's metaphor of the philosopher as butcher, "cutting Nature up at the joints"-- in other words, where it is easiest to cut. A moment's consideration of the last metaphor might give us pause, as it makes use of a structural level of organization in vertebrates-- i.e., one containing skeletal elements or organs or tissues --that arguably should have been in the previous inventory. The existence of one or several 'extra' intermediate levels, however, does not warrant the conclusion that nature is homogeneous across different scales, or that the main structural levels are "artifacts" of observational categories, techniques, or apparatus. Since the analogies at hand are based on the results of empirical investigations of different levels of organization, and since these investigations have defined a really quite limited number of basic classes of "objects" (e.g., (bio)molecules, cells), it is perhaps less surprising that relatively few basic frameworks should exist.[1]

The framework adopted in this investigation (see fig. 7), in contrast to that of several authors, is conspicuously "incongruent"; it results in comparisons between entities (cells and persons, single biomolecules and large scale brain activity patterns) at very different levels. An interesting question, suggested by the levels of organization perspective is whether there exist other, plausible, but more "congruent" analogies in between the ones already presented. One way to examine the spectrum of possible analogies, starting with the cell/person alignment as an extreme, would be to increase the size of the smaller system. Thus, we might try organs or bones instead of cells as the "objects" to compare to a language speaker or a scientist. There

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[1] This discussion has only skimmed over many interesting and subtle issues about "levels of organization" and reductionism that are treated in more detail elsewhere (e.g., Dresden, 1974; Hooker, 1975; Wimsatt, 1976, 1981; Bantz, 1980). The position taken here is similar to that of Wimsatt (1976).

are probably some interesting insights to be gained by thinking of, say, a scientific community as an articulated skeleton (though the image of the scientist as organ (e.g., liver, intestine) seems less palatable). An obvious problem with an analogy at this level (besides the ghoulish imagery) is that bones and organs just do not have enough internal structure to be very interesting as models of language users, scientists, or their conceptual systems. For example, the 'perceptual system' of a particular bone seems too rudimentary-- especially when compared to the elaborate 'perceptual systems' of cells --to be of much help with issues of coded sequence processing, or theory and evidence. Another increase in the size of the smaller system brings us back to the organism/scientist (e.g., Hull) or organism/language-speaker (e.g., historical linguistics) level examined in Chapter I.

An equally plausible way to find intermediate analogies would be to reduce the size of the larger system. Thus, we might try comparing cells with organs-- as cells are constructed out of different types of biomolecules (like amino acids and nucleotides), organs are made up of different cell types. A brief consideration of the "topology" of organs and tissues, however, reveals nothing remotely similar to the linear, polymeric structures-- DNA, RNA, proteins --that are so characteristic of cells. The architectonics of interacting cells are more sensibly defined in terms of two-dimensional sheets and three-dimensional networks. Of course, sheet-like structures-- e.g., membranes --are of fundamental importance in cells as well, but it is difficult to avoid concluding that one of the primary defining feature of subcellular architecture (i.e., the coding and decoding apparatus and its products) has no analogue in the organization of cells (now taken as units) into tissues and organs.

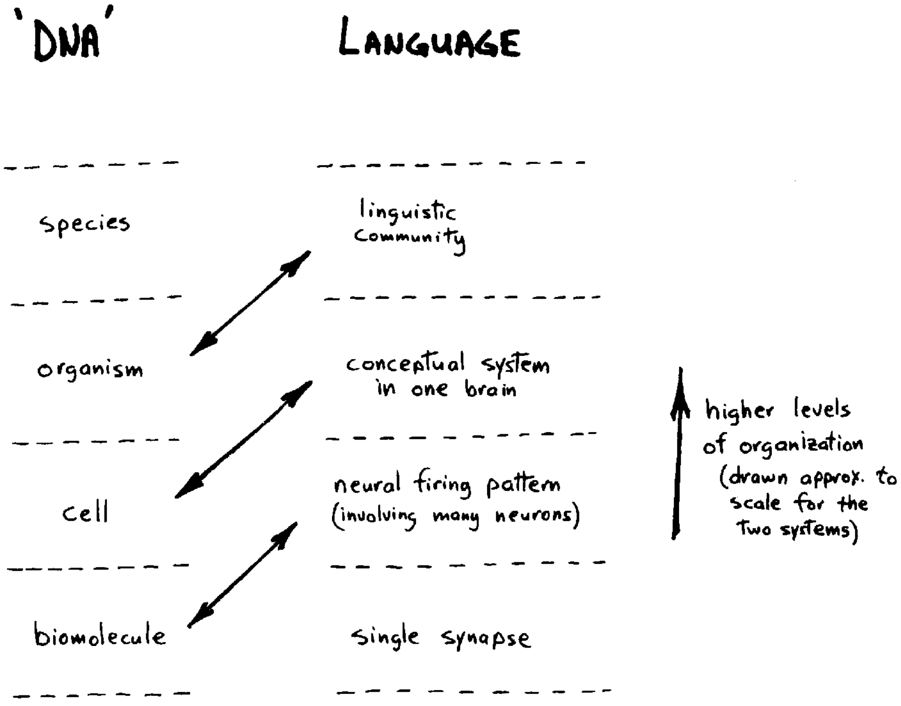

FIG. 7: Levels of Organization in the Present Framework

In a brief discussion, I could not claim to have covered all the possible analogies between biological, psychological, linguistic, and sociological entities, even given that discrete levels of organization reduce that number considerably. However, if one accepts that cellular genetic apparatus as a starting point for the small end of the analogy--and the universal existence of the apparatus and the code in virtually all cells, which is presumably traceable to the origin of life, lends a certain weight to this view --then, I am willing to argue that nothing like cells and the symbolic-representational system that each contains, arose until the origin of human language in hominid brains, about three billion years after the origin of cellular life, and over half a billion years after the origin of multicellular organisms. Such a system is clearly not to be found at the multicellular tissue or organ level, as argued above; but it also seems not to have arisen in the nervous systems of any other animals, not even in the closely related brains of the great apes. The topic of "language" in primates and other animals will be discussed at greater length in Chapter III and V. The main tasks of this chapter will be first, to briefly review previous attempts to produce a general analysis of symbolic systems, and second, to present a detailed framework and terminology aimed at capturing just what it is that cellular and human symbolic-representational systems have in common. That framework will serve as an outline for the empirical examination of the two systems in the succeeding chapters.

Previous Treatments of Sign and Symbol

In considering structure and meaning in language and linguistic behavior, it is difficult to avoid noticing similarities with many apparently nonlinguistic phenomena. Philosophers, psychologists, linguists, anthropologists, and aestheticians among others have attempted to gather up and explicate the different instances and types of "signs", "symbols", and "meanings" and provide, in contrast to the analogies between specific systems discussed in the last chapter, a general definition of all forms of symbolic activity. A brief perspective on this topic could hardly be other than narrow and biased. Furthermore, the various proposed frameworks and systems, though ostensibly intended to be general, have often been fitted to particular tasks, philosophical or otherwise, that were rather different than mine. I would like here just to to mention enough about some previous treatments to indicate some sources of building materials for the present framework whose task is to describe the common features of cellular protein synthesis and human language perception.[2] The topics discussed here have been reviewed from many different standpoints. Lyons (1977) provides a wide-ranging but somewhat uncritical treatment of a number of the issues, and a lengthy bibliography.

Of the many extant works on signs and symbols, the writings of the American philosopher Charles Peirce have been particularly influential. In particular, the baroque intricacies and terminology of Peircean "semiotics" have attracted attention lately, in contexts as disparate as an analysis of the 'labyrinthine' architectural style of the Minoan civilization on Crete (Preziosi, 1983) and sensorimotor programming in linguistic utterances (McNeill, 1979). Peirce's stated intent was, in fact, quite general; he wanted to produce through description, and then subsequent generalization, and account of

> the characters of all Signs used by a "scientific" intelligence, that is to say by an intelligence capable of learning by experience (1897, CP 2.227-- references are to the Collected Works (1931-1958) by date, volume, and paragraph).

This task was carried forward in the framework of Peirce's ontology, which recognized three modes or categories of being-- "Firstness", which is "positive qualitative possibility", "Secondness", which is "actual fact", and "Thirdness", which is a law-like existence that will "govern facts in the future". In Peirce's well-known discussion of the triadic Sign relation, for example, the "Representamen" (= "sign" in the

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[2] Ideas about the nature of human linguistic signs have, of course, been examined experimentally and extensively discussed in contemporary cognitive psychology, psycholinguistics, and linguistics proper, and these perspectives have been influential in developing the framework presented at the end of this chapter. However, discussion of that work will be postponed to the following chapters where empirical support for the framework is marshalled. The ideas discussed here are more explicitly philosophical, and partly serve as a historical introduction to these issues.

restricted sense) is a "First", its "Object" is a "Second", and it determines an "Interpretant", which is a "Third". Peirce then considers three parts of the sign relationship that vary-- these are 1), the 'substance' or nature of the sign itself, 2), the basis of the sign-object relation, and 3), what the sign indicates about the category of the object. Each of these parts are further subdivided into three subheadings with respect to Firstness, Secondness, and Thirdness. The best known subdivision is that of 2), the basis of the sign-object relation. Thus we first have an "Icon" (e.g., a pictorial traffic sign for lane narrowing), which resembles its object (i.e., it "qualitatively" suggests the "possibility" of the object-- a relation which falls into the category of Firstness). Next, we obtain an "Index" (e.g., a weather vane to indicate wind direction), which is connected to and really affected by its object (i.e., a relation which is of "actual fact"-- hence, Secondness). Finally, we have a "Symbol" (e.g., a spoken word), which refers to its Object by means of a law (i.e., its relation is in the category of Thirdness). Two lesser-known applications of Peirce's categories of being to 1), the nature of the sign itself, and 3), what the sign indicates about the existence of the object, yield Qualisigns, Sinsigns, and Legisigns, and then Rhemes, Dicisigns, and Arguments. The 27 possible combinations of the three trichotomies are further augmented by distinguishing Replicas (i.e., tokens) and "direct and indirect involvement". Overlaps reduce the count to ten "classes of sign"-- happily, a Pythagorean decad, which is the way Peirce drew it. In his later work, though, Peirce went further. Langer (1942) comments

> Charles Peirce who was probably the first person to concern himself seriously with semantics, began by making an inventory of all "symbol situations" in the hope that when all the possible meanings of "meaning" were herded together, they would show empirical differentia whereby one could divide the sheep from the goats. But the obstreperous flock, instead of

> falling neatly into a few classes, each according to its kind, divided and subdivided into the most terrifying orders of icons, qualisigns, legisigns, semes, phemes, and delomes, and there is but cold comfort in his assurance that his original 59,049 types can really be boiled down to a mere sixty-six (p. 54).

This is surely somewhat unfair to Peirce, as is my implication that Peirce was motivated only by a Procrustean desire to fit and refit various phenomena into his ontological categories; in fact, Peirce's treatment of signs contains a number of interesting insights, some of which will be noted later on. Nevertheless, the Peircean framework remains unsuitable for the present task for several fundamental reasons.

Peirce's proposed "starting point" is the spectrum of human and linguistic abilities-- e.g., the categorization of objects, or the perception of contiguity that must be presupposed as part of the mechanism by which an arrow indexically indicates its object. Indeed, Peirce often adopts a rather 'phenomenological' approach (CP 1.284-287, for example). He then proposes to analyze all linguistic as well as non-linguistic "sign-situations" from this vantage point. Two points are important here. First, this is fundamentally a "philosophical" occupation in which one is relatively unconcerned with the explicitly psychological or physiological details of the mechanisms underlying symbolic behavior, or linguistic symbolic behavior in particular. Now Peirce rather casually suggests in this regard that a sign stands for its object

> not in all respects, but in reference to a sort of idea.... here to be understood in a sort of Platonic sense, very familiar in everyday talk [!]; I mean in that sense in which we say that when a man catches another man's idea... [or] recalls what he was thinking at some previous time... [or] continues to think anything, say for a tenth of a second. [I]n so far as the thought continues to agree with itself during that time... it is the same idea, and it is not at each instant of the interval a new idea (1897, CP 2.228).

To contemporary ears, this passage seems to suggest the interesting notion of a segmented thought stream. Peirce is not, however, more specific elsewhere, and in numerous writings is quite critical of "psychologistic" explanations of logical thought, for example. Second, he is relatively unconcerned with exploring the possibility of other symbolic systems:

> A Sign is a Representamen with a Mental Interpretant. Possibly there may be Representamens that are not Signs.... But _thought_ is the chief, if not the only mode of representation (1902, _CP_ 2.274).

By contrast, I will be interested precisely in what is known of the mechanisms and substrate of human language perception or what might be called the underlying 'architecture' of the system. My emphasis is on the structure and function of the symbol processing device itself (presupposed by Peirce) and not so much on a categorization of the variety of linguistic and nonlinguistic "sign situations" that the device is capable of operating in, except as these situations relate to the origin and ontogeny of the system. Thus for the most part, only one basic "sign situation" (see below) will be of interest here. Also unlike Peirce, I will have an overriding interest in making a point-by-point comparison of language with the other major symbolic system in nature, discovered, of course, well after Peirce's time-- that involved with DNA, RNA, and protein.

Before discussing ideas about the concatenation of signs, it is useful to contrast Peirce's notion of a sign with the contemporaneous formulation by the linguist Ferdinand de Saussure (1916/1959). Saussure produced a well-known diagram (top of fig. 8) illustrating two people conversing, and then proceeded to distinguish five different parts of the "circuit" involved (bottom of fig. 8). These parts are 1), the "physical" sound waves, and then the "physiological" processes involved in 2), phonation (speech articulator movements), and 3), audition (detection of sounds in the peripheral auditory system), and finally, the "psychological" processes involved in activating 4), the word sound-image (also called the "signifier"), and of 5), the concept (also called the "signified"). The sound image calls up the concept in language perception, while the concept calls up the sound image in productive speech.

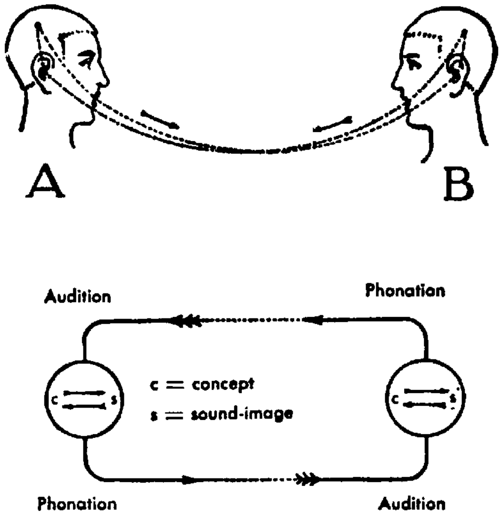

FIG. 8: Scheme from Saussure (1916/1959)

Although the top diagram shows only one dot inside each person's brain, Saussure clearly envisioned two quite distinct "psychological" entities:

> Indeed, we should not fail to note that the word-image stands apart from the sound itself and that it is just as psychological as the concept which is associated with it (1916/1959, p. 12).

From the point of view of Peirce's scheme, the "interpretant", a unitary phenomenon, has been split in two, yielding sound-images and concepts. By contrast, the external Peircean "object" that is signified by the sound waves does not even explicitly appear; in fact, Saussure actively downplays the role of external objects in the genesis of concepts:

> Psychologically, our thought-- apart from its expression in words --is only a shapeless and indistinct mass. Philosophers and linguists have always agreed that without the help of signs, we would be unable to make a clear-cut, consistent distinction between two ideas. Without language, thought is a vague uncharted nebula. There are no pre-existing ideas, and nothing is distinct before the appearance of language (1916/1959, p. 111-112.).

Audition is separated off from the "interpretant" while phonation might in some cases be viewed as part of the "representamen". Probably the most nearly equivalent entity in the two schemes is the external sign or "representamen" in the case of speech perception-- i.e., the sound waves that constitute the spoken word.[3] For the present purposes, the most important new emphasis is a specific bifurcation between a concept and an arbitrarily related internal sound image. In contrast to Saussure, however, it will be argued that prelinguistic "thought" is far from being "a shapeless and indistinct mass".

Returning to the problem of concatenation of signs, it is difficult to ignore the fact that normal linguistic behavior almost invariably involves long chains of signs. Peirce, however, did not express much

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[3] I have probably exaggerated the differences here. Peirce, for instance, allows an "interpretant" to also be the "object" of a "higher interpretant" in a recursive fashion (see below); therefore, one could equate the Saussurean "concept" with what was an "interpretant", but which was then taken as an internal "object" of a higher "interpretant". The Sausurean "sound image" could then be seen as an internal "repsentamen" signifying the internal "object for the higher interpretant. In spite of this, I think it is fair to say that the main thrust of the two expositions differ; and in any case, there are still two Peircean entities in the equation just made-- i.e., the original external "representamen" and the "higher interpretant" --for which no equivalent exists for Saussure.

interest in natural language syntax much beyond a word or two. In turning to his initial discussion of an "ordinary proposition" (a "dicent symbol"-- the ninth sign class), we find that he basically treats it as if it were a unitary sign. The paragraph in question (CP 2.262) must surely qualify as one of the major injuries the language has sustained. The difficulty stems from Peirce's strictly recursive method for describing more complex structures; any interpretant could be looked on as an object of another, "higher" interpretant. He states this rather opaquely as follows:

> The Third [i.e., the first, lower Interpretant] must indeed stand in such a relation [i.e., a hierarchical relation] and thus must be capable of determining a Third [i.e., a second, higher Interpretant] of its own; but besides that, it must have a second triadic relation in which the Representamen or rather the relation thereof to its Object shall be its own (the Third's) Object and must be capable of determining a Third [i.e., the higher Interpretant] to this relation. All this must equally be true of the Third's Third and so on endlessly; and this, and more [!], is involved in the familiar idea of a sign (CP 2.274).

In general terms, "meanings" are described here as what could be called the media and not objects of thought; thus, as one "objectifies" a meaning, it ceases to function as a meaning and instead, is referred to by another newly created "higher" meaning. A similar notion was developed, for example, by Husserl in his Logical Investigations (1913/1970; see p. 327-333). The problem from the perspective of the current task, is that the infinite regress inherent in such descriptions is not very congenial to linguistic, psychological, neurological (or biochemical) model building-- at least in the absence of other principles of organization.

It is therefore somewhat surprising that the relentlessly recursive aspect of Peirce's simple scheme has been so enthusiastically embraced by contemporary semioticians with linguistic and psychological tendencies. Eco (1976), for instance, seems to argue that infinite hierarchies are mandatory (e.g., p. 68-71). In his more recent book (1984), he even took up the question of the genetic code, concluding that, in spite of its lack of "communicative function", the process of protein translation resembled linguistic codes in having a syntactic system (an "s-code") as well as a coupled system of interpretation or meaning extraction (a "code with inference"). The committment to recursive infinities, however, remains; he endorses protein systhesis as a "case of semiosis though not unlimited [i.e., not truly language-like] (p. 84)". McNeill (1979), in the quite different context of a model of language development, describes the "semiotic extension" of concrete sensorimotor ideas to more abstract meanings using the recursive Peircean framework. McNeill, however, only envisions a few levels of recursion. Here the question is not so much what to do with the infinity problem (which is taken care of by other parts of the theory) but whether the rather monotonous and undifferentiated architecture of Peirce's chains of higher and higher triads explains enough about the complex linguistic (or other) facts at hand to be interesting. Some practitioners of the semiotic technique apparently think so-- Shapiro (1983, p. 100), for example, proclaims that "all the rules of linguistic structure [i.e., phonological, morphological semantic] are <u>isomorphous</u> as to the principles of organization". Nevertheless, most linguists (including Saussure) and psychologists have looked elsewhere for suitable frameworks or apparatus (see Chapters IV and V). The argument developed here, is that the better understood functional architecture of the entities that arise at the cellular level, when analogues of concept units are concatenated, can get us off to a better start on the problem of language comprehension. In contrast to the repetitive and uniform architecture implied by a hierarchy of Thirds running loose in the head, cellular biochemistry offer us an architecture that is variegated enough and complicated enough to be taken seriously. As such, it may provide the best currently available model of what defines a "language" in the broad sense.

The synoptic works of Cassirer and Langer on symbolic forms should be mentioned in connection with Peirce; however, they turn out not to be very helpful in providing a framework for the present purposes. The schemes proposed by both of these philosophers put much emphasis on developing a description of what are essentially unitary symbols consisting of a sign and a signification, but of a highly general nature, capable of application not strictly to human language, but also to myth, religion, art, music, and science. The German Neo-Kantian philosopher, Cassirer, in his gigantic _Philosophy of Symbolic Forms_ (1923, 1925, 1929) recognized three modes of "symbolic representation": 1), the "expressive function" (i.e., myths and religion) where the perceptual sign and the signified meaning are merged and not consciously realized to be separate, 2), the "intuition function" (i.e., ordinary natural language), which differentiates the perceptual world, spatially and temporally into material substances-- i.e., into more or less abstract _objects_, resulting in a great proliferation of new perceptual signs (Cassirer spends much time in this regard discussing the semantics of single words), and 3), the "conceptual function" (i.e., science), whereby the system of substances (and attributes) is replaced by a system of _relations_, where a principle of ordered concatenation is developed, and where the distinction between sign and signified is most consciously recognized and exploited. The more general framework of Cassirer (compared to Peirce or Saussure) is, rather ironically, not as comfortably generalized to the molecular level of organization-- it is not specific enough in places where similarities exist between language and the genetic code, but then is too closely tied to human cognition elsewhere to make a great deal of sense on a different level of organization. The interesting discussions in Langer (1942, 1972) on the origin of human symbolization are relevant later (Chapter III), but the general scheme presented is not more suitable than Cassirer's, and for similar reasons. Langer mainly distinguishes "discursive" (concatenated, linguistic, word-like) symbols from "non-discursive" symbols. The latter do not involve anything even metaphorically like a word, and one cannot define non-discursive symbols in terms of one another (e.g., pictures, parts of a musical composition). Though Langer covers a great deal of ground, as did Cassirer, there is little development of a specific framework for symbolic systems beyond a basic bifurcation between the signifier and the signified; her main emphasis is rather on restoring non-discursive symbolic analysis as an equal partner to the more familiar discursive or linguistic mode.

The final framework considered here is due to Hockett (1958, 1966), who described a set of so-called "design-features of language." In striking contrast to the often explicitly 'mentalistic' notions of signs and symbols described above, Hockett's perspective is behavioristic, and with a vengeance--

> The assumption that... elements [such as <u>and</u>] must denote something just as do <u>man</u>, <u>sky</u>, <u>honor</u>, or <u>unicorn</u> has generated much bad mentalistic philosophizing, populating the universe with abstract entities or the human mind with concepts, both of which are as useless as the luminiferous ether (1966, p. 21).

In spite of this, he ends up covering similar ground, but with different terminology and from a complementary 'external' perspective. It is interesting to see how Hockett's features map onto the frameworks reviewed above.

The original list of seven features or key properties was extended to sixteen in later publications (1966); however, a nucleus of four features are most relevant here-- these are arbitrariness, duality, discreteness, and displacement. By "arbitrariness", Hockett meant only that the relation between the external physical sign and its object was not "iconic" or "geometrically similar" in some "objective sense"; this contrasts, for example, with the internal arbitrariness between Saussure's "sound image" and "concept", and with Peirce's notion of a law-like or "symbolic" relationship between a sign and its object, which exists only by virture of an internal interpretant.

"Duality" or "duality of patterning", refers to the existence of two levels of structural organization, roughly phonological and lexical, that are arranged so that a particular small group of lower level units (phonemes) is mapped onto a single higher level unit (morpheme); the large number of possible permutations of a few elements taken a few at a time allows many upper level units to be mapped using a small number of lower level units. This notion does not even appear, for example, in Peirce's definition of a symbolic sign relation.

"Discreteness" means that the "possible messages" form a discontinuous (discrete) spectrum. This was meant to contrast, for instance, with the "bee-dancing" signals investigated by von Frisch, which vary continuously (and which have to rely on "iconic" meanings). Clearly, phonological units could be "discrete" independently of any possible meanings they happened to be conveying, but Hockett is not explicit here. In any case, discreteness does not appear in Peirce's definition.

By "displacement" Hockett means that linguistic messages "refer to things remote in time or space, or both from the site of communication (1966, p 11)". Peirce's elaborate systems recognizes a large range of "proximities" between a sign (representamen) and its object (in fact, that is what the system seems to be best suited for). But in Peirce's analysis of an "ordinary word" (i.e., a symbol-- e.g., "give", "bird") displacement is clearly built in:

> any ordinary word.... does not in itself identify [what it refers to]. It does not show us a bird, nor enact before our eyes a giving, or a marriage, but supposes that we are able to imagine those things and have [previously] associated the word with them (CP 2.298).

In fact, Peirce's "symbols" cannot even "indicate a particular thing" when the thing is not displaced, but only a kind of thing; it turns out that a word with an immediate referent (an 'extraordinary' word?) like a demonstrative pronoun (e.g., "that") is not even a "symbol" for Peirce but rather an "index" with a non-arbitrary connection to its object. For Hockett, "that" would not exhibit "displacement" if it referred to an object at hand, but it would certainly show "arbitrariness".

The remainder of Hockett's features are less relevant here-- several are exceedingly general and loosely defined ("productivity", "semanticity"), others involve language production (e.g., "complete feedback") or language learning, and several others seem to give inappropriate emphasis to particular uses of language (e.g., "prevarication"-- the ability to lie, or "reflexivity"-- the ability to talk about language itself) that seem secondary to its general descriptive function admitted by all parties.

The very abbreviated discussion of attempts to construct a framework for signs and symbols, if nothing else, should serve to emphasize difficulty of the task. There is not a lot of agreement in what a theory should explain, or on what devices should be used to do the explaining, or on how they should be employed. Different frameworks overlap in ways that are difficult to disentangle. Much of the difficulty is due to the fact that the processes underlying the comprehension and production of symbols in man (and animals) are so poorly understood. This is not to paint a crudely reductionistic view of these processes; but it seems unlikely on the other hand, that philosophical views of the questions will remain untouched, after, say, several hundred more years of progress in neurobiology-- at least if the history of the last several hundred years of philosophy and physics is any guide. A second difficulty is that we are constrained to examine our symbolic system using the system itself. I do not think that this implies that there are any well-defined _a priori_ roadblocks to neurobiological, psychological, or linguistic inquiry. But it does imply that progress will be more difficult than it is even in physics or biochemistry where it is somewhat less of a problem to objectively study something. In this light, one of the main motivations behind the present project-- given that it can be established that there are fundmental similarities between the molecular genetic system and human language comprehension processes --is that we can use the more "objective" results from the first system as a preliminary but refreshingly concrete model for the underlying processes involved in the second.

Framework for a Symbolic-Representational System

The framework developed here has two purposes. First it establishes a straightforward terminology and a simple visual scheme to which all the subsequent, more detailed, comparisons in the following chapters will refer. Second, it is also a summary of those investigations and in the end should be judged on its empirical adequacy. It is presented before the arguments on which it is based to provide a roadmap; there are enough of them to make the reverse order unhelpful. The final framework below is reached by successive approximation, to better show how it relates to previous ideas about these issues.

The context of the present analogy is quite specific. Roughly, we want to compare the <u>perception</u> of spoken (and signed) language by the human brain to the "perception" of the DNA "language" by the protein translation machinery of the cell. No previous treatment has explicitly stated the context of the comparison in this way. Rather, all accounts essentially start by making two lists of entities to be compared. On one hand variously have been alphabets, the Morse code, phonemes, words, sentences, paragraphs, sentences, and books, and on the other have been DNA, nucleotide bases, codons, bacterial operons, genes, amino acids and proteins. Once the lists are at hand, a piecemeal comparison usually commences. Rarely has anyone even taken the time to specify the overall context of the comparison. As a result, the nucleotide bases that make up DNA strand have been haphazardly compared to letters (i.e., to written representations of linguistic sound groups), to Morse code dots and dashes (i.e., to a peculiar recoding of those written representations of spoken language sounds designed specifically for telegraphic transmission) and to phonemes (i.e., to the, at least presently, rather abstract entities the phonologist postulates to explain the distribution of groups of similar speech sounds in spoken language). In each of these cases, there is a different but unstated context that I have tried to indicate parenthetically. Furthermore, a given author is often not internally consistent, shifting from one context to another as he proceeds up the hierarchy. The context I am arguing for-- and that I want to claim is in some sense, the most fundamental --does not correspond to any of those just listed because it is intimately concerned with the presently poorly known structure and function of the neural substrate of language (in addition to the phonology, syntax, and semantics of language)-- in fact, it is impossible to make sense out of the cell/person analogy without considering this level at some point.

There seem to be two reasons why the present analogy has hardly been considered previously. The first seems to have arisen as a natural consequence of the commonly observed fact that different parts of a scientific field progress at different rates and often in fits and starts. In constructing an analogy <u>between</u> fields, it is quite unlikely that the (putatively) correlated parts of the two fields will parallel each other in degree of "progress" or elaboration as well; rather, we might expect independent development to have produced uncorrelated "holes". Resulting complementary distributions of areas of ignorance could effectively conceal what might eventually turn out to be an obvious alignment. This in fact seems to have occurred in the two fields of 'cell' and 'person' research. It was already lamented that our present understanding of the underlying neural mechanisms of language comprehension is rudimentary; our understanding of the analogous part of cells-- i.e., the structure and function of biomolecules --by contrast, is further along. On the other hand, information about "possible functional sequences" of units (see below) is actually more accessible in linguistics than in biochemistry.

To flesh out these points, it helps to consider what one of the fields would look like if it had developed like the other. If modern protein biochemistry and molecular biology were like linguistics, for instance, (assuming for a moment the analogy in its final form) then biochemists and molecular biologists would spend their time trying to construct a set of rules that would account for all the possible amino acid sequences (and <u>only</u> the sequences) capable of producing a functional protein or protein fragment (e.g., a catalytically active enzyme) after having been synthesized and allowed to fold up in solution. The linguist-like biochemist would be able to synthesize and analyze different sequences of amino acids within seconds instead of weeks, months, or years, allowing huge numbers of sequences to be assayed. The analysis, however, would be indirect; different sequences could be compared only by observing their effects on a whole cell. A major goal, of course, would still be to understand the structure and function of the proteins themselves.[4] A useful strategy would be to compare sequences differing in only one or a few units.

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[4] Actually, rather indirect techniques were commonly used in biochemistry before the crystallization of subsequent structural characterization of DNA and proteins. Of course, biochemists had long been able to isolate molecular species and physically characterize them; but the three-dimensional structures of nucleic acids and proteins were completely unknown for the first half of this century. The first x-ray crystallographic structures for proteins in the late 1950's and 1960's came as a considerable shock. Previous models based on theoretical calculations and spectrographic and chemical data were highly underdetermined. It is interesting in this light to examine the early interpretations of very low resolution X-ray data, which reveal expectations of extremely regular, geometrically simple structures containing parallel bundles of rods (Perutz, 1949) or a flat layer of rods (Bragg et al., 1950). The initial reactions to the first higher resolution pictures are also telling. Kendrew et al. (1958) dryly commented "the arrangement seems to be almost totally lacking in the kind of symmetry one instinctively anticipates, and it is more complicated than has been predicted by any theory of protein structure". Perutz, who devoted much of his life to hemoglobin, was more forthright: "could the search for ultimate truth really have revealed so hideous and visceral looking an object? Was the nuggett of gold a lump of lead?" (1964, p.70). Perhaps when it becomes possible to examine the neural firing patterns underlying language comprehension (see Chapter V), they will be found at first equally "unsymmetrical" and unexpectedly complex, possibly even "visceral"!

By contrast, the biochemist-like linguist would have direct access to the firing patterns that underlie experiences of meaningful, well-formed sentences, but these could only be examined on at a time, and the process would take a very long time. As a result, only a few sequences could be examined in a year. On the other hand, such analyses would provide mechanistic, dynamical explanations not only for how the neural firing pattern was built up during the linguistic input but also how it affected pre-existing patterns in the network. Thus, one would known a great deal about the comprehension of some sentences, but much less about rules describing what sort of input sequences could be understood.

Obviously, the inverted "developmental orders" in the two fields could probably never have occurred. On the other hand, it is very likely that 1), the neural patterns underlying language comprehension will come to be investigated, and 2), the "sequence space" of possible protein structures will eventually be examined in great detail. The main point is that the actually occurring developemental orders can temporarily make two fields look more different that they really are by making certain types of explanations-- e.g., rules to generate sequences --easier to construct.

The second reason that the present analogy has been mostly overlooked has to do with what I think is a genuine difference between the two systems-- that is, the utter lack of "language" production, either internal or communicative (fig. 9) at the cellular level. At first sight, the notion of a language without production, and hence, without a direct communicative function seems a bit peculiar.

Among other things, it appears to compromise intentionality. It is difficult even to imagine what strictly perceptual language would be (but see below). Nevertheless, the idea that communication is the *sine*

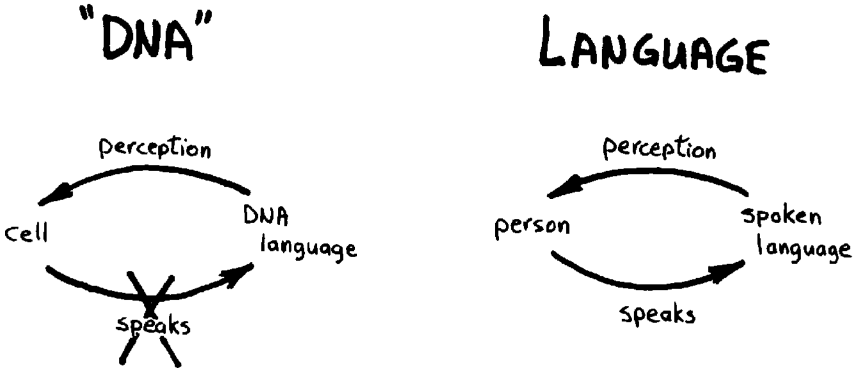

FIG. 9: No Language Production in Cells

<u>qua</u> <u>non</u> of language has been challenged by linguists among others. Chomsky, for example, disputes the notion that the "essential purpose" of language is communication (1980, p. 230-231), but only concludes at length that

> it is difficult to say what "the purpose" of language is, except, perhaps, the expression of thought, a rather empty formulation. The functions of language are various. It is unclear what might be meant by the statement that some of them are "central" or "essential" (p. 230).

Sapir is more emphatic:

> The primary function of language is generally said to be communication.... [but] the purely communicative aspect has been exaggerated. It is best to admit that language is primarily a vocal actualization of the tendency to see reality symbolically, that it is precisely this quality which renders it a fit instrument for communication... (p. 159).

Positions such as these are of course, less at variance with the ideas promoted at the end of the last chapter.[5] To more graphically point out the differences between the systems traceable to the lack of production, it helps to envision language without production, or cells with it.

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[5] These issues will be discussed at greater length in the context of the comparative anatomy of human and primate brains and ideas about specifically language-related adaptations.

If persons were actually like cells in this regard, then no one would be able to talk (or write), though everyone would have the ability to understand language. The source of coded input strings would be internal (like DNA); each person would store hundreds of thousands of different sound sequence messages inside his or her brain in a permanent magnetic-tape-like form. These independent libraries would be inherited. During daily activities, messages appropriate to various situations could be carefully accessed and meanings generated from them internally. However, no new messages could arise during a person's lifetime, except as a result of random deterioration of the stored messages-- e.g., "mutations" of a message unit, accidental inversions of portions of the stored message sequences. Obviously, cultural evolution would be immensely slowed. Producing a message the length of, say, a scientific paper, from scratch would involve a tedious selection process spanning thousands or millions of generations; and at long last, one could only have it "read" by one's offspring.

Alternatively, it is possible to conceive of cells with production. In the first place, it would be possible for cells to synthesize proteins de novo without the need for a coded message (i.e., without DNA or messenger RNA), in addition to using the more familiar process that depends on a message strand. Furthermore, a highly non-random protein, appropriate to the task at hand could be made, after a few tries. So far the cells have just started to "think to themselves". Full-fledged production of the DNA language would require also that the cells had a brand new chunk of enzymatic machinery for turning the amino acid sequences that constitute a protein (generated de novo or otherwise) back into coded DNA strings containing one triplet of nucleotide bases per amino acid.[6] Then the cell would be able to communicate directly with other cells by injecting the DNA strand into them, and having them generate a protein from it. Such a system comprises a more thorough-going minute-to-minute Lamarckianism, than has ever been conceived for biological organisms. Cells (and probably to a lesser extent, multi-cellular organisms) would be capable of evolving at a lightning-fast pace, adapting in a directed, Protean manner to external environmental and "social" conditions, and moreover, passing on the acquired knowledge to cells unrelated by descent.[7]

The scenarios above are perhaps even more uncomfortably reminiscent of science fiction that the previous pair. Nevertheless, I think they effectively point out a second reason why the analogy has not previously been examined from the present context; the presence of production in only one of the systems would make them look very different, in spite of the fact that they might be based in a strong sense on very similar

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[6] Even in the early years of molecular biology in the 1950's, before the genetic code had been deciphered, the existence of such a subsystem was never stringly argued for (e.g., there was no genetic evidence for it). on the other hand, it was not explicitly denied until Crick put forward the "central dogma of molecular biology" in an influential and forward-looking paper, in which he stated that "once 'information' has passed into protein <u>it cannot get out again</u> (1958, p. 153, his emphasis)". A decade later with the discipline solidified, Crick observed that the discovery of the prohibited transfer "would shake the whole intellectual basis of molecular biology, and it is for this reason that the central dogma is as important today as it was when it was first proposed (1970, p. 563).

[7] Notice that the productive aspects of language make it doubly different from the genetic code; not only can humans produce new meanings by "directed mutation", but they can also <u>communicate</u> them. Cultural or conceptual evolution has often been characterized as "Lamarckian" but it could presumably be so without the communicative function of language. To make the point graphically, if whole animal phenotypes evolved like human mental "phenotypes" do, then not only would a giraffe's neck elongate as it tried to reach the higher branches, but the animal with the newly acquired long neck would be able to instantly "communicate" such a neck to other short-necked members of the herd.

architectural principles on the comprehension side (e.g., concerning the way in which sequences of meaningful units are assembled into functioning "structures"). From the present point of view, mere conversation or even a few moments of thought to oneself results in immediate "evolutionary" change in the mental "phenotype" potentially capable of transmission. Combined with the differential availability in the two systems of certain types of empirical information, the differences resulting from the unilateral presence of production has lead most responsible thinkers to conclude that the similarities between the two systems must be very superficial. The risk in postulating a similar underlying architecture for two phenomena is that the amount of fiddling needed to arrive at different instantiations can sometimes be so extensive that one is loathe to conclude that the underlying architecture is very explanatory after all. I want to argue here that the predictive power of the present framework arises precisely from the common architecture and not-- to use a well-worn metaphor -- from the "epicycles" added to save the phenomena.

The basic common scheme is now given. Put very crudely, it involves different levels of organization than evolutionary epistemology; it uses a different way of building up internal structures than Peirce; it postulates a more direct relation of signified to objects than does Saussure; it has more parts than the schemes of Cassirer and Langer; and it eschews the excessively behavioristic stance of Hockett. In the scenarios given above to help locate the context of the comparison, a variety of analogies and types of units were implied. At the risk of being excessively elliptical, the next section gives those units (very) straightforward names and indicated the nature of the relationships that hold between them using a few features. The empirical data in the following chapters will be used to argue for, explicate and draw predictions from that analytical scaffold. It is first described approximately synchronically-- from the perspective of a time slice in the operating system --and then diachronically-- but across "perceptual" rather than the usually implied evolutionary time.

In the scheme, the simplest linguistic (in the general sense) symbol structure minimally has five parts-- the external symbol (S), the internal symbol-representation (SR), the "3-dimensional connector" (C), the internal "thing"-representation (TR), and the external "thing" (T) (see fig. 10). Each of these five types of parts has a specifiable, "homologous" relationship with the next part in the two systems. For reference, the more complicated 8-part 'ontology' needed to describe linguistic <u>production</u> as well as comprehension, is also illustrated (see fig. 11). Further discussion of the productive aspect of linguistic systems is however postponed to the section on contrasts between DNA and language; the remainder of this section is concerned only with the symbol structure common to DNA and language.

We start with the external symbol (S). It is defined to have a non-arbitrary, causal relation with (or toward) the internal symbol-representation (SR). This relation is non-arbitrary in the sense that is is not defined by the symbol system itself but depends on a pre-existing, relatively deterministic processes. In this case, it is a one-to-one transformation. The relation is causal in the sense that a given symbol (S) relatively automatically and reliably 'calls up' its internal representation (SR).

By contrast, the internal symbol-representation (SR) has an <u>arbitrary</u>(<u>2</u>), causal relation with the internal "thing"-representation (TR). This relation is arbitrary in the sense that there is no

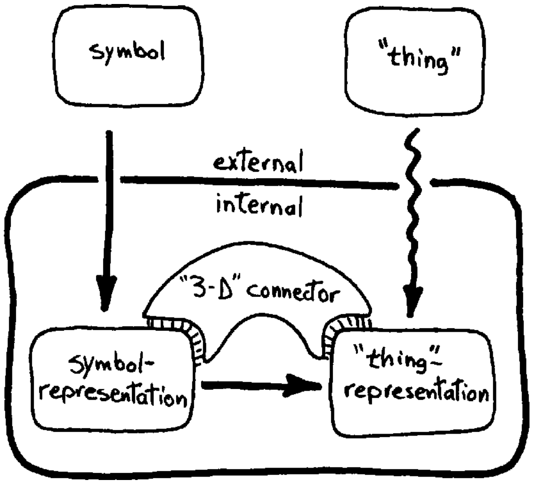

FIG. 10: Basic Common Scheme

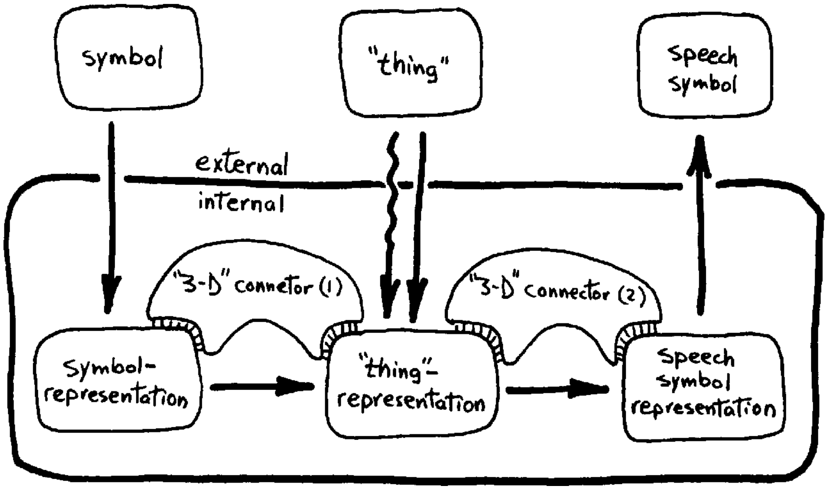

FIG. 11: Basic Common Scheme With Production

deterministic, pre-existing (i.e., prelinguistic) reason why a particular internal symbol-representation (SR) will be preferentially connected to any of the various internal "thing"-representations (TR's). What initially determines what parts get connected is a fifth entity that is capable of recognizing in a non-arbitrary way, the "3-dimensional" structure of a given internal symbol-representation (SR) and then connecting it up by means of an arbitrary(2) bond to a particular internal "thing"-representation-- this entity is the "3-dimensional connector" (C). This is also a one-to-one connection. By "3-dimensional recognition", I mean to refer to a connection that involves a large, variable (or non-standard) region of a part in the system; it stands in contrast to an arbitrary bond, which involves a smaller, standardized subregion of the part. The two connecting regions (arbitrary(2) and "3-dimensional") are in different "places" on both the symbol- and "thing"-representations (SR and TR). The internal "thing"-representation (TR), however, has a much more variegated "3-dimensional" structure (it is much less standardized) than the internal symbol-representation (SR). The internal "thing"-representation (TR) then also has a non-arbitrary relation with the external "thing" (T) or "things". Again, this means that the relation is not defined by the symbol system itself, but depends on a pre-existing, pre-linguistic transformation. Unlike the two relations described above, however, the connection between the external "thing" (T) and the internal "thing"-representation (TR) is often one-to-many-- a group of "things" (T's) is often connected to a single "thing"-representation (TR) by a relatively deterministic, pre-linguistic "perceptual" transformation. This relation is not causal in a linguistic context because the external "thing" or "things" are not necessarily present (often they are not); the internal "thing"-representation (TR) is, as noted above, causally 'called up' in normal operation only by the internal symbol-representation (SR).

What has been described so far is something like an instantaneous "time slice" of an operating symolic-representational system. To see the whole system, we must look at it "diachronically". It is at this juncture that my treatment diverges most from Peirce's. Up to now, the scheme resembles a modified Peircean triangle with a 3-part Interpretant. Basically, the method is to simply "attach" together a linear sequence of internal "thing"-representations (TR's) by means of arbitrary(3), standardized connections and then allow this chain to "fold" upon itself into a rather large "3-dimensional" structure. The assembly process itself is carried out by a a "chain assembler" that makes temporary arbitrary(2) bonds with each symbol-representation; it is itself built around a folded chain of symbol-representation segments, but also contains folded "thing"-representation chains. The 3-dimensional connector is itself a folded chain of "thing"-representations. "Folding" refers to a process by which non-adjacent "thing"-representations (TR's), each with specific properties, are spontaneously (i.e., without further intervention of the assembly apparatus) brought into "closer" contact, producing a much more complex overall connectivity than a one-dimensional chain, and giving rise to several levels of "3-dimensional" organization. The internal "thing"-representations (TR's) are conceived of as having "backbones" by which the arbitrary(2) connections are made and which provide a ready-made "syntactic" scaffold (i.e., a small number of generalized folding patterns) and then "side chains" which are important in determining <u>particular</u> "folding" patterns as well as eventual "semantic" function (which arises only after "folding") with respect to the "world" <u>via</u> interactions with a wide variety of internal "substrates". One main type of "semantic" function is to alter the "3-dimensional" structure of a "substrate".

Backtracking now, we find that the external symbols (S) are themselves connected into linear sequences by arbitrary(1) bonds and exhibit a backbone-sidechain structure as well.

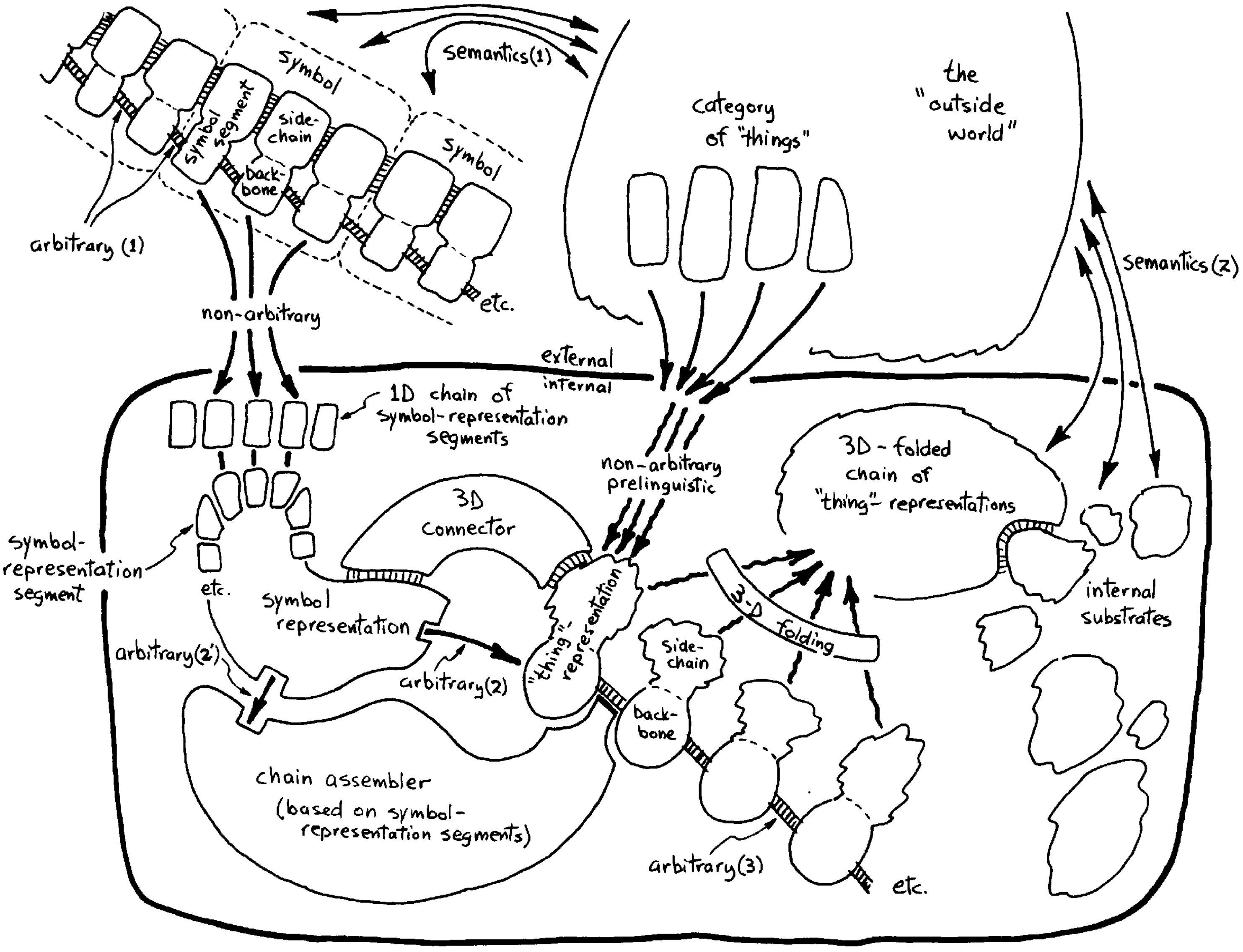

FIG. 12: Basic Scheme in Operation

Finally, since an external symbol (S) automatically calls up an internal symbol-representation (SR) which automatically calls up an internal "thing"-representation (TR), then the external symbol (S) order is responsible in a sense for the ordering in the chain of internal "thing"-representations (TR's). This diachronic picture is illustrated in Figure 12, which provides a summary of all parts, relationships, and their salient characteristics discussed in this section except that the apparatus for assembling the "thing"-representation (TR) chains.

I have tried to be as concise as possible omitting all the details of the two systems and using a combination terminology that draws, however, more extensively from the concrete, more localizable chemical entities than from neural or or linguistic (in the narrow sense) phenomena. What the parts terminology lacks in delicacy, it makes up for in directness. This enterprise should not be construed as a attempt to provide an abstract framework for symbolic behavior of 'all kinds' but only for the peculiarly linguistic (in the wide sense) kind that occurs, as far as I can tell, only at two specific levels of organization. The purpose of such an elliptical exposition is simply to establish the basic structure on which empirical details will be exhibited. I do not want to argue for the analysis using internal "philosophical" criteria but only on the basis of how well it is supported (or extended) by the comparative data.

CHAPTER III

SYMBOLS AND SYMBOL SEGMENTS

In this chapter, the more empirically exposed parts of the analogy are developed. An important task throughout will be to precisely indicate the proper level of specificity of the comparison. For instance, it seems highly unlikely that a particular bond torsion angle in a protein will imply anything about the dynamic electrical behavior of a certain type of pyramidal neuron in human auditory cortex. On the other hand, the source of constraints on bond torsion angles in a biopolymer, for example, might fruitfully be used to infer the source of contraints on serial interactions between neural firing pattern units in auditory cortex. In other words, we want to concentrate more on relations between units than on the unit properties, as suggested in Chapter I. The problem is that sometimes, there is not a sharp boundary between "properties" and "relations", but only a continuum of levels of specificity of the comparison. This is especially troubling when one is trying to make predictions about hidden processes. A way out is to carefully determine the appropriate level of analogical specificity for exposed parts of the comparison so that predictions of reasonable specificity can be made about covert phenomena.

The topics in this chapter are centered on the nature of the symbol (S). The processes by which it is internalized or "perceived" (S => SR), and the nature of the resulting internal symbol representation (SR), and its association with a "thing"-representation (SR => TR), are mainly treated in later chapters. However, it is difficult to discuss these topics in strict isolation and a zig-zag path is occasionally unavoidable. For each subheading, cellular and molecular phenomena are presented first and the parallel aspects of human language second. This pattern will be followed throughout the later chapters. Unless noted, terms like "symbol" will be used only in the sense introduced at the end of the last chapter and summarized in Figure 12.

The main comparison here is between the information bearing nucleotide chains at the cellular level, and sequences of pressure waves that humans perceive as speech sounds. There are, of course, several other linguistic media-- e.g., visuomanual signs in various sign languages, written language, finger-spelled spoken language, Morse code, and so on. Only the first of these, sequences of forelimb and facial configurations, will be examined for analogical purposes; sign language alone is a primary linguistic system, like spoken language. Written language, in contrast to signed or spoken language, is clearly secondary. It is preceded in both cultural evolution and individual development by the perception of spoken or signed language, and is peculiar (relative to the first two) in several ways-- for example, lexical units are clearly marked off from each other. Also, it is common for a person to understand spoken but not written language, but the converse situation has probably never existed in pure form. On the other hand, it is difficult to avoid considering written language. The origin of writing is a landmark in the development of modern civilizations and written language has coevolved with a number of languages for thousands of years. More recently, a majority of contemporary psycholinguistic work has been on written language (the spoken word in this regard is usually considered a "degraded" stimulus in comparison with written words). And it seems absurd to deny that something quite similar happens at some level or levels upon hearing and reading the same linguistic string. Therefore, reading research will not be neglected. Other specialized coded forms of language, however, will not be considered and for strict analogical purposes, I will deal mostly with the primal forms of spoken and signed language.

The nature of the symbol is discussed under six headings--segmentation, linearity, arbitrariness(1), backbone and sidechain structure, prebiotic/prelinguistic substrate, and propagation and evolution. The first three are concerned more with relations between units in the symbol chain, the next two more with the nature of those units, and the last with some significant differences between the biochemical and linguistic systems.

Segmentation of the Symbol Chain

One of the major characteristics of external symbols is that they are segmented apart from any specialized linguistic or "perceptual" mechanisms. In some respects, this is so obvious a feature that it is not accorded any special status; nevertheless, in the present comparative context, this feature forms the basis for a number of subtle parallels. The chemical and linguistic details of segmentation will be treated in particular detail to provide a background for the later topics, which are concerned with many of the same phenomena, but from different perspectives.

DNA Strands and DNA Segments

Segmentation is first treated in a compositional sense and then in a dynamic sense.

Compositional Segments in DNA

It is well known that the DNA (deoxyribonucleic acid) symbols (i.e., what the molecular biologist calls "codons"-- see below) are composed of subunits or segments known as nucleotides, each of which consists of the sugar 2'-deoxyribose with a phophate group esterified at the 5' position and one of four aromatic bases at the 1' carbon (the bases are of two types-- i.e., the purines adenine and guanine, and the pyrimidines, cytosine and thymine). The segments are connected into phosphate diesters at the 3' sugar carbon. Figure 13 shows a flattened as well as a 3-dimensional representation of a DNA molecule-- in both cases a single segment (one nucleotide) is circled and the sugar, phosphate group, and the aromatic base is indicated. A space filling model of a free nucleotide and the numbering scheme is also shown.

That nucleotides were the proper subunits or segments of DNA had been clear before Watson and Crick (1953) discovered the stereochemical nature of DNA. It was known in fact, even before DNA was thought to be the information carrying component of the genetic substance; the polymeric structure of nucleic acids had been taken as evidence that these substances served as an inert scaffold, with a simple repeating sequence (the "tetranucleotide hypothesis"), upon which hypothetical proteinaceous coding elements were arrayed (Olby, 1974; Judson, 1979). The revelation of the double-helical anti-parallel structure of B-DNA solidified the earlier essentially correct segmentation scheme. The composition of each phosphodiester strand is unambiguous; the polymer differs from a sequence of free nucleotides only in that a total of one water molecule per nucleotide is removed in the formation of the covalent intersegment bonds. Thus in a strictly compositional sense, DNA (and RNA) have very nearly non-overlapping subunits that can be

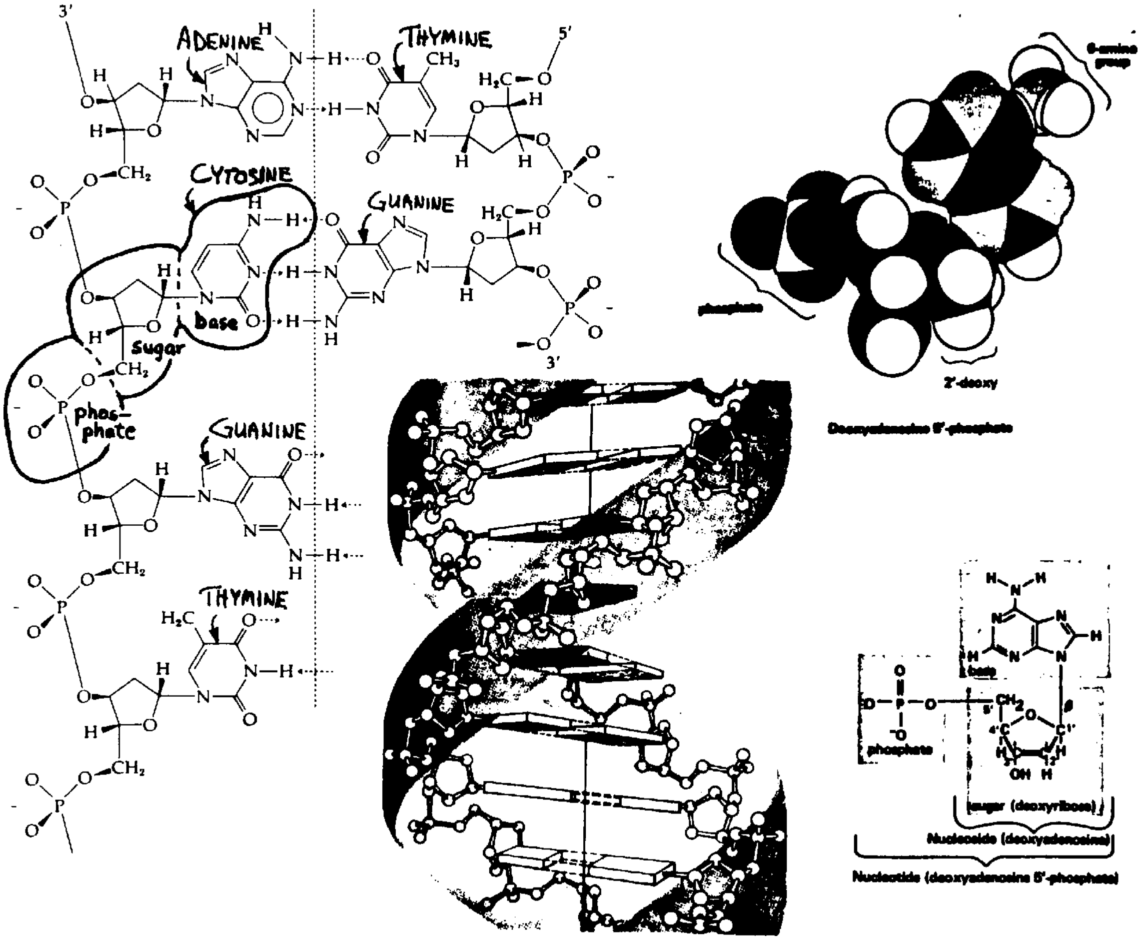

FIG. 13: Units of DNA

recognized by a structural chemist without invoking biotic mechanisms or processes.

Dynamical Segments in DNA

A more dynamic definition of 'where the prebiotic subunits or segments are' in a molecular chain can be gotten from the relative stability of the various covalent and non-covalent links in the chemical context of a prebiotic chemical soup (often visualized as an aqueous solution, at near to modern earth-surface temperatures and pressures, under reducing conditions, and subject to unshielded ultraviolet radiation and lightning-- e.g., Miller and Orgel, 1974). The more detailed parameters of such an environment are presently not well known (see Schopf (1984) for an extensive review) and it would be rather impractical to duplicate them precisely for extended periods of time, even if they could eventually be determined. Nevertheless, one can begin to get an idea of the "ecologically" relevant stabilities by considering a few of the many simpler "soups" to which organic chemists have exposed DNA (reviews: Brown, 1974; Dugas and Penney, 1981; Saenger, 1984).

For example, the 3',5'-phosophodiester linkage is especially vulnerable to hydrolytic cleavage in polynucleotides. In single-stranded RNA chains in particular, acid- or base-catalyzed hydrolysis of the 5'-phophoryl linkage goes to completion, resulting in a mixture of 2'- and 3'-phosphate nucleotides. A similar reaction is catalyzed by various metal ions (e.g., Ca^{2+}, Zn^{2+}, Ba^{2+}, Pb^{2+}). Thus, in the context of very simple aqueous "soups", the inter-segment bonds in RNA are clearly less stable than the within-segment bonds (e.g., glycosidic alkyl-oxygen linkages).

But in considering the segmentation of DNA chains by acid/base hydrolysis, it turns out to be less clear. Single-stranded DNA is much more stable than RNA in alkali because it lacks a potential alkoxide function beta to the 3'-phosphate (i.e., it only has -H on the 3'-carbon instead of -OH); this does not allow the formation of a strained 2',3' cyclic intermediate (see fig. 14) that is seen during RNA hydrolysis (the two possible ring openings of this intermediate account for the mix of 2' and 3' products). Base-catalyzed chain scission still occurs (probably mostly as a result of hydrodynamic distortion of intersegment nucleotide bonds into an analogous intermediate state) but only at the infinitesimal rate of one break per 10^9 daltons per hour (Hill and Fangman, 1973).

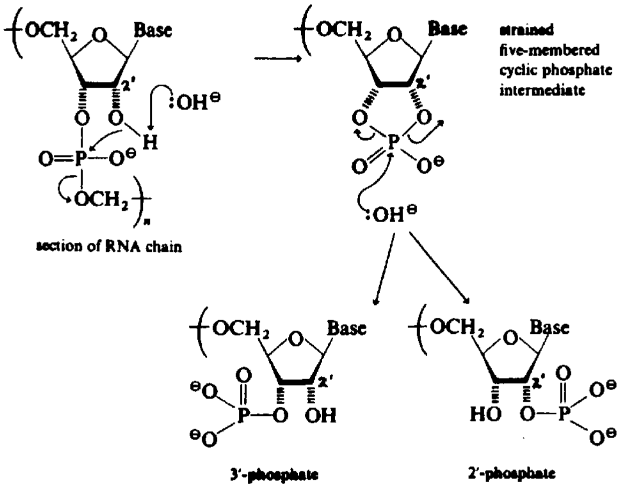

FIG. 14: Hydrolysis of the Internucleotide Linkage

In acid (or at elevated temperatures), on the other hand, the purine glycosidic bonds are the least stable, resulting in "apurinic acid", followed by eventual chain scission at sites of base removal. Many other reagants that destabilize the glycosidic linkage (e.g., methylating agents, hydrazine) lead to base loss, unmasking of the sugar aldehyde group, and subsequent acid- or base-catalyzed chain scission (by way of several different intermediates), which results in a number of endgroups that are not always complete nucleotides. Also, on the basis of studies with model compounds for the phosphate linkage (e.g., dialkyl phosphate) it has been suggested that the slow hydrolysis of internucleotide linkages in DNA (as opposed to RNA) can occur by alkyl/oxygen (i.e., within-segment) cleavage in addition to the usual phosphoryl/oxygen (i.e., between-segment) cleavage in RNA (Brown, 1974). Thus, although the segments or subunits of the three-base symbols (codons) in DNA are as clear as they are in RNA from a "compositional" viewpoint, the greater stability of the intersegment bond in DNA complicates the "dynamical" picture of where the segments are.

Contrasts with Linguistic Symbol Segments

Before moving on to linguistic segmentation, several differences between chains of speech sounds and chains of nucleotides are first considered. In explicating how DNA is different, some of the interwoven constraints on molecular level segmented symbol chains can be brought into clearer focus.

The first main difference is that the primary cellular symbol segment sequences are located inside living cells, in contrast to the basically extra-organismal location of speech sound waves (actually, the sound does pass through the skull, but the physical vibration of the brain by speech of normal volume has relatively little effect on ongoing activity). It is difficult to be sure about the initial location of DNA. One idea is that it was secondarily incorporated into protocells; in fact, this is probably one of the few points about which the "DNA-first" and "protein-first" factions in origin of life research agree. Nevertheless, prebiotic synthesis of DNA and RNA has met with limited success (see below) and even the bases are somewhat difficult to synthesize. It is not even entirely implausible that nucleorides were synthesized *de novo* in protocells. But whatever the resolution, it is clear that the internal location of DNA in current cells makes for an entirely different looking system than is seen with language.

Linguistic symbol chains were never internalized in human brains, and instead, a dynamic and interactive (but sometimes lamentably impermanent) method of information use was retained. This contrast will be explored at greater length at the end of this chapter.

The second main difference is that cellular level symbol chains are much more stable through time than the rapidly dissipating pressure wave sequences described below that are perceived as speech. In this respect, DNA resembles tape-recorded language more closely than the sound sequences themselves. As previously noted, humans invented a secondary written form of language that was stable and non-dissipating; it proved to be unexpectedly useful, developing in a short time, a life (metaphor, not pun) of its own after a rather inauspicious birth in the form of irrigation records and state inventories (Gelb, 1963). However, the stable form of human language never became the primary symbolic medium in the same way that DNA is primary in cells. Thus, the "extra" stability of the <u>primary</u> DNA chain relative to speech sounds seems to demand an explanation.

One way to make sense of the situation is to separate out the different effects of the removal of the 2'-OH. Some effects-- i.e., the increased conformational flexibility of DNA relative to RNA --seem to have analogues in linguistic symbol chains, and will be discussed at length in the next section on linearity of the symbol chain. Other effects-- i.e., a much more stable intersegment linkage --could be seen as "derived" relative to a hypothetical, primitive symbol chain with RNA-like segmentability and stability, but with DNA-like flexibility and tendency not to fold. It is somewhat artificial to describe the molecular level system in terms of a hypothetical "primitive" molecule that could not exist; nevertheless, I think it can help to clearly point out how the two systems differ. Another way of phrasing the difference is that it is an "accident" of the molecular realm that going from a 2'-OH to a 2'-H produces both increased flexibility (linearity) and increased stability.[1] We shall see that these two states can be varied independently at the linguistic level.

Given that the two systems are different, there might well be some question why we should refer to the RNA and hypothetical RNA-like states as "primitive" and real DNA as "derived". Actually, in contrast to the case of whether the DNA chain was primitively external or not where there was little empirical information on which to base a decision, there is some information about the probable prebiotic condition of the 2'-position. Some treatments (e.g., Miller and Orgel, 1974; Day, 1984) have hardly distinguished RNA and DNA in discussing prebiotic syntheses. Nevertheless, evidence form several angles suggests that RNA was in fact primitive. First, the lack of a beta-hydroxyl on the sugar ring prevents the formation of a reactive cyclic phosphate intermediate. This was already mentioned in explaining why DNA is more stable; in addition, it makes DNA monomers very unreactive and almost useless in prebiotic polymerization experiments (see e.g., Schuster, 1979, p.33; Dugas and Penney, 1981, p. 176-177); all successful polymerization experiments (e.g., van Roode and Orgel, 1980; Inoue and Orgel, 1983)

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[1] Another "accident" that potentially could have caused a lot of trouble is the destabilization in DNA of the purine glycosidic (base-sugar) linkage in acid. From the retrospective view of the currently existing cellular system, it turns out to be easier, with a double-helix that is carrying sequence information, to replace lost purine halves of base pairs (the stable pyrimidine halves remain and preserve the sequence information) than to try to somehow reattach the free ends of a chain that has been cut all the way through (this can actually be done, but if there is more than one cut, the information is degraded). And in fact, large numbers of lost purines (10,000 per day in a mammalian cell) are routinely replaced by DNA repair mechanisms (Kornberg, 1980).

have had to use RNA monomers or derivatives. Second, there is a clue from the metabolic pathways in modern cells, which synthesize deoxyribonucleotides from complete ribonucleotides (by removing the oxygen with ribonucleotide reductases), but synthesize the ribonucleotides themselves from smaller precursors (Follmann, 1982). Finally, Eigen and Schuster (1979) using less direct arguments also identify the segmentable and less stable RNA as primitive.

To conclude, we thus have rather objective, empirical measures of segmentation in DNA symbols; that is, we can define what the segments are on the basis of physical properties (clearly from a compositional viewpoint but somewhat less so dynamically) <u>without reference</u> to the rest of the complex biochemical machinery within which it is normally embedded <u>in vivo</u>-- or in linguistic terms, without reference to language-specific perceptual mechanisms. Another way of putting this is that the segments are capable of being specified using only "lower level" properties (see Wimsatt, 1976). In addition, we have a rationale for why the segments are not as clear dynamically in DNA. As we will see later, prebiotic criteria cannot be used to specify the boundaries of the 3-segment codons or "words" of the DNA code, which turn out to be defined only in the context of the biochemical machinery in the nucleus and cytoplasm.

Segments in the Speech Stream

The 'objective' or prelinguistic segmentation of the stream of complex sounds that constitute the external symbols of spoken language is more problematic than in the molecular case; the question, in fact, has been the subject of a rather polemical debate in acoustic phonetics that dates at least to the early 1960's. I will argue in the next section that the acoustic speech stream is objectively segmented into units (approximately, vowels and consonants) apart from any specifically linguistic perceptual considerations, much as was more clearly the case with the segmentation of DNA symbols into nucleotide bases. As before, segmentation is discussed from a "compositional" and then a "dynamical" perspective.

By way of introduction, we might note that the average person who has not studied acoustic phonetics or seen a spectrogram would have relatively little difficulty accepting the proposition that auditory linguistic signals like words are segmented, since perceptually, the speech sounds of one's native language are so distinct and concrete; vowels seem quite separable from consonants and a given perceptual segment (what some linguists might call a phoneme) seems much the same from word to word.[2] the development of sound spectrographic methods of speech recording in the late 1940's provided a method of evaluating more objectively the segmentation of the external acoustic symbols of speech analogous to the rise of crystallographic techniques for the study of nucleic acids) and finding how it related to perceptual segments. Some of the results relatively unambiguously corroborated what European linguists had become aware of in the 19th century and what the Sanskrit grammarians of the Panini tradition had known over two millenia earlier. For example, "p" and "t" had long been described as 'unvoiced' versions of "b" and "d"; and this is actually the case-- the vocal chords begin

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[2] Morais et al. (1979) claim to show that illiterate speakers (Portuguese of "peasant origin") apparently do not perceive speech as a sequence of phones (consciously, that is); they could not carry out a task involving adding or deleting single initial phones. Nevertheless, the prevalance of often elaborate pig latins in many languages and cultures, and of other similar phonological games makes their results somewhat suspect. As the author is of Portuguese extraction himself, he is loathe to comment further on the implied phonological deficiencies of his peasant countrymen.

vibrating and producing periodic sound simultaneously with lip-parting in "b", whereas this is delayed about 80 msec for a "p", during which time there is a burst of broadband noise (along with voiceless formant transitions and a few other minor complications). Here, the spectrographic records only quantified what was an essentially correct notion. Other revelations of the spectrograph were more disconcerting, however, especially with respect to consonants. It turned out, in general, to be extremely difficult to relate the intuitively obvious perceptual segments to discrete things or cues in the speech wave.

Compositional Segmentation

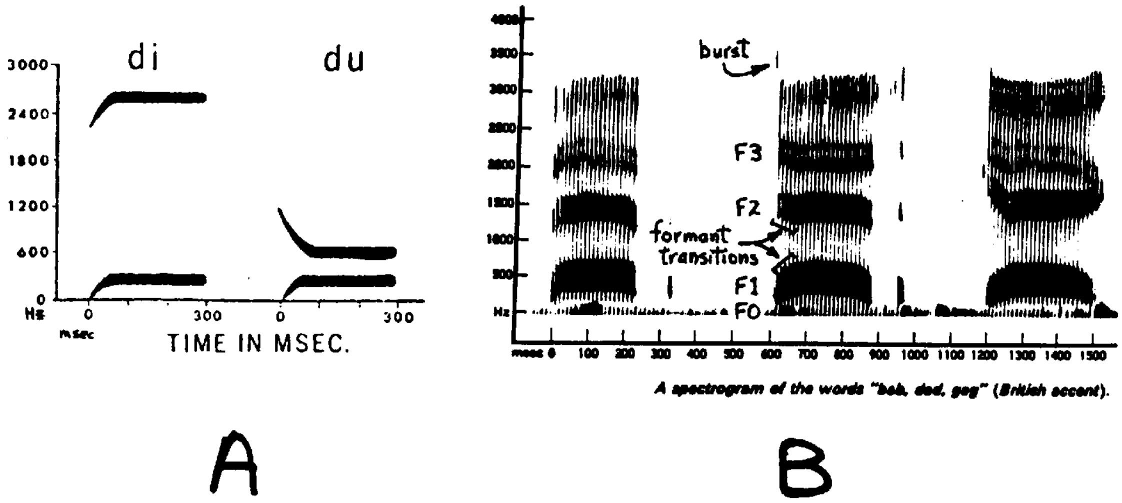
A widely accepted view (e.g., review by Pisoni, 1978) that came out of several decades of this research (especially on stop consonants and mostly using synthetic speech stimuli) was that phonemes do not exists as compositional, non-overlapping segments in the speech stream. That view implied not just that there was no one-to-one mapping between sound and perceived segment but that there existed an almost complete lack of correspondence between any given segment of the speech stream and a given phoneme-- the result of articulatory gestures being compressed, oeverlapped, and merged. In the terms of the present inquiry, acoustic segments simply did not appear to have an objective existence, independent from the perceptual system. Hockett (1955) made this point in a well known passage as follows:

> Imagine a row of Easter eggs carried along a moving belt: the eggs are of various sizes, and variously colored, but not boiled. At a certain point, the belt carries the row of eggs between two rollers of a wringer, which quite effectively smash and rub them more or less into each other. The flow of eggs before the wringer represents the series of impulses from the phoneme source; the mess that emerges from the wringer represents the output of the speech transmitter. At a subsequent point we have an inspector whose task it is to examine the passing mess and decide, on the basis of the broken and unbroken yolks, the variously colored bits of

> shell, the nature of the flow of eggs which previously arrived at the wringer (p. 210).

As a rather tame, laboratory example of what Hockett was talking about, Figure 15A shows hand-painted spectrograms that will produce the perceptions of a rather tinny sounding "dee" and "doo" (phonetically [di] and [du]) when played back on a speech synthesizer. The straight bands are the first and second "formant" (determined in real speech mainly by tongue position) whose relative and absolute frequencies determine what vowel is heard. The stop consonant [d], however, is signalled in these reduced stimuli apparently only by the syllable initial "formant transitions" (which result in real life from the tongue moving quickly from the place of consonant articulation to the stable vowel position). Consequently, the objective physical reality of two perceptually <u>contiguous</u> segments is that the consonant appears to overlap the vowel almost completely. To make matters worse, the second (higher frequency) formant transition is quite different in the two cases illustrated in Figure 15A, though [d] is invariantly perceived. Liberman et al. (1967) describe the consonant [d] as highly "encoded" in the syllable. The notion that there are no discrete feature for particular phonemes, arrived at mostly by studying synthetic stop consonant perception, has been generalized to other phonemes and is currently held by many workers to be an essential characteristic of speech--

> Acoustic cues for successive phonemes are intermixed in the sound stream to such an extent that definable segments of sound to not correspond to segments at the phoneme level. Moreover, the same phoneme is most commonly represented in different phonemic environments by sounds that are vastly different. There is in short a marked lack of correspondence between sound and perceived phoneme (Liberman et al., 1967, p. 432).



A spectrogram of the words "bab, dad, gag" (British accent).

FIG. 15: Artificial and Natural Syllables

Several researchers, however, have held a dissenting position in arguing that if one examines <u>natural</u> speech signals (see for example, fig. 15B), one finds that there are cues-- eliminated in the synthetic syllables --that constitute the sought after invariant, context-independent acoustic attributes of phonemes (Fant, 1973; Stevens, 1975; Cole and Scott, 1974; Blumstein and Stevens, 1980). The experiments of Cole and Scott (1974) involved splicing tapes of the initial aperiodic noise bursts (present in a number of voiced and unvoiced stop consonants) that <u>precede</u> the formant transitions, onto various steady state vowel "environments" and showed invariant identification of [b], [d], [p], [t], and [k] (but not [g]) across the [i]-[u] environments. Bursts had been known for quite a while (Schatz, 1954) but the early experiments with them failed to show invariance--probably as a result of using artificial bursts with spectral compositions quite different from the natural bursts (Blumstein and Stevens, 1979).

The tape splicing experiments generated a considerable stir and quite a bit of criticism. Dorman et al., (1977) for instance, claimed that the spliced burst also contained the onset of formant transitions embedded in the noise, while Dorman and Raphael (1980) have shown that formant transitions of the vowel *preceding* a stop consonant can be used to identify a stimulus made ambiguous by juxtaposing the burst which normally signals one consonant with an opening formant transition that normally signals another. Essentially, these critics have re-emphasized the context-dependent, overlapping nature of the acoustic events responsible for phonetic perception.

Nevertheless, in a recent series of experiments, the position that relatively invariant, localized feature in the acoustic stream underlie perceptual invariance has been quite convincingly argued (Stevens and Blumstein, 1978; Blumstein and Stevens, 1979, 1980). The main point is that the cues for place of articulation (as in [b] versus [d] versus [g]-- among the most thoroughly studied consonants) could be present in the gross, short-time spectral characteristics of the speech signal very near the onset of the syllable. These invariant spectra can be produced by initial noise bursts, by the earliest parts of the formant transitions-- which notably are constant in the context of different vowels (see fig. 16 from DeLattre et al., (1955) showing that the onset of the second formant for a given consonant always *starts* at the same frequency (e.g., approximately 1800 Hz for a [d]) --or by both bursts and transition onsets. What Blumstein and Stevens (1980) showed was that synthetic speech stimuli for the onset of the syllable as short as 10-20 msec (roughly half the time needed for a formant transition) in fact can be reliably identified for place of articulation whther the second and higher formants contain moving *or straight* transitions, and whether or not an initial burst is present.

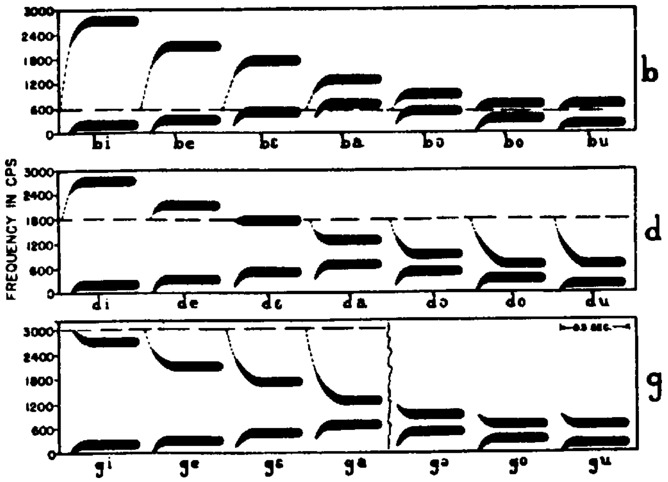


FIG. 16: Stop Consonants in Different Vowel Environments

These results are quite consistent with a speech perception theory (e.g., Fant, 1973) that postulates invariant relatively non-overlapping cues for consonants present in the 10-20 msec time window adjacent to consonantal onset or offset (note that the very ends of offset formants often closely approximate the very beginnings of of onset formants for a given consonant-- which could explain Dorman and Raphael's (1980) result). In light of this, Blumstein and Stevens (1980) offer a different interpretation of formant transitions. Basically transitions seem to provide acoustic material that smoothly links the transient events at onset to the slowly varying spectral characteristics of the vowel. If one hypothesizes that abrupt onsets and offsets in the speech stream act as markers signalling points in time where relevant invariant spectral information should be sampled, then formant transitions can be seen as a way of assuring that no further abrupt discontinuities in the spectrum occur following the initial transient at the release.

More recently, Mack and Blumstein (1983) extended such an analysis to a stop-glide contrast (i.e., [b] versus [w]; [d] or [g] versus [y]). Here they showed that the onsets of the stop consonants as opposed to the glides are characterized by a marked transient increase in acoustic energy in all vowel environments examined. Furthermore, perceptual experiments with synthetic stimuli showed that such an amplitude spike could override the vowel-overlapping cues (slower formant transition rate, longer transition duration) previously thought to signal glides. Thus a stimulus with the frequency, formant transition rate and duration characteristics of a [w] but with the amplitude envelope of a [b] was usually perceived as a [b], and _vice versa_. Once again, invariant, local non-overlapping segments of the sound stream can apparently be located. The general conclusion that the best-researched stop consonant are signalled by context-free cues has been supported by recent experiments using synthetic stimuli that are even closer to real speech. The main implication is that the cues are not static, but involve _changing_ (though invariant, context-free) onset spectra (Kewley-Port et al., 1983).

To summarize, so far there appears to be some evidence that speech streams are composed of segments, just as there was good evidence for many years that DNA chains were composed of segments.[3] In contrast to the biological case, many of the arguments for the objective segmentation of speech streams have employed 'devices' containing operating symbolic-representational systems-- i.e., human subjects --as well as more 'objective' apparatus (e.g., spectrographs) to assay the symbol chain. The justification for having included human experiments

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[3] In the biological case, in fact, biochemists knew about the segments well before they knew that they were assembled in (long) chains.

and synthetic, reduced stimuli (sometimes even with conflicting cues) in the preceding discussion of the <u>compositional</u> analysis of speech streams (compare the strictly physical-- i.e., prebiotic --characterization of compositional segments in DNA given previously) is simply that a great majority of the research has been done this way. The field was dominated until rather recently by a notion that even the low level auditory processing of speech streams involved language-specific mechanisms,[4] and a great majority of the work employed humans. A purely prelinguistic approach to natural speech sound streams analogous to X-ray crystallographic or biochemical analyses of biopolymers is simply not yet practical because the "natural" underlying segments and their constituents-- compare, nuclear and electronic structure of nucleotides --are not yet known. Debates have centered not just on the character of the external segments but, as exemplified above, on whether such units even exist, and although the studies cited suggest that they do, the verdict is not yet unanimous. Compared to our knowlege of the chemical "universe" of which biochemistry is a part, our developing knowledge of the "universe" of which language is a part-- including sounds and the way they interact with prelinguistic nervous systems --has not yet produced foundational theories. Thus, there is still a distinct unease in contemporary acoustic phonetics that visually inspected spectrographic representations, for example, might not tell us what is "really there" for the prelinguistic auditory system. By contrast,

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[4] This view grew out of attempts to explain the apparent lack of invariance in the speech stream. One prominent idea of this sort was the "motor theory of speech perception" (e.g., Liberman et al., 1967), which argued that a listener's tacit knowledge of how segments interact when spoken in succession (i.e., knowledge of how the apparent one-to-many relation between intended articulatory movement and variable context-dependent acoustic result arises) could help in the low level decoding of a perceived stream.

there is rather less unease about the appropriateness of the mathematical representations in the quantum mechanics of prebiotic atoms and molecules. As is turns out, when acoustic phoneticians began to examine the low level perception of speech sounds by animals (e.g., Miller, 1977; Kuhl, 1979), remarkable parallels with the human results were uncovered. This is particularly salutary in the present context since it now appears that much of the more detailed human experimentation cited in support of the idea that speech streams are composed of objective segments probably did succeed in engaging mostly prelinguistic mechanisms. The animal experiments are examined next in explicitly considering the dynamic segmentation of speech streams.

Dynamic Segmentation

In parallel with the biological case, a dynamic definition of 'where the prelinguistic subunits or segments are' can be built up relative to a prelinguistic "soup" of some sort. Most accounts point to the origin of language (see Lieberman (1984) for a recent review) sometime in the last 100,000 years in essentially modern Homo sapiens brains. Thus, the "soup" for language consisted of neural interactions in prelinguistic hominid brains and the perceptible features of the physical environment the hominids inhabited (including, of course, other hominids). Clearly this is about as directly accessible as a chemical description of the substrate on Earth 3.5 billion years ago that gave rise to life. As was the case with DNA chains, acoustic phoneticians-- that is, simpler, currently existing "reagents" embodied in the brains of mammals as models of the true prelinguistic "soup". At the molecular level, non-enzymatic hydrolysis of biotic 3'-5' chains was examined. In a similar manner, we shall first examine how speech sound streams are segmented by animals (chinchillas and macaques, in particular).

An obvious way to determine dynamic prelinguistic segmentation of speech is to use animal listeners. The use of animal listeners in speech perception research, however, is suprizingly recent. For example, as late as 1972, Liberman et al. could write:

> Unfortunately, we know nothing at all about how animal other than man perceive speech. Presumably they lack the special processor necessary to decode the speech signal. If so, their perception of speech must be different than ours. They should not hear categorically, for instance, and they should not hear the [di]-[du] patterns [see fig. 16 above] as two-segment syllables which have the first segment in common (1972, p. 324).

Actually, there were a few earlier studies (reviewed in Miller (1977)) but key experiments done in the mid-1970's on chinchillas showed convincingly that Liberman et al.'s prognosis was incorrect (Kuhl, 1979, 1982; Kuhl and Padden, 1983). For the present investigation into dynamic segmentation, ideally we would know in detail how our "reagents" worked-- i.e., how the very complex auditory system of an animal processed a speech stream so that the segments stood out and the intersegment boundaries were represented at some level in the system. Currently we must rely on less direct psychophysical and in the case of animals, behavioral approaches. Three phenomena related to dynamic segmentation-- categorical perception, perceptual constancy, and sensitivity maxima -- will be discussed using voice onset time perception (/da-ta/), vowel perception (/a-i/) and place of articulation perception (/ba-da-ga/).

Kuhl and Miller (1975) showed that chinchillas perceive speech sounds <u>categorically</u>, just as do humans. The chinchillas produce sigmoid identification functions when presented with exemplars from a linear continuum of voice onset time stimuli ranging from 0 msec voice onset time (a good /da/, for example) to +80 msec voice onset time (a good

/ta/). An abrupt change in the labeling function occurs at just the voice onset time (about +30 msec) at which human listeners begin to perceive /ta/ instead of /da/. The existence of categorical perception of speech sounds in animals does not directly indicate that they segment any given stream (e.g., /da/) into its constituents (/d/ and /a/) but the fact that they can so readily <u>classify</u> small speech streams on the basis of a change in one segment just as humans do is quite suggestive. Also the location of the boundary changed when different pairs of consonants were used, again paralleling the human data. For example, the location of the bilabial boundary (/ba-pa/) occurred at a lower voice onset time (about +25 msec) than the alveolar boundary (/da-ta/). The results suggest that "reagents" in the prelinguistic "soup" of the mammalian auditory system dynamically define segment boundaries, at least in these simple instances.

Perceptual constancy experiments, also with chinchillas (Burdick and Miller, 1975), show that the animals quickly generalize a learned distinction between spoken examples of /a/ and /i/ to new talkers with different fundamental frequencies (e.g., male and female). Thus, the animals ignore the same differences that human listeners do. More convincing evidence of segmentation itself comes from experiments (Kuhl and Miller, 1975) in which animals were trained to distinguish sets of syllables (/ti/, /ta/, /tu/ <u>vs</u>. /di/, /da/, /du/). This training generalized to new vowel environments (/te/, /ta/, /to/ <u>vs</u>. /de/, /da/, /do/). This is exactly the task mentioned by Liberman et al. (1972); clearly the animals <u>are</u> capable of hearing one or the other sets of stimuli (at some level) as "two-segment syllables which have the first segment in common".

Finally, the recent experiments of Kuhl and Padden (1983) showed that macaques have enhanced discriminibility for small changes in cues for place of articulation (/ba-da-ga/ continuum-- the cue was starting frequency of the second formant with synthetic stimuli) precisely at the "phonetic boundaries" that separate the categories /b/ from /d/ and /d/ from /g/ for human listeners. Previously, enhanced discriminibility at phoneme boundaries in humans had been taken as evidence of speech-specific mechanisms. Again, the existence of such categorization of one segment in a small speech stream provides indirect evidence that they are capable of segmenting the stream without the specialized higher level apparatus for language comprehension that humans have.

It is useful to pause briefly to compare the techniques used here with what would be there counterparts in nucleic acid chemistry if they existed there. The biochemist as animal acoustic phonetician would synthesize a set of dinucleotides containing a range of structures that varied smoothly between say, pApC and pGpC, and then degrade them with various chemical reagents to find the units. In comparison to the linguistic case, it is not actually possible to produce a smoothly varying series of chemical structures because of the existence of quantum phenomena at that scale. On the other hand, the acoustic phonetic experiments above suggest that humans and animals are not able to detect speech-like stimuli as continuously varying, except under special conditions. Thus, in a sense, the continuum of stimuli does not exist in the world of linguistic phenomena either (see Wimsatt (1980b) for a related discussion). Experiments using such continua can then be seen as a way to find out what the units really are; the molecular biologist, by contrast, already knows the real units. These differences are due mostly to scale; since linguistic phenomena are much more nearly our size, we are at leisure to manipulate the underlying "hidden variables" in a way closed off to the chemist, but concomitantly have more trouble seeing the real units.

Linearity of the Symbol Chain

Symbol chains, in contrast to symbol-representation and "thing"-representation chains, are basically linear or "one-dimensional". Again, this might seem like such an obvious property in some respects (for example, it was more or less assumed in the previous section) that it might not seem worthy of comment. Actually, it is quite an interesting and non-trivial exercise to produce a definition to cover both the molecular and linguistic cases.

DNA (and RNA) Helicies

Levels of Structure

Molecular biologists and protein chemists have already devised terms for the different levels of structure in biopolymers. For proteins, these levels are "primary structure" for the sequence of segments, "secondary structure" for a few types of simple repeating (i.e., helical) three-dimensional structures that arise through constraints on local interactions, and "tertiary structure" for complex three-dimensional architectures resulting from non-local interactions between portions of the chain that are themselves partly organized into secondary structures. These terms were used early on by Eyring (1935) with essentially their modern meanings and explicitly applied to proteins by Linderstrom-Lang (1952), over a decade before the first X-ray crystallographic structure of a protein was solved. The three levels have been applied to nucleic acid chains as well (see fig. 17). One main difference is that the secondary structure configuration in nucleic acids involves not one but two associated strands of segments. A brief glance at Figure 17 seems to indicate that DNA chains possess complex three dimensional structures (even "tertiary structures" in this illustration from a popular advanced text) just like proteins, and it may thus seem paradoxical to label them linear or "one-dimensional". The property referred to, however, is brought out upon comparing the internal architecture of DNA 'tertiary structures' to RNA tertiary structures (folded symbol-representation chains) and protein tertiary structures (folded "thing"-representation chains). RNA and protein structures are discussed at much greater length in Chapters IV and V to which reference should be made.

From a structural point of view, the important fact that makes DNA symbol chains linear or approximately "one-dimensional" is that they do not fold up into stable, three-dimensional structures that involve non-local interactions between segments. Another way of saying this is that DNA strands do not have true "tertiary structure". There are several reasons for this. The first is that DNA often consists of two exactly complementary base-paired strands. This allows the segments making up the two strands to have their sidechains located in the interior of the structure and their standardized backbone parts exposed. This was a rather novel concept in the early 1950's before the structure of DNA had been discovered because the exact opposite had been found to be the case with the alpha-helix (one of the main components of secondary structure in <u>proteins</u>), which has an internal backbone and exposed sidechains.[5] The inward turned sidechains are rather

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[5] It is perhaps not surprizing, then, that the model constructed for DNA by Linus Pauling (who earlier has discovered the alpha-helix) as well as one of the unsuccessful models of Watson and Crick consisted of

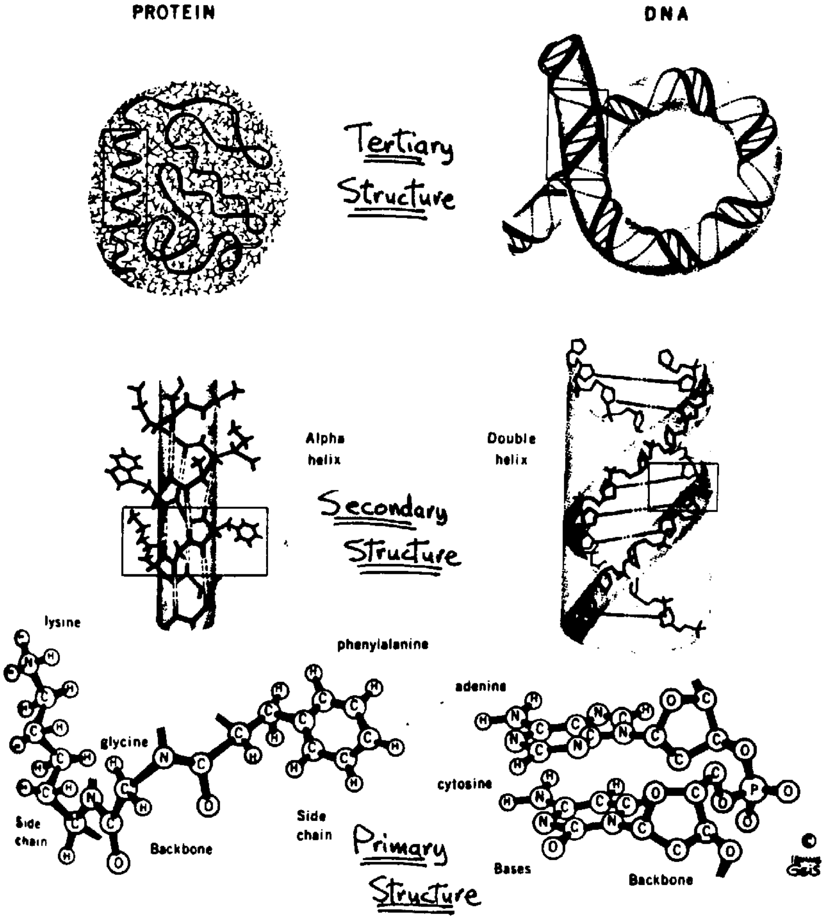

FIG. 17: Levels of Structure

inaccessible to the solvent and the things in it, including other parts of the chain itself, in contrast to the situation in proteins where the exposed sidechains interact with the solvent and each other and are intimately involved with directing folding patterns. RNA, however, has inward turned sidechains, yet also appears to support a degree of true

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multiple polynucleotide strands with the backbones internal and the sidechains (bases) dangling out (Olby, 1974; Judson, 1979). This allowed no base pairing among other things.

tertiary structure, a point to which we shall return. A second reason cited until recently (see e.g., Cantor and Schimmel, 1980, p. 176) for the paucity of true folded tertiary structures in DNA was that all DNA sequences assume only one basic secondary structure-- i.e., a right-handed double helix --while in proteins, peptide sequence determines which of several secondary structures arise. Finally, a third difficulty in folding DNA chains is that the exposed backbone groups fairly bristle with negative charge. Since it is thermodynamically unfavorable to "bury" like charges inside a compact structure in aqueous solution, there is a tendency for the polynucleotide chain to be extended. In proteins, the exposed sidechains can be uncharged (as well as positively or negatively charged); and since exposed uncharged residues result in the nearby water molecules assuming more ordered, ice-like configurations, it is actually thermodynamically favorable for these residues to be "buried", allowing for energetically favorable folding.

The New DNA Structures

Recent crystallographic data about DNA, however, has lead to a major overhaul of concepts of DNA structure. Most molecular biologists were stunned by the revelation of an X-ray crystallographic structure for lift-handed Z-DNA (Wang, et al., 1979); the initial reaction was that that the structure must exist only under very special un-biotic conditions. Then it was shown (Nordheim et al., 1981) that antibodies to Z-DNA bind to the interband regions of *Drosophila* polytene chromosomes. A flood of investigations and results followed (see e.g., the *Cold Spring Harbor Symp. Quant. Biol.* 47 (1983), "Structures of DNA"). Z-DNA seems to be involved, for example, in the regulation of

DNA supercoiling (known to regulate transcription) and its formation is promoted by methylation (a known inhibitor of transcription) (review: Rich, 1983). The sequence of events was somewhat ironic since the structure reported by Wang et al. represented the first long-awaited single-crystal structure for double-stranded DNA longer than two bases; studies of long DNA strands up until then used oriented but non-crystalline fibers. After a few years (and another Z-DNA crystal) a single-crystal structure was finally reported for the "classical" B form (Rosalind Franklin's "wet" form, Watson and Crick's model) and A form (similar to the RNA helix; Franklin's "crystalline form) (see fig. 18). In the process, it became apparent that DNA was quite a bit more conformationally diverse than had previously been realized (for review see Saenger, 1984).

Recent molecular modeling has also emphasized the local mobility of the DNA double helix allowed by the large number of independent internal rotations about bonds for each segment in the backbone, as well as reaffirming the previously demonstrated macroscopic stiffness that is caused mainly by energetically favorable base-stacking (Olson et al., 1983; Conner et al., 1984). The local flexibility is great enough that the right => left, B => Z transition-- which involves extensive conformational adjustments at each segment --can occur without significant "melting" (i.e., separation of the strands by breaking of the Watson-Crick base pair bonds) (Tran-Dinh et al., 1984). Molecular dynamics simulations on a short B-like DNA double-helix by Levitt (1983) also showed an extremely flexible structure that bent smoothly and only occasionally showed a "kink" of the general sort previously postulated to account for bends in what had been thought to be a stiff helix (e.g., Sobell et al., 1977). Also in contrast to previous conceptions, the

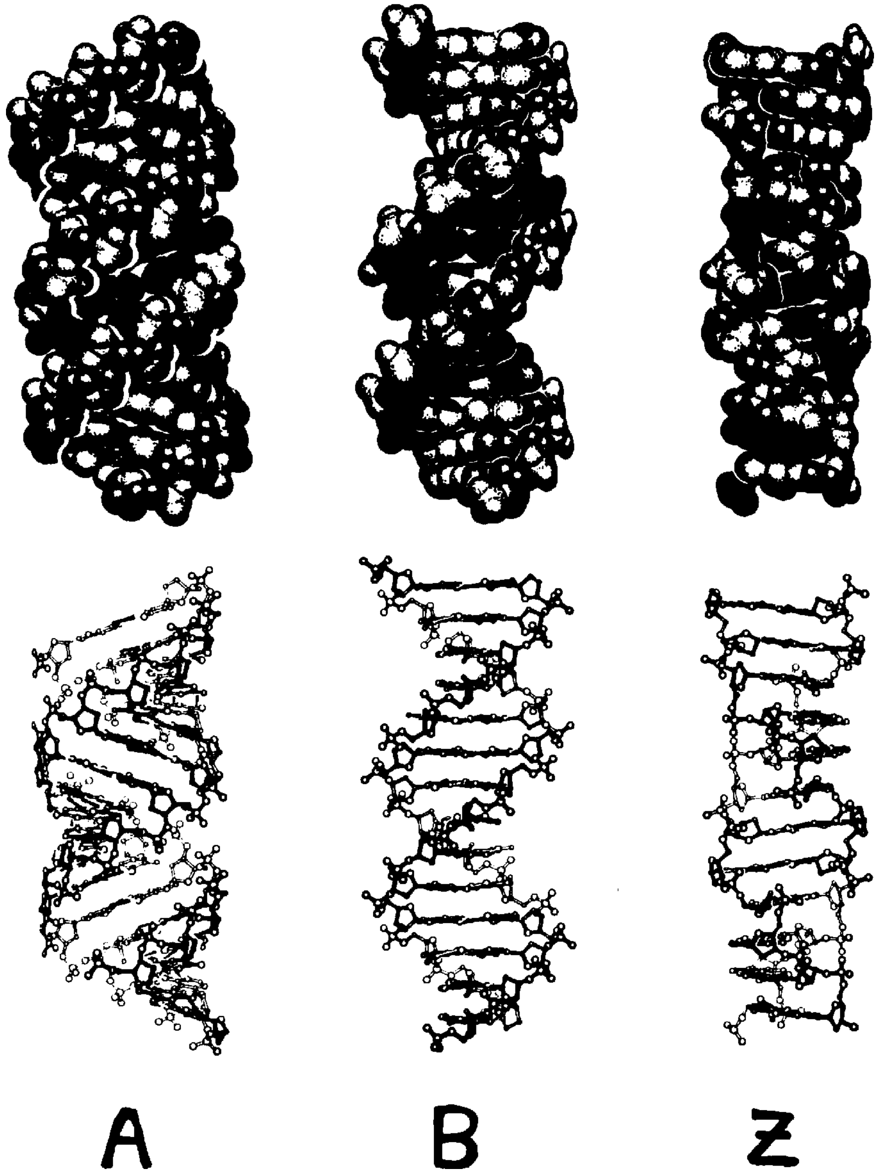

FIG. 18: Structures of DNA

model showed no partial local melting; the base pairs remained hydrogen bonded and stacked during all flexing motions.

Finally, crystallographers have pointed out that the B-DNA structure (still thought to be the most common) shows clear sequence-induced local variation in helix parameters (Dickerson and Drew, 1981). It has been suggested that if such effects are generally applicable, they might be important in sequence-specific recognition of DNA by proteins. RNA, which only assumes an A-type helix conformation, does not show these effects (Holbrook et al., 1981) and neither does A-DNA itself (e.g., Conner et al., 1984). Thus Dickerson et al. (1982) suggested

> if these variations do play a role in recognition by proteins, then it may be that DNA evolved as the primary storage medium for genetic information rather than RNA, precisely because its structure was more malleable and expressive of base sequence (p. 484).

In the clamor over the new almost protein-like results in DNA structure, the fundamental differences between DNA and protein structures have not been emphasized. It is worth reexamining the three main differences cited earlier (inward turned sidechains, one secondary structure, no true folding) in light of the new data. Clearly the second point is no longer true-- a Z-type helix (about 12-fold left-handed) constitutes a type of secondary structure as distinct from a B-type helix (about 10-fold right-handed) as is an alpha helix (3.6 fold right-handed) from a beta-strand (actually a 2-fold helix) in protein secondary structure. There are also a number of differences between the DNA and the protein secondary structures in addition to those cited parenthetically. For example, the structural classes in DNA (especially B-type helicies) seem to be fuzzier-- e.g., in terms of allowed bond torsion angles --than for protein structures, which seems to be partly a reflection of the extreme local mobility noted above. One reason it is difficult, however, to directly compare DNA and proteins is that the main secondary structural elements are quite different in size-- e.g., an 18-23 angstrom diameter B-DNA double helix compared to a 6-10 angstrom diameter alpha helix; thus, what an evolutionary morphologist would call "allometric effects" have to be distinguished from "real", scale-independent differences. RNA on the other hand, resembles proteins in its ability to form complex, stable, partly folded tertiary structures (e.g., ribosomes, transfer RNA), yet is nearly identical to DNA structurally. By comparing the DNA symbol chain with RNA, the symbol-representation chain (see Chapter IV for a description on its own terms), then, we can more easily identify why DNA is linear or "one-dimensional".

DNA Compared to RNA

Single strands of RNA clearly play a structural role in cells. Transfer RNA (tRNA), ribosomal RNA, 7S RNA (in signal recognition particle), and probably intron RNA ("self-splicing RNA") and other mesenger RNA's assume complex, stable three-dimensional tertiary structures (with double-stranded sections arising from self-complementary sequences) that not only serve as scaffolds one which proteins can be mounted, but may in some instances have true catalytic functions by themselves. DNA, by contrast, seems to have a much more limited structural repertoire, at least in currently existing cells; single-strand-based DNA structures so far appear to be confined to small, mostly hypothetical "hair pin" loops that are thought to be important in transcription initiation in circular single-stranded viral DNA.[6] There are, of course, the extensively studied DNA and protein structures-- nucleosomes --that consist of

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[6] Pure double stranded DNA will condense into supercoiled fibers, fibers with thick beads, and finally large diameter maggot-like particles as it is precipitated out of ethanol solutions of gradually increasing ionic strength. It is possible that these structures are related to the tightly packaged DNA in the heads of large bacteriophages. Hearnshaw et al. (1978), however, suggest on the basis of electron microscopic and X-ray diffraction evidence that the DNA forms a simple, large coil. In any case, these double stranded structures are quite unlike either folded polypeptide chains or folded RNA's in their great size and lack of determinate structure.

double-stranded DNA wound at intervals aroung cores of basic proteins called histones. Just under 2 turns (146 base pairs) are wound around each core, and there is one core about every 200 base pairs. The DNA-wound cores themselves aggregate into as yet poorly understood higher level structures (review in Saenger, 1984). Thus contrary to the initial expectation that the DNA would be coated by histones (e.g., Pardon and Wilkins, 1972), DNA/protein structures are organized exactly the opposite from RNA/protein structures-- it is the nucleic acid that is mounted on a protein scaffold. Furthermore, DNA sequence appears to have little `effect on nucleosome structure (although it might control nucleosome placement), while RNA tertiary structures are clearly determined by sequence. The lack of stable, folded, initially single-stranded structures in DNA is apparently more than just a "frozen accident" in contemporary cells-- single strands of DNA with the same sequence as structural RNA's have not been observed to fold into the corresponding particles.

The remarkable differences in RNA and DNA tertiary structure stem entirely from the difference in the substituent at the 2' position of the sugar ring: -OH in RNA and -H in DNA. The previous section on segmentation emphasized the role of this reactive ribose hydroxyl in determining the stability to hydrolysis of the intersegment links in polynucleotide chains, but paid relatively little attention to overall conformation. Here, we consider how removing the bulky oxygen from the 2' position essentially makes DNA into a linear, "one-dimensional" molecule. At the risk of some artificiality, I would like to argue that the "linearization" of DNA by the removal of the 2' oxygen can be seen as a "primitive" characteristic of a symbolic-representational system, in contrast to the stabilization of the intersegment bond, which although it happens to arise from the same action, appears "derived" in the context of the present analogy.

RNA, in contrast to DNA, has only one basic secondary structure, which closely resembles the DNA A-helix. Thus in high salt solutions--which cause an inversion of the circular dichroism spectrum for DNA that has been interpreted as a B (right-handed) to Z (left-handed) helix transition --the RNA spectrum remains unchanged (Pohl and Jovin, 1972). Likewise, RNA does not show the A to B helix transition seen in DNA as the salt concentration is lowered from moderate to low levels (or the humidity is increased in fiber preparations.[7] The 2'-OH thus keeps the RNA helix in the A-form. The exact explanation for why this occurs is not clear. One possible reason that RNA doesn't undergo an A to B transition is that the bulky OH group provides steric hindrance that constrains the sugar ring in each monomer to adopt one particular conformation out of the many observed to occur in B-type helicies.[8] The

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[7] Conner et al. (1984) have suggested on the basis of X-ray crystallographic observations that the reason DNA adopts the B-helix when well solvated (=low salt conditions or high humidity) is that water molecules stick into the minor groove of the helix and form a spine there that holds the groove open; this keeps the base pairs centered near the helix axis and the C3'-C4' sugar ring bond parallel to the helix axis, As water molecules are withdrawn, the groove closes, probably cooperatively, allowing the base pairs to slide to an off-center position and the C3'-C4' bond to tilt to follow the helix backbone, producing a typical A-helix conformation.

[8] The furanose ring in nucleotides is a strained 5-membered structure with a tendency to "pucker". Since it is also unsymmetrically substituted, potential energy "wells" are created that define preferred modes of puckering. X-ray diffraction data for the 12 base pairs in a B-DNA double helix revealed many different puckers in the sugar ring, spanning the entire range from C2'-endo to C3'-endo-- i.e., the 2'-3' ring bond is twisted to varying degrees in or out of the ring plane Dickerson and Drew, 1981). By contrast, nucleotides in the A-DNA helix (Conner et al., 1984) or in the RNA A-type helix (Kim, 1981) are much more tightly constrained and adopt only the C3'-endo pucker. The aspect of the 2'-OH that keeps RNA in the C3'-endo pucker might include its ability to take part in energetically favorable internucleotide H-bonds via bridging water molecules as well as the steric hindrance suggested above (Saenger, 1984).

reason RNA fails to undergo a transition to the Z-form is somewhat mysterious since the 2'-OH position would point outwards from the helix, suggesting little steric hindrance (Wang et al., 1979). It is possible that there is a substantial and possibly prohibitive kinetic barrier since the RNA helix does not form the intermediate B-helix and is probably restricted to the more difficult direct A to Z transition.[9]

These observations may at first seem paradoxical because the presence of stable tertiary structure in RNA is correlated with a lack rather than a variety of different available secondary structures, as there exist, for example in proteins. The apparent contradiction is reconciled if a clear distinction is made between the local and global effects of stiffness in building a folded tertiary structure. Thus, in discussions of the one example of a nucleic acid tertiary structure that has been crystallized and that diffracts to a high resolution-- the yeast phenylalanine transfer RNA molecule (for review see Kim, 1981)-- various authors have commented on the remarkable flexibility of the nucleic acid backbone (see fig. 19), especially as it winds its way through the loop regions. However, when the double helical portions of the molecule are examined (Holbrook et al., 1981), they are actually much less conformationally variable than double helical B-DNA.

A recent study comparing local mobility in A-RNA and B-DNA double helicies (Holbrook and Kim, 1984) showed that although the types of mobility were similar for the two, the magnitudes of the motions were an order of magnitude greater in B-DNA (something the authors hardly comment on). The differences are probably somewhat exaggerated by the

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[9] Recently, it was shown that Z-RNA can form under the appropriate conditions; however, the conditons required were more extreme than were needed to effect the transition to the Z form in DNA. Thus, the character of the RNA as conformationally "stiffer" is still supported.

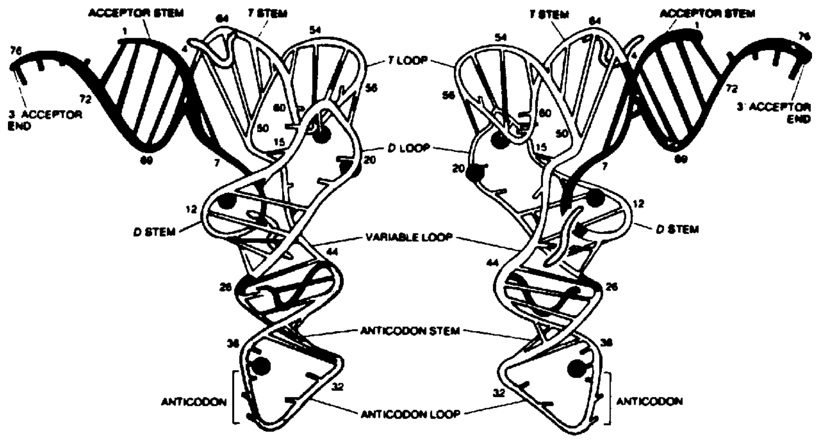

FIG. 19: Tertiary Structure of Transfer RNA (tRNA)

different sources of data. Nevertheless, the differences suggest the following resolution-- locally stiff secondary structure segments are required in order to induce the other parts of the globally stable folded molecule to take up, by comparison, strained configuration. From this perspective, the reason DNA structures show less conformational variation globally (in contrast to their greater local variation noted by Dickerson et al. for example, in the quote above)-- i.e., one of the reasons the great majority of the stable DNA structures in cells appear to be "linear" or "one-dimensional" --is that the helix is too flexible to 'force' the existence of a true stable "three-dimensional" folded molecule (i.e., with specific non-local chain interactions). This is probably one reason ribosomes, for example, couldn't be made of DNA.

From the view of the present analogy, this "flabbiness" is an absolutely necessary attribute of symbol chains-- it protects the information in them from sequence dependent, site specific degradation because the soup has no three-dimensional structure to selectively condition its attack. Another way of saying this is that true protein-like tertiary structure would compromise the otherwise intrinsically arbitrary(1) nature of the intersegment connection (see below). This of course is what happens with RNA, which has arbitrary(1) intersegment bonds but which can exhibit a certain amount of true tertiary structure. Only by keeping an arbitrary chain one-dimensional does it become possible for it to accumulate <u>information</u> (about three-dimensional protein configurations in the context of a nascent symbolic-representational system) without the soup "seeing" it as such, and thus dissipating it.[10]

The Linearity of the Speech Stream

It is not very controversial that speech sounds are linear in some sense. Saussure (1916/1959) made it one of the two "primordial characteristics" of the linguistic sign (p. 67-70), the other being its arbitrary nature. However, at first, it might seem that they are linear in a different sense than the persisting strands of connected nucleotide segments discussed above. Speech sound streams are linear only through time whereas DNA strands seem atemporally linear. It was noted in this regard in the section on segmentation that the especial persistence or stability of DNA contrasts markedly with the more transiently existing and less stable RNA, and also, that the extra stability to hydrolysis of DNA seems to be a "derived" character that resulted from the same change

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[10] Note that this is a more restrictive notion of information than is found in information theory, where information turns out to be closely allied formally with entropy, and thus, in principle, is defined for almost any given system (e.g., non-biotic as well as biotic). The restriction here, roughly, is that "naturalistic" information appears to be scale-specific; it would seem to be much more difficult to have a symbol segment chain made out of, say, atoms or elementary particles, on one hand, or macromolecules on the other.

that "linearized" the molecule. Nevertheless, even RNA chains do not degrade nearly as fast as speech sound streams (especially if they are folded); and different sections of a single chain can sometimes be simultaneously "comprehended" ("translated" in the terminology of molecular biology) before the chain is finally destroyed. This results in multiple copies of the coded-for protein. In spite of this apparent difference, there is a straightforward sense in which the molecular level chain functions fundamentally as a temporal sequence-- the perception and comprehension apparatus is only capable of interacting with the chain locally, a few units at a time, and must therefore process the chain sequentially. In no sense can the cell access its symbol chains literally as templates.[11] The details of the apparatus will be discussed later; for now a vivid illustration of this is the process of "linear diffusion", which has been shown to occur for a DNA sequence-recognizing protein (Winter et al., 1981). Such a protein can bind non-specifically to the DNA and then slide rapidly along the strand until it recognizes a certain short sequence (the reduced dimensionality of the search greatly speeds the recognition process when concentrations are low). This process would be analogous in language to something like monitoring a speech stream for a short (meaningless) sequence of segments (one or two syllables).

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[11] Interestingly, several initial attempts at the coding problem involved just such an hypothesis (e.g., Gamow, 1954). The great complexity of the apparatus needed to specifically access the information even one unit at a time was unexpected. Crick's (1958) early adaptors, for example, were envisioned as just a few nucleotides long (in reality they are about 70); and it was only gradually realized how complex ribosomes (thousands of nucleotides long) and their associated proteins (totalling many thousands of amino acids in length) actually were (See also Chapter IV).

Linearity in Listening and Reading

The persisting nature of the DNA strand was previously compared to written language; the similarity can be exploited here to illustrate the essentially temporal linearity of the symbol chain from another angle. Written language like a DNA strand, is processed locally and sequentially. A number of different experiments (see Rayner (1983) for a review) have shown that as the eye fixates a point on a page, it is only possible to see about 10 to 20 character positions at a time well enough to actually distinguish letters (gross word shape is available from slightly farther out). When subjects read "carefully"-- for the purpose of comprehending and remembering text -- they essentially fixate every content word (but not words like "the" and "is"). Speed reading, by contrast, involves fixation of one or a few strategic (at least in principle) words per line. The end result (of careful reading) is thus rather similar to listening to speech streams. The most obvious differences are that small batches of segments are fed into the system in parallel at each fixation instead of one at a time, and that word boundaries are explicitly represented in the stream (see below). The main point here is that reading, like auditory speech perception and the "perception" of DNA, involves highly localized sequential interactions with the linear symbol chain-- which for all practical purposes need only exist transiently and locally. Assuming for now that local sequential pickup is necessary, it is easy to see why the perception of "auditory writing" did not evolve (before the invention of tape recorders)-- it is simply not practical for the auditory system to sequentially scan a stationary spectral "display" as does the eye. That is, in vision, eye movements can direct a majority of the visual receptors (i.e., the fovea) to small pieces of the persisting array on a page in a sequential manner; by contrast, it is impossible for the frequency-mapped auditory receptor sheet to perform a similar piecemeal scan of a persisting acoustic array (an acoustic "page") consisting of several hundred simultaneously and continuously articulated words(!) because there is no way to concentrate most of the receptors on just one part of such a cacophony. The difficulty is due simply to the greater wavelength of hearable pressure waves compared to seeable electromagnetic waves, which dictates that the acoustic array or "page" be much larger than a written page; the necessary distance between hypothetical sound sources constituting each segment (or even word) makes it impractical for the acoustic receptor sheet to scan them--i.e., to be moved past them --at a reasonable rate (20 segments per second in the case of heard speech) at least in the absence of the ability to fly. We shall return momentarily to these issues (but not flight) in the process of defining higher levels of structure in speech streams.

Levels of Structure Past Sequence (Primary) Structure

It is possible to define structural levels in the linguistic symbol chain just as we did for the molecular symbol chain. The definitions of primary, secondary and tertiary structure that are used for molecular chains are actually quite abstract and general, and can be applied profitably to linguistic sound sequences, once the proper translations into levels of *temporal* structure are made.

The previous discussion implied that the notion of "primary" (or sequence) structure has a clear correlate in the temporal sound streams of auditory linguistic segments; linguistic correlates of secondary and tertiary structure, however are initially less obvious. The question of levels of structure in linguistic phenomena is an incredibly difficult and contentious one compared to the parallel question in molecular biology. What I want to do here is merely examine levels of structure in the symbol stuff itself, as much as is practical from the perspective of a prelinguistic "assay". Therefore, since there is no prelinguistic indication in the speech sound stream of word boundaries[12] (i.e., they cannot be specified without the help of a linguistically competent listener or spectrogram reader who knows the language he is reading), the word level is not relevant here. Notice that in the case of DNA, the "word" level-- i.e., the nucleotide triplet or "codon" --was equally absent from the discussion of levels of structure in the symbol chain. Three levels of organization in speech sound streams that are larger than the segment and pre-linguistically evident are in order of increasing size-- the syllable, the stress group, and the "breath group."[13] Some of these phenomena-- e.g., the breath group --are clearly peculiar to speech production and like some other suprasegmental phenomena, they are not indicated explicitly in writing (though a breath group, for example, might often respect a syntactic phrase or clause boundary). The justification for treating the three in a comparative

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[12] This is especially apparent in listening to an unfamiliar foreign language; without the usual automatic word recognition mechanism in operation, it is much easier to perceive speech as the continuous stream of sound segments that it really is.

[13] This taxonomy differs somewhat from the distinction between segmental features (e.g., voice onset time) and "suprasegmental" features (e.g., pitch, stress, and duration) of speech streams. Suprasegmental features are usually defined as those whose domain extends over more than one segment (Lehiste, 1970; Ladefoged, 1982). The syllable itself, however, is sometimes not thought of as a suprasegmental unit, though a syllable (or rather the segments in it) might carry stress. The "breath group" on the other hand, though extending across many segments, is often considered to be a non-linguistic concomitant of speech production not related to underlying linguistic knowledge (e.g., Hyman, 1975).

context with DNA structure is that they appear to be universally occurring basically prelinguistic levels of organization common to all (natural) auditory symbol streams. How and at what level these phenomena code for meaning, or even if they are very important for this purpose (cf. their lack in writing) are separate questions that will be pursued later.

Levels of Structure (Secondary)

The syllable, a unit consisting of a few segments (often a consonant and a vowel), seems an obvious enough unit of organization, and considerable evidence exists regarding this most widely discussed "suprasegmental"; yet as Bell and Hooper (1978) note in a recent review "the syllable has a long and troubled history in the development of phonology (p. 4)". Some influential treatments (e.g., Chomsky and Halle, 1968) have not even recognized a unit between the segment and the word. The evidence that syllables are real or natural units ranges from the existence of perceptual and productive speech errors (Fromkin, 1980) involving syllabic interchange and the historical prominence of syllabaries in the origin of writing (Gelb, 1963) to a variety of observations on the phonotactic distribution of segments in words within languages, between languages, and in language development that point among other things, to the existence of a basic unmarked consonant-vowel unit. On the other hand, a major argument against syllables as units is that a difference in the location of a syllable boundary in a word is never "contrastive"-- i.e., there are no pairs of morphemes (meaningful units) that differ only in syllable boundary location (but not phonetically), paralleling a pair of morphemes like "pit" and "bit" that differ only in the voicing of the initial bilabial stop consonant. Of course, since pure contrastive syllabication would have no surface phonetic realization, it would have to be detected by other criteria and distinguished from whole word homonymy (cf. Hyman, 1975). A second reason given for ignoring syllables is that phonological rules referring to the syllable boundary can easily be rewritten using the features consonant, vowel, and the word boundary.

It is interesting to consider a possible "syllabic" level of organization in DNA-- i.e., a unit of organization comprising a few nucleotides. We might take the pyrimidine/purine distinction (the most basic structural dichotomy) tentatively as something like the consonant/vowel distinction (see next section). Naturally occurring sequences of the 4 nucleotides appear quasi-random, and since pyrimidines and purines are usually present in about equal proportions, the result is that they approximately alternate. One could visualize the DNA strand as a sequence of some set of mononucleotide, dinucleotide (16 possible) and trinucleotide (64 possible) syllables.[14] As is the case with trinucleotide codons ("words"), there is no indication in the DNA chain itself where the boundaries between putative "syllable" units are-- the only prebiotically salient boundaries are those between mononucleotide segments; and there is nothing to distinguish a within-codon intersegment bond from a between-codon intersegment bond (apart from an operating symbolic-representational system). Thus, in moving past unit sequence structure-- i.e., primary structure --the first salient level of organization we get to is the double helix-- i.e., secondary structure. DNA secondary structure is based on a repeating unit (one turn of the helix) that is rather larger than a

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[14] See section on "arbitrariness" below for a discussion of patterns of dinucleotide "syllables" that argue for the presence of weak intrinsic sequential constraints.

codon-- there are about 10 segments per turn in B-DNA, for example. This suggests that we should look for a regularly recurring unit in language that is bigger than a syllable and even extends across more than one word.

A possible candidate for "secondary structure" in speech streams is the "stress group" or "measure". In a language like English, stressed syllables[15] recur at approximately equal intervals of around 500 msec; this tendency is often called "isochrony" (review: Lehiste, 1977). The group of syllables including the stressed syllable and any that occur in the interstress interval is sometimes called a stress group. In English, an average stress group contains about 3 syllables. These observations have been extended to a number of different languages (e.g., Dauer, 1983). There appears, in fact, to be a language universal tendency for stresses to recur at an average interval of just under 500 msec with a standard deviation of about 150 msec. In Dauer's (1983) study, there were no statistically differences in variances between English, Spanish, Greek, and Italian speakers. Data for English, Thai, Spanish, Greek, and Italian show that the average number of syllables per stress group varies between languages-- less than 3 syllables/stress in Thai to over 4 syllables/stress in Spanish. The tendency to modify segment duration so as to produce more regular interstress intervals

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[15] The actual acoustic correlates of stress turned out to be somewhat elusive. Initially, it was presupposed that a stressed syllable simply has more intensity that unstressed syllables, and quite elaborate systems of analyzing stress with up to four levels of stress were developed a number of years ago. However, experimental investigations showed that (longer) duration and (higher) pitch of the syllable were much more important cues. Recently, in experiments that played off syllable duration cues against pitch cues and pause cues (Nooteboom et al., 1978), syllable duration overrode pitch as well as pause cues. In general, fewer levels of stress are now recognized and many acoustic phoneticians (e.g., Ladefoged, 1982) distinguish only stressed versus unstressed syllables.

occurs even in languages like Spanish (Manrique and Signorini, 1983) that previously had been thought to be organized around equal length _syllables_ ("syllable-timed") rather that equal length interstress intervals ("stress-timed"). The apparent greater regularity of syllable length can be attributed to differences in syllable structure (tendency to simpler, more uniform syllable structure in "syllable-timed" languages) and patterns of unstressed syllable reduction (loss of consonants rather than centering of vowels).[16]

So far, stress-timing has been discussed primarily as a productive phenomenon that likely reflects an underlying rhythmic organization to speech and other motor phenomena (Allen, 1975). There is, however, a perceptual component to isochrony as well (Lehiste, 1977)-- i.e., listeners tend to hear interstress intervals as more alike in duration than they really are, a sort of categorical perception for interval. Thus, in languages like English where stress is often used to indicate syntactic boundaries-- e.g., the two different senses of "The queen said the knight is a monster" would normally be disambiguated by syllable duration stress cues --experiments show that speakers must overcome the tendency to perceptual uniformity by rather dramatic alterations.

Returning to the notion of the stress group as a possible analogue of the secondary structure unit in DNA (one turn of the helix), it can be seen that approximately the same number of segments are present in each unit-- 10 segments per helix turn in DNA and an average of 8 segments per stress group. There are, however, fewer words (cf. codons) per unit in language (2 or less) than in DNA (over 3). At first, the uniformity of the helix (it looks similar from all directions) would seem to argue

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[16] This does not explain, however, why some radio announcers (e.g., Howard Cosell) appear to use a more syllable-timed rhythm in English.

against any "stress-like" emphasis of certain segments. However, in the case of sequence specific DNA binding proteins (Matthews et al., 1983; Lewis et al., 1983) where specific "perceptual" interactions involving DNA have been studied in the greatest three-dimensional detail, it seems likely that the helix is basically contacted from one side. In this light, it seems less bizarre to view the repeating spiral of DNA (from a particular side) as a rhythmically emphasized chain of segments. As with speech, the rhythmic emphasis can be applied (i.e., a helix can occur) to any meaningful sequence. The only known constraint is that Z-DNA (with a larger number of segments per turn) can only occur with alternating pyrimidine/purine sequences.[17] This is not to claim that local sequence specific effects on the helix (including twist, for example) do not occur; that they do is an interesting just-revealed fact about DNA (see above). But then there are parallel segment induced effects on stress-timing as well that could account for the considerable local variations in timing that are observed. The point is rather that all symbol chains, regardless of segment sequence seem to be able to express a rhythmically repeating "secondary structure".

Levels of Structure (Tertiary)

In the case of DNA symbol chains, higher levels of structure are observed-- e.g., nucleosomes in eukaryotes --but these were distinguished from true folded tertiary structures of the sort seen in RNA and proteins. It is worth noting in passing that the so-called "breath group" (Lieberman, 1967, 1984) in speech streams constitutes a possible analogue. Speech is produced in discrete chunks of up to 5 or

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[17] It would perhaps be overwrought to point out that in language as well, simpler alternating CV (cf. pyrimidine/purine) sequences are correlated (e.g., in Spanish) with a larger number of syllables (and segments) per interstress interval.

6 seconds in duration during which lung volume undergoes a slow, linear decrement with time. The boundaries between such "breath groups" are marked with quick inspirations (preceded by momentary drops in pitch) which are quite audible in normal speech if one listens for them. Breath groups can mark off syntactically related groups of words; however, such marking does not seem to be required for speech to be intelligible, and inspirations can sometimes occur at unusual places in a sentence. The number of segments in a breath group varies, but is usually on the order of 100 or more. The arrangement of DNA on nucleosomes is more stylized-- exactly 146 segments per nucleosome core and about one core every 200 segments. Nevertheless, the nature of the constraints involved seems broadly similar. Both speech streams and DNA chains are fundamentally linear; but certain practical considerations-- the limits of the respiratory apparatus, and the problems of packing a very long linear molecule into a small place --dictate that the linear sequences of symbols be organized into groups larger than the basic unit if secondary structure.[18]

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[18] There are a number of other higher level units of speech streams that could be defined by a combination of intonational contoms, pauses, and intensity differences, that are characterized by a closer relationship to the syntactic structure and meaning content of the ongoing discourse. There have been attempts, for example, to define a "phonemic clause" on the basis of F0 patterns. Such higher level units that respect boundaries in the coded symbol stream that are apparent only <u>after</u> decoding are actually unlike the so-called tertiary structure units in DNA-- the nucleosomes --which, as far as can be determined presently, pay no attention to boundaries in the coded chain that correspond to functional groups (e.g., the sentence-like secondary structural elements) in the decoded protein product.

Defining 3-D Folding at the Linguistic Level

I earlier characterized DNA (the symbol chain) as a "one-dimensional" molecule, in contrast to proteins ("thing"-representation chains) and structural RNA (symbol-representation chains), which fold into true three-dimensional tertiary structures. In turning to language, it was suggested that linguistic symbol chains (and DNA looked at from a molecular "perception" perspective) were in a sense linear through time. It remains here to get an idea of what it would mean for a temporal stream of spatially delocalized phenomena to be "folded" into a true "three-dimensional" or "tertiary" structure. Since this is something symbol chains do <u>not</u> do, we shall compare them to the closely related symbol-representation chains that initially arise in the auditory system during speech perception (see section below for more complete definition), and which <u>are</u> capable of "folding".

The definition of true folding adhered to with DNA versus RNA and proteins essentially was that it required a stable (i.e., repeatably produceable) juxtaposition and interaction of non-neighboring segments of a locally-generated, initially linear chain. In <u>temporal</u> terms, this translates to a repeatably produceable pattern of interaction between temporally non-neighboring unit phenomena (e.g., persisting patterns of firing in a neural network) that that were generated in a particular sequence. In the molecular case, an important fact is that the original chain of segments retains its intersegment bonds after it has been folded. In temporal terms, this means that "folding" interactions between persisting unit phenomena preserve and depend on the initial, "local" interactions between each unit and its immediate temporal neighbors. Also, in the molecular case, a given unit will interact directly with only a few non-neighboring units. In temporal terms, this means that the persisting unit phenomena (e.g., firing patterns) do not indiscriminately interact with every other unit but instead have strong interactions with only a few temporally displaced units. This analogy, which seems to suggest "folding up" one-dimensional time in a 'space' containing 2 more dimensions of time, is less arcane than it first appears to be when it is applied to concrete examples like speech sounds or neural network models; an essentially similar extension of "time" to more dimensions is routinely carried out when, for example, mathematical models are used to display the overall dynamical behavior (i.e., all the possible "one-dimensional" trajectories) of a system on a plane or in 3-space for comfortable viewing. DNA and protein molecules, of course, change through time (especially during initial folding, for example) just as do neural network patterns. However, in the case of chains of ribonucleotides or amino acids, it is possible to represent some fundamental aspects of their folded structures (e.g., bond angle geometry) in a relatively straightforward way in 3-space (with all the caveats about the "real" delocalized quantum mechanical situation). With this as a "starting point" so to speak, one can procede to embed the system in more complex spaces to more realistically model its behavior. There is presently no similarly straightforward or "natural" baseline representation of important aspects of the delocalized and superimposed spatiotemporal patterns in neural networks that can be visualized as a structure in 3-space with distinct parts and "bond-angles". A main impetus for trying to establish the present analogy is that we might be able to use the more tractable and comprehensible "model" of three-dimensional folding Nature has already provided for us in cells as just such a starting point.

Lack of Folding in the Symbol Stream

Speech sound streams are not "three-dimensional" because the basic units in them dissipate too rapidly to interact with any but the neighboring units. This has long been recognized as a characteristic of spoken language; one of Hockett's "design features", for example, is "rapid fading". Nevertheless, it was thought to be a peculiarity of spoken language not present, for example in written language. As we have seen, written language is functionally just as "one-dimensional" as spoken language as a result of how it is accessed. In each case, a discrete series of patterns is applied to a receptor sheet; the main difference with writing is that the patterns are available for repeated (one-dimensional) perusal. If speech sounds were actually "three-dimensional", the pressure waves that constitute one segment would directly interact with the pressure waves of selected segments generated 10 or 100 segments later; something like this happens in a particularly reverberant echo chamber. As pointed out in a different context, the resulting cacaphony would be difficult to understand, as speech at least. One can also consider what written language would be like if it were truly "three-dimensional" in the sense above. In this case, the patterns of light emitted by pairs of non-adjacent words would be superimposed, as would occur, for example, in trying to read a page through an unevenly corrugated plate of glass. Thus, both spoken and written language seem clearly "one-dimensional" and are disrupted by "unnatural" and capricious "three-dimensional" transformations. The question remains if this is necessarily the case-- i.e., are three-dimensional symbol chains perhaps impossible or impractical to construct? Before turning to this, we briefly compare symbol chains to symbol-representation chains, which <u>are</u> capable of folding, to see what constraints generate "naturally" folded structures.

"Stiffness"

The difference between DNA symbol chains and RNA symbol-representation chains at the molecular level is that the DNA chains are more flexible; RNA, by contrast, exhibits a stiffer helix, which somewhat paradoxically allows it to fold into stable tertiary structures. A correlate of "stiffness" in speech symbol chains and symbol-representation chains is found in the phenomenon of categorical perception. Categorical perception was previously discussed as indirect evidence of the ability of pre-linguistic animals to perceptually segment speech streams. Here we shall be interested more in the categorization process itself.

What categorical perception of speech sounds means, is that a variety of somewhat different instantiations of a particular speech sound are perceived as the "same" thing. Roughly, this implies that at some level (we shall be more specific later) a unitary category representation (the symbol-representation segment) is activated, indicating that any one of a number of possible examples of that speech sound has occurred. The existence of coarticulatory effects (interactions between adjoining segments resulting in alterations of one or both segments) early on suggested the need for such a device.[19] As discussed above, at least some of the categorical boundaries seem to be generated in animal auditory systems as well, indicating that speech categorization is probably just one example of a more general phenomenon in nervous systems. Also, it is relatively easy to construct a robust neural network model (using symmetrical feedback) that will exhibit this

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[19] The recent experiments reviewed in the section on segmentation argue for more invariance (in spite of coarticulation), than had initially been thought to exist, but have certainly not eliminated the problem completely. For example, it appears that several different (though individually relatively invariant) cues can signal a given segment.

behavior (e.g., Hopfield, 1982, 1984). When a quiescent network of this sort is presented with a certain firing pattern or even a degraded piece of a pattern, it "relaxes" to the nearest stable firing-pattern in state space (i.e., the appropriate, or at least the best guess category representation). These ideas will be discussed in more detail in Chapter V. The main point here is that there are many more possible input states (i.e., exemplars of a category) than there are output states (i.e., the category representations themselves). As described previously, there is a similar relationship between the many conformational states of DNA segments (i.e., input states) and the few conformational states of RNA segments (i.e., the output states or symbol-representation segments); in the case of the nucleotide chains, however, the natural way to describe a reduction in sequence specific conformational states is as an increase in <u>stiffness</u>. Thus, in a sense, the chains of neural firing patterns evoked (at the segment identification level or levels in the auditory system) by chains of coarticulated speech sound are less variable and less affected by local context than those sounds, or by analogy, "stiffer".

So far, the variability in molecular and linguistic symbols segments and symbol-representation segments has been described as if it was entirely <u>internal</u> to the segment. In nucleotide chains, there does appear to be a significant contribution to chain stiffness by within-segment bonds (Saenger, 1984, p. 62-65). However, there is probably also a contribution to chain stiffness by between-segment interactions (e.g., steric hindrance of 2'-OH involving next segment; intersegment H-bonds by water molecule bridges). This suggests that the recognition of speech sounds may actually be easier (i.e., the categories will be better defined, the internal representations of the chain "stiffer") in the context of a continuous chain, whether meaningful or not. There is no evidence to my knowledge for this (in the auditory modality) but a reasonable experiment would be to see if there was a nonsense syllable superiority effect in a phoneme monitoring task (see below).

The important conclusion in the molecular case was that only the stiffer RNA chains are capable of forming three-dimensional structures. The interesting possibility of an analogous capacity of internal speech sound representations will be considered in the next section on symbol-representations alongside an explicit discussion of RNA tertiary structure. The present implication is that something like "stiffness" may be required at the linguistic level as well to support "naturally folded" neural firing patterns in the human higher level auditory system.

Conclusion

To conclude this discussion of the linearity of the speech stream, we return to a question raised before-- that is, why do speech streams need to be "one-dimensional"? The answer to this question given in Chapter I was that symbolic-representational systems need to "hide" or "camouflage" information (about how to make three-dimensional reaction-controlling devices) from the dissipative attack of the "soup". These are mostly chemical metaphors but they can be restated in linguistic terms. If speech streams somehow were "three-dimensional"-- i.e., consisting of persisting units capable of non-local temporal interaction --then the "soup" instantiated in prelinguistic hominid perceptual systems would treat them as complex objects with global properties, rather than segmented chains, and thereby preferentially divide them up between certain segments (on the basis of accidental "three-dimensional" implications of the sequence for the perceptual system that arise when the sequence is folded/superposed). If that happened, the sequence information would be lost, just as it would be lost from a molecular chain that is attacked in a site-specific manner as a result of it having folded up. The information is "destroyed" in the perceptual system when it is initially subdivided in a way that depends on sequence; if the stream has no non-local "tertiary" interaction, on the other hand (and has properly arbitrary connections and so on) then it can get into the perceptual system unscathed (or else divided into smaller chains in a random, sequence-independent way). The symbol stream must not be 'seen' to contain higher levels of organization by the prelinguistic perceptual system in order for the sequence to be used as a vehicle to stand for something else that will actually end up being three-dimensional. One implication is that the evolution of human language may have passed through a bird-song like stage in which long elaborate "one-dimensional" sequences of speech-like sounds (or endogenous sound-representations) were generated for non-linguistic purposes. Subsequently, they could have been taken over for use as symbol chains (or symbol-representation chains).

An obvious question might have occurred to the reader here-- namely, why doesn't the system simply skip the symbol-representation step and go directly to the units ("thing"-representations) that will eventually be used to build up the three-dimensional reaction-controlling devices? One answer is that the units suitable for building the reaction-controllers are especially easy to generate prebiotically or prelinguistically (in contrast to symbols and symbol-representation segments-- see below) and have built-in relations to broad classes of phenomena in the soup-world. The only way to access them directly (i.e., starting with symbols or other external phenomena) would be to use these built-in relations, which, as we shall see is very inconvenient, if not impossible. It is somewhat artificial to consider this problem in isolation, but difficult to discuss it in context before the rest of the system has been sketched out, and wee shall return to it later.

Arbitrariness(1)

"Arbitrary", being a useful word, has a number of meanings in different contexts. As is customary in philosophical investigations, for example, I want to specify several restricted and rather distinct contexts in which the word will be used. This procedure can be quite aggravating when carried to an extreme-- the reader is held hostage until he or she agrees to learn all the various restrictions. Abbreviating all of this can force an almost complete standstill (see e.g., Chomsky, 1981). On the other hand, certain fields like mathematics seem to have made considerable progress by following just such a program quite strictly.[20] The present project is not mathematical, but the juxtaposition of widely different disciplines does result in new and rather unusual contexts for some words. In the case of "arbitrary", I would like to distinguish 3 different types of connections in a symbolic-representational system that can be so called, yet that are distinct enough to warrant separate numbers.

The dictionary says only that "arbitrary" means 'selected at random and without reason'. Most linguists, however, have used the word in a more specific context. Saussure (1916/1959), for example, makes it one

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[20] Sometimes the new context for a word can be rather jarring, as in the case of "surgery on manifolds".

of two fundamental principles:

> The bond between the signifier and the signified is arbitrary.... The idea of "sister" [the signified] is not linked by an inner relationship to the succession of sounds s-o-r which serves as its signifier in French; that it could be represented equally well by just any other sequence is proved by differences among languages and by the very existence of different languages.... (p. 67-68).

He also points out that

> The term [arbitrary] should not imply that the choice of the signifier is left entirely to the speaker (we shall see below that the individual does not have the power to change a sign in any way once it has become established in the linguistic community); I mean that it is unmotivated, i.e. arbitrary in that is actually has no connection with the signified (p. 68-69).

Saussure's relation is between two different classes of internal phenomena-- the "sound-image" and the "concept". Hockett's (1966) "arbitrariness" holds between two different kinds of phenomena as well, but as previously pointed out, they are both strictly external-- sound waves and actual things.

There is another sense of "arbitrary" that is implicit here, and in the writings of many other linguists that involves "bonds" (to use Saussure's term!) between units of the same class. Thus, just as any given sound could in some hypothetical language be bound to any given concept, any given sound can follow any other sound (be bound to it) within certain weak limits. Similarly, many alternate orderings of "concepts" could be imagined, and many actually do occur. These last two cases and especially the last might at first seem to involve much less "arbitrariness" than the relation explicitly mentioned in the passages above; however, if one only considers <u>pairs</u> of units as did the authors in the first case, it is easy to see that this is largely an illusion. The obvious difference, of course, is that the within-class bonds of sound (or sound-image) units to each other, and concepts with each other naturally define long chains rather than pairs. A second seeming violence to linguistic intuition is that the "bond" between sound-image and concept seems like it should belong to a different category than a bond between two concepts, or especially between two physical pressure wave patterns. This apparent discrepancy is largely due to the tendency to view sound-concept relations as static, atemporal structures; in reality, it is quite likely that during the processing of a speech stream, for example, there is a sequential relation between sound-image and concept that is measured in the same hundreds of milliseconds that define the transition between two concepts in a comprehended sequence, making the situation seem a lot more like the molecular case, where these relations at issue can be characterized as a single type of chemical bond (covalent).

Having approached the issue in a sidelong manner, we can now try for a more explicit definition of these different senses of "arbitrary" implied above that is applicable to both linguistic and molecular phenomena. Arbitrariness(1) applies to the bonds between segments in symbol (S) chains and symbol-representation (SR) chains: these bonds connect units of the same type; each unit can make bonds with 2 other units (i.e., a chain can be generated); and the variable parts of each bound unit (i.e., the "sidechains") interact with those of their neighbors in the chain. This type of arbitrariness will be discussed here. It contrasts with two other sorts of arbitrariness discussed in later chapters. Arbitrariness(2) applies to bonds between complete symbol-representations (SR's) and "thing"-representations (TR's): these bonds connect units of different types; and each unit makes only one bond. Arbitrariness(2) is most like the Saussurean notion cited above. Finally, arbitrariness(3) applies to bonds between "thing"-representations (TR's): these bonds connect units of the same type; each unit can make bond with 2 other units; and the variable parts of each bound unit (the "sidechains") do <u>not</u> interact directly with those of their neighbors, but since they are "exposed", they partly compromise the intrinsic tendency of the non-variable part of each unit (the "backbone") to form arbitrary bonds.

In the present context, a connection is said to be "arbitrary" in general if there are only small differences in the relative "stability"-- judged by a prebiotic or prelinguistic assay --of linkages between different pairs of units. In the case of arbitrariness(1) (and arbitrariness(3)), the comparisons are made between the different possible links of what can be a long chain; with arbitrariness(2), each pair of units is discrete. The idea is basically the same in the two instances, but the criterion is inherently more stringent with chains because of the possibility that small unit differences with relatively minor local effects can result in large differences in complex "folded" tertiary structure and loss of strict arbitrariness. This, of course, was the case with RNA and is even more pronounced with proteins in their native state. Therefore, it is useful to distinguish local and global arbitrariness. The different global types were numbered and described in general terms above. Each type, nevertheless, is characterized by the same sort of "standardized connection" responsible for an 'underlying' arbitrariness that is local but absolute.[21]

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[21] An alternate hypothetical way of achieving arbitrariness would be to start instead with a variable, non-standard "backbone" with intrinsically or locally non-arbitrary connections and then 'fine tune' them to equal stability by fiddling with the also variable "sidechains". This has clearly not occurrred anywhere at the molecular level in spite of the fact that alternate backbones are available prebiotically (e.g., beta-amino acids-- Miller and Orgel, 1974). Again, a rather ad hoc appeal could be made to "processing constraints"-- the very complex apparatus that "perceives" and generates the existing chains of

Nucleotide Sequences

Relative Stability

The symbol chain and the symbol-representation chains at the molecular level are made up of 4 nucleotides. Therefore, there are 16 possible dinucleotide linkages to compare. Probably the most obvious gauge of the almost equal stabilities of these linkages is the long time that it took to develop a practical DNA sequencing technique. In the case of acid- or base-catalyzed hydrolysis, there is less than an order of magnitude difference in rate between the fastest and the slowest dinucleotide (reviewed in Brown, 1974); these are very slight differences in the biomolecular world where an enzyme commonly increases the rate of a reaction by a factor of 10^{12} (twelve orders of magnitude) relative to the rate of the uncatalyzed reaction. In the previous section on segmentation, it was noted that with DNA, the internucleotide linkages are all much more stable than in RNA; and the different stabilities of the sugar/base (glycosidic) linkage are emphasized.[22] Thus, in acid, the DNA backbone is stable and the less stable purine glycosidic linkages are hydrolyzed. The chain positions that lose a base are destabilized and more easily hydrolyzed themselves, not by

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standardized parts would seemingly have to be quite a bit more complex to deal with non-standard parts. In the molecular case, some of the other backbone types are less suitable for other reasons as well-- e.g., they possess too much conformational flexibility (Schulz and Schirmer, 1979, p. 6).

[22] The chemical method of DNA sequencing (Maxam and Gilbert, 1977) further plays on these differences. To cut prefenentially at adenosine residues, for example, the purines are first methylated. Since the glycosidic bond of methylated adenosine is less stable than that of methylated guanosine, gentle acid hydrolysis cleaves off more adenines. Subsequently, treatment with alkali results in preferential hydrolysis of the backbone at the sites of base removal-- i.e., where there had been an adenine.

cutting at the intersegment bond, but probably by opening a sugar ring (i.e., sometimes cutting through the middle of a segment); since segmentation is compromised, it is difficult to assess the arbitrariness of the intersegment bond itself. It was previously suggested that this "extra" stabilization of the intersegment bond in DNA was a "derived" condition peculiar to the molecular level system.

Even these few observations point up a problem; there is really no useful context-free way to define relative stabilities-- they can only be defined in a given chemical environment. Earlier it was claimed that a canonical environment would be a "prebiotic soup"; but being inaccessible, we turned to the "environment" of the nucleic acid chemist's laboratory. Certain things about the laboratory designed specifically to exploit small differences in stability, however, are clearly unusual from a prebiotic perspective-- like the sequential exposure of a molecule to baths of purified reagants (cf. DNA sequencing) and the extreme temperatures and pH's often employed. And in many cases, the most relevant experiments for the present purpose-- e.g., measurements of the relative stability of different nucleotide linkages in cold, dilute solutions at near neutral pH --have simply not been done (the experiments would be time-consuming and the information of no present practical value). Most estimates of prebiotic stabilities (see e.g., Miller and Orgel, 1974, p. 118-128) are thus extrapolations from data taken under more rigorous conditions. In conclusion, the data available point to noticeable though not large differences in relative stabilities of different intersegment bonds in DNA symbol chains, but only very slight differences in RNA symbol-representation chains-- both exhibit local arbitrariness, but it is compromised to a certain extent in DNA, in return for increased overall stability.

Every dinucleotide (and nearly every trinucleotide of the 64 possible) in fact appear in coding sequences. In language, by contrast, we shall see that there are language specific phonetic and phonological sequential constraints on the segments in the symbol chain. Recent work with nucleotide sequences, however, has revealed some statistical tendencies in the appearance of dinucleotides that suggest the existence of weak local sequential constraints at the molecular level as well. In prokaryotic DNA sequences, for example, the dinucleotide AG is less common that expected on the basis of the mononucleotide content. This tendency occurs in the first and second dinucleotide reading frames (AGx and xAG; i.e., within "words") as well as in the third reading frame (xxA-Gxx; i.e., betweeen "words") (Nussinov, 1981). The restriction on AG in the first frame could be due to the abundance of AGx amino acids in the coded-for proteins. However, since the restriction persists in the second frame despite the well-known degeneracy of the third base, and especially since it appears in the third frame across the word boundary, it appears to be due to a constraint intrinsic to the symbol stuff itself-- one that is not directly traceable to constraints on possible meaningful sequences. In this respect, it resembles a phonetic or phonological sequential constraint. The more recent investigations of Nussinov (1984) suggest that the avoidance of other dinucleotide sequences is due to steric repulsion between nearest neighbor purines on opposite strands (see below); thus, pyrimidine-purine sequences and purine-pyrimidine sequences are disfavored in general over purine-purine and pyrimidine-pyrimidine dinucleotides (this does not explain the constraint on AG, a purine-purine sequence).

The Standardized Connection

The "standardized connection" at the molecular level is the 3'-5' internucleotide linkage. Its important characteristic is that the 16 possible versions of it that can connect the 4 nucleotides all contain a phosphodiester linkage of approximately the same geometry; this was presupposed, for instance, in the previous discussions of the typically helical conformation of DNA and RNA, and it partly accounts for the slight differences in relative stability of the 16 linkages. Such a standardized connection characterizes all types of arbitrariness. The two features that distinguish arbitrariness(1) are the availability of two non-equivalent bonds per unit, and the presence of interactions between neighboring sidechains. The non-varying sugar-phosphate backbone of each nucleotide allows it to make two bonds-- one at the 5'-carbon and another at the 2'- or 3'-carbon. The two bonding sites, however, are not equivalent and there is thus a clear polarity to the chain, which is why, for example, 16 rather than just 8 different pairs of 4 nucleotides can be defined. The second feature of arbitrary(1) connections is that the variable part of each unit-- the "sidechain" or specifically in the case of nucleotides, the aromatic base-- also interacts with its nearest neighbors, just like the invariable backbone part (see next section for an explicit discussion of the general backbone/sidechain distinction). Like the backbones, the sidechains make "standardized" connections with their two neighbors. However, compared to the backbone connection, the sidechain connection-- i.e., base-stacking --is more symmetrical; it is harder to tell the polarity of the chain only by examining the stacked bases (there is a pseudo-dyad symmetry in the plane of the bases approximately perpendicular to the base-pair H-bonds).

Lack of Word Boundaries

An important consequence of arbitrariness(1) is that the higher level units in the segmented symbol chain-- i.e., the three base symbols themselves --are not marked off in any distinctive way. Since no chemical or conformational cues distinguish within-codon dinucleotides from between-codon dinucleotides, an elaborate apparatus is needed to recognize each codon in sequence. One way out of this would be to have a non-overlapping "comma-less" code (proposed early on by Crick et al., 1957)-- i.e., where a sequence would have only one possible decomposition into meaningful codons and hence, where all between-codon sequences would be meaningless. In reality, 61 out of 64 codons have an amino acid "meaning" (the remaining three are stop codons) and so the code is almost completely overlapping. This means that a meaningful message can be read off starting anywhere on a strand. However, since all codons (words) are the same length (in contrast to the linguitic situation), there are only three different messages possible for a given strand. The true message is often called the "open reading frame" because it will not contain any stop codons.[23] The strictly overlapping nature of the code and the uniformity of word size puts a high premium on "starting in the right place" and cells have a number of elaborate mechanisms to ensure this. But it is just as important that each codon be recognized accurately in order for the system to be able to tell where the beginning of the next codon is. In turning to language, it will be seen that the "code" is less overlapping (though certainly not comma-less), words have variable lengths, and there is nothing quite

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[23] Notice that the presence of 3 stop codons out of 64 total will cause messages read in the 2 non-coding frames to contain stop codons on an average every 20 bases (assuming that the coding sequences are pseudo-random).

like a stop codon (which would immediately prevent the listener from hearing anything more after it had been heard!); nevertheless, just as in the molecular case, it is of overriding importance that each word be recognized in turn in order to tell where the beginning of each next word is, since in most human languages, as in the DNA language, there are no cues for word boundaries in the stream of segments that constitute symbols. These issues will be discussed in more detail when we consider symbol-representations.

Speech Segment Sequences

Relative Stability

In parallel with the molecular case, we would like to know for language, what are the relative "stabilities" to "attack" by a prelinguistic perceptual system of all the possible pairs of linguistic segments. By "attack" is meant early, stimulus-dependent processing, and differences in "stability" correspond to differences in the degree to which the two segments in a stimulus appear as distinct, automatically generated firing patterns in the peripheral mammalian auditory system. There exists a body of data on the representation of a small number of consonant-vowel syllables in the firing patterns in auditory nerve fibers of the cat (e.g., Sinex and Geisler, 1983). Preliminary models of cross-fiber firing patterns using experimental parameters (e.g., Delgutte, 1982) show that aspects of these speech segments that are known to be important for phonetic distinctions in humans are in fact prominently represented in these patterns. These studies will be reviewed in detail in discussing the internalization of the symbol chain. For now, we note that these results correlate well with the earlier cited behavioral studies on the perception of two-segment syllables by other mammals (chinchillas and monkeys). However, they are not much help in directly assessing the <u>relative</u> "stability" of the different intersegment linkages in speech streams-- i.e., one of the things we need to know to determine that these linkages show arbitrariness(1). This is mostly because of the larger number of segments and therefore, the number of possible two-segment sequences. The actual number of distinct sounds that are counted to appear in speech streams varies, depending on factors like whether non-contrastive phones (e.g., aspirated and non-aspirated [p] in English) are both included and on how diphthongs (markedly non-stationary vowels) are treated. Perhaps 36 would be a minimum number of contrasting segments (24 consonants and 12 vowels) for a relatively unabstract analysis. Ladefoged (1982) lists 44 contrasting segments while Klatt (1980), who includes some allophones in a pragmatic analysis designed for a computer speech recognition system, ends up with a list of 55 segments. This means that there are at least 1000 to perhaps over 3000 possible two segment sequences in language (i.e., English) compared to 16 in DNA (or a few times that many if modified (e.g., methylated) bases with the same coding value are included (cf. allophones)). Klatt (1980), for example, included in his system about 2000 diphones (i.e., 2/3 of all possible) as occurring in English speech streams (i.e., both within and between words). So far only a very small number of these have been examined electrophysiologically and perceptually in animals (see above). Even in humans, very few perceptual experiments have attempted to directly measure the relative ease with which the several thousand different diphones are perceived as two segments, and as in the case of the analogous experiments with biomolecules, there is not a great deal of current theoretical interest in such data. Therefore, we must turn to the less direct method of examining the distribution of actually existing sequences in English and other languages.

A brief glance at some sequential constraints and at cross-linguistic patterns will serve to illustrate the rather small differences in "stability" that appear to characterize many of the possible two-segment sequences. English, for example, contains the words "brick" and "blend" which begin with the sequences [br] and [bl], and these sequences occur within and between other words. The fact that there are no words "blick" and "brend" thus appears to reflect a random underuse of the available subset of allowed sequences. Certain other pairs of segments, by contrast, are not found at the beginnings of any words; thus the absence of a word like "ndick" seems less random-- it doesn't even seem to be a possible word in English because it begins with [nd]. However, this appears not to reflect a significant difference in the tendency of that sequence to be perceived at two segments (i.e., a difference in "stability") compared to [br] and [bl] since [nd] can occur in speech streams within words (e.g., "standard"), at the ends of words (e.g., "blend") or across word boundaries (e.g., "ten dimes"). Furthermore, it occurs at the beginnings of words in other languages like Swahili (e.g., ndizi 'banana'). Similarly, there are systematic differences in the distribution of segments-- like [p] and [p^h] in English ([p] has a shorter voice onset time than [p^h], an "aspirated p"). --that do not contrast. Thus, "spin" is pronounced [spIn] but "pin" is pronounced [p^hIn]; but as before, this is probably not due to the intrinsic segmentability of [sp^h], which occurs, for example, in "six pins", pronounced [$sIksp^hInz$]. Finally, there are some sequences that occur very rarely in English, even across word boundaries. Klatt (1980) counting some allophones estimated that 1/3 of the 3000 possible sequences do not occur. However, if only contrasting segments are counted, the number is lower, probably less than 1/4 of the 1200 to 1500 such sequences. Catford (1977, p. 219-220), for example, lists 80% of all possible consonant-consanant sequences as occurring across the word boundary. In general, though, there has been less work on constraints on between-word sequences and it is therefore to be definitive here.

When a large sample of languages is examined, certain cross-linguistic preference patterns within word can be discerned. Greenberg's (1978) study of initial and final consonant cluster sequences revealed a number of statistical tendencies; however, many if not most seem to have an articulatory rather than a perceptual explanation. The observation that homorganic (i.e., involving the same place of articulation) nasals+obstruents (e.g., [nd]) are preferred over heterorganic nasals+obstruents (e.g., [md]) seems rather straightforwardly attributable to a diachronically expressed difference in ease of articulation of these two classes of sequences. Since there is no production in cells, the relative ease of producing (as opposed to perceiving) different pairs of segments has been left out of the definition of arbitrariness(1). Again, most language universals work has concentrated on within-word constraints.

The main difference between the molecular and linguistic symbol chains is in the amount of "sequence space" that is used up. Molecular symbol chains use 4 segments taken 3 at a time, which gives 64 possible sequences, to code for 20 amino acid "meanings". All of the sequences are used since there is a well known redundancy in the genetic code. In the linguistic case 35 or 40 segments are taken in variable size groups, usually at least 2 segments long but sometimes up to 10 or 15 segments (and commonly so in polysynthetic languages like Greenlandic Eskimo--see the examples in Sadock, 1980). There are about 1200 to 1500 theoretically possible two segment words, about 50,000 possible three segment words, about 2 million possible four segment words, 100 million possible five segment words, and billions and billions of possible six segment words. It is difficult to say how many word meanings there are in a language (especially in English with the existence of many technical vocabularies) but perhaps 20,000 would be a ballpark estimate for one person (2000 is too few and 200,000 too many). Thus, even subtracting out clearly impractical 'possible words' like [kkkkk], there are still orders of magnitude more available sequences than are absolutely required, compared to only 3 times as many in the molecular case. In this light, it is easier to see why a much more elaborate set of patterned constraints on within- and between-word segment sequences--i.e., a phonology --is able to exist in the case of language (I have hardly discussed these constraints or the formal apparatus for demonstrating them-- for recent summaries, see Hyman, 1975; Kenstowicz and Kisseberth, 1979). There is simply not enough room for such things at the molecular level; the only sorts of intrinsic sequential constraints present are the rather weak statistical tendencies revealed, for example, in the work of Nussinov (1981, 1984) discussed above.

To summarize, then, there is indirect distributional evidence that the relative "stabilities" of the 1500 or so pairs of segments in the early stages of auditory processing probably do not greatly differ. The prominent cross-linguistic correlations mostly appear to reflect articulatory constraints. Within a language specific constraints related to word boundaries are common, but sequences not permitted within word or morphemes often appear across these boundaries. Since the auditory system must initially (and finally in non-linguistic animals) process these two classes of sequences the same way (there usually being no word boundary cues) we tentatively take the weaker between-word sequences constraints as evidence of arbitrariness(1).

The Standardized Connection

As in the molecular case, the probable existence of relatively small differences in stability of the various segment pairs implies that there must be a "standardized connection" possible between any two segments. The situation is more complex in the linguistic case because of the greater variety of the segments, but it is nevertheless possible to examine patterns of transitions between segments in detail using acoustic phonetic techniques. The remarkable fact to keep in mind is that the 40 odd segments of a language can be processed at rates up to 20 or 30 segments per second in almost any local order and furthermore to a degree of precision that permits single segment mispronounciations to often be detected (e.g., Cole and Jakimik, 1980).

For each biochemical symbol segment, molecular biologists long ago defined a constant backbone part and a variable information-carrying sidechain part. A similar analysis can be made (with little violence to accepted notions) of acoustic segments (see succeeding section), many of which consist of a relatively constant backbone part-- the fundamental frequency (F0-- perceived more or less as the ongoing pitch of an utterance) --and a variable, information-carrying "sidechain"-- a set of "formants" (defined broadly to include stop bursts and characteristic spectra of fricatives and affricates as well as vowels and sonorants) that emphasize various harmonics of F0 or bands or noise.[24] Rather than

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[24] Such a bifurcation does not of couse hold strictly for tone languages (e.g, Chinese, many Bantu languages) where F0 is used in a

duplicating the later discussion, I would like to draw a limited analogy between the nature of the "backbone" and the "sidechain" <u>interactions</u> in the two cases. The molecular backbone is decidedly polarized-- the two connections available are not equal and one can tell the direction of the chain. In the case of language, the F0 contour "backbone" has a very complex phenomenology and it is responsible for many alterations of the baseline meaning of an utterance (e.g., a rise in F0 at the end of a sentence usually indicates a question in English (but not French)). Nevertheless, the unmarked pattern in English (and possibly cross-linguistically) is a fall in F0 across the duration of a sentence (other patterns can include, for example, "resetting" at a major syntactic boundary, a dip to indicate a syntactic gap (Sorenson and Cooper, 1980), and so on). Thus, the "connection" afforded by F0 is inherently asymmetrical in many instances, as in the molecular case.

The neighboring sidechains of molecular symbol segments interact unlike their amino acid counterparts) by symmetrical base-stacking. In turning to the 40 odd linguistic "sidechains", we find that they are much more complex and variable than the 4 closely related nucleotide bases. However, in the case of simple (and common) consonant-vowel and vowel-consonant syllables, there is a clear interaction between the two segments (due to coarticulation) that often results in a "symmetrical bond" (noted already in the first section on linguistic segmentation)-- i.e., a similar appearing transition in the vowel formant structure at either vowel onset or offset. Such effects here, and in other cases (e.g., involving rounding) rarely extend over more than two segments, and in this respect resemble the fundamentally local character of the

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phonologically contrastive way. Even in those langauges, though, a majority of the contrasts are carried by "formants", since it is rare to have more that four levels or contours of tone.

analogous base-stacking interaction. I do not want to claim that the acoustic result of coarticulation is always symmetrical-- that one always has trouble telling the direction of time in running speech spectra with the fundamental frequency removed (most good readers would have no problem since F0 does not even show up well on most spectrographs) --or hardly that one can always tell the correct direction from the fundamental frequency contour itself. But is seems fair to identify a tendency along the stated lines.

Lack of Word Boundaries

Finally, as with DNA chains, the multi-segment units of meaning are not marked off in any way. This has already been mentioned but it is also important to stress the implications of it for recognition of the word level units. A strict demonstration of the non-existence of word boundaries would be to find similar processing of within- and between-word segment sequences in the prelinguistic animal auditory system. Nevertheless, quite a good demonstration of the fact can be had simply by listening to an unfamiliar foreign language; it is in general quite impossible to tell where one word ends and another starts, though other prelinguistically conditioned aspects of the speech stream like stress groups are at the same time clearly distinguishable. In parallel with the molecular case, a possible way out of the recognition problem would be to have a non-overlapping or "comma-less" linguistic 'code', in which any but the correct divisions of the segment stream yielded meaningless sequences. Although the linguistic 'code' is not completely overlapping like the molecular code, it is often possible to produce several alternate subdivisions of the speech stream locally (see e.g., Cole and Jakimik, 1980). In some cases the restrictions on word initial or final segments or sequences help. Thus, "this rope" [δIsrop] cannot be mistakenly recognized as "thi srope" [δI srop] or "thrisr ope" [δIsr op] because [sr] appears neither word-initially nor word-finally and [I] cannot appear in an open syllable. On the other hand, [aImekI...] could be the first 6 segments of "I'm aching...", "I'm making...", "I make it...", "I may continue..."-- i.e., a boundary can occur after any of the segments but the first. In fast conversational speech, there are no cues for these boundaries, which must be actively recognized. The topic of word recognition will be explicitly taken up in considering symbol-representations; for now the key point is that arbitrariness(1) means that there are no higher level marks.[25]

Probably the most obvious question occurring to the reader making saccades across these clearly demarcated words is, why does arbitrariness(1), if it is an important defining characteristic of auditory symbol chains and DNA symbol chains, not apply to written language? Furthermore, it does not not even seem possible to perform the sort of analysis above on the "stability" of different linkages, and so on, because during reading, the segments are processed in parallel in batches of 10 or 20. One answer to the question seems to be that the present occurrence of arbitrariness(1) in the primal form of both systems is probably the reflection of a "bottleneck" (perhaps the birdsong-like stage suggested earlier) in the initial evolution of a symbolic-representational system. It was probably necessary, for instance, that symbol chains have nearly arbitrary connections (and no word markers) in order that they remain invisible long enough to build

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[25] This would have to be modified somewhat to apply to language like Hungarian, which is said to have the first syllable of each word stressed, and thus to have an overt mark at word boundaries. Nevertheless, such a "demarcative" function for stress (in the sense of Trubetzkoy) has been downplayed (e.g., Bolinger, 1978).

up enough complexity to get the system off the ground. Once in operation, the primate bearers of the system were free to plan out or stumble upon variations on the symbol stuff at their leisure. By most accounts, the last mentioned, leisurely non-writing stage of language accounts for most of its history. Nothing quite like written language seems to have evolved at the molecular level, though, probably a result of the inability of cells to "think on their own" (see Chapter II). Some independent evidence for the "bottleneck" theory is the structure of the symbol chain in another primary (i.e., "effortlessly" learned, unlike reading and writing) form of human language-- visuomanual sign language(s); symbol chains in ASL consisting of "holds" and "movements" (cf. consonants and vowels) appear (Liddell, 1984) to be much more like their sequential marker-less, auditory counterparts than was even thought quite recently (e.g., Klima and Bellugi, 1979).

Backbone and Sidechain Structure

So far we have considered three properties-- segmentation, linearity, and arbitrariness(1) --that are primarily characteristics of the connection between the units in the symbol chain though considerable detail about the units themselves had to be introduced. In the next two sections, we consider properties that are more associated with the units themselves, even in isolation. The first property is given a name that comes from structural chemistry because no convenient equivalent term exists in the literature of acoustic phonetics although it will be argued that quite similar notions are employed there. The notion of a constant "backbone" or baseline against which different "sidechains" can be seen is not strictly confined to biomolecules or human speech sounds. In the molecular case, for example, there is a family of synthetic, chain-like molecules based on modified ethylene units. When these units are polymerized, a uniform aliphatic (single bonded) carbon chain backbone results, with various possible sidechains on every other carbon. The polymers with uniform sidechains are most familiar-- e.g., no sidechain (Polyethylene), phenyl sidechain (Polystyrene), cyano sidechain (Orlon), two-piece methyl and methyl ester sidechain (Plexiglas) --but copolymers, that is, molecules with a uniform backbone and variable sidechains are also possible (and profitable). It is harder to say is non-biological polymers existed prebiotically; prebiotic chemists, however, have succeeded from time to time in generating possible candidates although the presence of such products is usually a sign that the experiment has failed (i.e., to produce biotic polymers) and therefore will be difficult to publish. Similarly, at a prelinguistic level, there are phenomena in the vocal repertoire of some birds demonstrating a primitive backbone/sidechain type of organization-- some quiet parrot vocalizations (non-whistling type) consist of a constant fundamental frequency and slightly differently emphasized harmonics (Nottebohm, 1976) that have acquired well-known interpretations by humans as speech sounds. We will return to related topics in more detail in considering the probable prebiotic and prelinguistic substrates of symbols.

Phosphate-Sugar and Aromatic Base

Constant Backbone

In DNA, the backbone part of each unit is, of course, a sugar connected in ester linkage to a phosphate. The same piece of molecular structure appears in each link but its conformation varies, depending on base sequence and other less well understood longer range effects associated with supercoiling and winding on a nucleosome core (discussed in section on linearity). In the crystallized dodecamer of double-helical B-DNA, the main variation in the backbone due to base sequence apparently arises nearest neighbor purine sidechains from opposite strands hindering each other (Calladine, 1982; Dickerson, 1983). This happens because each base pair tends to twist (in the same direction) like a propellor, but a propellor with unequal length blades (long purines, short pyrimidines). Thus, as long as the "propellors" are stacked with the long blades all on one side, there is no clash; with an alternating long-short arrangement, there is maximum interference between the inner parts of the long blades. The result is that the 6 backbone bond torsion angles in each nucleotide in such a sequence 'give' enough to allow the longer blades to stick out of the stack a bit, and to reduce the twist of the stack. The resulting local adjustments, however, are rather regular and predictable. When we turn to language, similar local and relatively monor effects of "sidechains" on the configuration of the linguistic "backbone" occur; the main difference is that the effects are less regular because of the existence of 8 or 9 times as many possible sidechains. Also, the effects arise by different mechanisms because the linguistic symbol chain is not "double-stranded" in any sense.

Variable Sidechain

The sidechains of DNA have already been mentioned many times-- they are the four aromatic bases-- adenine (A), cytosine (C), guanine (G), and thymine (T) (uracil in RNA). Now we can explicitly consider them as information-bearing devices. The genetic code is based on a very simple system of 4 (by themselves) meaningless segments, each of which has only

2 "distinctive features", as it were. The first feature is the distance the base sticks out from the backbone (not the same as the backbone bulges described above)-- there are long purines, A and G, and short pyrimidines, C and T. The second feature is the number of possible hydrogen bonds-- there are 3 bonds possible with C and G and 2 possible with A and T; for this reason, CG or GC base pairs are stronger than AT or TA base pairs. Thus, the hypothetical "Prague School" molecular biologist might designate adenine, for example as having two binary features, [+long] and [-strong]; similarly, cytosine would be designated [-long] and [+strong]. In addition, there are as already noted, several variants of the bases-- e.g., 5-methyl cytosine --that have the same effect as the unmodified base when encountered in the chain; these would be something like molecular "allophones" or perhaps allobases. Thus, there would be a more abstract category /C/ that marks off a set of bases that all have the same effect when it comes to coding for meaning. /C/ could be "realized" as [C] or [^{Me}C] but both [GG ^{Me}C] and [GGC] stand for glycine. This is something like the situation in language that a phonologist calls "free variation"-- e.g., [map] and [map^h] can both be used to mean 'map'. I do not want to imply more similarities than have been explicitly stated here, however, because there are significant qualitative as well as quantitative differences between the two systems-- e.g., there is no sign in language of the prominent redundancy seen in the genetic code (see Chapter IV).

This is hardly the first time that "distinctive feature" have been 'discovered' outside of a strictly phonological milieu-- such an analysis has been performed on things as disparate as kinship terminology and letter shape. Furthermore, it is hardly clear that features and rules are the appropriate framework even for understanding speech sound perception and production; Klatt (1980), for example, argues strongly against using them. Part of the reason for the exercise is to emphasize what such an alternate, more abstract level of analysis looks like when applied to a system where the underlying principles are rather well understood. This is not to condemn the use of such an analysis but to get a flavor for how the much more complex "underlying principles" of language might relate to it when they are uncovered.

Double Strandedness

A prominent feature of the molecular symbol chain is that is consists of two complementary strands. Surprisingly, this apparently fundamental arrangement is nowhere to be found in linguistic level symbol chains (though something like it could occur in internal, folded symbol-representations). The difference can be considered in light of the lack of production at the molecular level. A complementary double strand has two big advantages for a molecular system without production. First, it is much more stable than a single strand. This is important in cells, which "listen" only to their own permanently stored set of symbol chains. If a sequence is lost, so is the "meaning" that that sequence codes for, since there is no way for cells to generate new "meanings" de novo. The second advantage of a double strand guessed almost immediately by Watson and Crick, before any of the required enzymic machinery was understood, is that a complementary double strand can be "semi-conservatively" replicated; the parent double strand is duplicated by splitting it in two and then synthesizing the complementary halves for each single strand. This allows there to be a strong covalent backbone holding together the sequence information for each new strand at all times. There is nothing quite like replication in language in its native state before the invention of writing (and xeroxing). Language propagation depends on entirely different mechanisms; it requires neither a stable symbol chain, nor direct copies of the whole thing (which is about as long as a 1000 page book at one letter per nucleotide even for a mere bacterial cell). These differences are explored in the section below on replication and evolution.

Now it should be pointed out that the notions of backbone and sidechain just discussed, as well as segmentation and arbitrariness(1) for the most part were defined in terms of a single strand. Important structural determinants like base stacking and helix formation occur in single strands (though single stranded structures are slightly different form the structure of one of the strands in a double helix-- e.g., the single strand would naturally not be expected to show the effect of opposite strand clashes). Furthermore, during the actual operation of "perceiving" DNA, the double strand is unwound, and only one strand is read. Thus, a number of the properties discussed so far seem independent of double-strandedness. However, it is not possible to cleanly factor out double-strandedness from the discussions of 3-dimensional folding of polynucleotides; folding seems to depend partly on the formation of double-stranded base paired stretches, and much of the discussion revolved around differences in the flexibility of the double-stranded structure (though these differences are at least partly intrinsic to each strand). Since there is no double-strandedness in the linguistic level symbols, and since double-strandedness at the molecular level is inextricably wound up, so to speak, with linearity, it is clear that the detailed architecture of the two systems is somewhat divergent here. This fact does not undermine the usefulness of a concept like "linearity" but it does indicate that in some instances, it may not be possible to neatly sort out and line up the parallel reasons. Given the large number of interlocking pieces in each system, it is perhaps surprising that this situation has not obtained (I think) more often.

Fundamental Frequency and Formants

Constant Backbone

The acoustic spectra of many of the sounds of speech have two distinct parts. At the low frequency end, there is a "fundamental frequency" component (abbreviated F0) that will be compared to the constant phosphate-sugar backbone, and at higher frequencies, there are emphasized spectral band called "formants (labeled F1, F2, F3, ...) that will be compared to the variable information-bearing aromatic base sidechains. These two are considered in turn.

The fundamental frequency-- i.e., what is perceived as the pitch of a voice --is generated by the periodic flapping motions of the vocal folds (the glottis). This frequency averages near 100 Hz for an adult male, over 200 Hz for an adult female, and can go over 1000 Hz for a screaming child. Since the volume of air per unit time allowed through the vocal folds varies more like a sawtooth wave than a pure sinusoid, a large series of harmonics that are integer multiples of the fundamental frequency are also generated. It is the selective emphasis of certain harmonics that constitute vowel formants. Many speech sounds contain a fundamental frequency (27 out of a basic list of 36 in English). These include 12 vowels, a total of 7 nasals, liquids, and glides, which are vowel-like, and 8 voiced obstruents, which have a secondary constriction in the vocal tract (beyond the glottis) that constitutes an additional but aperiodic (noise) sound source. 9 sounds without a fundamental frequency remain; 8 are unvoiced versions of the voiced obstruents, and the last could be called a glottal obstruent. Thus, normal connected speech consists of stretches of higher frequency segment "sidechains" (i.e., formants) underlain by an F0 "backbone" that is interrupted from time to time by the presence of unvoiced obstruents. Some unvoiced obstruents in English (e.g., [s]) occur more often than their voiced partners (i.e., [z]); and since there is also a moderate cross-linguistic preference for unvoiced obstruents (Greeberg, 1978), the periodic lack of a "backbone" appears not to be unusual in the speech symbol stream. Gaps occur in DNA backbones as well where they are called "nicks". They are normally closed after a time by enzymes (ligases). Furthermore, in almost all of the DNA crystal structures that have been reported, the small (5-15 base) chains line up end to end, just as if they had a continuous backbone, indicating the importance of base stacking in chain structure. Nevertheless, there is a clear quantitative difference; natural DNA chains rarely have as many "nicks" as speech chains have pauses in voicing.[26]

In contrast to the formant "sidechains", the fundamental frequency "backbone" usually does not carry contrasting phonetic information. This was also the case with DNA where the main things that count in coding are the biochemical features of the particular bases in a sequence (i.e., long or short; 2 or 3 bonds possible); backbone

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[26] It is quite possible to understand whispered speech, which completely lacks a fundamental frequency (the vocal cords are lax and do not vibrate during whispering; instead, they generate broadband noise which is, however, filtered in the same manner as the series of harmonics generated in speaking aloud. Stacked free nucleotides or bases rarely occur in cells and they certainly cannot be transcribed. The difference points up the greater flexibility of the linguistic as opposed to the molecular system. In any case, the "backboneless" speech streams produced during whispering are certainly not the norm.

variability has no effect on what amino acids are coded for. As a demonstration of this in speech, it is easily possible to pronounce a vowel (e.g., 'eeee' at a variety of different levels of pitch (i.e., different fundamental frequencies) and always have it sound like the same vowel. The situation is not quite so simple in languages that have different pitch levels or contours (called "tones") as contrastive elements-- e.g., in Nupe, an African language, high-tone [ba] means 'to be sour' while low-tone [ba] means 'to count' (example from Hyman, 1975). The overall range of an F0 contour for a given sentence in such a language, nevertheless, can be moved up or down without changing the words that are signalled; and a certain amount of non-contrastive variation is allowed even within a single breath-group (e.g., lowering at the end of a sentence).

Under normal circumstances, fundamental frequency changes continuously and is quite complexly patterned; one only need pronounce a sentence or two with a steady pitch to see how odd and mechanical it sounds. First, there are some direct local effects of certain segment sequences on F0. Sorenson and Cooper (1980), for example, showed a slight fall in F0 both within and across words during the first 50 msec of a vowel after a prior voiceless consonant. This effect is reminiscent of the local base-sequence dependent modifications of the DNA backbone noted above; interactions between certain classes of "sidechains" affect the F0 "backbone" in a predictable way. At a slightly larger scale, there are usually small pitch increases on each stressed syllable (see e.g., Fujisaka, 1983); this was compared previously to the periodic cycles of the helix backbone. Finally, there are superimposed, longer range changes in slope. These can substantially alter the overall meaning of an utterance. For example, Ladd (1980) distinguishes a "contradiction" contour from a "fall-rise"--the first adds the "meaning" of questioning the assumptions of the hearer, while the second serves to focus on one member of a set mentioned by a sentence and can thus effect things like the scope of negation. The question of exactly what type of "meaning" is conveyed by intonation is much disputed; Ladd's position is unusual in emphasizing how similar intonational meaning is to the meaning of some words--modals, for instance. Nevertheless, a major distinction between intonational meaning and normal word meaning that is of interest in the present context and that is granted by any analysis, is the method by which the two types of meaning get into the system-- "normal" word meaning by "sidechain" (i.e., formant) sequences, and intonational meaning by the contour of the F0 "backbone". A similar distinction in 'input pathways' appears at the molecular level. Sidechain sequence is "perceived" via base pairing (i.e., by detecting the distinctive features of the bases) as normal "word meaning" (i.e., amino acid meaning), while the overall shape of the backbone (cf. an intonation contour) is "perceived" more holistically by a considerable number of control proteins. Initial models of the second pathway of meaning extraction at the molecular level postulated recognition of the somewhat exposed sides of the base-paired sidechains themselves (e.g., Lewis et al., 1983; Matthews et al., 1983) but other recent work (Nussinov and Lennon, 1984) suggests that the particular shape of the 'constant' backbone might be just as, or more important. Another similarity is that a given sidechain sequence (cf. a sentence) can sometimes assume more than one backbone configuration (cf. several different intonation countours applied to it) by undergoing a B => Z transition, for example, though more subtle variations are possible too. Again there are differences here. For example, much of the supposed "intonation-like" meaning at the molecular level appears at present to be involved with deciding how much to "listen" to particular sequences (i.e., with control of transcription initiation)-- a somewhat more restricted function than is served by linguistic intonation. And the "contours" of the DNA backbone compared here to the F0 contours that signal intonational meaning are predictable from local base sequence while in language, these last two things can be determined independently.

Variable Sidechains

The linguistic symbol segment sidechains have been referred to as a group as "formants". Since the term was introduced in the late 19th century with reference originally to vowels, we start with them. he vocal tract is essentially an adjustable (by the tongue, for example) resonant cavity with a driver, the glottis at its base. Formants, then are defined for a particular adjustment of the cavity as its 4 or 5 lowest resonant frequencies (which are always higher than F0 in most adults). During phonation, the vocal folds generate the fundamental (e.g.-- 100 Hz) and a long series of harmonics (in this case-- 200 Hz, 300 Hz, etc.). The harmonics that happen to land away from a resonant frequency are attenuated (the vocal tract can be thought of as filtering them out) while those that land on or near a resonant frequency are passed and appear in the total output spectrum as emphasized bands or "formants". What vowel is perceived is determined mostly by the relative and absolute frequencies of the first two formants. Since men, women, and children have different sized vocal tracts, the resonant frequencies for the same oral gesture differ. Therefore, in order to interpret a given pattern of formant frequencies as the vowel it was intended to be, an estimate, as it were, of the size of the speakers vocal tract must be made early on. This is somewhat akin to estimating the distance of an object to tell how big it really is. Already, the system is much more complex than with nucleotide bases where only two features are needed and where there is no "sexual dimorphism" in nucleotide chains. A popular, quasi-articulatory based method of describing vowels in English (12) uses 4 features-- "height" (high, mid, low), which is inversely proportional to F1 frequency, "backness" (front, back), which is proportional to the difference between F1 and F2, and "rounding" (rounded, unrounded) and "tenseness" (tense, lax), which have complex acoustic correlates. A more straightforward acoustic specification (Ladefoged, 1980) would involve 6 continuously varying "features"-- the amplitude and frequency of F1, F2, and F3.[27]

Two-thirds of the contrasting sounds in English-- the consonants --remain. Briefly, these can be divided into vowel-like and obstruents. The vowel-like group (7) includes nasals, liguids, and glides. All of thses have sets of vowel-like formants that differ, however, in their patterns of intensity, frequency, or rates of change from those in true vowels.[28] The largest group of consonants are the obstruents (17) in which there is a secondary constriction in the vocal tract past the glottis that generates a turbulent air flow and thus, unlike most glottally generates sounds, an aperiodic (i.e., noise-like) spectrum. The main motor variable is the "place of articulation", which can range

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[27] The 12 vowels commonly distinguished in English are found in the words-- teak, tick, take, tech, tack, tock, talk, took, toke, "tuke", turk, tuck. Phonetic symbols for them are, in order-- i, I, e, ɛ, æ, a, ɔ, U, o, u, ɚ, ə.

[28] The 7 vowel-like consonants distinguished in English are found at the end of "sun", "some", and "sung" (nasals), and at the beginning of "lat", "rat" (liquids) and "yet", "wet" (glides). Phonetic symbols in order are-- n, m, ŋ, l, r, y, w.

from the lips all the way to the glottis itself. From a sensory point of view, different locations in oral cavity constriction result in a different spectral profile for the noise and often one or more "formant" peaks in the noise. Two other distinguishing features of obstruents are whether or not "voicing" (a periodic sound generated simultaneously by the glottis) accompanies the noise, and the degree of abruptness ("manner") of the onset and offset of the noise.[29] This is an oversimplified summary since several speech sounds appear to have multiple cues. Nevertheless, recent work has emphasized the particular importance of the cues listed above. In the case of stop bursts, for example, Repp (1984) showed that listeners are remarkably sensitive to even very weak release bursts (i.e., short noise formants).

To summarize, a total of at least 10 features are conservatively needed to describe the 36 segment "sidechains" listed here, in contrast to 2 features for the 4 nucleotide sidechains. The more abstract well-known analysis of Chomsky and Halle (1968), for comparison, uses 13 binary features for English to describe 46 different sounds, while Ladefoged (1980) lists 15 continuously varying strictly acoustic features, and Ladefoged (1982), 20 traditional features to describe over 100 sounds present in one or another of the worlds languages. Clearly, there is a major quantitative difference here between the linguistic and molecular systems in the number of sidechains and in the number of ways that they differ (i.e., their features). There is, of course, a proportional difference in the number of word meanings coded for. The

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[29] There are 17 obstruent consonants distinguished in English. They are listed (as the prevocalic sound in each word) in voiced and unvoiced pairs, and in order from most distal to most proximal (i.e., near the glottis) place of articulation-- pin, bin; fin, vim; thin, then; Tim, dim; sing, zing; shun, genre; chin, gin; come, gum; him, (no unvoiced version possible). The phonetic symbols for these sounds in order are-- p, b, f, v, θ, ð, t, d, s, z, š, ž, č, ǰ, k, g, h.

interesting similarity is that for a given feature, there are rarely more than 2 or 3 different "levels" of it (pace Chomsky and Halle et al. who would allow only two and Ladefoged who prefers the accuracy of continuously variable parameters); even "place of articulation", with 7 possible levels is rarely used by itself to distinguish more that 3 or 4 otherwise similar sounds in a language. Initially, it might seem perverse to think that there is a common explanation for why molecular level symbol chains weren't based entirely on 4 different sidechain lengths, or alternatively on four different types of base pair bonds, or in the case of language, why speech sounds weren't more "rationally" designed with, say, 6 levels of F0 and 6 levels of F1 (i.e., for 36 possible combinations) or even better, 36 levels of F0. There are plausible enough reasons in each case why this didn't happen. With DNA, for example, 4 different base lengths would probably be hard to fit into a uniform helix, or too similar to allow reliable recognition and base pairing. With language, 6 levels of F0 (much less 36) would be difficult to produce in an arbitrary sequence and hard to distinguish. But stated this way, a certain similarity should be more apparent. A way to phrase the common constraint in the present framework is that the conflicting requirements of being a symbol chain-- i.e., the need for units uniform enough to allow segmentation, linearity, and arbitrariness(1) versus the need to have reliably distinguishable units --conspire to make it impratical for there to be more than a couple levels of a given feature.

Prelinguistic/Prebiotic Status of the Symbol Stuff

Prelinguistic and prebiotic criteria have already been invoked in discussing segmentation, a property of the connection between symbol segments; in this section, I would like to examine the prelinguistic and prebiotic availability of the symbol segment itself. Somewhat surprisingly, complete symbol segments (and symbol-representation segments) turn out to be substantially more difficult to produce or observe prebiotically or prelinguistically than complete "thing"-representation units (amino acids, word meanings-- see Chapter V) that they stand for. The symbol segment and symbol-representation segment are thus more "derived" than the "thing"-representations, which, by contrast, are facilely generated prebiotically and prelinguistically, and can be thought of as constituting a ser of naturally occurring (i.e., "primitive") representations of categories of phenomena in the previously existing "soups".

Origin of Nucleic Acids

Scientists have long speculated about the origin of life from non-living matter (see Farley, 1977). Opinions about the likelihood of such a process or on what organisms it would produce have varied greatly over the years. In the nineteenth century with the rise of evolutionary thinking, the idea that simple life could arise de novo became rather widely accepted. Pasteur's experiments after mid-century suggested that spontaneous generation probably did not occur either in rotting meat or in contemporary bogs; nevertheless, it seemed clear to many that the concept of evolution by natural causes implied at least the spontaneous generation of the first organism or organisms. Speculation about what sort of prebiotic chemical reactions might have given rise to life accompanied the explosive development of biochemistry in this century. However, the ideas of Oparin, Haldane, and others went virtually untested until the well known electric discharge experiment of Miller

(1953) that succeeded in generating amino acids from a mixture of ammonia, methane, hydrogen, and water. Subsequent to that, many more experiments were performed (reviews: Miller and Orgel, 1974; Fox and Dose, 1977; Dillon, 1978; Day, 1984) and literally millions of different compounds have been synthesized starting with more or less plausible prebiotic reactants, catalysts, and energy sources. In this section, attempts at the synthesis of nucleic acids are described first, and then viewed in the context of the earlier syntheses of amino acids.

Symbol Segments

Many prebiotic researchers have supposed that the building blocks of DNA and RNA chains must have existed before the origin of life. Eigen and Schuster (1979), for example, in a theoretical examination of a class of nonlinear reaction networks ("hypercycles") with possible prebiotic relevance, state

> Here we simply start from the assumption that when self-organization began all kinds of energy rich materials were ubiquitous, including in particular: amino acids in varying degrees of abundance, nucleotides involving the four bases A, U, G, C, [and] polymers of both the preceding classes (p. 65).

Similarly White's (1980) model assumes "steady or periodic availability of free energy and monomers (amino acids and nucleotides)" while Kuhn and Waser (1983) postulate a "suspension of energy-rich nucleotide-like compounds". Many other examples could be cited. In spite of this, the prebiotic synthesis of nucleotides has proved exceedingly difficult and no satisfactory synthesis currently exists. In 1974, Miller and Orgel concluded

> The origin of nucleosides and nucleotides remains, in our opinion, one of the major problems in prebiotic sysnthesis (p. 115).

This conclusion has recently been reiterated (Follmann, 1983; Shapiro, 1984). The reasons are intriguing.

Electric discharge experiments failed to generate even trace amounts of nucleosides (i.e., sugar plus base) or their components (sugars-- i.e., part of the backbone --and bases-- i.e., the sidechains). However, several syntheses of the adenine sidechain were achieved early on by the oligomerization of pure HCN in concentrated aqueous solution. HCN occurs in abundance in the electric discharge experiments if the concentration of hydrogen is kept low. Adenine can even be synthesized starting with realistically dilute solutions of HCN if they are frozen. The reaction mixture must be afterwards hydrolyzed for hours at 110° in dilute acid to actually get the adenine (Feris et al., 1978). Another photochemical pathway without hydrolysis, however, is also plausible (Miller and Orgel, 1974). On the other hand, formaldehyde-- also a product of the electric discharge experiments --can be polymerized in alkali to give a variety of sugars, with ribose making up a few percent of the total sugar (deoxyribose, the sugar in DNA is not produced); a catalyst like alumina allows more realistic concentrations. The problem is that the base cannot be coupled to the sugar in aqueous solution. Purines and a sugar can be coupled non-specifically and in low yield if they are heated together dry with a magnesium salt (sea salt) catalyst. This process does not work with pyrimidines.

There are several problems with these procedures. First, there are conflicting reaction requirements; the best synthesis of a purine requires an initial cold alkali step followed by a hot acid step. Second, sugars are so unstable it is unlikely that they could have accumulated prebiotically (Miler and Orgel, 1974). Third, the simultaneous systhesis of purines and sugars is unlikely to have occurred; this is because their respective precursors, HCN and formaldehyde (which were, of course, both generated in the electric discharge experiments), preferentially react with each other to give amino acids, rather than with themselves, to give purines and sugars. Fourth, the base-sugar condensation reaction is not prebiotically satisfactory as it uses pure reagents; Shapiro (1984) points out that if the poorly characterized, heterogeneous raw products of the purine and sugar syntheses were used as reactants, over 2,500 different nucleosides would be possible using conservative estimates of the raw product diversity. Finally, to produce the complete DNA or RNA segment, the base-sugar molecule must be phosphorylated; and as noted previously this can occur at 3 different positions. Phosphorous salts are also exceedingly insoluble in water, though phosphorous is more common in the dissolved volatile fraction of many (molten) igneous rocks and can appear in higher concentrations in volcanic pools, for example (as noted by Day, 1984). None of these restrictions are completely prohibitive. Thus, prebiotic reactants might have been fractionated, sugars might have been continuously synthesized, heterogeneous product mixtures might have been fractionated, everything might have come together in a volcanic pool, and so on; since there is relatively little direct information on the absolute plausibility of these various complex fixes, it is probably best to rely for the time being on <u>relative</u> measures--for example, as determined by comparing the syntheses above to syntheses of other biotic monomers.

"Thing"-Representations

A most obvious comparison is with amino acids. After the initial experiments of Miller, is is not too inaccurate to say that it has been difficult to avoid producing amino acids in prebiotic experiments, and they have even been found on meteorites. Amino acids are produced in good yield from mixtures of simple gases, with a variety of energy sources, including electric discharges, ultraviolet light, and shock waves. Conditions for the syntheses are much less restricted than those for the syntheses described above, which often require that one or another class of probably ubiquitous molecules (e.g, formaldehyde in the case of adenine synthesis) be excluded before the reaction will proceed. The main requirement is that the gas mixture is reducing with some methane present (Schlesinger and Miller, 1983). These experiments will be discussed more fully later. The important observation here is that the amino acids facilely produced are complete, each containing both a constant backbone part and most of the biotically observed sidechains. Thus, it is much easier to generate an entire "thing-representation unit that even the sidechain part of a symbol (or symbol-representation) segment (e.g., adenine). This seems to represent a fundamental difference between the two types of units and has stood up to almost 30 years of experimentation in this field. Certainly, there will be new discoveries and new syntheses, but for now, we will assume the distinction is valid. It is intriguing that an analogous situation seems to hold at the linguistic level.

The Origin of Speech Sounds

Man has probably speculated for as long about the origin of language as about the origin of life (Harnad et al., 1976). There has been a similar waxing and waning of ideas about the origin of the various components of language, the context in which language arose, and the order of events. By virtue of its close association with the developments of the modern human mind, discussion of the language origin question has often taken place in an even more emotionally charged atmosphere than the origin of life question. The controversies surrounding the various "ape language" projects are a case in point. As above, we shall try to circumvent some of the more acrimonious debates for the time being by sticking more to an assessment of the relative rather than absolute difficulty of the acquisition of different components.

However, since production of the code occurs in addition to perception of it at the linguistic level, the issue of the pre-systemic status of the symbol segment stuff is inherently more complex than at the molecular level because of the possibility that there were influences on the final nature of the linguistic symbol segment related to the ease of production (the molecular counterpart or the symbol chain, DNA, must of course be "produced" in a sense-- during replication, for example --but this is very different from "true" production, which involves encoding rather than mere copying). One way of visualizing this is as a contest to decide whether the peripheral perceptual or the peripheral production system will change more in the transition from the prelinguistic to the linguistic condition. If the peripheral production system were to hold its ground, so to speak, constraining the perceptual system to change, then we would expect considerable disanalogies with the molecular level perception-only situation. By contrast, if the peripheral perceptual system was little affected by production constraints, then we might expect more parallels with the molecular case. The second situation seems to better describe what occurred. Lower level perception of speech by primates and other mammals reviewed above suggests that peripherally at least, the lower level auditory system was relatively little modified to perceive language; by contrast, there appear to have been more substantial alterations of the peripheral apparatus for production, as we shall see (a number of authors have argued a similar position-- e.g., Kuhl and Padden, 1983; Stevens, 1983). The conclusion here is that it might be possible to assess the pre-systemic availability of the symbol segment stuff (speech sounds) relative to the "thing"-representations ("concepts", category representations) just as was done at the molecular level, in spite of the presence of production.

The scenario outlined above basically derives from two observations. First, when speech sounds are played to primates (or cats or chinchillas), these subjects seem to initially perceive them in a manner similar to humans. On the other hand, primates (and other mammals) seem quite unable to produce speech-like sounds (cf. the difficulty of the prebiotic synthesis of nucleotides). The first named experiments were discussed earlier in this chapter; now we consider the second set of observations. An advantage at the linguistic level is that some members of a different group of amniote vertebrates-- the birds --have in effect achieved a "prebiotic synthesis" of the symbol segment in their ability to control the production of speech-like sounds; this provides, if nothing else, an independent perspective on the prelinguistic availability and conditions for such phenomena.

Symbol Segments

Within the ape language industry, one of the most burning issues has been whether the apes are capable of understanding or comprehending symbol sequences; by contrast, the question of interest here-- that is, whether speech-like sounds can be generated using prelinguistic "reagents" in simian oral, pharyngeal, and neural structures --is not disputed much today. In the aftermath of the almost complete failure of several exhaustive attempts to teach chimpanzees to make human speech sounds (Hayes, 1952; Kellogg, 1968), it has been generally accepted that apes can generate speech-lke sounds only with great difficulty (their capacity for vocal learning is much inferior to many songbirds), and subsequent investigations all employed some form of visual-manual communication. There has been less agreement on why this is so. For a number of years, Lieberman (review in his (1984)) has contrasted the relative suitability for speech of the primate larynx and glottis with the unsuitability of the configuration of the supra-laryngeal cavity. The argument is basically that although the non-human primate glottis seems capable of generating a fundamental frequency with a usable harmonic spectrum, the essential primitive mammalian condition of the supralaryngeal (pharyngeal and oral) airway-- i.e., a high larynx, small size of the pharyngeal portion of the airway --results in a much reduced capacity to independently modulate formant frequencies (i.e., resonant frequencies of the air space) by moving the tongue body. In humans, a lowered larynx and therefore, a substantial pharyngeal cavity above the larynx whose size can be modified independently of the size of the oral cavity (by tongue body movements) allows a much greater range of vowels to be produced. The most strenuous debates have centered on the nature of these cavities in _Homo erectus_ (1.5 to 0.4 million years before present) and _Homo sapiens neanderthalensis_ (125,000 to 40,000 years before present). Unfortunately, the cavities occur in soft tissue that is rather loosely suspended underneath the jaw and in front of the vertebral column, and are thus preserved only indirectly in the shapes of these bones. An intriguing clue from development is that the supralaryngeal cavity of the human newborn (like other primate babies) starts off in the primitive mammalian condition; newborn humans and other mammals are obligate nosebreathers during quiet respiration. There is then a gradual descent of the larynx that is quite visible by 3 months and is complete after several years. The tongue retains the same large size as in other primates though it is mounted in a relatively shorter jaw; this is possible because the tongue curves and its posterior portions have followed or perhaps pushed the larynx to its low position within the pharyngeal cavity. Other primates, by contrast retain the "standard plan" airway into adulthood.

Clearly, this is not the whole picture; the scenario hardly mentions consonants, which account for a majority of the segments in most languages, and which require extremely delicate motor control (e.g., to maintain the frication noise of an [s] or to properly control the rapid opening of the seal between the tongue and the roof of the mouth for a [t]) that other primates seem to lack. There is indirect evidence that something similar to what occurred in the evolution of neural control of finger movements in primates also occurred in the evolution of neural control of thoracic, glottal, pharyngeal, lingual, jaw, and facial movements involved in human speech. In the first case, it has been possible to directly examine both the central nervous systems of animal without fine digit control (e.g., cats) as well as those of animals with increasing degrees of such control (e.g., raccoons, monkeys, great apes).

A reasonably consistent picture of the neuroanatomical changes in the final few levels of synapses involved in distal limb control has been established (review: Weisendanger, 1981). Briefly, in a cat, the descending neural pathways from the cortex (and from the brainstem) synapse primarily on interneurons in the spinal cord; those interneurons then directly contact the motoneurons controlling various muscles. In raccoons, monkeys, and apes, there is an increasing tendency for corticospinal neurons to contact motoneurons directly (while still contacting the interneurons to a degree). Now it is known that the spinal cord itself is capable of generating quite complex coordinated activity of the sort involved in locomotion, for example, and has been hypothesized to contain one or more essentially self-contained "pattern generators" somewhere in its interneuronal circuitry (the pattern generating circuitry might even include some of the motoneurons). A clearly over-simplified but heuristic model of how locomotion works is that the supraspinal pathways transmit a somewhat non-specific motor signal to the spinal pattern generators, which then fill in the details and take any perturbations into account (see Gallistel (1980) for a history and discussion of this idea). In the cat, any signal from the cortex must be "filtered" through the patterns generators, and as such, is more on a level with the other brainstem inputs (e.g., reticulospinal, vestibulospinal) that also contact the interneuronal network. In primates, by contrast, cortical signals can activate specific sets of motoneurons directly to, as it were, "break them out of" the global, coordinated firing patterns associates with whole hand locomotion to make it possible also to delicately manipulate small objects (or facilely generate manual signs in ape-language experiments for that matter).

In considering the control of speech movements, the evidence is less direct; nevertheless, something similar seem to have taken place. Neural pathways of sound production in mammals are quite complex but in the case of the control of the larynx in primates, some of the immediate output pathways have been rather extensively explored (review: Muller-Preus and Ploog, 1983). The motoneurons controlling the larynx are in the brainstem nucleus ambiguus. An important source of input to the nucleus ambiguus is the dorsal part of the midbrain periaqueductal gray, where neurons can be found with reponses that are time-locked to onset of EMG activity in laryngeal muscles active just prior to, and during vocalization (Larson and Kistler, 1984). Stimulating there in rats, bats, cats, monkeys, and the gibbon evokes natural-sounding vocalizations that are spectrographically indistinguishable (in the case of the monkey) from naturally elicited calls. Lesioning there in the same animals produces mutism. A pre-callosal, medial limbic cortical area involved with vocalization (stimulating it produces vocalization, lesioning it produces mutism) projects to the periaqueductal gray both directly and via 4 other subcortical and thalamic structures. None of these 5 projections, however, directly contact nucleus ambiguus motoneurons. In monkeys, then, it appears that cortical influences in laryngeal gestures must all be "filtered through" the periaqueductal gray (which incedentally, is probably better known for its involvement with pain-- neurons there have opiate receptors and lesions or stimulation induce analgesia). In humans, by contrast, lesioning or stimulating the central gray (which had formerly been done to alleviate pain) produces no obvious deficits or effects on speech. The probable reason is that there are more direct cortical projection to motoneurons in humans. Stimulating the cortical larynx area, for example, causes vocalization in humans but not monkeys (summarized in Jurgens, 1982). The appearance of a small direct projection from the precentral larynx area to the nucleus ambiguus in chimpanzees (Kuypers, 1958), and the devastating effect on the motor control of motor and premotor cortex lesions in the larynx and face region in man (similar lesions have no effect on monkey vocalizations) suggest that a substantial direct motor cortex to nucleus ambiguus connection, analogous to the direct motor cortex projection to spinal motoneurons exists in man.[30]

We have only been considering the final output links involved in producing the symbol segment streams in man. Yet the considerable differences between the human and prelinguistic primate vocal tract and between the neural control pathways in the two instances could partly explain why the primate most closely related to man have such difficulty producing speech and make it unlikely that speech sound were readily available prelinguistically; this closely parallels the difficulty experienced in trying to prebiotically synthesize DNA segments. As in the biochemical case, it helps to compare the availability of these units to the pre-systemic availability of another type of unit that was incorporated into the final system-- the "thing"-representation.

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[30] Interestingly enough, a similar process, in which the forebrain gains more direct access to motoneurons, seems to have occurred in the evolution of the neural pathways involved in sound production in birds. Vocal learning has evolved independently in at least three bird groups (review: Nottebohm, 1972). In most of the remaining 24 orders of birds, vocal ontogeny pretty much excludes environmental influences, and a deafened bird will often develop a normal repertoire (as will, incidentally, a deafened monkey). The repertoire is thus largely controlled genetically and hybrids have even been observed that develop songs "in between" those of their two parents. In the two orders where vocal learning is prominent-- songbirds and parrots --it was found that the forebrain output pathway most important for sound production (the pathway from a nucleus in the basal dorsal ventricular ridge to the reticular formation) had come to directly contact motoneurons controlling the sound-producing syrinx (not homologous with the larynx) which are located in the hypoglossal nucleus (Nottebohm et al., 1976; Paton et al., 1981). This contrasts with the situation in pigeons (Zeier and Karten, 1971) and ducks (Arends and Dubbeldam, 1982) where the same pathway terminates only in the surrounding reticular formation, which then projects to the motoneurons.

"Thing"-Representations

For now, we shall define the "thing"-representation at the linguistic level as an internal category representation that exists in the form of a tendency of a cortical neural network to end up in a certain stable firing-pattern state; the tendency becomes apparent when the network is brought anywhere "near" to that firing pattern by the stimulation of a particular external thing, action, or other phenomena. Concrete proposals for the location and properties of these so-called "thing"-representations are made in Chapter V; for now, these units can be identified with what many cognitive psychologists would call "concepts" (see e.g., the definition in Anderson, 1981)-- i.e., unanalyzed building blocks, primitives, or nodes for an internal cognitive structure, usually associated with words. The argument is that these units appear to be much more easily obtained in a prelinguistic milieu than symbol segments, just as was the case at the molecular level.

The ape language experiments have generated much controversy over the question of what sort of internal representations were involved in the behaviors-- language-like and otherwise --that have been observed (see, for example, two recent collections edited by Griffin (1982) and de Luce and Walker (1983) and the review by Premack (1983)). Nevertheless, a certain consensus seems to have been reached on at least one point-- namely, that chimpanzees (and probably the two other great apes, gorillas and orangutans, as well), seem capable of acquiring a number of unitary concepts referring to classes of real world objects and actions, as well as the ability to internally "activate" one of these concepts (bring one of them to mind even when a real world example of the concept is not present) upon viewing a non-iconic symbol for it that had been previously learned. The carefully controlled experiments of Savage-Rumbaugh et al. (1983) are particularly convincing in this respect (see Chapter V). The number of concepts that have been carefully investigated this way is not large (under 100) but includes not only concrete categories like "banana", "sweet potato", "wrench", and "stick", but a few, more abstract concepts like "same", "on (top of)", and "toy" (Premack, 1983) or "food" and "tool" (Rumbaugh et al., 1983). It is clearly more difficult to assess the structure of the more abstract categories (e.g., to determine what the sign for "tool" really indicated about internal representations when many of the other learned signs refer to only food and tools). However, I agree with Ristau and Robins (1982) who conclude in a critical review that the labeling phenomena exhibited in these experiments point to the acquisition of unit concepts that are rather like human concepts in the concrete examples (e.g., banana) though probably not as rich in the abstract cases as human concepts (cf., very useful concepts such as "line" or "make").

An important point about the experiments described above in the present context is that they almost always require more than just the development and maintenance of an internal category representation or concept. First, the animal must be able to recognize an external symbol. Savage-Rumbaugh et al.'s (1983) results indicate that this is not always easy by any means, and visually similar symbols were confused and sometimes inspected repeatedly to be sure of their identity. Then the internal representation of the symbol (which has to be more general that the different possible symbol tokens-- i.e., different tokens are viewed from different angles, and so on) can call up the internal representation of the appropriate concept. In addition, the chimpanzees were taught to generate a specific button press upon various forms of direct activation of a concept (e.g., a photograph of an example of that concept). Again, this is a different, non-trivial skill from simple concept learning and had to be taught separately, even after receptive processing of symbols in the paradigm was possible; it seems quite possible that a manipulation of a third internal representation is involved here-- approximately, a category of motor patterns or goals that result in the pressing of a button with a certain symbol. In the previous discussion of prebiotic chemistry, amino acids (compared here to internal concepts) turned out to be much easier to generate than nucleotides (analogous to speech sound segments). At first, the difficulty of teaching chimpanzees to use symbols for straightforward categories like "banana" in a truly referential way might seem to argue against a similar conclusion at the linguistic/prelinguistic level. However, much of the difficulty could be due simply to the complexity of the task (requiring coordination of perhaps as many as three different classes of internal representations), rather than to the difficulty of generating internal "thing"-representations (concepts) _per se_. It seems quite plausible that concept-like representations (e.g., of classes of edible berries, predator types, etc.) are routinely generated in primate and probably other animal brains, perhaps as facilely as are amino acids from prebiotic atmospheres. The challenge is to devise tests to examine such "natural categories" without having to introduce all the complexities associated with learning symbols to stand for them. Results in artificial category experiments with pigeons conducted for a number of years suggest that such an ability to construct categories (at least relatively unabstract ones based on local features) may be quite widely distributed (Cerella, 1982). By contrast, the ability to use a large set of non-iconic symbols productively and receptively, and with displacement, even one at a time, is probably not widely teachable, and it certainly is virtually non-existent in natural animal populations of any kind. But then, prebiotic synthesis experiments have never uncovered any sign of naturally occurring instances of nucleotides or other symbols "standing for" or "calling up" amino acids, when prebiotic starting materials were used. There have been a class of prebiotic synthesis experiments more akin to the ape language experiments, where biotic monomers and polymers of various types (including those that are nearly impossible to synthesize prebiotically) are mixed and reacted; this is a little like artificially "teaching" the prebiotic soup something about symbols. These experiments will be discussed in Chapter V where there is also a more detailed discussion of some of the difficult questions about word meaning that were so rapidly passed over here.

Propagation and Evolution of the System

In this section two major differences between the biological and linguistic symbolic-representational systems that mostly involve the symbol chain are discussed. The first is the lack of anything at the linguistic level to compare with the stylized and comprehensive replication of the entire symbol chain. There is, in fact, nothing quite like a unitary linguistic "genome" in each person (cf. cell) that is unchanging throughout life. Conversely, there is nothing like language development in cells. Second, there is only one major mechanism of evolution in currently existing cellular life, but four quite distinct modes possible at the linguistic level (one of these is the same as the cellular mechanism). Both differences are traceable to the presence of language (in the broad sense) production only at the linguistic level.

Replication and Evolution at the Molecular Level

DNA Replication

DNA replication is a fundamental fact about cells (review: Kornberg, 1980). Isolated bacterial cells make an exact copy of their entire double-stranded DNA genome consisting of about 3 million base pairs every time they divide, which can be every 20 minutes if nutrients are available. Since there are uniformly 3 nucleotides to a "word", the bacterial genome consists of 1 million "words", which are arranged into groups of several hundred, each group coding for one protein (i.e., a total of about 5000 proteins). In more complex eukaryotic cells, there can be much more DNA-- orders of magnitude more --but it is thought that it might not code for that many more proteins. In multicellular organisims, cell differentiation occurs, resulting in up to 200 different cell types; in the process, a given cell often divides only a certain number of times and then persists in a differentiated state without dividing for the remainder of the life of the organism. In man, most neurons, for example stop dividing soon after birth though they continue to change shape, for example; skin cells, by contrast, are continually generated throughout life. The important feature of the cellular symbolic-representational system is that in most cases, all the symbol seguences the cell will ever "listen to" are stored within it in a permanent form that persists throughout the cell's life (red blood cells, which lose their nuclei and DNA as they mature in some species would be an exception). Furthermore, all the cells interacting in the "society" of a multicellular organism contain rigidly identical copies of this long, comprehensive message. In general, the symbol chain is transferred verbatim along with any mutations it might have picked up to the two daughter-cell offspring when the cell divides. A major exception to simple linear transmission occurs in sexual reproduction where a single cell (a "zygote" in eukaryotic organisms) ends up with a combination symbol chain, part of which came from a non-parent cell and the remainder from the parent cell. There are many complex embellishments on these themes discovered in the past century (see e.g., Alberts et al. (1983) for an overview), but the salient feature of interest here is the extreme conservatism of the transmission process, the prominent restrictions on the mixing of symbol chains from different cells, and the great formality of the sexual mechanisms (at the molecular level) involved with such mixing when it occurs. Because of these factors, it is often possible to define higher levels groupings of organisms (e.g., species).

During cell division, a cell gives to its offspring not only a self-contained "library" of all the proteins the offspring will need to make, but also, all the apparatus-- e.g., ribosomes, tRNA, thousands of enzymes --that it will need to decode the symbol chains in the library. Thus, "newborn" cells can immediately "comprehend" the genetic code; there is no "language learning" stage. It turns out that in complex eukaryotic cells like a fertilized egg, the cell does not immediately begin "perceiving" its own DNA (it waits until gastrulation); but when it does begin to do so, the architecture of the process is almost indistinguishable from DNA "perception" (i.e., transcription and translation) in other older cells. There are many elaborate and as yet poorly understood mechanisms that control the order and timing of the "perception" of the different parts of the chain, but there is no stage in which the cell does not know the DNA language-- i.e., lacks the apparatus that relates particular groups of symbol segments to particular amino acid "meanings".

Mechanism of Evolution

The main "mechanism of evolution" at the biological level, from the bottom-up point of view of the symbolic-representational system, is a change in or a addition to the sequence of symbol segments. This is the main way in present day cells that variation in fitness can be transmitted to offspring. Fitness could be defined as the contribution an individual makes to the next generations gene pool (e.g., Roughgarden, 1979), which depends both on reproductive ability as well as viability. Needless to say, in the case of multicellular organisims, the causal chain between sequence changes and eventual population level outcomes resulting from interaction among billions of cells in an environment will often be rather opaque; nevertheless, with static sequences, evolution would not be possible and only environmentally induced oscillation about an unchanging mean (or simple elimination of a lineage) would occur in the absence of changes in other parts of the symbolic-representational system. When we examine those "other parts" at the biological level, it seems that a variety of theoretically possible changes that would alter fitness (i.e., in addition to changes in the symbol segment sequence) have not occurred, or only rarely occurred. For example, a perfectly plausible "strategy" would be to change or add to the list of the 4 currently employed symbol segments or the 20 currently employed amino acid "word meanings"; such an innovation, hwever, has never been detected in any organism. Another strategy would be to change the mapping from particular symbol segment sequences to particular amino acids. This has actually occurred on a small scale in mitochondria (which have a decoding system that is largely separate from the main system in the cytoplasm); the mammalian mitochondrial genetic code, for example, differs in the mapping of 3 (out of 64) codons (review: Kroon and Saccone, 1983). The general reason given that changes like these are rare is that they are too disruptive. Thus, it is perhaps surprising that these very changes have occurred on a massive scale at the linguistic level. We shall see that having a system for production of symbol streams (in the context of a system with more word meanings) not only makes such changes possible, but actually promotes them through its interaction with language development and continual language learning.

The Propagation of Language and Language Change

Language Learning

In broad outline, humans resemble cells in transmitting to their (linguistic) offspring both a mass of information as well as the means of decoding it; however, there are striking differences in the particulars. First, there is nothing in language propagation to compare with the one-shot process of DNA replication. Rather, parents transmit linguistic information to their offspring over a long period of time. But there is also a fundamental difference in the nature of the transmission process. In cells, a simple copy of the information is transmitted; in humans, by contrast, virtually all transmitted sequences are generated anew from meaning-like sequences and there is little sign of a significant store of uninterpreted sequences.[31] Of course, it is possible for a human parent to emulate the cellular parent by simply parrotting a sequence to his or her linguistic offspring that had been formerly been transmitted to the parent, and certainly such a process has a role to play in child rearing. Nevertheless, it is possible to transmit brand new highly non-random, road-tested sequences as well; there is none of the rigid uniformity of symbol chain sequences from person to person in human societies that was seen in cell "societies". Compared to the cellular system, the human linguistic system is much more flexible; if a difficulty comes up, an appropriate sequence can often be generated on the spot. The cellular transmission system, by contrast, has to pack everything necessary for life (literally) into a single bundle; if something gets left out or gets copied incorrectly (as often enough happens) there are no second chances. This unilateral presence of language production thus results in major differences in the "style" of the two systems; the linguistic system is free-wheeling, interactive, and inventive, while the cellular system is by comparison rigid, pre-programmed, and conservative.

A second difference has to do with the way in which the decoding apparatus is transmitted. Human babies, like cells, acquire the coding system from their parents; but unlike them, babies must laboriously learn their parents' coding system almost from scratch over a number of years. Human language learning, however, is not quite as "from scratch" as would be a hypothetical newborn cell lacking a genetic decoding apparatus. This is because the symbolic-representational systems at the

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[31] Perhaps the closest linguistic analogue of a genome would be the possible storage of the long sequences of speech sound segments impled by the truly prodigious human capacity for the oral transmission of myths and poetry. However, it is unlikely that any bard stored such sequences in a strictly uninterpreted form as do cells.

molecular and linguistic levels are somewhat entangled at the locus of language learning. Of course, the entirety of the human brain consists of cells and in a sense is completely "explained" by the lower system; but this is little different than the relation between cells and the lower level atoms and molecules of which they consist, and which "explain" cells from the bottom up as well. In both cases, the higher level system has found a way, as it were, to "trick" its lower level constituents into doing its bidding without breaking any of the deterministic rules; this is just what was in Chapter I identified (from a more bottom-up perspective) as the <u>sine qua non</u> of a symbolic-representational system. In both cases, the higher level information is mostly "hidden" from the lower level "soup". This implies that the two systems should be largely insulated from each other since the molecular level system is just part of the background "soup" that the linguistic system grew out of. There is one major point of entanglement, already pointed out in Chapter I; it is the <u>genetic</u> predisposition to develop a language. That is, although a parents's speech to his or her offspring is key to the development of a language (just as is the parent cell's transfer of the genetic decoding apparatus to its offspring), there is an additional source of information that comes up from the molecular level system in the form of a capacity of the human brain (as opposed to the chimpanzee brain) to learn a language. Nothing like this happens in cells; there is no evidence for an underlying submolecular symbolic-representational system that has evolved so as to predispose molecules to arrange themselves into a decoding apparatus, and so on-- at least in the scientific literature. The biochemical-linguistic entanglement, however, seems to be limited to the capacity for language development or to a general modulation of language-like abilities (e.g., mathematical aptitude), but appears to be almost completely insulated from the content of linguistic labors (mathematical theorems, novels, the articles in last week's issue of Science). In Chapter IV, we shall consider just what the genetic endowement might involve.

The third difference in the mechanisms of language transmission between the molecular and linguistic systems was implied in the discussion of language production above; explicitly, it is the human ability to comprehend the symbol streams of not only one's parents, but the symbol streams of any other person who happens to speak the language. From the point of view of the molecular system, this looks like a wild free-for-all; and the highly "promiscuous" mixing of the symbol strings from different persons at the linguistic level makes it quite difficult to define anything like a "species" there. The mixing is so effortless, there is hardly any need for the formalities of sexual reproduction, which surround the much more restricted mixing allowed at the molecular level. There are of course many new, highly complex "formalities" that have arisen in the development of human cultures and which have restricted mixing to a greater or lesser extent (e.g., social class); but it is fair to say that such mixing is the norm in a local group and a human raised without it in the "cellular" fashion (perhaps using only one long tape recording), would be a most unfortunate and pathetic soul.

Mechanisms of Evolution

The "mechanisms of evolution" are diverse at the linguistic level; at least four rather distinct processes can be distinguished. The first, involving changes in symbol segment sequences is most like the genetic mechanism of organic evolution. The difference here is in the nature of the changes, which have a random character at the molecular level but which can be highly directed or appropriate at the linguistic level, since new symbol chains are capable of being effortlessly produced from internally generated, already functional meaning "chains". Molecular level changes result from undirected modification of the sysmbol chain since to reference to the 3-dimensional protein "meaning" is possible.

A second mechanism of change that is very different from anything seen in currently existing cells involves the incorporation of new types of symbol segments. This has happened repeatedly in a rather short time (thousands of years), with the result that the groups of 20 to 40 segments that characterize each of the worlds approximately 5000 languages are all slightly different from each other in a variety of ways. Different languages have different numbers of total segments, different numbers of consonants or vowels or other subclasses; some languages have relatively "exotic" sounds like "clicks" (Khoi-San languages), front rounded nasal vowels (the vowel in French "un"), the vowel in English "bird", labiovelar stops, and so on; even rather similar sounds exhibit small regularly occurring differences from one language to another (e.g., F1 and F2 for the vowels [i], [e], and [a] in Danish and English-- Ladefoged, 1980, p. 449). Things are not completely chaotic; for example, almost all languages have the vowels [a] "hot", [i] "heat", and [u] "hoot" and certain unvoiced stop consonants are also popular.

A third type of change seen in language occurs but only very rarely in cells; this is a reworking of the mapping between particular segment groups and particular meanings--i.e., the coding scheme. A brief comparative glance at dictionaries for even closely related languages like French, Spanish, and Italian will serve to emphasize the thoroughness of such rearrangements. A good deal of the variation, especially in comparing closely related languages, can be understood as resulting from a semi-stochastic exploration of possible coding schemes driven by often rather well understood, nearest neighbor interactions that occur during perception and production. An example of such an interaction is the commonly documented "sound change" called <u>metathesis</u>-- a simple reordering of adjacent segments (e.g., [askt] => [akst] for "asked"). It might be thought of as reflecting a slight probability that the neural patterns involved in generating sequences of coordinated muscle contractions for each segment get reordered into an "easier" sequence before output. Over time, the new sequence eventually gets "fixed" in both the production and perception apparatus. Other common changes are <u>assimilation</u> and <u>dissimilation</u>, where adjacent segments become more similar or more different, and <u>segment loss or addition</u> associated with change in stress patterns. Sound patterns can get altered rapidly even by these simple mechanisms; for example, an unstressed vowel might be lost, resulting in two consonants being juxtaposed; if they differ in voicing, one might undergo voicing assimilation; subsequently, they could metathesize, or a get a different vowel reinserted between them. Since these changes often occur simultaneously in many different words, each with different phonetic environments, a nice logical system tends to get messed up pretty quickly. Furthermore, it is not uncommon for a "messed-up" system to be <u>reanalyzed</u> into a more regular one. Non-local sound changes (like umlaut) are possible as well. The end result is that the meaning carrying segment groups are in a constant ferment, in sharp contrast to the almost universal genetic code.

A fourth type of change in language that has not been seen in any currently existing organism is the annexation of new concepts or word meanings ("thing"-representations) into the system. Again, this is a ubiquitous process in any language, perhaps most strikingly demonstrated by the de novo generation of huge number of new words in the context of scientific and technological advance. It is a non-trivial task for college undergraduates to acquire several thousand of these new meanings in order to begin to make sense of the literature in a given field. More or less arcane examples, depending on one's field of specialization can be gleaned from traditional etymological studies; the fossilized metaphors that gave rise to many common words (e.g., "wind's eye" => "window") point to a constant ferment in these units as well, again in sharp contrast to the 20 amino acid "meanings" at the molecular level that have most likely persisted unchanged for over 3 billion years.

CHAPTER IV

SYMBOL-REPRESENTATIONS AND SYMBOL-REPRESENTATION SEGMENTS

The comparisons in the previous chapter between the "external" molecular and linguistic symbol chains (see fig. 12) involved phenomena that were reasonably well exposed in both systems. As we turn to symbol-representations and "thing"-representations in this and the next chapter, the objects of comparison become progressively more hidden in the linguistic case but remain equally exposed in the molecular case. Thus, we can begin to make some predictive use of the analogy. I am not implying that there is nothing 'really' known about word recognition or syntax or semantics; but the analogy as presently construed most directly addresses internal neural phenomena about which there is less and less information as one moves "inward"; and for now at least, there is hardly a glimmer of what even the overall outlines of a neural-like model of comprehension might look like. The promise of the present investigation is the possibility of coming up with some concrete proposals for the overall architecture of the comprehension system.

It is important to keep in mind the differing scales of the two systems. As we saw in the last chapter, there is a considerable quantitative difference in the number of symbol segments (4 *versus* 30-40) as well as the number of word meanings (20 *versus* 5000 or more). However, I do not think the molecular system is too simple by any means. Even a bacterial cell is enormously complex, containing thousands of different enzymes and molecular species that interact in a coordinated way; and it is the very same 20 word system that supports the development of the 50 or 100 billion neurons in a primate brain, which differentiate into hundreds of different cellular subtypes, each with distinct morphology and connections. In fact, a major benefit of the analogy is to move our model into the right ballpark of complexity. Everyone knows that the brain must be doing something pretty complicated during language comprehension; but the tendency, given the present lack of technique in neurobiology, is to fall back on an implicit, comfortably amorphous image of what is going on. The obstinately detailed picture presented by the 4-segment/20-word molecular level system without production is a good corrective for this-- not only to stress how complicated the interactions between even 20 words can be, but to point up at the same time how far one can get with such simple starting materials. The main task in the next two chapters is to make some suggestions as to where those "simple" starting materials come from in language.

The Transition from 1-D to 3-D

RNA as Message and Structure

RNA strands, like DNA strands, are composed of nucleotide segments. In the treatment of DNA in Chapter III, several important differences between the two were already discussed. We now turn explicitly to the phenomenology of RNA.

Introduction

Perhaps the most striking aspect of the molecular organization in cells is the fundamental involvement of RNA at the interface between one-dimensional message and three-dimensional functional architecture. On one hand, RNA serves-- like DNA --as a one-dimensional strand carrying coded sequence information that is accessed linearly by the other parts of the symbolic-representational system. On the other hand, RNA is capable-- like proteins -- of folding up into determinate three-dimensional structures that serve structural and catalytic functions. By contrast, there are no known determinate three-dimensionally folded particles based on DNA (see Chapter III), and there is no known instance where one-dimensional sequence information is extracted from proteins (see Chapter V). The intermingling of roles in RNA is very ancient and seems to have changed little since the origin of life (Woese, 1983), especially in comparison to protein function. Barbieri (1981) has even suggested in a theoretical paper that we distinguish a "ribotype" as a necessary mediator between the one-dimensional genotype and the three-dimensional phenotype (his experimental work has been on ribosome structure). I think that this is a good way to make the point. Three functions of RNA-- mRNA, tRNA, and rRNA -- thickly involved in the "transition to 3-D" are central to the definition of a symbolic-representational system-- these are the one-dimensional use of RNA strands as <u>internal messages</u> (active messages), the 1-D to 3-D bridging function as <u>word recognizers</u> (i.e., symbol-representations), and the explicitly 3-D use as <u>chain assemblers</u> (to connect together "thing"-representations).

This division of RNA functions into internal message (messenger RNA--mRNA), word recognition (transfer RNA--tRNA), and chain assembly (ribosomal RNA-- rRNA) is reflected in a similar three way subdivision of the mechanisms by which the cell accesses its DNA sequences for these three types of RNA's. Thus, there are three different RNA polymerases in eukaryotes (I, II, and III) to make rRNA, mRNA, and tRNA respectively (summary in Alberts et al., 1983). The subsequent processing of the transcribed RNA's is also distinct for each class-- rRNA can be spliced by enzyme-like folded RNA's ("ribozymes"-- see below) coded for in the spliced-out portion, mRNA splicing probably involves small RNA's sticking to consensus sequences at the splice junction, and tRNA splicing depends on the 70 to 90 base sequence folding into its mature shape while still a part of a larger precursor, which is then spliced by a "ribozyme" coded for elsewhere (review; Cech, 1983). These basic subdivisions seem to be very old and preliminary data suggest that archaeobacterial introns might be similar.[1] Each of these functions will be treated separately. Before doing that, however, a short discussion of the recently changed ideas about RNA structure and function is given.

Recent Perspectives on RNA Structures

The roles of RNA as message and structure in the process of "perceiving" the molecular level language was known in outline by 1960, eight years after the discovery of the DNA structure (see Judson, 1979, pp. 348-446, for an account); nevertheless, RNA has suffered for a long time from a subtle prejudice of sorts-- it was always a mere subordinate (or just a messenger!) of the important, centrally-located DNA sequences that commanded it. Early workers consistently underestimated the complexity of the RNA apparatus. Crick's postulated adaptors, for instance, were only a few nucleotides long, and really only a short step away from the direct template hypothesis of Gamow (1954); they turned out to be 70 to 90 nucleotides long. Similarly, the ribosome was initially conceived of by Watson and Crick as an empty pot, something akin to a phage head, with protein synthesis going on inside (Judson, 1979, p. 424). The historical prejudice, moreover, continued into the next decades as

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[1] The streamlined, probably secondarily simplified system in eubacteria like E. coli, by contrast, has no introns and only one RNA polymerase.

researchers began to investigate the mode of operation of ribosomes; work concentrated mainly on the protein complement (over 50 proteins in bacterial ribosomes). The RNA was visualized as an inert, rather amorphous scaffold on which were mounted the proteins that did all the real work (cf. discussion in Woese, 1980). Over the years it turned out to be quite difficult to associate any of the ribosome's activities with the many proteins mounted on it; by contrast, small mutations in the RNA often produced all-or-none effects. Another idea was that the proteins biased the RNA to assume certain conformations, the implication being that by itself, the RNA would be considerably underdetermined. Although this picture is certainly partly true-- there is data, for instance, that some proteins cause functionally important local unwinding --recent results suggest that bare ribosomal RNA under physiological conditions closely approximates its overall native protein-covered structure (Cantor, 1980; Thompson and Hearst, 1983).

It was not really until the recent demonstration of binding site specificity and reaction rate acceleration in a folded RNA "ribozyme" (Bass and Cech, 1984; review: Altman, 1984) that the protein-like three-dimensional properties of RNA were taken seriously. At the same time, functions have begun to be assigned to the 15 or 20 well characterized small nuclear and small cytoplasmic RNA's (review: Reddy and Busch, 1983). It is interesting that the best attested function for these RNA's are closely tied up with internal message RNA, word recognition RNA, and chain assembly RNA.[2] Finally, the complex

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[2] Two examples are 7S RNA and a pair of 4.5S RNA's. 7S RNA folds into a particle and associates with 6 proteins (Walter and Blobel, 1983). The complete 11S particle recognizes certain hydrophobic sequences on newly forming polypeptide chains that signal that the protein being synthesized should be inserted through a membrane. The 11S particle (the "third subunit" of the ribosome) then binds to the active ribosome, preventing further chain elongation until the ribosome is attached to a

self-assembling, membrane-independent, RNA-containing apparatus called the nucleolus should be mentioned here. It was recognized by the earliest cytologists, but takes on a different significance (cf. Barbieri, 1981) in light of the recent results. The nucleolus makes ribosomes, and is apparently held together by the specific binding of unfinished ribosome precursors to each other in a poorly understood fashion[3] (summary: Alberts et al., 1983, pp. 424-428). All this is not to downplay the role of the proteins (even ribosomal proteins), which of course, perform a much wider range of functions than three-dimensional RNA's; rather it is to emphasize that 1) RNA's are capable of forming determinate, protein-like 3-D structures, and 2) such structures are involved at key points in the 1D => 3D transition that defines a symbolic-representational system.

"Message" and "Structure" in the Auditory System

The foundational, archaic nature of the three-part role of the symbol-representation stuff (RNA) at the molecular level-- i.e., as <u>internal message</u>, <u>word recognizer</u>, and <u>chain assembler</u> --suggests that we look for something similar at the linguistic level. The first task

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membrane (displacing the particle) where elongation continues, extruding the newly formed protein through the membrane (Gilmore and Blobel, 1983) (it would be much more difficult to stuff a complete, folded protein through the hydrophobic layer of a membrane although it can be done). This would be an interesting turn-about-- with 3-D RNA recognizing amino acid sequences --if the RNA component turns out to be directly involved. The second example is a recently isolated 19S particle named the "prosome" composed of two 4.5S RNA's and 10 proteins that is apparently involved in completely inhibiting mRNA translation (Schmid et al., 1984).

[3] The lack of the requirement for a membrane around the nucleolus as well as its key function in synthesizing one of the major components of the symbolic-representational apparatus (the chain assembler) is thought-provoking in a prebiotic context. Barbieri (1981) suggests in light of this that membranes may not be primitive, in contrast to the received opinion (e.g., Eigen and Schuster, 1979) that the acquisition of a membrane was necessary to individuate early protocells.

is to find the symbol-representation stuff-- the RNA analogue.

Symbol-Representation Segments in the Auditory System

These were identified in Chapter III as patterns of activity in the auditory system evoked by streams of speech-like segments. However, the mammalian (neural) auditory system is a rather large place. It starts out with the line of hair cells in the cochlea. The mechanical and electrical properties of the cochlea result in an approximate spectral analysis being performed-- i.e., different hair cells respond to different frequencies. This information is then splayed out within tens of milliseconds across 25 or more distinct "representations" of the hair cell line (of varying topographic fidelity, some almost completely non-topographic) at various levels in the central nervous system.[4]

The brainstem areas are present in all mammals that have been examined in detail, and are relatively unchanged up to the thalamus even in mammals like echolocating bats that have functionally and behaviorally quite specialized auditory systems (Zook and Casseday, 1982). The cortical auditory areas are more specialized-- e.g., in bats (Suga, 1982)-- but also in humans (review: Braak, 1980). Like other primates (Brugge, 1982), humans have a strictly logarithmic frequency map in primary auditory cortex (AI) (Romani et al., 1982; assayed in awake humans with a neuromagnetic technique). However, the cytoarchitectonically distinct areas adjoining AI laterally and

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[4] A working list of auditory system "areas" would include-- 3 cochlear nuclei (DCN, PVCN, AVCN), 2 olivary nuclei (LSO, MSO), 2 peri-olivary nuclei (DPO+DPLO, LNTB+VPLO), 1 nucleus of the trapezoid body (MNTB), 3 nuclei of the lateral lemniscus (VNLL, INLL, DNLL), 4 nuclei in or near the inferior colliculus (ICc, ICe, ICp, NBIC), 5 nuclei in the auditory thalamus (VL, POL, Dc, M, Dd), and at least 6 and perhaps up to 12 contiguous cortical areas (AI and others) (summary in Merzenich and Kaas, 1980; Kaas, 1982; Galaburda and Pandya, 1983). This comes to a conservative total of 26 areas that could reasonably be called sensory.

posteriorly (which are driven by auditory stimuli in monkeys-- Merzenich and Brugge, 1973; Muller-Preuss and Ploog, 1981) are expanded relative to the size of AI in humans (Braak, 1978a; Galaburda and Sanides, 1980; Galaburda and Mesulam, 1983), and show a greater degree of lateralization than is seen in apes (one of these areas, called Tpt, can be up to 7 times as large in the left hemisphere as in the right-- Galaburda and Sanides, 1980). The area becomes markedly activated (bilaterally, but with a left hemisphere dominance) during speech perception and to a lesser extent during silent reading (Lassen et al., 1978, p. 69; Nishizawa et al., 1982). Unilateral left hemisphere lesions in this region causes lasting comprehension deficits for language, music, and nonverbal sounds (reviews: Kertesz, 1983; Damasio and Geschwind, 1984). By contrast, lesions in the primary area disrupt word repetition but leave comprehension intact (review: Damasio and Damasio, 1983). For now, then, we will define *symbol-representation segments* as a coherent, stimulus driven pattern of firing in the secondary cortical areas that would be evoked by the presentation of a speech sound to the auditory periphery. As discussed in Chapter III, the phenomenon of categorical perception (present also in animals) as well as neural network models like those in Hopfield (1984), suggest that the patterns evoked in these areas might be less variable (cf. stiffness in RNA *vs*. DNA) than the sounds that can call them up-- i.e., a given pattern would be evoked by a *group* of similar sounds.

Messages and Structures

As noted at the beginning of this chapter, there are many differences in detail between the chemical and linguistic systems. However, the ancient involvement of the symbol-representation stuff as a bridge between the one-dimensional symbol chain and the three-dimensional "thing"-representation chain is clearly a high level "relation" rather than a unit "property" and thus, by the heuristics set out for analogical comparison in Chapter I, ought to generate the most robust predictions. The conception of auditory linguistic processing that the analogy suggests is quite novel, and to my knowledge never before contemplated.

The three main roles of RNA are internal message string, word recognizer, and chain assembler. Each of these functions is in fact required in some form by almost any theory of language perception-- they are 1) the internalization of the speech stream as a sequence of segments, 2) the recognition of small groups of segments in this internal stream as standing for meanings, and 3) the construction of some sort of representation out of the sequence of meanings that are called up. What the present analogy suggests is that all three functions are performed in the main by chains made out of one kind of unit-- the symbol-representation segment --in the same volume of secondary auditory cortex. For the latter two functions, the chains would be stable and "folded"-- i.e., they would involve interactions between what were initially temporally non-adjacent units. The idea, restated, is that several key functions underlying language comprehension (word recognition, chain assembly) are mediated by complex, stored neural activity patterns across secondary auditory cortical areas that are initially built up by the simple concatenation of unit patterns, each of which is nothing more than the pattern that would arise in those areas in response to a particular speech-like sound. Even at the molecular level, structural symbol-representation segment chains are not the whole story behind the "comprehension" of DNA (e.g., structural RNA in modern organisms is often associated with proteins as described above); and it seems likely that the linguistic system could turn out to be even more complex. Nevertheless, I would like to briefly follow up the unusual picture of language comprehension suggested by the analogy for each of the three functions listed above, in light of currently available information. The proposal is actually quite concrete and is subject to indirect investigation even with present-day techniques.

Internalization of the Symbol Chain

The first major step in "comprehending" a symbol chain is to make an internal, one-dimensional copy of it, segment by segment (see fig. 12), out of potentially three-dimensional symbol-representation stuff; the resulting internal message, however, is not supposed to fold (or is unfolded if it did fold) and is processed as a one-dimensional chain, albeit a "stiff" chain. This transformation is labeled "non-arbitrary" in Figure 12 because the symbolic-representational system has no say in the informational aspects of the copying process; a given symbol segment can only be connected to one particular symbol-representation segment most of the time (e.g., C (DNA) is usually paired with G (RNA), and so on). By contrast, multiple connections are possible in principle with arbitrary(1), arbitrary(2), and arbitrary(3) bonds; it is the rest of the symbolic-representational system that is responsible for deciding which connections are actually made.

Messenger RNA (mRNA)

In all cells, the one-dimensional messages in DNA are first copied into single-stranded "messenger" RNA's (mRNA's) before they are decoded (summary in Lewin, 1983; Alberts et al., 1983). Such a messenger was initially postulated to carry the information out of the DNA-containing nucleus in eukaryotic cells (e.g., animal cells) to the cytoplasm where protein synthesis occurs. However, mRNA was soon found in prokaryotic cells (e.g., bacteria) as well, where there is no nucleus, and the DNA floats around among the contents of the entire cell. There are several differences in detail between the two cell types. First, the eukaryotic message copy starts of as a giant precursor molecule which is spliced and modified before it gets out of the nucleus, while the bacterial message copy is used pretty much as is. Second, the eukaryotic messages are quite stable in undecoded form and may be sequestered in different places in the cell as a result of the common tendency to stick to the cytoskeleton. In special cases (e.g., eggs) mRNA may be kept around for weeks before being decoded, though more usual half-lives are measured in hours. Bacterial messages, by contrast, are degraded within a few minutes and are as a rule, immediately decoded, even as they are being made on the ribosome.

It is clearly a bit misleading to call DNA "external" and mRNA "internal" in modern cells. Both are within the same compartment in bacteria and though DNA is segregated from mature RNA in eukaryotes, it is a little peculiar to think of the cell nucleus as "external" to the cell. Nevertheless, in light of the difficulty of synthesizing DNA bases and strands prebiotically (much more difficult than even their RNA counterparts), the strategic abilities of RNA to act as message and 3-D structure, and the present derivation of DNA nucleotides from completed RNA nucleotides (Follmann, 1982), it seems quite possible that DNA was secondarily annexed for use as a symbol chain by a nascent symbolic-representational system. From the perspective of the newly evolving system, then, DNA might have been primitively external (cf. Eigen and Schuster, 1979), just as the speech stream is still today.

The Uninterpreted Message Chain in Auditory Cortex

Symbol-Representation Segments

In turning to language, there is a rather extensive literature on the representation of speech-like sounds in the mammalian auditory system (e.g., Sachs and Young, 1979; Young and Sachs, 1979; Sinex and Geisler, 1983; Delgutte and Kiang, 1984a-d; Delgutte, 1984). However, a great majority of the work has concentrated on the auditory nerve, and less is known about more central structures in this regard; the only existing single unit study of the representation of human speech sounds in the forebrain used mynah birds (Langner, et al., 1981). Probably the closest thing to a study of speech sounds in the mammalian forebrain is the detailed investigation into processing of bat sonar signals in bat primary and secondary cortex (Suga, 1982); the signals are often frequency modulated, with running spectra that closely resemble syllable final formant transitions-- i.e., like ultrasonic VC syllables. In this section, I would like to briefly examine the existing data about vowels, consonants and syllables in the auditory nerve, and vowels in the forebrain to get an idea of what the linguistic level symbol-representation segment might look like.

Detailed auditory nerve data was collected first for steady state vowels. An influential study was that of Sachs and Young (1979) who showed that the discharge rates of a population of frequency-specific nerve fibers can only represent spectral peaks (formants) at very low sound pressure levels; at normal speaking volume, or in the presence of background noise (Sachs et al., 1983), all the recorded fibers saturate and the formant peaks disappear.[5] A way out was suggested by Young and

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[5] It is rather ironic, in light of the traditional lament of the

Sachs (1979) who showed that if the localized <u>sychronized</u> firing rate (i.e., the magnitude of phase-locked firing at a particular frequency) is computed, formant peaks survive at conversational speech levels (see also Sinex and Geisler, 1983; Delgutte and Kiang, 1984a). Localized sychronized rates also represent voice pitch (F0) better (Sachs, 1984). A problem with all these studies is the choice of only the most sensitive fibers and barbiturate anesthesia which depresses middle-ear muscle and especially cochlear efferent activity; it is quite possible that higher threshold fibers with an awake central auditory system could give a usable rate profile. A study of a secondary cortical area (P) in cats showed that neurons with well-defined best frequencies are commonly "tuned" to different intensity ranges (Philips and Orman, 1984) indicating that even in the anesthetized cat, information from higher threshold fibers must be getting through (some neurons had best intensities of 80 dB SPL or more, which is well into the conversational range).

Experiments with fricatives and CV and VCV syllables (Delgutte and Kiang, 1984c,d) show that simple running rate profiles often contain sufficient information to distinguish place and manner of articulation; in fact, computed sychronized rates were ineffective in distinguishing fricative formants. Auditory nerve firing patterns to syllable prominently show the effects of short-term adaptation-- i.e., effects on nearest neighbor segments. Adaptation effects are often thought of as defects that make the auditory system a poor spectrograph; actually, they turn out to be properties to be exploited. A nice example involves

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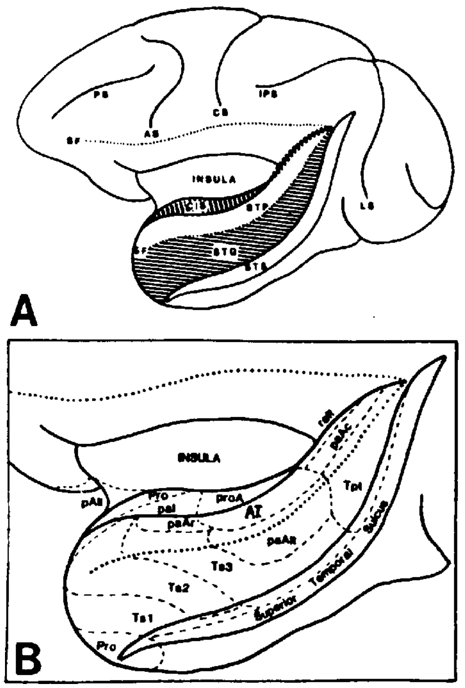
acoustic phonetician that a particular cue is barely visible for a soft or shortened segment (see e.g., Ladefoged, 1982), that auditory physiologists ended up spending so much time looking for firing patterns that were not saturated at normal volumes!

the distinction between the consonants "ch" and "sh", which is thought to be based on "ch" having a faster rise time, and this is reflected in ongoing firing rates. However, acoustic phoneticians found in perceptual experiments that a longer silent gap between the preceding vowel and the frication noise can serve as another apparently independent cue for "ch". The auditory nerve data suggest a simple explanation; what probably happens is simply that the fibers get more of a chance to recover from short term adaptation with a longer silent interval, and thus can give a stronger burst at frication onset. Thus, from the auditory system's point of view, two "unrelated" cues that "trade" with each other end up having indistinguishable effects already by the level of the auditory nerve.

There is much less information on the representation of speech-like sounds in the primate forebrain; however, it is possible to make some suggestions on the basis of experiments done so far on primates and other animals. The best data is from birds and bats. Langner et al. (1981) recorded from neurons in the primary, tonotopically organized forebrain auditory area (Field L in the dorsal ventricular ridge) in "talking" birds during presentation of a range of steady state vowels. Many neurons responded best when a formant coincided with their "best frequency" assayed with pure tones, regardless of where the other formants in the vowel were located. In neurons located in more superficial and deep layers of this structure, many units showed multiple best frequencies and thus were often selective for a particular vowel whose formants coincided with these frequencies (lest the reader be irate, the natural vocal repertoire of many birds includes syllable-like units with multiple spectral peaks-- see e.g., Scheich et al., 1983). Langner et al. (1981) did not systematically map these multiple best frequency neurons. Suga (1982), however, has shown that there are two specialized subregions of bat secondary auditory cortex that actually have topological maps of such neurons (tuned to pairs of formant frequencies in reflected bat screams); thus, different three formant bat "vowels" activate loci at different x- and y-coordinates in maps where x and y are two different formant frequencies (the bats use the information to analyze Doppler shifts in their reflected echolocating signals).

Studies of primary and secondary mammalian forebrain auditory areas in other animals are surprizingly scanty. The most sophisticated experiments have been carried out by researchers inimical to the idea of distinct cortical areas (see e.g., Abeles, 1982) and who have, thus, made no attempt to determine which area they were in. Mapping experiments in cat secondary auditory cortex areas (A, P, VP, DV, V, and AII) have turned up units with multiple best frequencies, especially in the non-tonotopically organized AII, but these could not be studied in detail (Reale and Imig, 1980). Experiments with awake cats confirmed that many AII neurons are sharply tuned, with complex, stable response requirements (Diamond and Weinberger, 1983).

Turning finally to primates, primary auditory cortex and a few surrounding areas have been mapped (Brugge, 1982), but almost nothing is known about the physiology of secondary auditory cortical areas (paAlt, Ts3, paAc, Tpt in Galaburda and Sanides, 1983; see fig. 20) posterior and lateral to primary auditory cortex ("Wernicke's area") that in humans seems to be so important for speech comprehension, and of the equivalent of the cat area AII mentioned above (proA), which is located medial to primary cortex in primates.



Semistylized diagrams to show the gross surface (A) and architectonic (B) topography of the superior temporal region. The sylvian fissure (SF) has been opened to expose the plane of the circular sulcus (CiS) and supratemporal plane (STP). Below the superior temporal gyrus (STG) the banks of the superior temporal sulcus (STS) are also exposed.

FIG. 20: Primate Auditory Cortex

A rare bit of data was presented by Muller-Preus and Ploog (1981), who showed that neurons in areas lateral to primary cortex on the superior temporal gyrus (areas paAlt and Ts3) responded well to just about any of the monkey calls presented; however, they did not test any of the neurons with simple tones. Merzenich and Brugge (1973, pp. 277, 291) recorded a few units somewhat more posteriorly (areas paAlt, Tpt-- right in the middle of the monkey "Wernicke's area") and reported that there might even be tonotopic order in this region. Unfortunately, at the present time, there are very few experiments on the effects of sound (speech-like or otherwise) sequences in structures more centrally located than the auditory nerve (review of existing studies: Moller, 1983).

To conclude, there is presently not enough evidence to produce a detailed model of the neural representation of a speech-like sound in secondary auditory cortex-- i.e., a model of the symbol-representation segment. Nevertheless, several preliminary conclusions can be drawn. First, the representation of a sound is most likely spread across a number of different cortical areas, each with somewhat distinct response properties. Second, in some of these areas, activity due to spectral peaks in the stimulus is likely to be non-topographically arranged; however, it is possible that specializations like those in bat cortex actually result in local spatial maps of different combinations of spectral peaks (i.e., different vowels represented at different loci), or of other parameters of the input. Third, the responses of many neurons in the areas examined is quite prompt (well under 50 milliseconds, even in the "higher" areas like paAlt), and in principle seem capable of supporting a representation of an input chain of sound segments as a chain of discrete activity-pattern "segments", albeit with significant nearest (temporal) neighbor interaction. Fourth, psychological evidence (e.g., Crowder, 1983) suggests that such representations may be be able to be activated without any auditory input.

Persistence Time of Uninterpreted Messages

Compared to the message chains of symbol-representation segments at the molecular level (mRNA's-- equivalent to complete paragraphs), which last from minutes in bacteria or hours or days in eukaryotes, the internal message chains in human brains appear to be much more transitory.[6] There is no relevant neurophysiological information about this. However, a variety of experiments done by cognitive psychologists have addressed related questions; specifically, we want to know how long uninterpreted speech sound representations can be retained. This is not an easy question since the initial linear representation of the speech stream is almost immediately processed to many levels (see e.g., Marslen-Wilson and Tyler, 1980; Bierwisch, 1983). The exact same thing happens, for example, in bacterial cells that immediately synthesize a protein from a message; only it is considerably more difficult to "purify" the resulting mixture at the linguistic level (using only psychological techniques) to get out just the uninterpreted message.

Over the years, a variety of experiments using lists have suggested that only a rather short chain (several segments) can be retained and only for a brief period of time (several seconds) in a "pre-categorical acoustic store" or in "echoic memory". The estimates of persistence time have been revised somewhat upward (tens of seconds) if the input is not overwritten by more auditory input (review: Broadbent, 1981; Gardiner, 1983; Monsell, 1984). Bates et al. (1980), however, showed recognition memory for the surface forms of sentences (i.e., whether a pronoun or the actual referent was used) from a 15 minute natural discourse with a 15 to 30 minute delay. This brings to mind the fanciful ideas put forth by Penfield and others about people having a verbatim memory for everything that ever happened to them. A follow up experiment by Bates

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[6] In case the comparison of absolute time seems unjustified, it should be pointed out that word recognition occurs at almost the same rate in humans and eukaryotic cells; bacteria are about 5 times faster, however.

et al. (1980) using written transcriptions, though not directly relevant to the issue of auditory persistence, suggests nevertheless, that rather high level representations, well beyond and uninterpreted chain must have been involved. Both subjects reading the original text, as well as those reading a reversed form of the text (with pronouns substituted for nouns and vice versa) showed better memory for the surface forms at locations where marked forms (i.e., nouns) occurred in the original text; clearly such context dependent "highlighting" phenomena could not have been present in the uninterpreted sequence.

It seems likely that the earlier estimates-- a few segments lasting a few seconds --are better estimates of the length of the chain that can be stored without interpretation and without long-term consolidation processes (obviously, even a nonsense sequence can be memorized). Indeed, some experiments suggest that the true 'presemantic' storage time might be even shorter-- Huggins (1975) showed that the integration of successive bits of speech too small to be intelligible by themselves (something akin to a moving glance at an object behind a picket fence) was prohibited by silent gaps longer than about 200 msec. Thus, in contrast to the situation in cells where a whole population of paragraph-sized messages (mRNA's) may be stored uninterpreted for hours, the internal message of chains of linguistic symbol-representation segments is much more short-lived, as was the case with the external symbol segment chain itself (Chapter III).

Word Recognition Devices

The second major step in comprehension in the broad sense, is word recognition. This is the process by which small groups of symbol-representation segments are recognized to stand for units of a completely different type-- the "thing"-representations --that are the building blocks for the majority of the "three-dimensional" structures found in the system. As noted at the beginning of this chapter, the message-like symbol-representation segments are heavily involved in this process-- in fact, in cells, the word recognition devices are entirely made out of them. Word recognition is understood in outline at the molecular level; there are many details to be filled in, but most of the major components have been identified and in many cases, their interactions are known in great detail. By contrast, at the linguistic level, the neurobiology of word recognition is rudimentary; the units, and even the general region of the brain where it occurs are in dispute. On the other hand, there is a large and sophisticated literature in psycholinguistics on word recognition or "lexical access". The task of this section is to provide some suggestions on the nature of the underlying units. The main comparison is between transfer RNA (tRNA) and the as yet hypothetical neural correlate of what some psycholinguists refer to as a "logogen" (review: Morton, 1982). there are four main topics-- word templates, the basis of arbitrariness(2), loading the "meaning", and interactions during chain assembly (arbitrariness(2')).

Transfer RNA (tRNA)-- The "Adaptor"

Transfer RNA's are remarkable molecules; though they are only 70 to 90 nucleotide segments long, each one has at least four functionally distinct binding regions (see "symbol-representation" in fig. 12), which is more specific sites than many enzymes with three times as many residues. It is all the more remarkable in this light that they should be made out of the relatively homogeneous nucleotides rather than the diverse amino acids. The four topics listed will direct attention to each region in turn (review: Schimmel, 1980). With tRNA, we have a literal bridge between one-dimensional nucleotide message chains and three-dimensional proteins. At one end, tRNA's recognize one-dimensional nucleotide triplets, while at the other end, a three-dimensional amino acid "meaning" is loaded by means of an arbitrary bond. Though all 3 entities are drawn about equal size in Figure 12, the body of the tRNA actually dwarfs both the recognized triplet as well as the loaded amino acid "thing"-representation. If similar general "size-relations" obtain at the linguistic level, the implication, in view of the rather coarse techniques for measuring activity in human brains, is that "internal message" activity or "word meaning" activity during word recognition has probably escaped detection (by e.g., blood-flow techniques or ERP's) so far, and much of what we presently see is only activity due to word recognition devices. Furthermore, the other symbol-representation segment containing device--the chain assembler (ribosome) --is even bigger than the word recognizers.

Codon-Anticodon Recognition: the Word Template

In tracing a line starting with internal one-dimensional message and ending with one of the word meaning subunits of a three-dimensional chain (see fig. 12), the first "connection" is the complementary base-pairing between three segments in the message (mRNA) called a codon, and three segments (out of 70 to 90) from the symbol repsentation (tRNA) that are called an anticodon (see fig. 19) (there are 61 possible anticodons, though most cells have less-- around 40 --because of the possibility of "wobble" (see below)). This is emphatically not the actual order the connections are made; the order followed here rather reflects the topology of the schematic reconstruction. For the most part, codon-anticodon recognition is a straightforward template matchup-- i.e., a non-arbitrary connection (just as was the previously described symbol segment => symbol-representation segment match-up); there are no alternate possibilities of connection that could be specified by the rest of the system. The connection is based on the combinations of the 2 nucleotide "features" (long or short base; 2 or 3 H-bonds) presented by the codon. However, in a number of instances, the system will tolerate a mismatch. With very few exceptions, this type of "degeneracy" (actually, a bit of arbitrariness) is allowed only in the last position of a three segment word; it is called "wobble" and is probably made possible by the conformational flexibility of the tRNA anticodon loop. Interestingly, an analogous degeneracy of end of the word segments apparently exists at the linguistic level (Marslen-Wilson and Welsh, 1978; Marslen-Wilson and Tyler, 1980). In general, the actual RNA word that gets recognized tends not to depend on context. However, so-called "context effects", in which the surrounding sequence alters the efficiency or actually changes what RNA word is recognized at a site do occur (see e.g., Murgola et al., 1984; Carrier and Buckingham, 1984); the mechanism is obscure and could involve tRNA-tRNA interactions, "accidental" folding of the message, or even interactions involving the growing "meaning" chain.

Loading the "Meaning": Aminoacyl-tRNA Synthetases

The second connection involving the symbol-representation is the recognition site for the "3-D connector". One of the main determinants of the mapping scheme in currently existing organisms is a set of 20 or so enzymes called aminoacyl-tRNA synthetases, each of which non-arbitrarily binds a particular amino acid as well as one or more of several tRNA's, and then attaches them together (see Schimmel, 1980; ATP is also involved) by an arbitrary(2) bond (see next subheading) prior to the codon-anticodon recognition and chain assembly steps. These enzymes are the 3-D connectors in Figure 12. Interestingly, these enzymes do not recognize the tRNA anticodon itself (which is of course the major determinant of what word the loaded tRNA will eventually recognize during chain assembly); rather, they bind to large regions on other parts of the tRNA molecules that also vary (along with the anticodon) from tRNA to tRNA (review: Schimmel and Soll, 1979). The location of the site used by an enzyme to recognize a particular tRNA is not standardized; it is different for different tRNA's and sometimes even includes one base of the anticodon. This is a non-standard non-arbitrary connection (in contrast to the standard non-arbitrary connection at the codon/anticodon) and is indicated in Figure 12 by many short parallel lines. It involves a sterospecific interaction between large parts of the two participants. In contrast to the strong, local, oriented, covalent bonds described earlier (e.g., in the nucleotide backbone), the three-dimensional "stickiness" described here involves much weaker interactions that must be evaluated over a much larger surface area; and that surface normally exhibits a much more complex topography than the one or few atoms directly involved in a covalent bond).

The 3-D connectors (the enzymes) load each tRNA with its appropriate amino acid meaning before the word-recognition/chain-assembly process begins, probably because they would get in the way if the entire operation was simultaneous. One way of describing the situation is that the multifarious amino acid meanings each get a convenient, standardized tRNA "handle" (all tRNA's are about the same shape) attached to them to automatize the assembly process; furthermore, each "handle" has a standardized representation (the anticodon) of the highly non-standard 3-D meaning of the amino acid it carries.

The second major source of degeneracy in the code (the first being "wobble" at the anticodon) arises in the meaning-loading step. Most of the 20 aminoacyl-tRNA synthetases (i.e., one for each amino acid) recognize more than one tRNA out of the 40 or so tRNA's (this does not imply overlaps-- usually a tRNA is only recognized by one synthetase). The end result of both types of degeneracy is that the 61 coding triplets are recognized by ~40 tRNA's to stand for 20 amino acids. Degeneracy of this magnitude does not occur at the linguistic level within a dialect; however, the ability to easily recognize words in other quite different dialects suggests that considerable degeneracy can be supported by the linguistic word recognition apparatus as well.

An interesting fact about the meaning-loading step is that although the end result (i.e., which anticodon gets associated with which amino acid) is mostly the same in all cells (minor differences in eukaryotic organelles, for example), the details of the process differ considerably from organism to organism (see e.g., Gabius et al., 1983). In fact, if one simply takes all the 40 or so different tRNA's from one organism and gives them to one aminoacyl-tRNA synthetase from a different type of organism, the reaction is surprizingly non-specific-- instead of picking out a few tRNA's as the enzyme does under normal conditions, it tacks on its preferred amino acid to almost every one of the tRNA's (Ninio and Chapeville, 1980). The picture that emerges is that the apparently static coding specificity is maintained by an ongoing, dynamic tuning of the loading reactions in evolutionary time. In turning to language, such an ongoing tuning of the relation between "sound" (more specifically, internal symbol-representation) and meaning must also exist; the difference (and the clearest argument for the dynamic nature of the relationship) is that, in contrast to the situation in cells, the "end result" is allowed to change. This seems to be due to the increased flexibility of the system as a result of production (see the end of Chapter III) and a larger set of sounds and meanings.

The tRNA to Amino Acid Linkage: Arbitrariness(2)

The third connection on the way from one-dimensionality to three-dimensionality is the bond between the symbol-representation and the "thing"-representation; at the molecular level, this is the "aminoacyl linkage". The end of the tRNA molecule opposite the anticodon is constant for all known tRNA's (it is always -CCA and is labeled "3' acceptor end" in fig. 19). The constant backbone part of an amino acid "thing"-representation is attached onto this end by the enzyme just described. The bond between tRNA and the amino acid, in contrast to both the standardized codon-anticodon connection and the non-standard interaction with the 3-D connector is arbitrary. Nothing about the bond itself determines which amino acid is attached to which tRNA (there are ~800 possible combinations of the 20 amino acids and ~40 tRNA's); rather, other parts of the system (the 3-D connector) determine the particular 40 or so connections that occur. At the beginning of Chapter III, this sort of situation was identified as arbitrariness(2)--i.e., where two classes of units form pairs (as opposed to a single class forming chains).

As with arbitrariness(1), it is possible to point to the nearly equal stabilities to hydrolysis, or tendencies to form, among the various pairs. Although all 800 possible pairs have not been tested, preliminary investigations (Kinjo et al., 1984) have turned up only slight differences. The large number of different human languages could involve in part, different mapping schemes across this bond.

To the extent that arbitrariness(2) is compromised, we might say that an "iconic" relationship exists between a particular tRNA (and hence a particular few codons) and a particular amino acid. Actually, there has been considerable effort expended in origin of life research on trying to find plausible "iconic" explanations for the genetic code. Several ingenious schemes have demonstrated correlations between amino acid shapes and cavities somewhere on tRNA. For example, Shimizu (1982) produced tRNA cavities by sticking two tRNA's together, head to tail, while Hendry et al. (1981) investigated the shapes of cavities made by taking out the middle base from an anticodon made from DNA. Others (Jungck, 1978; Weber and Lacey, 1978; review: Lacey and Mullins, 1983) have uncovered correlations between the slightly differing chemical properties of anticodons (e.g., bulkiness, hydrophobicity) and the more diverse properties of amino acids. These results do not directly address the question of the "iconicity" of the present day tRNA-amino acid bond; however, they have been used to suggest that an earlier stage in the evolution of life, the connection between primitive word-recognition devices (presumably containing only an anticodon) and amino acid meanings might have been non-arbitrary. Another possibility is that the connection in question was always arbitrary and that the apparently non-arbitrary correlations (in hydrophobicity, for example) are entirely due to the 3-D connector (which could have, for example, hydrophobic sites for both parties-- cf. Jungck, 1978). It is important to emphasize that compared to truly non-arbitrary connections (e.g., codon-anticodon interaction; tRNA-connector interactions) the present day tRNA-amino acid bond looks quite arbitrary. There is a similar debate about the origin of human language, and similar evidence of limited iconicity or sound symbolism.

Interactions During Chain Assembly: Arbitrariness(2')

Finally, we come to the fourth and last connection involving the symbol-representation-- i.e., binding to the chain assembler. Like other instances of arbitrariness, the connection involves as set of nearly equally stable standardized connections; and like arbitrariness(2), the two things being connected belong to two different classes, and they form pairs instead of chains. However, there is only one member in one of the classes (i.e., only one chain assembler) so this connection will be called arbitrary(2'). All 40 of the different tRNA "handles" with their loaded meanings must be capable of sticking into the same binding site on the chain assembler (actually, all tRNA's can stick into either of two sites on the ribosome). A fundamental trade-off should be obvious here; the tRNA's must be different enough to be recognized and appropriately loaded, but at the same time, they must be similar enough to all fit into the chain assembler.[7]

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[7] Actually, the situation is more complicated because the tRNA's probably interact with each other while binding adjacent codons (see e.g., Labuda et al., 1984). They also associate with a variety of other protein factors during chain assembly (e.g., EF-Tu in prokaryotes; summary in Lewin, 1983, pp. 87-162).

A Linguistic "Adaptor" in Secondary Auditory Cortex

The novel aspect of the cellular word recognition device is that it is made out of the very same units (albeit some secondarily modified in tRNA) as the internal one-dimensional message. In this section, I would like to investigate the interesting model of word recognition that this relationship points to at the linguistic level.

Adaptors Made Out of Speech-like Units

The peculiar involvement of persisting internal representations of speech-like sounds in language processing is granted in some form by many cognitive psychologists. In the "standard model" of the previous decade, the short term memory "box" was visualized as involving predominantly auditory or auditory-articulatory based phenomena (Lachman et al., 1979). The situation is more complex today (see e.g., Morton, 1984, for a review) and many models now have more boxes usually including, for example, something that could qualify as a visual short term memory. Nevertheless, a special place for auditory-articulatory phenomena was retained in concepts of "working memory" and has been argued for from several different perspectives (Crowder, 1983; Gardiner, 1983). For the most part, these models have been concerned with relatively short chains of segments-- on the order of a few words, perhaps 5 or 10 segments. However, it has rarely if ever been proposed that simple speech-sound representations functioned as anything but one-dimensional streams of information.[8]

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[8] It is true that learning theorists have for some time postulated the existence of higher order units, even in an essentially uninterpreted memory store. An example is the venerable idea of hierarchical "chunking" in short term memory (Broadbent, 1975; Estes, 1978) to overcome inherent capacity limitations. Nevertheless, these and other similar proposals have never gone as far as to suggest that the resulting higher level units themselves mediate processes like word

The unorthodox suggestion made by the present analogy is that chains of speech-like sound representations (thought of in a concrete way as patterns similar to those that could be evoked by actual speech sounds) in addition to serving as internal messages, can also "fold up" into persisting "three-dimensional" firing pattern states that are available to recognize words in the unmarked segment stream of an internal message. Both the message and the word recognition "device" would be made out of the same type of unit and would exist as firing patterns, latent or overt, in the same group of secondary auditory cortical areas (see above). These devices would initially be generated by sequences much longer than a word (the tRNA symbol-representation is from 20 to 30 words in length before folding).

Before trying to explicate "binding together" and "folding" of firing pattern units in more explicitly neurobiological terms, I would like to counter the claim that the simple concatenation of sensory-like patterns isn't suited to such sophisticated tasks such as word recognition, meaning activation, and so on. My main response is that I think that many people have been much too liberal with the types of units they want to explicitly or implicitly put into neural networks. The fact that the brain is complex and poorly understood is often used as a license to imagine a visual or auditory area firing in completely arbitrary ways relative to normal externally driven conditions. It seems just as likely that the neural firing patterns come in only a few pedestrian varieties, much as prebiotic soups end up generating really quite modest variations on a theme.

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recognition or the construction of sentence meaning; rather, most workers have described ways in which hierarchical memory organization impinges on what presumably are even higher level cognitive mechanisms.

A similar sort of situation existed with respect to the anatomical as opposed to the physiological organization of "association" cortex prior to the detailed mapping studies of the last decade. The earlier feeling was that association cortex contained a sublime organizational principle that would not be particularly comprehensible even when it was found out. Instead, dedicated "electroanatomy" turned up a surprisingly straightforward pattern of predominantly unimodal maps of receptor surfaces, with increasingly degraded topography. Certainly, there remain many questions about how such map-networks work (there are virtually no models); and the details of connectivity and between-area differences, much less the names of the areas are hardly simple (see e.g., Symonds and Rosenquist, 1984a, 1984b). Nevertheless, I would like to claim that the basic principle of how association cortex is set up did turn out to be rather pedestrian, so to say; the answer was not very surprising given the nervous system's well known ability in more peripheral stations to generate topological inter-areal connections. Furthermore, the overall system looks complicated enough (in contrast to the sublime, but essentially featureless picture held previously) to be interesting. The moral for the present task might be to look for 'simple' (the word is used advisedly in view of the hundreds of millions of neurons involved) firing pattern units, and then get all the needed complexity from standardized, between-unit interactions, just as can be seen to happen at the molecular level.

Folding Once Again

Molecular folding requires that the units in a chain be bound together by strong covalent bonds-- free-floating units, in temporary linear arrangements or otherwise, cannot fold. Thus, a major task is to develop a notion of the "bonding" of successive activity units in a neural network to one another; as at the molecular level, a simple juxtaposition (sequential activation) of units won't do. Each unit must interact strongly with exactly one other unit-- namely, the immediately preceding one --in such a way that both units are modified along some sort of "axis" between the two. Folding can begin to occur after a number of successive units have been "stuck together" in this as yet unspecified fashion. The result is that additional, but by comparison, less robust interactions (mutual modifications) occur between small groups of temporally non-neighboring units. The final result after all the units have been "stuck on" is a more complex but stable firing pattern that presumably can be stored complete in the network as a tendency for the network to fall back into that pattern upon appropriate stimulus.

I do not claim to have a mathematically articulate model of "bonding" at present (an explicit suggestion in this direction is given in Chapter V); but the basic outline of what it might involve can be stated simply, and it does no great violence to presently held (for the most part, equally qualitative) ideas about how neural networks function. Most every neural network model (see e.g., J.A. Anderson, 1984) admits some form of short term modification of effective connectivity between individual pairs of neurons; a simple example would be the venerable notion of a "Hebb synapse" for which there is some evidence for in invertebrates. Second, many models have suggested that neural networks might serve as classifying machines, reducing unruly, continuously varying inputs to a smaller number of discrete categories instantiated by particular, stable, firing patterns (again, see Anderson, 1984). The idea here is simply to produce a mutual modification of <u>two</u> such successively (or perhaps, partly simultaneously) activated, category-like firing patterns _with reference to an "axis" or "plane" between them_. The modification would be reflected by a short-term change in the connectivity of the network (Hopfield, 1984)-- roughly, in short term memory. One straightforward way to define such an axis begins by taking the firing rate of each neuron in the network as a component in a many-dimensional vector (one dimension for each neuron-- this is simply a convenient way to represent distributed activity patterns). A given firing pattern then corresponds to a particular vector in a many-dimensional state space. An obvious axis between two such patterns is the line that can be drawn through the tips of the two vectors. One proposal for a "modification with reference to this axis" (i.e., "bonding") would be to simply alter the connectivity of the neural network (for now in a _deus ex machina_ fashion) such that the two stable states represented by the two vectors were moved a little closer to each other in state space as measured along that line. To construct the second link in the chain, a similar process of pairwise modification could be carrried out with reference to the axis between the already once modified second unit, and a new as yet unmodified third unit. "Folding" would then be represented by spontaneous transitions in the stability of certain firing patterns arising after network connectivity changes (one for each bond) had accumulated in the course of processing at least 10 units, or so. Folding would be complete after 100 or more units had been bonded together.

The Source of the Sequences

The basic alignment given above opens the way to a number of predictions about how auditory cortex symbol-representation ("adaptors") might work that are based on the analysis of the four types of "connections" made by molecular level symbol-representations (tRNA's) in the previous section. However, before we can proceed, there is the pressing problem of a plausible source for these symbol-representation chains, one of which would be needed for each word or small group of words, and each of which is made out of perhaps an order of magnitude more segments than a word. At the cellular level, the ~40 word recognizer sequences are simply coded for in the DNA (tDNA), and like all the other meaningful sequences in the genome, they are handed in a single "package" to the "baby" cell. The human baby as noted at the end of Chapter III is born mostly lacking a linguistic "genome", as it were, and only gradually acquires not only DNA-like message strands, but also part of the apparatus to decode them over a number of years. A problem for the analogy is that studies of parents' (and others') speech to their children have not turned up utterances that could unambiguously be identified as an analogue of tDNA-- i.e., several tens of words long, and a slightly different sequence for each word that needs to be recognized. Parents' speech and "motherese" is quite complex, and quite different from normal adult speech (see e.g., Malsheen, 1980; Eliot, 1981, pp. 149-163; Schatz, 1982) but none of the work to date points to the existence of long, stylized sequences like those that code for tRNA in cells.

Several points need to be made here. First, the human baby, unlike the cell, has and needs a long time to learn a language; even the peak rates of word acquisition are only on the order of a couple of new words a day. By comparison, a newborn cell must often begin comprehending its stored DNA in the adult fashion within minutes. In this light, it seems entirely possible that the ongoing transfer of coded information described at the end of Chapter III applies not only to "regular" ("thing"-representation based) meaning but to decoding apparatus meanings (symbol-representation segment based) as well. By itself, however, this is not an explanation for how we could get specific sequences. A second point is that although is takes several years before babies overtly begin to acquire adult-like sound-meaning mappings, it appears that the infant's auditory system begins to process the sounds themselves in an adult-like manner much earlier (see e.g., Jusczyk, 1982). Thus, for over a year before adult-like word recognition begins, the infant's auditory system experiences on the order of a million firing pattern sequences (i.e., RNA-like chains) that have some adult-like character (the same thing goes, of course, for an adult learning a language in a foreign country). Third, babies learn to speak, unlike cells, and give evidence of the internal generation of quite complex sound sequences on their own during the pre-speech period called "variegated babble" (Stark, 1980), commencing at the end of the first year.

These observations suggest a possible explanation for the origin of auditory "adaptors" at the linguistic level-- namely, that they "evolve" anew in each brain as it learns a language, by a process of selection. At the molecular level, there was evidence that just this sort of thing was happening in evolutionary time; in contrast to the fixity of the code, the adaptors and the adaptor-recognizing 3-D connectors (loading enzymes) showed signs of continual evolution. Furthermore, such a comparison, between events in evolutionary time at the biological level and events in the life of a single person at the linguistic level is in line with the framework argued for in the Chapter II scenarios. In this view, auditory "adaptors" (each made of tens or a hundred symbol-representation segments) would gradually and idiosyncratically crystallize over a period of several years as the child (or adult) learns to automatically recognize words with them. The initial source could be extrinsic (overheard speech), intrinsic (internally generated sequences of speech-like sound percepts), or both.

Clues from Neuropsychology of Language

The sample size of aphasic patients with both CT-scans and clinical examinations has grown considerably in recent years and at least six general types of aphasia with reasonably distinct cortical (and subcortical) and clinical pictures (Kertesz, ed. 1983; Damasio and Geschwind, 1984). The names for these six types are, however, old or misleading, and tend to obscure comparisons with other primate brains. They are Wernicke's aphasia (secondary auditory cortex lesion), conduction aphasia (primary auditory cortex lesion or auditory cortex => motor cortex pathways), Broca's aphasia (motor and premotor cortex--face area), transcortical sensory aphasia (secondary visual cortex lesion), transcortical motor aphasia (premotor cortex lesion anterior and dorsal to Broca's lesions), and mutism (limbic premotor-- the equivalent of the monkey vocalization area). The most severe, lasting deficits in language comprehension (including reading) result from secondary auditory cortex lesions. The phenomenon of aphasia after strictly visual cortex lesions (e.g., inferotemporal cortex) is discussed in Chapter V. The present hypothesis is that not only the internal message, but also the word recognition devices and the chain assembler all exist in approximately the same region of secondary auditory cortex (approximately, Wernicke's area as defined by Braak, 1978a). A lesion damaging this area would be expected to have catastrophic effects on language understanding and probably silent, language-like thought as well, considerably beyond what would be expected if only an internal auditory message stream had been disrupted. In a cell, such a lesion would be equivalent to damaging all three types of RNA. The main difference of the conception presented here and the standard view on Wernicke's aphasia-- which envisions the area as performing abstract, "higher", amodal functions on internal message streams --is that, as in the molecular model, it may be possible to perform all these functions without invoking anything other than internal (auditory) message streams themselves, albeit some of them "folded".

Notes on the Symbol-Representation

There is a well known quip of Neils Bohr's wondering if a just-proposed idea was "sufficiently crazy to be right". Understandably, it has been appended, as an implicit recommendation from an artisan of crazy but sometimes right ideas, to many proposals that couldn't even be described as wrong. In this light, I think is would be crazy and wrong to think that the mechanism of word recognition in auditory corticies will turn out to be exactly isomorphic to those involving internal messages, word recognizers, and chain assemblers at the molecular level. Nevertheless, it is sometimes helpful to start off by describing what the hidden parts of system B would look if they were in fact isomorphic to those in A (as was done in Chapter II); empirically directed pruning and grafting can then hopefully bring the model into greater accord with reality.

In the following sections I would first like to describe some differences concerning the internal message => meaning mapping. The genetic code demonstrates a regularly occurring redundancy here.

Redundancy of this kind within a linguistic dialect is mostly restricted to college students participating in certain types of psycholinguistic experiments, and rarely appears in real life linguistic experience. Then I would like to give preliminary linguistic analogues of some of the "connections" described for the symbol-representation at the molecular level (tRNA), when possible, in light of psychological evidence on human word recognition. Four entities were described that make a connection with the symbol-representation: 1) the internal message strand (non-arbitrary), 2) the 3-D connector (non-arbitrary), 3) the "thing"-representation (arbitrary(2)), and 4) the chain assembler (arbitrary(2')).

Redundancy and the Number of Word Templates

The large number of words in language show a variety of regularities that have engaged linguists for many years, often in attempts to economically describe them using rules that generate the total word list from a smaller set of underlying forms. Though not explicitly advanced as psychological descriptions, these notions were and are very attractive to psychologists constructing models of word recognition. Chomsky and Halle's (1968) claim seemed eminently reasonable and testable:

> Regular variations such as this [i.e., the pronounciation of "telegraph", "telegraphic", and "telegraphy"] are not matters for the lexicon, which should contain only idosyncratic properties of items, properties not predictable by general rule (p. 12).

The results of recent psychological experiments suggest to the contrary that both base forms and derived forms may have separate "representations" at some level in the recognition system-- i.e., every word the speaker knows might have its own recognition device. There are grouping effects for related forms to be sure in various tasks, but there is little evidence for a special place for the uninflected base form (review: Butterworth, 1983). In this view, the ability to generate a non-word pronounciation or a new derivation would have to be seen as something of a "fall-back" procedure not used in "normal" automatic word recognition.

All the "extra" representations might be thought of as a kind of redundancy; nevertheless, the redundancy at the level of the genetic code is of a different type. Thus, because of "wobble", the first level redundancy, differences in bases that would "contrast" (i.e., cause a different amino acid meaning to be signalled) at the beginning of a molecular word are not detected at the end of a word, and thus one tRNA will often recognize more than one codon; however, the amino acid meaning signalled is exactly identical, which is certainly not the case with derivationally related forms in language. The second level redundancy-- of having multiple codons for an amino acid even after "wobble" has been accounted for --might initially seem to recall the derivational regularities above since there is regularity to the pattern of which codons alternate; nevertheless, the coded-for meanings are again exactly identical, unlike the linguistic case. In Chapter V, it is argued that there is nothing analogous to a clitic or to derivational morphology at the molecular level; instead, higher level structures are built up entirely on the basis of word order (as is mostly the case in some languages-- Chinese, for example).

Linguistic "Codons" and "Anticodons": Neural Templates

The first connection of the symbol representation starting from the symbol side (as opposed to the "thing"-representation side) is that between a few segments of the internal message and a small region of the symbol-representation. At the molecular level, this connection involves a segment-by-segment template match (codon-anticodon base pairing). A possible analogue of this process in a neural network might be developed in which a bond-like interaction occurred between two firing patterns states (or parts of larger states-- cf. Anderson, 1984) and where a good template match might be defined as a two-part bound firing pattern substate (a "codon-anticodon" pair) whose state space configuration closely resembled the average of the set of other good matches-- i.e., the set of lowest energy pairs of, on one hand, word sequence segments (in the internal message stream) and, on the other, small 'complementary' regions of "folded" symbol-representation firing patterns. If such a model could be developed, it would give a curious concrete interpretation to linguistic oppositions-- i.e., they might be directly involved in word recognition in the sense that a particular segment in the internal message stream would interact with its best complementary opposite in the word recognition device (the same segment, of course, would sometimes be part of the message, and at other times, part of the recognizer).

Loading the Meaning (Weak Three-Dimensional Bonds)

The model of the second connection of the symbol-representation (meaning loading) literally suggested by the molecular level situation is quite novel. The process would be an actively maintained one-- i.e., auditory cortex word recognition devices would have to be continually "loaded" with their amino-acid-like visual cortex meanings (see Chapter V) throughout life. The three-dimensional connectors responsible for maintaining this specificity would be other stored, folded patterns located in secondary visual cortex as well-- also made of amino acid-like visual category units.[9] The characteristic of the connection between the tRNA word recognition device and the loading enzyme was that large, non-standard regions of the molecules were involved; in contrast to the aminoacyl bond (arbitrariness(2)), or the internucleotide linkage in mRNA (arbitrariness(1)), there is no obvious way to draw a bonding axis between the two entities involved because weak stickiness (van der Waals forces, hydrophobic "bonds", matched dipoles) must in practice be evaluated over a complex three-dimensional surface created by several units. I already suggested a network analogy to the strong, oriented covalent bond, in terms of modification of the connectivity matrix of the neural network so as to move the stable states of the bonded units in a regular way with respect to the "axis" drawn between the tips of their state space vectors. In the case of the weaker, three-dimensional (stereospecific) stickiness, a neural network analogy might be sought in terms of a less robust "bonding" (e.g., one that does not involve modifying the location of the stable states of the network) taking place with respect to the two surfaces (in the mathematical sense)-- one for each folded chain --drawn through the tips of the vectors representing

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[9] The situation must be different from the molecular system at some point, since it seems unlikely that people hear sound sequences capable of generating the 3-D connectors to "load" the meanings (onto auditory cortex symbol-representations-- approximately, logogens) of all the words they will recognize that day. Two possibilities are-- 1) the 3-D connectors are less ephemeral than in cells, and 2) the symbol-representation => "thing"-representation bond is more permanent. There is, in any case, psycholinguistic evidence that mechanisms involved in word recognition may require constant renewal. For example, there is a long-lived (hours or days) word repetition effect in lexical decision tasks (word/non-word choice) that is thought to give rise to the very robust word frequency effect (high frequency words are recognized faster) (reviews: Henderson, 1982; Butterworth, 1983; Monsell, 1985). This long-lived, somewhat modality-specific priming suggests that a pool of meaning-loaded 'word-recognizers' may be actively maintained at the linguistic level as well.

the units involved in the bond. This is really only a suggestion of where to look for a model; it would need to be made much more concrete before it could be rigorously analyzed and evaluated in an actual model network.

At the molecular level, there are reasons why the amino acid "meanings" might have to be loaded ahead of time-- the loading enzymes (which are very diverse in size and subunit composition) would get in the way; furthermore, it would probably be kinetically unfeasible to do everything at once even if the loading enzymes could be standardized (i.e., made to have an arbitrary(2') bond with the chain assembler). It is possible that similar classes of constraints exist at the neural network level-- e.g., it might be unfeasible to make visual cortex 3-D connector firing patterns (which "stereospecifically" locate a word meaning firing pattern in secondary visual cortex and its matching standardized "adaptor" in secondary auditory cortex) of similar enough configuration themselves not to interfere with arbitrary(2') bonding with the chain assembler during the chain assembly process. There are enough variables running wild here to make even a hardened interdisciplinarian like myself wince; nevertheless, I think the redeeming value of the exercise is that is provides a full-bodied scent of what the eventual explanations of word recognition in terms of neural network dynamics are going to have to involve.

The Word-Recognizer to Word Meaning Link: Arbitrariness(2)

At the molecular level, the 3-D connector makes a strong, directed covalent bond between the standardized tRNA "handle" and the varible amino acid "meaning"; it is an arbitrary bond, in principle, possible between any combination of the two kinds of units. At the linguistic level, it is well known that in different languages, a given meaning like "man" can be signalled by a variety of sound groups. This has long been taken to infer that somewhere in the brain, internal sound representations and internal concepts are capable of being bonded together in any combination. In the present model, the arbitrary(2) bond is made between symbol-representations (i.e., folded chains of symbol-representation segments) in secondary auditory cortex, and "thing"-representations, the prelinguistic category representations located mostly in secondary visual cortex (see Chapter V). In monkeys, the direct connections between secondary auditory cortex and secondary visual cortex are really quite modest; much more prominent pathways are available via a loop through premotor cortex or through the cortical areas on the parahippocampal gyrus (summary and references in Pandya and Yeterian, 1984). Blood flow studies during listening to words with the eyes closed show activation of the frontal areas in question (parahippocampal activity is not assayed because of the particular artery that is used for isotope injection) (Nishizawa et al., 1982; see also discussion in Lassen and Roland, 1983). A literal interpretation of the present analogy suggests that a similar "directional bonding" process (involving adjustment of stable state locations) between two firing pattern units as was postulated to occur between a pair of units <u>within</u> secondary auditory cortex can also occur <u>between</u> a pair of units located in two different modalities.

<u>Interactions During Chain Assembly</u>: <u>Arbitrariness(2')</u>

The main idea here is that a major function of the hypothetical symbol-representation based word recognition devices in secondary auditory cortex-- besides providing a template to match to sequences of segments in the internal representation chain --is to present a standardized surface (a sort of "handle") to the chain assembler during the actual bonding together of the meanings. At the molecular level, the template matching part of the symbol-representation is actually diminuitive with respect to the rest of the molecule; a long chain of symbol-representation segments is used to recognize just a few of them. The implied relation here is that most of the activity observed in secondary cortex during word recognition (Nishizawa et al., 1982) might actually have little to do with the internal message sequence, and might consist mostly of activity related to word recognition device "handles" and the chain assembler.

Conclusion

The proposals given in the previous section for possible properties of linguistic word recognition devices were perhaps a bit overdrawn; for instance, though I think it eminently plausible to conclude by analogy that internal speech-sound representation units might be involved in word recognition as more than message streams, there seems little pretext to go about predicting their exact length (about 25 words in cells). Clearly the way to find out more about the logogen-like word recognition units for which psychologists have collected considerable evidence is to do neurophysiological experiments. The prospect is not so distant as one might expect. MacKay (1984), for instance, was able to detect localized activity in striate cortex to a spatial resolution of about a centimeter using a closely spaced array of scalp electrodes, only a few tens of sweeps per stimulus, and a current-souce density computation. It is intriguing to contemplate studies of word recognition using a larger array, especially in light of the millisecond temporal resolution available with this technique. When such data begins to be collected, the exuberant hypotheses can begin to be pruned. But one needs something to prune. The currently extremely pessimistic picture painted by Morton (1984), with regard to localization would not be much help in interpreting such data, which preliminary studies suggest will contain complexly varying spatial patterns (Gevins et al., 1981, 1983). I think the ideas presented here might serve as a better starting point.

The Chain Assembler

The third major component of comprehension in the broad sense is chain assembly. This is the process by which "thing"-representations are actually bonded together. In cells, the symbol-representation stuff makes up a major part of the apparatus. The chain assembler is the most complex apparatus that has a definitive composition in cells and there are good general reasons to believe that the mechanisms involved in assembly of linguistic meanings are equally complex with reference to other brain functions. The chain assembler is not even well understood at the molecular level relative to the other parts of the cell; therefore, we will have to pass briefly over what is one of the central parts of a symbolic-representational system.

The Ribosome

The ribosome is a very complex device. There are 4 quite distinct versions of ribosomes in living things, and really, by consequence, 4 different types of living things-- namely, eocytes (sulfur-dependent bacteria), archaebacteria, eubacteria (e.g., _E. coli_), and eukaryotes (Henderson et al., 1984). Compared to other definitive macromolecular assemblies, the ribosome is huge, containing between 4500 and 7500 RNA nucleotides (symbol-representation segments) and between 55 and 80 distinct proteins (i.e., about 1/2 RNA by weight). It accounts for the majority of the nucleotides (DNA and RNA included) in a cell. It has a small and a large part in all organisms that stick together during chain assembly. Figure 21 shows the probable folding of the RNA components of the subunits and tRNA molecules drawn to scale. The ribosome binds two tRNA word recognition devices and one mRNA internal message at one time. The growing amino acid chain is always attached to a tRNA. As each new loaded tRNA binds (as determined by codon-anticodon recognition on the bound internal message) the chain is popped off the old tRNA and added on to the end of the amino acid brought in by the new tRNA (see fig. 22). The bare tRNA is then ejected to make room for a new one. The ribosome operates in a sea of different loaded tRNA's, which pop in and out at a very high rate until the right one is found. The rate of assembly is about 2 or 3 word meanings per second in eukaryotes and about 6 times that fast in bacteria. The growing chain of amino acid meanings begins to protrude from the ribosome after about 25 or 30 word meanings have been concatenated, at which time it is completely exposed to the solvent and begins to spontaneously fold.

A Chain Assembler in Secondary Auditory Cortex

In drawing an analogy with the cellular chain assembler, the most unusual implication has to do with its size (several thousand symbol-representation segments long). At the linguistic level, this would correspond to the pattern of activity evoked in the cortex by several minutes of continuous speech. Since so little is known about the simpler effects of a few auditory cortex segments on each other, it seems a bit premature to speculate at length about the possible

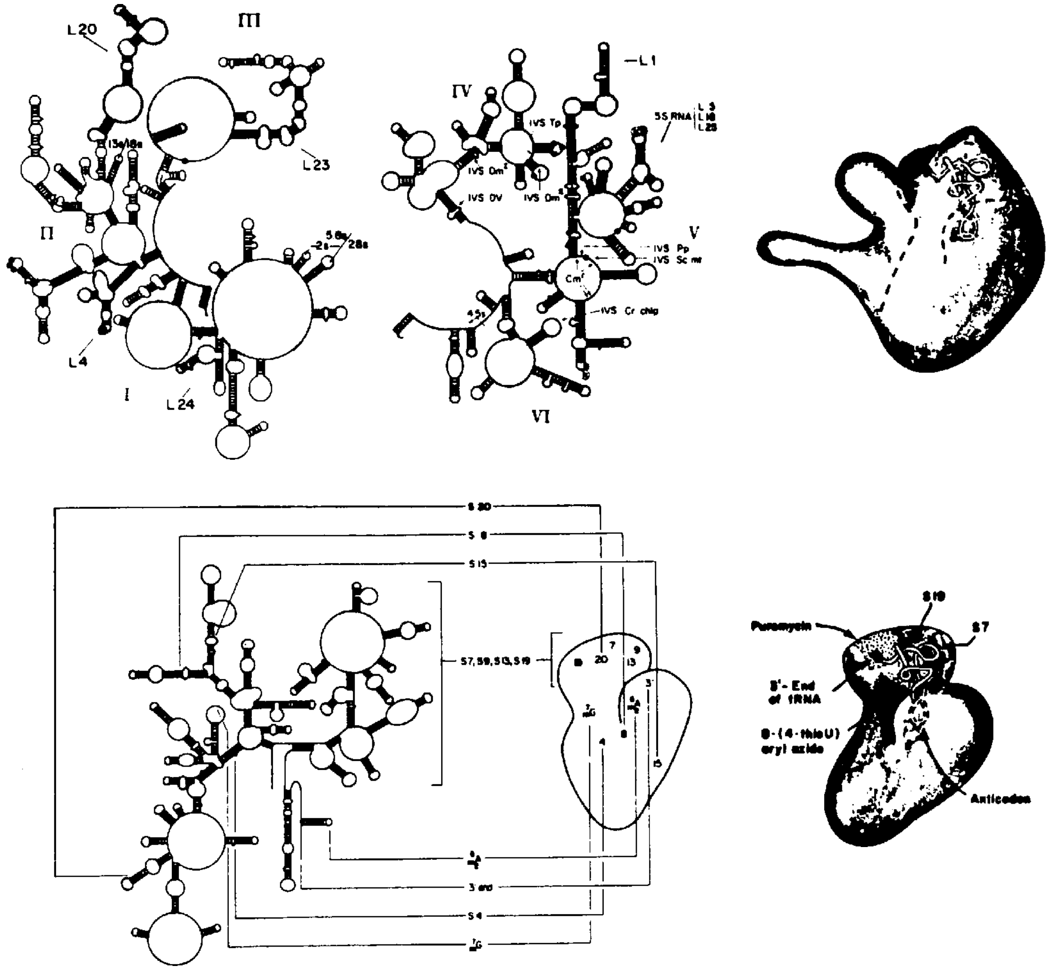


FIG. 21: Ribosomal Subunits and rRNA

structure of such a huge thing, especially when it is so little understood even at the molecular level.

My comments here are limited mostly to considering if such a large thing, involving minutes of connected activity, is even plausible. In this respect, it is worthwhile pointing out that the origin of the chain assembler at the cellular level is mysterious-- it is difficult to see

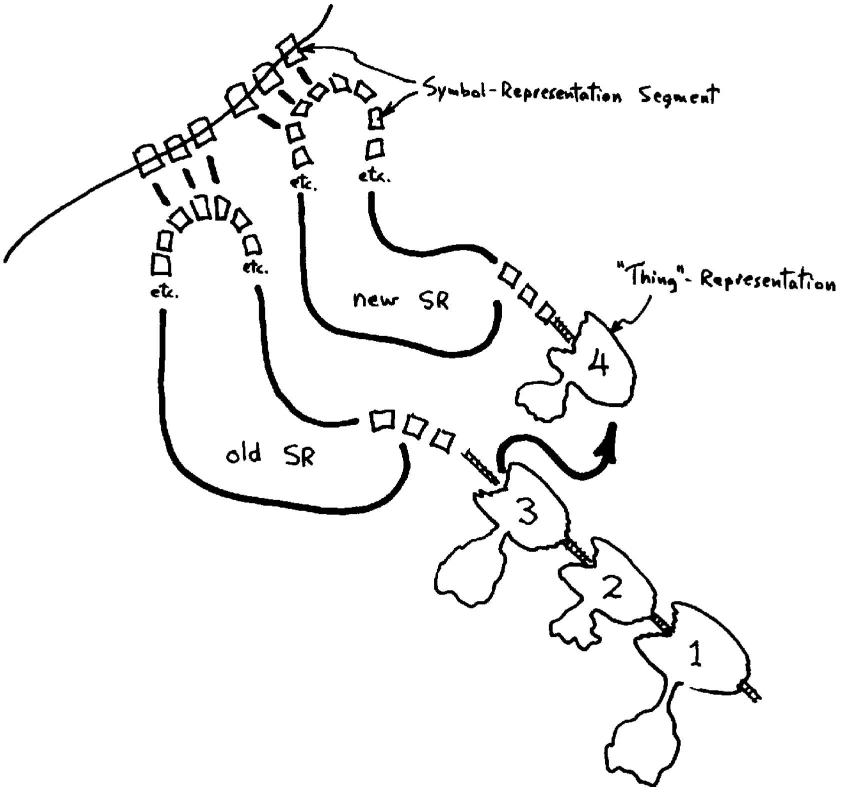


FIG. 22: Chain Assembly

how something so complicated ever "got off the ground". There are really no plausible models of what a smaller, "primitive ribosome" might have looked like. With the complex tangle of RNA chains in the nucleolus in mind, it might be better to think of ribosomes as haviing "crystallized" out of an extremely complex, heterogeneous matrix of approximately replicating molecules as Barbieri (1981) has suggested. Most workers have simply ignored the problem-- e.g., Eigen and Schuster's models (1979) concentrate only on tRNA. Returning to the linguistic level, there is the additional problem that such a thing would have to be generated anew in each brain (it seems unreasonable to think that such a long sequence would be able to be genetically transmitted) as it learned language. A fact to keep in mind is the remarkable ability of humans to memorize hours of speech streams involving many times the number of segments at issue here. The peculiarly human musical abilities are possibly relevant here as well. Certainly, there are no precedents in the prelinguistic world (e.g., in birdsong) involving chain anywhere near the same magnitude (in terms of segments). An analogue of the "crystallization from complexity" argument suggests that human language might have arisen in the context of the production, perception, and perhaps internal generation of very long chains of segments.

CHAPTER V

"THING"-REPRESENTATION UNITS AND CHAINS

In this chapter, we consider the units that, after concatenation into chains, spontaneously "fold" and become capable of controlling "reactions". These devices are far more functionally diverse than those described in the previous chapter; they are fully "three dimensional". A perceived (and rather highly charged) gap between cognitive psychology and neurobiology is first described. Then, four topics are considered in order of increasing complexity; these are isolated "thing"-representation units, levels of structure in folded chains, "substrates" and function, and higher level coordination and interaction.

Psychology and Neurobiology of Language

Cognitive science and neurobiology have for a long time had an uneasy relationship with respect to language. In the early days of computer models of cognitive processes, an oft-cited argument was that since the particular type of hardware running a program-- e.g., hypothetical hydraulic CPU *versus* tube CPU *versus* integrated circuit CPU --was completely irrelevant to an understanding of the logic of the program, a similar situation might exist in the case of hypothetical programs of the brain and the actual neural "hardware" that ran them. In addition, there was the strong implication that the programs in the brain and in CPU's might have important similarities. The implied transition from tube CPU to semi-conductor CPU to "neural CPU" today seems less clear, and the great discontinuity between the second and third step has been reemphasized (see e.g., Hinton and Anderson, eds., 1981). At the same time there has been more interest in trying to take some of the inherent properties of the brain "CPU" seriously in psychological theorizing--e.g., massive parallelism, slow switching, lack of a clock. Nevertheless, despite the existence of hopeful titles like <u>Neural Models of Language Processes</u> (Arbib et al., eds., 1982), <u>Handbook of Cognitive Neuroscience</u> (Gazzaniga, ed., 1984), and <u>Biological Perspectives on Language</u> (Caplan et al., eds., 1984), there has been rather little progress made toward a model concerning natural language that could interest both a psychologist and a neurobiologist. Neurobiologists have often made, let us say, indelicate use of psychological concepts (e.g., Ojemann, 1983) and psychologists for their part have understandably been ready to kick neurobiology out the back door again on short notice. Lehnert (1983), for example, described the relationship this way:

> To put it bluntly, the neurophysiologist and the AI (artificial intelligence) researcher still have nothing to say to one another, at least as far as natural language processing is concerned. I suspect we should keep checking in on each other periodically.... so that we'll be ready to talk when there's something to talk about. In the meantime, at least for language specialists, it's enough to know that we're not missing anything (pp. 215-216).

Similar sentiments have been expressed by psychologist and philosopher Pylyshyn (1984), who reasserts the program/hardware distinction:

> So far... <u>all</u> the functions that have been modelled by such mechanisms [i.e. brain-like connectionist models as in Hinton and Anderson, 1981] are cognitively impenetrable [i.e., dependent only on hardware constraints]; they are chiefly functions like memory retrieval. The rigidity of these functions makes it doubtful that they are anything but properties of the functional architecture...
>
> The preceding remarks also suggest that the proper place to look for neurophysiological constraints on cognitive models is precisely in functions hypothesized as part of the functional architecture-- transducers, parsing, lexical access processes, aspects of phoneme recognition in speech, an so on... In the case of representation-governed regularities, such as those

> involved in understanding natural languages... any part of the achievement can depend crucially on anything one believes or knows. This massive holism makes it unlikely that topographic or structural constraints will show through in any direct way in the observed regularities. In such situations, anything, it seems has at least the potential of being functionally, and hence structurally, connected to anything else (pp. 215-216).

Despite the fact that my sympathies lie with the expelled neurobiologists, I agree that a distinct gap does currently exist between neural-network-like models and psycholinguistic or AI models of language processes; and it is the intent of this chapter to make a stab at putting something in this gap. I would first, however, like to point out what I think is a misconception, exemplified in the Pylyshyn quote, of just where the gap is.

In the context of the present analogy, the dichotomy between rigid lower level units and completely free higher relations imported directly from the architecture of a von Neumann computer is particularly misleading. With a computer, we can write any sort of program and then make the computer slavishly follow it. The relation between the "outside world" and the computer's "internal representations" is almost entirely up to the programmer; there are virtually no pre-existing "thing"-representations in the computer. By itself, this might not seem like a liability; but if we look at the molecular level symbol representational system, as well as the less exposed version in people, I will argue that the "basic mechanism" of language in the broad sense is to control the ordered assembly of these pre-existing units. The resulting highly complex functional "devices" are generated spontaneously by means of interactions between the pre-existing units and very general "rules" of the sort-- "find the conformation with the lowest energy". This strategy allows a highly specific, complex device to be built without having to explicitly specify where all the parts "end up" (cf. Schulz and Schirmer, 1979, p. 5; Pattee, 1982).

The reason computers aren't capable of this is that their pre-existing units are so impoverished and flexible that they need to be told explicitly what to do by the programmer; there is no possibility of letting between-unit interactions "take care of the details".[1] Quite obviously, this is because they were designed just this way, so they would be able to do long tedious computations involving context-free manipulation of single low-level details. At the molecular level for comparison, a computer-like device would have to be able to modify the locations of any one out of a large set of atoms without affecting the surrounding structure at all. Real enzymes, of course, are not afforded such luxury; contexual interaction ("allosteric effects") are not only the norm, but are heavily exploited as as means of controlling ongoing operations. Similarly, the brain "CPU" is more inflexible and recalcitrant toward attempts to 'program' it than is a real CPU; but this of course is exactly how it is possible to get so much more structure out of order symbol string inputs than can be gotten by feeding the same string (and nothing else!) to a quiescent computer.

The viewpoint I am arguing here is that the real gap which currently exists is not between rigid low level hardware mechanism and high level program-like rules, but the lack of a model to take us from <u>isolated</u> lower level neural-like units to <u>concatenated</u> lower level units with high level functional properties. It is remarkable how many of the

---

[1] There have been some interesting projects in AI that could be thought of as attempts to emulate the more brain-like strategy of allowing rather complex lower level units to directly interact "on their own terms". One proposal is the "word expert parser" of Small (1983), in which smart word demons interact with each other (e.g., one of them might look elsewhere in the sentence for an implied instrument or subject, and so on) until a consensus is reached. All the detailed proposals made to produce a serial simulation of this (usually several million steps per sentence) seem to have less to do with the way the brain would do it; but the overall approach is a move in a brain-like direction.

neural-like models that have been discussed (see e.g., Hinton and Anderson, 1981; Amari and Arbib, 1982; Marr, 1982; Ballard et al., 1983; Hopfield, 1984) could be described as "one-unit" models. Many of them of course store multiple memories or multiple categories, and some of them have interaction among units (usually as a consequence of the network getting too "filled up"); nevertheless, very few attempts have been made to investigate the <u>interactive</u> <u>concatenation</u> of successively actived units- where each unit "bonds to" or specifically interacts most intensely with its nearest temporal neighbors. In one respect, the criticism of Pylyshyn and others is thus valid in pointing out that language understanding involves more than isolated instances of categorization resulting in a single active unit pattern. This is emphatically not a reason, though, to abandon the rich, hardly explored dynamics of the neural network for the almost featureless dynamics of a von Neumann machine; it should rather be a challenge to find ways of getting the, at present, isolated units in networks-- which already have attractive properties-- to interact. What we eventually would like is a neural-like model of what happens after 50 or 100 unit word meanings have been presented to "working memory". The argument of this thesis is that a currently available, fully articulated, model of this is a polypeptide chain.

<u>The Isolated "Thing"-Representation</u>

In this section, an analogy is drawn between the set of amino acids and an as yet hypothetical set of stable firing pattern states of secondary visual cortical areas in the human and in other primate brains. First, the basic structure of this internal "meaning" unit in the two systems is described. Second, the implications of the easy prebiotic availability of these units are developed, especially in the context of their central importance in controlling most of what goes on in a symbolic-representational system. Finally, the notion of "polysemy"--the apparent (but not actual, it will be claimed) multiplicity of meanings of a word --is discussed using examples from both systems and argued to be one of the hallmarks of a language in the broad sense.

Amino Acids-- Molecular "Thing"-Representations

Amino acids are the building blocks for proteins, which have the most varied functions of any of the constituents of a cell. Proteins not only serve as thousands of different, highly specific "reaction controllers" (enzymes), as was emphasized in the previous chapters, but also as fibrous, non-catalytic structural elements (e.g., by weight, the most common protein in a vertebrate is often collagen). The incredible structural and functional diversity of proteins, however, depends for the most part, simply on the order in which a mere 20 different types of subunits are concatenated. In the next three parts, the basic structure of these units, their prebiotic availability, and their unit properties in the context of a protein are considered (summaries: Schulz and Schirmer, 1979; Walsh, 1979; Cantor and Schimmel, 1980; Dugas and Penney, 1981).

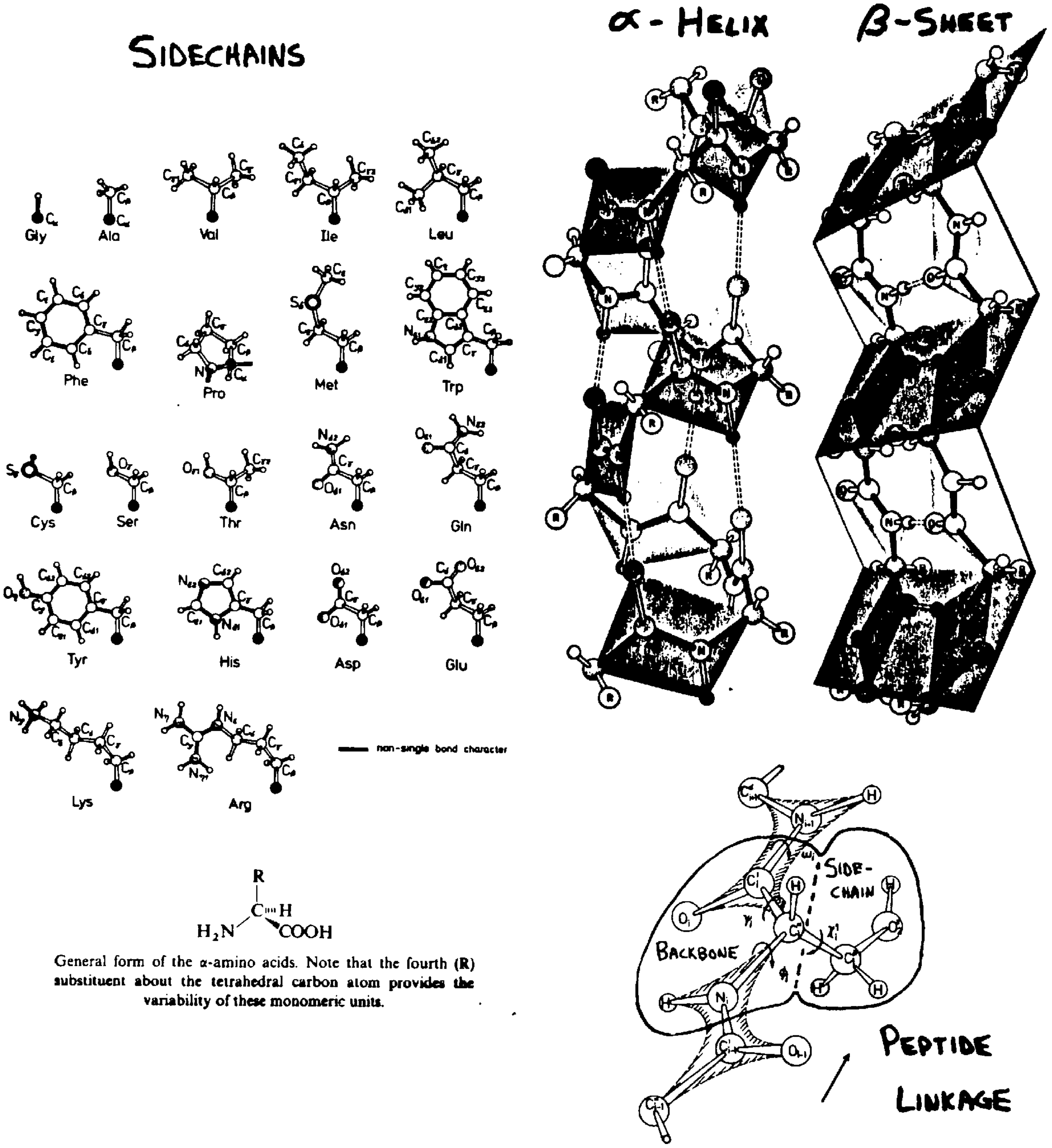
Basic Structure: Backbone

Like nucleotides, amino acids can each be divided up into a constant backbone part that is capable of making an asymmetrical directional bond to two other units, and a variable sidechain part. Since two bonds can be made per unit, since they occur between similar types of units, and since the 400 possible versions of the bond are of similar stability (less so than in nucleotides, though), it resembles the arbitrary (1) bond; however, since the side chains of adjacent units do not interact, but instead stick out in different directions, it was distinguished as arbitrariness (3) (this is discussed further in the section below on concatenation).

The structure of an amino acid is quite simple and in general they are smaller and more compact than nucleotides. The backbone part of an amino acid consists of a central carbon atom (the "alpha-carbon") with 4 groups attached to it, one of which is the sidechain. The remaining three groups are an amine group, a carboxyl group (the acid part), and a hydrogen (see fig. 23). The two distinguishable bonds made by each amino acid involve the amino group and the carboxyl group (cf. 5'-phospate and 3'-carbon in nucleotides). The one exception to this picture is proline, which can be thought of as having its sidechain curled back and stuck to the backbone amino group (as well as to the alpha-carbon); this displaces one of the hydrogens there (instead of an amine group, proline has -NH-).

Basic Structure: Sidechains

Again like nucleotides, each amino acid has a variable sidechain. Compared to the 4 similar sidechains in nucleotides, the 20 amino acid sidechains are more variable (see Fig. 23), ranging from a single hydrogen, to a group that is twice the weight of the backbone part. The sidechains can divided up in several ways. An important distinction is between polar and non-polar sidechains (about half and half); probably the most important overall determinant of protein structure is the pattern of polar and non-polar sidechains (which usually approximately alternate). The polar residues tend to remain at the surface of a folded protein in contact with the solvent, while the non-polar residues



General form of the α-amino acids. Note that the fourth (R) substituent about the tetrahedral carbon atom provides the variability of these monomeric units.

FIG. 23: Amino Acids and Amino Acid Chains

remain buried. Another important feature distinguishing the sidechains is simple bulkiness; this is also quite important in determining folding patterns (e.g., it shows up in substitution patterns in homologous proteins from different species). The charged sidechains (subset of the polar group) can be subdivided into acidic (negatively charged) and basic (positively charged). Other partly cross-cutting distinctions are based on polarizability (aromatic *versus* non-aromatic), presence of hydroxyls, or of amides, "special" sidechains like imidazole, or the proline ring. In comparison with the straightforward analysis of the features of nucleotide sidechains relevant to the system, the feature of amino acid sidechains present a much more complex picture. Furthermore, they are highly context dependent, unlike those of the nucleotide sidechains. Weber and Miller (1981) give a good self-contained discussion of the "semantics" of the 20 amino acids in the course of giving reasons for the occurrence of the 20 biotic amino acids (out of the somewhat larger group available prebiotically).

Implications of Prebiotic Availability

The easy prebiotic availability of amino acids was already remarked upon in Chapter III. An additional sign of the generality of the electric discharge experiments is the discovery of amino acids on meteorites (reviewed in Weber and Miller, 1981) in similar proportions; synthesis of these racemic (not optically active and therefore non-biotic) amino acids is probably datable by the age of such meteorites, which are older than any terrestrial rocks (Hutchinson, 1983) and are often used as a date of the origin of the solar system.

The philosophical implications of the ease of prebiotic synthesis of amino acids have, I think, been underplayed. In the context of the present analogy, one could look at amino acids as palpable prebiotic representations of *categories of reactive collisions* in the primordial prebiotic "soup" or atmosphere. In a sense, amino acids are descriptions of the chemical phenomena that exist in such soups. Of course, any one chemical species is, to a certain extent, a description of the rest of the chemicals present by this definition; what makes amino acids special is that they so readily arise and dominate such mixtures. Since the amino acids are category representations of what are really rather complex quantum mechanical transitions, I have called them "thing"-representations with quotes. At the linguistic level, there are some perfectly good things to be represented, but there are also phenomena that aren't very thing-like-- e.g., "giving", "on (top of)" --so quotes are appropriate there, too. The word "thing" was retained for clarity and because language so commonly allows one to treat abstract objects the same as if they were things ("I gave him the idea" or "a piece of my mind" and so on-- see Lakoff and Johnson (1980) for many more examples).

Molecular "Polysemy"

"Polysemous" words at the linguistic level are those with many meanings (e.g. "put", with 54 different senses listed in the OED). It is interesting to examine this notion using the concrete entities at the molecular level. Thus, we could think of an amino acid "word" as having a number of different shades of molecular meaning when placed into chains of different amino acid contexts and folded up. In fact it is a common point of amazement in the introduction to most biochemistry texts that so many different and specific reactions can be run with so few basic building blocks. To make the point another way, if one gave a chemist who had no knowledge of living things the task of setting up a system to catalzye thousands of different interlocking reactions, and then gave him only the 20 not very exotic amino acid units to work with, the answer surely would be that it was in principle impossible to do. The perfectly good reason cited would be that the chemical properties of most amino acids by themselves are quite undistinguished. For example, most are rather unreactive (some have billion year half-lives in aqueous solution). Organisms, of course, currently run those thousands of reactions, using mostly the 20 amino acids, and in examining the enzymes they have construced, it is clear that a given amino acid takes part in a large variety of very specific chemical interactions, either directly as a catalytic group or by providing a surface to bind to in the active site, or indirectly as a factor in determining the folding pattern supporting the catalytic site (see next section). Thus, although amino acids are almost "meaningless" in isolation, they can develop a number of highly specific "meanings" in the context of a folded polypeptide chain. The amino acids nevertheless are still quite localizable as nearly the same group of atomic nuclei (minus one water molecule per residue) in the folded chains as they are in isolated form in solutions; and none of this is to suggest that the form of the folded chain results from anything else than the (very complicated) sum of the interactions between the amino acids in the chain and the surrounding solvent.

In the context of the present analogy, I think these observations provide more than just a commentary on the good design of living things; I think they give us a powerful way to think about linguisitic entities. At the molecular level we can clearly distinguish the unit itself, either isolated or concatenated, from its very different functions in those two cases. With language, however, we do not now have that option because the relevant neural phenomena are mostly hidden. As a result, it is more difficult to sort out what might be constant units from their various functions in context. It would be easy to mistakenly attribute the modified, more specific functions of a unit in different contexts to the unit itself (e.g., as "different" word meanings). The molecular system shows us instead, that we can get different, but _specific_ "meanings" out of the same well-defined unit when placed in different contexts, but also, that if we isolate the unit, we find it to be almost "meaningless". The implication at the linguistic level is that there might be similarly _well-defined_ _singular_ units that in the context of a chain take on much more specific and varied functions or meanings than they have in isolated form.

Subunits of Cellular "Thing"-Representations

The notion of a covalent bond is, of course, quite general and applies as well to within-unit bonds as it does to between-unit bonds. Thus, amino acids are themselves constructed of smaller units (atoms) held together by covalent bonds similar to (though for the most part, more stable than) the peptide linkage. Most amino acids consist of only four atoms-- carbon, oxygen, hydrogen, and nitrogen (two contain a sulfur atom as well) --averaging approximately 19 atoms apiece. This decomposition of the cellular level "word meaning" units suggests a somewhat unorthodox approach to components of meaning that is developed in a little more detail later. The basic idea is that there may be a rather small number of extremely minimal meaning "atoms"; in contrast to many other related proposals, the present analogy suggests that these "atoms" may be too simple to stand alone a word meanings. The paucity of free atoms in a prebiotic soup furthermore implies that these subunits may not even appear in isolated form in prelinguistic brain activity in animals.

Firing Pattern Units in Secondary Visual Cortex

In this section I would like to use the analogy and available indirect evidence to make a preliminary but concrete proposal for what a "thing"-representation might be at the linguistic level. Basically, the idea is that "thing"-representations are prelinguisitically conditioned tendencies of primate secondary (including non-topographic) visual cortical areas to "fall into" stable firing pattern states that correspond to categories of visually perceived phenomena (i.e., "things").

The Modality of the Meaning

The problem of concepts and categories is not new, and enough has been written and thought about it that one tends to step more gingerly than usual. Nevertheless, it is difficult to avoid the topic, especially in the case of the present project. What I would like to do here is not so much to reinvent old notions as simply to graft some of them onto new ideas about the layout of the primate cortex.

An influential framework for representation of concepts, categories, and their interrelations in cognitive psychology was the "semantic network" model of Collins and Quillian (1969). Structurally, these models consisted of nodes and links. The content of a node was a "concept" (see also Anderson, 1981), which most often corresponded to a single word, usually a noun. The emphasis on nouns has continued to the present in psychological research on concepts and categories to the almost complete exclusion of verb-like notions (see e.g., review by Medin and Smith, 1984). Possible links included subordination ("is a") as well as conjuction and disjunction. A major innovation was the idea of "spreading activation" (review: Collins and Loftus, 1975) developed in several different contexts, whereby the activation of one node would cause a radial spread of activation to other nodes, decaying with distance and number of other nodes attached. These models have a great intuitive appeal and various versions of them have persisted to the present (J.R. Anderson, 1983). They have usually been interpreted rather abstractly as representing propositions with only an arbitrary relation to the thing referred to. Experimental support for these ideas came from the robust phenomenon of short-lived (several seconds) semantic priming effects in word recognition, demonstrated a number of years ago with words (Meyer and Schvaneveldt, 1971) and more recently with pictures (Rosch, 1975; Vanderwart, 1984).

During the same period on a completely independent front, electrophysiological mapping experiments in the "association" cortex of primates and other animals revealed that contrary to earlier conceptions of diffuse intermodal association areas (an excellent statement can be found in William James' Principles of Psychology), a good part of the non-primary "sensory" cortex (behind the motor cortex) was filled up with repeated, heavily interconnected maps of the receptor surfaces (Merzenich and Kaas, 1980; Kaas, 1982; Symonds and Rosenquist, 1984a, 1984b); furthermore, even the "higher", apparently non-topologically organized areas (e.g., inferotemporal cortex in the visual system) seemed to be predominantly unimodal-- i.e., driven almost exclusively by visual input in anesthetized and awake animals (see Richmond et al., 1983, and references therein). Poly-modal cortex exists, but mostly as thin strips separating the large uni-modal regions-- i.e., visual cortex, somatosensory cortex, and auditory cortex --and in the projections into the limbic system. Furthermore, there is currently no reason to doubt that this sort of organization is present in human posterior cortex. The studies of Braak (1978b), for instance, show a clear architectonic transition in the human superior temporal sulcus similar to that seen in monkeys where this region is occupied by a poly-modal strip in the sulcus separating a large stretch of visual cortex ventrally (inferotemporal cortex) from a large auditory cortex dorsally. The blood flow studies of Lassen and Roland (1983) on humans engaged in intermodal perception show only spatially distinct modality-specific activation posteriorly; the only poly-modal area activated was in frontal cortex.

The juxtaposition above is rather heavy handed; but is suggests that the place where psychologists, philosophers, and neurobiologists have always wanted to put their higher meanings and concepts (see e.g., Fodor, 1983, pp. 118-119) just might not exist in the brain. Continuing in this fashion, it seems that we might have to stick all the concepts, semantics, and other abstract stuff into one or the other of the three main modalities, which brings us finally to the question of which one(s). This is not as outrageous a request as it might seem at first, especially with regard to concrete concepts. Psychologists, for example, think nothing of using <u>pictures</u> in concept and category research. From the point of view of the cortex, the two other main input types are auditory representations of objects (not words, but things like cackling chickens and creaky chairs) and somatosensory representations of objects (how they feel). A moment's thought shows that there is quite an asymmetry here-- consider for a moment, the purely auditory representation (without words) of "chair", "line", "give", "big", "many", "on (top of)". These and many other concepts seem much more easily conveyed in pictures, and rightly so, since primates are highly visual animals. Bats, on the other hand, would have quite a respectable acoustic representation of a chair, just as platypuses have a finely detailed somatosensory representation of many objects (they normally forage underwater with their eyes and ears closed using only an exquisitely sensitive bill which gives them their name). The straightforward conclusion is that in primates in particular (but in many other diurnal animals as well) many of the meanings might be comfortably be put into visual cortex. Of course, blind people have concepts, too; but their concepts could be predominantly somatosensory, as has been suggested in other contexts (try the same set of words as somatosensory objects-- they seem to work much better than as auditory objects). As far as I know, there hasn't been a case of a human deprived of vision and somatosensation, to be able to tell whether purely auditorily initiated concepts could, for instance, allow a language to be learned (cf. Helen Keller, who did quite well with only somatosensory input to posterior cortex).

Visual Cortex and Aphasia

Until quite recently, the perfectly reasonable hypothesis that a majority of word meanings might be based in the visual system seemed quite at variance with the localization of lesions in aphasia. According to that hypothesis, a secondary visual cortex lesion might be expected to considerably disrupt language understanding, yet such lesions were downplayed in most texts in comparison with secondary auditory cortex lesions. Recent reports (Hier et al., 1980, and especially, Rubens and Kertesz, 1983) show that left-hemisphere lesions located entirely within visual cortex reliably produce a syndrome that is inconveniently called "transcortical sensory aphasia" (i.e., "across from" the language area!), in which patients show very poor auditory comprehension, yet paradoxically, have preserved repetition (unlike Wernicke's aphasics and conduction aphasics, who have impaired repetition). Probably the main reason this wasn't reported before is that in contrast to severe Wernicke's aphasia (sometimes called "jargonaphasia"), severe transcortical sensory aphasia more often goes away, partially or completely after a few months. One reason may be that since the visual cortex shows less obvious anatomical asymmetry than secondary auditory cortex areas (especially Tpt), it may be functionally less lateralized and hence, it might be easier for the preserved right hemisphere secondary visual areas (as opposed to the right hemisphere secondary auditory cortical areas) to take over, or to operate by themselves. The fact that bilateral inferotemporal cortex lesions are needed to produce a lasting deficit in object recognition and pattern discrimination may be relevant here (review: Dean, 1982).

"Thing"-Representations

Preliminary neural network models like those of Anderson (1984) and Hopfield (1984) show that it is possible to store a large number of content-addressable patterns in a neural network in terms of the values in a connectivity matrix that specifies the strength of connection (back and forth) of each pair of neurons in the network. What this means is that a piece of one of the stored patterns, or a pattern that resembles one of the stored patterns, is "presented" to the network (i.e., the network is made to fire that way) then, the network will spontaneously evolve (along non-mixing trajectories) to the nearest stable state (i.e., a local energy minimum). The main requirements for stability are that the matrix is approximately symmetrical (i.e., connection X => Y is similar to Y => X) and that the neurons do not excite themselves too much (Hopfield, 1984).

Clearly, these models are highly oversimplified both quantitatively (30-100 neurons) and qualitatively (only one "area", only one "layer", no topography, no local circuits); yet their behavior is already a little brain-like in their high degree of parallelism and also of feedback (in contrast, for example, to "perceptrons"), their resistance to noise and damage, and their ability to generate discrete "categories" from continuously varying inputs. In the present analogy, the "thing"-representations are visualized as a set of complex, stable firing pattern states to which the neurons in the secondary visual cortical areas evolve, several hundred milliseconds after the presentation of different classes of visual stimuli, or after "direct" internal activation by an auditory cortex pattern, presumably, a symbol-representation (probably via a frontal or parahippocampal loop). The main evidence that the cortex does in fact sometimes exhibit discrete epochs of "relaxation" into more stable states comes from evoked potential studies (review: Desmedt, 1981). A working hypothesis is that a "thing"-representation might correspond to the synaptic activity responsible for the negative going (i.e., probably excitatory potential or potentials preceding a "P300" wave. The later P300 wave probably represents a momentary cortex-wide pause in activity; it has been associated in psychological experiments with a "resetting of short term memory Karis, et al., 1984). In line with the present proposal, Kutas and Hillyard (1983, 1984) have, in fact, explicitly identified a negative-going wave elicited in their experiments (sentences presented visually at 700 milliseconds per word) as a correlate of semantic priming.

An important aspect of these "thing"-representation patterns is that we would expect them to be generated prelinguistically as was argued in

Chapter III and as is the case for amino acids. The evoked potentials recorded from macaques are quite similar to those recorded from humans, and show early modality-specific negative waves and P300's (Neville and Foote, 1984), offering some indirect support for the notion that other primates (and probably mammals in general) develop cortical network activity patterns that might be similar to isolated word-meaning activition in humans.

A second point is that the constraints on folding-- approximately visible as word order syntax in language --arise from the simple juxtaposition and bonding of prelinguistic units. From this, we might predict that many of the "phenomena" in human language that are gathered together under the rubric of "syntax" may in fact eventually come to be identified as constraints on constructing "foldable", self-assembling sequences of prelinguistic neural firing pattern units. This conception of syntax differs from the current picture promoted by Chomsky and his followers (summaries: Lightfoot, 1982; Newmeyer, 1984) of an "autonomous"-- i.e., strictly language-specific --"organ" containing a set of syntax "modules". Natural language syntax might instead be described as the opportunistic exploitation of the properties of chains of prelinguistic units-- properties that are, in a sense, inherent in these units. The prebiotic availability of "thing"-representations was used previously to argue that the major advance in the origin of life may not have been to invent such units, but to have found a way of attaching them together. The argument here goes even further-- i.e., there is little reason to think that the properties of the "folded" chain may be any more "autonomous" with respect to visual perception and cognition than are the basic word meanings themselves (cf. Jackendoff, 1983).

Polysemy

A suggestion implicit in the discussion of "molecular polysemy" is that polysemous words in language like "go", "get", "sweet", "line", and so on, are actually all instantiated by virtually the same pattern of visual cortex activity during assembly of the "thing"-representation chain. The reason that they appear to have such different meanings in context--e.g., "line" (of sight, of rope, of flight, of march, of trees, of battle, of kings, of duty, of work, of merchandise, of argument, of thought, of poetry, of type) --is from a tendency to attribute the properties that only arise in the context of a chain (cf. the specificity of interaction of an amino acid in a protein binding site) to the unit itself (example from Miller, 1978). The actual experience of a single isolated word meaning (with thoughtlessness before and after!) is probably a rare event; by analogy with the molecular level, one would expect the experience to be almost contentless and apparently non-specific, though in reality, it would involve a small but repeatable and uniform content. The molecular system shows us in concrete detail how thorough-going context effects can be, even with only 20 different recognized words; with over 5000 recognized words at the linguistic level, the possibilities for "specificity of reaction" within the world of neural firing pattern units is even more prodigious. The position that polysemy is is more apparent than real-- that it might be more a reflection of context effects --has been argued (e.g., Miller, 1978), though rarely in the extreme form presented here (but see Catford, 1984).

Subunits of Linguistic "Thing"-Representations

An intriguing possibility is that the linguistic word meaning units (amino acid analogues) might be similarly constructed of subunits as are amino acids composed of atoms (around 20 each). That analogy, however, suggests an interesting sort of decomposition rather different from the semantic decompositions commonly carried out in linguistics and psychology.

There have been various attempts over the years to analyze word meanings into simpler components (e.g., Katz and Fodor, 1963; "generative semantics" (review in Newmeyer, 1980); Miller and Johnson-Laird, 1976; Dixon, 1982). One of the most ambitious decompositions (Wierzbicka, 1980) argues for only 13 semantic primitives. The characteristic strategy followed in those and in many other related projects in psychology, linguistics, philosophy, and dictionary-making involves defining word in terms of simpler units that themselves, most often are perfectly good words (e.g., "kill" => "cause to make not alive"-- a notorious generative semantics example; "I see a dog" => "something happens in my eyes because of something that can be said about a place; I can say something because of that about something that is now in that place; one thing that I can say about that something is this; it is a dog"-- Wierzbicka, 1980, p. 111). By contrast, the atomic subunits of amino acids could never themselves function as stand-alone "thing"-representation units. An alternative strategy of decomposition at the linguistic level based on an analogy with the situation at the biomolecular level might attempt to build up the basic word meaning firing patterns by "bonding together" much simpler, <u>sub-word</u> firing patterns; this would mean decomposing even proposed semantic primitives like CAUSE, SAY, and SOMETHING into simpler units too small to act as word meanings on their own. Even the venerable "red at time t" would be too complex to be "atomic". By analogy with the molecular prebiotic milieu where unbound atoms are rare, we might not even expect to see these hypothetical "atomic" firing patterns ("linguistic atoms") in a "free state" even in prelinguistic animal brains (which instead would already support a core set of unbound, but already "molecular" word meaning patterns).

"Thing"-Representation Chains: Levels of Structure

The topics of protein structure and folding, and natural language syntax and semantics are both inherently much more complex than any considered earlier-- especially those topics concerned mainly with unit properties. This section must therefore be rather programmatic; there is only space to outline a few points of contact.

Levels of Structure in Proteins

Arbitrariness(3): Primary and Secondary Structure

At the molecular level, the local structure of an enzyme depends on the nature of the arbitrary bond that is generated between two amino acids. This bond is arbitrary in the sense that it can be formed between any of the 400 pairs of 20 amino acids. As was the case with the arbitrary(1) bond between symbol segments (deoxyribonucleotides) and symbol-representation segments (ribonucleotides), the stabilities of the 400 possible bonds are not greatly different (though they cover a greater range than the 16 possible internucleotide bonds). As with arbitrary(1) bonds, the two units involved are of the same type and each unit makes two bonds with other units (i.e., chains can be formed, in contrast to arbitrary(2) bonds, for example). The main difference is that the variable sidechains of each unit-- the R-group on each amino acid --do not interact directly with the sidechain of a neighboring unit (as is the case with nucleotides) but usually with the sidechains of non-adjacent units, or with the surrounding solvent. This difference is obviously correlated with folding behavior-- DNA with mostly local sidechain interactions tends to be "one-dimensional" while proteins with mostly non-local sidechain interactions, of course, are "three-dimensional".

The peptide bond develops pi (double-bonded) character, which causes successive groups of atomic nuclei in the chain to lie in planes; steric hindrance and restrictions on favorable H-bonding by backbone groups (NH and CO) then limits the rotation of these planar groups relative to each other. The end result is that there are only two readily available configurations of the chain (see fig. 23)-- the alpha helix (3.6 amino acids per complete turn) and the beta stand (2 amino acids per turn). These two structures describe much of the local geometry of the "thing"-representation chain (they appear as spirals and ribbons, respectively, in the schematic diagrams of protein backbones in fig. 24 (from Richardson, 1984)).

3-D Folding: Secondary and Tertiary Structure

Folded proteins exhibit a hierarchy of substructures, and several different definitions of these levels have been produced. In what follows, only two main levels of three-dimensional organization past the one-dimensional sequence structure are considered-- namely, the secondary structure element and the tertiary structure folding pattern

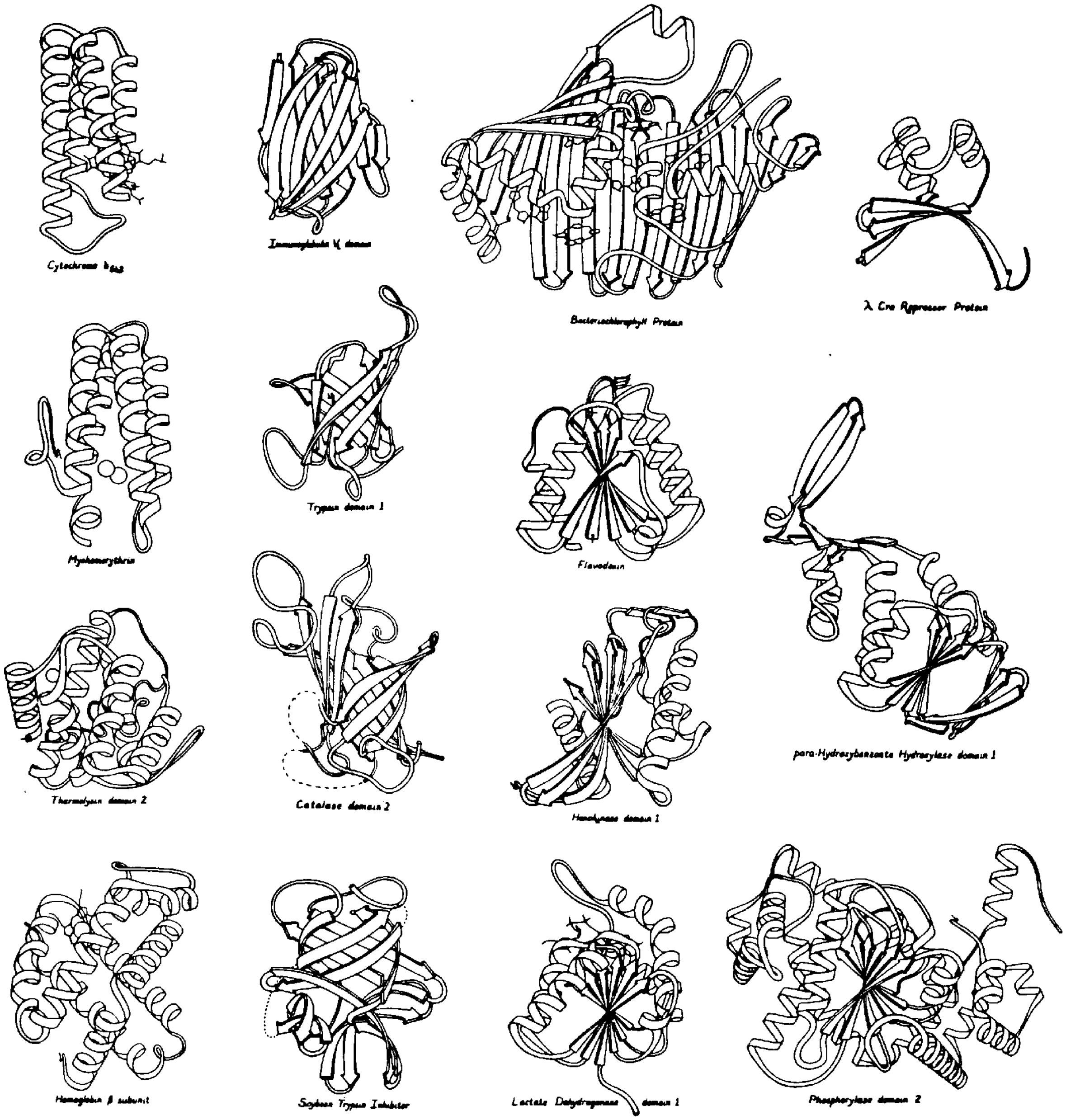


FIG. 24: Schematic Protein Structures (from Richardson, 1984)

within a domain. A <u>secondary structure element</u> is a continuous stretch (at least 4 or 5 units) of one of the two types of secondary structure.[2]

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[2] A significant fraction of the chain usually remains and is sometimes

A domain can be defined as a potentially independent, stable folding unit containing little free space (Richardson, 1981; see also, Sander, 1981; Go, 1983; Bajaj and Blundell, 1984). To anticipate, the first is approximately equivalent to a sentence while the second corresponds to a coherent discourse.

Secondary structure elements are usuallly rather short although occasional exceptions exist (e.g., an enormous stretch of alpha helix in an unusual viral cell surface protein). Taylor and Thornton (1984), for example, identified a reoccurring three-"sentence" fragment of folded tertiary structure (sometimes called a "supersecondary structure") consisting of two beta strands containing about 5 amino acids each and an alpha helix containing about 15 amino acids. Figure 24 (from Richardson, 1984) illustrates the variability in the number of secondary structure elements that may constitute a domain (each drawing represents one domain). Lambda cro repressor protein, for example, consists of just a few while bacteriochlorophyll protein has over 20.

There is a clear distinction between secondary and tertiary structure in folded proteins. The main difference is that secondary structure is not nearly as "three-dimensional" as tertiary structure measured in terms of the number of non-local interactions (i.e., interactions between units displaced a large distance from each other in the linear, unfolded chain). The contacts defining secondary structure are quite local; and this is reflected in the partial success of secondary structure prediction methods that are based solely on the empirically defined tendency of single amino acids to form an alpha-helix or a beta-strand (review: Schulz and Schirmer, 1979). Also, in a number of

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classified as "(random) coil". It is far from randomly organized, however-- e.g., in terms of backbone torsion angles --and might more informatively be called "mixed" secondary structure.

cases, small protein fragments have been found to fold into secndary structure elements of approximately native configuration (Wetlaufer, 1981). By contrast, tertiary folded structure is based on a large number of non-local contacts; as an example, each amino acid ("thing"-representation) in one well-studied protein makes contact with an average of almost 7 other such units that are 5 or more units removed in the chain (calculated from fig. 13 from Scheraga, 1981). One way to diagram the organization of a folded protein domain would be to list the string of "thing"-representations (analogous in some ways to "surface structure") and then draw lines between the units that interact directly (in the folded "deep structure"). This is not usually done because the average domain is between 100 and 200 units long (some are over 400 units) and would thus generate a formidable (and not very useful) tangle of intersecting lines; instead, a more abstract matrix representation is often used (a triangular "contact map" with each unit on both x and y axes). Even the smallest domains would require numerous crossing lines to indicate their connectivity in the first way, which, if nothing else, emphasizes their irreducible "three-dimensional" character.

Levels of Structure in Discourses

Arbitrariness(3): Word Order and Word Order Patterns

At the linguistic level, a crude model of how two patterns in a network could be "bonded together" along an axis between them was developed; the main idea was to change the location of the stable states relative to that axis by changing the connectivity matrix that determines the location in state space of the stable points. The connectivity matrix could be thought of as something like a "working memory" in which a "thing"-representation chain could be built up until it began to "fold". An important fact about molecular level "thing"-representations is that interunit bonding only involves the constant backbone. Thus, a distinction between the constant backbone part of a firing pattern and a variable sidechain part would need to be made.

Indirect evidence that there might be only a small number of "secondary structures" of the "thing"-representation chains comes from studies of cross-linguistic word order patterns that was stimulated by the seminal work of Greenberg (1966) (for recent perspectives, see Givon, 1984; Hawkins, 1984; Lugan et al., 1984; Maxwell, 1984). There has not yet emerged a consensus by any means on what the detailed rules of linearization might be, and the ability of inflectional morphology to essentially substitute for word order (see below) complicates the situation by loosening ordering constraints; nevertheless, the importance of simple ordering rules of the sort "always try to keep the 'modifiers' on one side of the 'heads' they modify" has been reemphasized-- even within the generative tradition (Jackendoff, 1977). It is important to keep in mind the indirectness of the connection between word ("thing"-representation) order and secondary structure. In proteins, where both are 'visible' in some cases, it is often virtually impossible to predict solely from the word order pattern whether a particular section of string will fold into an alpha helix or a beta strand, especially in the context of a longer string. Thus, even with the knowledge that the majority of protein secondary structure is unequivocally alpha helix or beta strand, molecular level "word order theorists" (for example, a protein chemist trying to predict the 3-D structure of a protein from a sequence-- actually a common goal in light of the paucity of known X-ray crystallographic structures) have had quite a difficult time. Since the neural mechanisms of language comprehension are unlikely to be simpler than the dynamics of protein folding, there is cause for sobriety. But at the same time, one can hold out the hope that the underlying "deep structure" of the folded "thing"-representation chain-- or at least, the first level of structure past the primary sequence --may turn out to be simpler than that "surface structure" has initially lead us to suspect.

3-D Folding: Sentence and Discourse Structure

At the linguistic level, one must obviously be more tentative in discussing the properties of as yet hypothetical neural substrates of language perception. Nevertheless, linguistic and psychological investigations point to a reasonably clear distinction between sentence and discourse structure. Perhaps the strict separation enforced by present day generative linguists is unwarranted; and surely the concomitant occupation with sentence structure to the complete exclusion of discourse structure is so. But, many parties grant at least a fundamental difference between the two. One indication of this is the difference in taste as to how linguistic structures should be graphically represented. Sentence linguists of many different persuasions-- e.g., Chomsky (1981) who retains transformations, Gazdar (1982) who shuns them, and Hudson (1984), who even disallows constituent structure (e.g., NP, VP) --employ the constraint that lines in a particular structural representation (of a sentence) shall not cross; their representations are somewhat restricted "two-dimensional" ones.[3]

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[3] Notice that even the connectivity of an alpha-helix "sentence" could not be represented as a two dimensional diagram without crossing lines if one is restricted to one side of the "surface structure" string-- i.e., if a tree diagram is used.

Of course, it is certainly going beyond the published intentions of most linguists to treat grammatical diagrams as representing actual facts about interacting neural firing patterns (but cf. Chomsky, 1980). It is still interesting, though, that discourse linguists and psychologists (Beaugrande and Dressler, 1981; van Dijk and Kintsch, 1983; Brown and Yule, 1983; Anderson, 1983) generally relax the "two-dimensional" tree constraint, either by using multiple diagrams of the same set of sentences, or by overtly permitting lines to cross. The clear implication of the molecular situation for the "connectivity" of linguistic discourse-- i.e., "tertiary" --structure (along temporal dimensions) in fact, is that each activiated word meaning assembled into a chain might end up interacting significantly with 5 or 10 other meanings at non-adjacent locations in the chain (in addition, of course, to "bonding" interactions with neighboring units).

Differences-- Word Length and Word Order

One clear difference between the molecular and linguistic chains is the development of a more complex word morphology at the linguistic level. The 61 molecular symbols (which stand for 20 meanings) are uniformly composed of 3 segments and almost all possible sequences are used. Linguistic words, by contrast, are much more complex; not only are they of different lengths, but they have budded off or tacked on various more or less independent excresences (e.g., derivational and inflectional affixes, clitics) that have come to perform a number of functions. Furthermore, in no known language are more than a fraction of the possible segment sequences used (see Chapter III).

A second difference has to do with the fact that functions performed by word order in one language can apparently be performed as well by morphological devices in others; the molecular level system, by contrast, is based strictly on word order. In English, as an example, the object is usually identified by its position after a verb-- e.g., "(the boy) hit the dog" --but usually has no inflectional mark to distinguish it from a subject-- "the dog hit (the boy)" --which usually comes before the verb. only a remnant of inflectional morphology persists in the English pronominal system-- e.g., "he hit him". By contrast, in Hebrew or Russion, for example, there are productive modifications of words like "boy" or "dog" that indicate (among other things whether the boy or the dog was doing the hitting, regardless of the order with respect to the verb (that order is then used to indicate other things like topic) (summary: Sapir, 1921; Comrie, 1981; Givon, 1984).

Inflectional and derivational morphology, and clitics are disproportionately affected by lesions in the production system; Broca's aphasics not only exhibit almost a total absence of them in productive speech but also have difficulty understanding them. This raises the intriguiging possibility that their lack at the molecular level might be related to the lack of production there.

Substrates and Function

Molecular Level Substrates

Once the chain has been folded, it acquires an extreme specificity for a substrate. The goal is more than recognition binding, however; often, it is the dissolution or formation of a covalent bond. To break a bond, for example, the shape of the active site is thought to be designed so that it best binds a high energy transition state of the molecule in which the bond to be broken is strained; if the bond then breaks, the products will tend to dissociate from the active site, preparing it for another catalytic cycle. In support of this picture, "transition state analogs" bind very well, but nothing happens to them (summaries: Walsh, 1979; Dugas and Penney, 1981). The variety of substrates is quite remarkable ranging from single "word meanings" (i.e., amino acids) to whole proteins, to other molecules in the symbol-representational system (e.g., nucleotides), to non-proteins and non-symbols (e.g., energy-rich molecules, metabolic intermediates, carbohydrates, lipids, and so on).

Neural Firing Patterns as Substrates

A major goal for the future is to develop the concept of "catalytic" modification (i.e. the forming or breaking of "bonds" as discussed previously) of one pattern by another in a neural network. It may be possible to articulate a unified description of "bonding" between neural firing pattern units general enough to apply not only to the construction of "3-D folded" chains but to the actions performed by such structures (created in short term working memory upon hearing a discourse) on their substrate patterns in the same network. As with the molecular case, the range of substrates may be enormous compared to the modest diversity of the units (i.e., "thing"-representation) that make up the reaction controllers themselves. These could include not only part of the symbolic-representational system like other stored "folded" discourse meanings now acting on substrates, and uninterpreted symbol representation segments and chains, but also other non-system units like emotional meaning firing pattern (presumably originating in the limbic system, but then fed into upper level visual cortex to "react"), images, and many other associated pattern units in what we might visualize as a sort of mental "intermediate metabolism", whose overall function might be to interconvert or dispose of various firing pattern 'fragments' generated in the course of a day's thought. These are highly speculative ideas, but they present an intriguing glimpse of what the brain's actual "operating system" might look like. It is quite a different picture than that implicitly suggested by the regimented, clock-pulse driven, compartmentalized, dynamics of a von Neumann machine.

A topic only briefly touched upon at the network level is the notion of "recognition binding" as opposed to bond dissolution or formation. Recognition binding is all important in a network crowded with myriad overlapping patterns; in fact, it is the ability of enzymes to specifically recognize their substrate rather than the ability to catalyze a reaction that most clearly distinguishes them from non-biotic catalysts. Unfortunately, recognition binding is not even very well understood at the molecular level, at least in comparison to covalent bonding; this is partly because recognition (like 3-D folding) involves the simultaneous satisfaction of a large number of weak constraints, while covalent bonding involves stronger, more localized constraints--and hence, responds well to treatments that ignore context. Nevertheless, a notion of pattern-pattern recognition binding at the network level distinct from the pattern-pattern "bonding" presented earlier will eventually have to be developed.

Higher Levels of Coordination and Interaction

Two parallels are striking at higher levels of organization. First, both systems control many "reactions" all at the same time and thus have both developed a high degree of specificity for recognizing various "substrates". At the molecular level, the basic network of reactions has been worked out in some detail (see fig. 25-- an abstract representation of the reactions in a cell). Anderson (1983) for comparison has estimated that the human "cognitive system" might contain on the order of 100,000 "productions". Although "productions" are clearly quite different in form (they are LISP programes) from the protein analogues in secondary visual cortex argued for here, they are of comparable complexity.

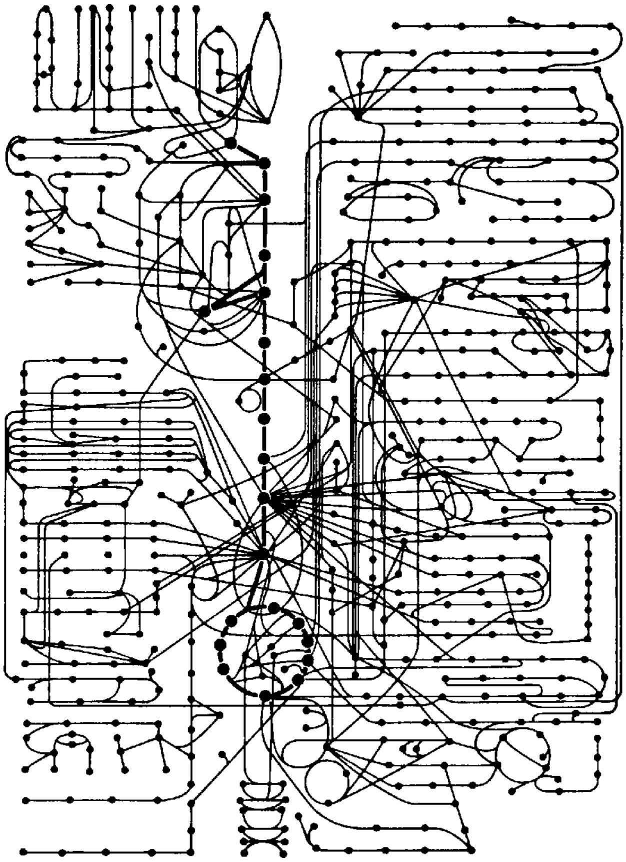

FIG. 25: Schematic Metabolic Network (from Alberts et al., 1983)

A Secondary "Symbiotic" Symbolic-Representational System

A second interesting parallel between the molecular and linguistic levels is that in both cases there is a secondary, partially autonomous symbolic-representational system associated with the main system.

Nucleus and Organelles

In eukaryotic cells, there is a central nuclear-cytoplasmic system and the secondary organelle system. The second system depends to a great extent on protein products from the first system. Nevertheless, many of the central components of the symbolic-representational system-- e.g., ribosomes, tRNAs and loading enzymes --are all completely distinct from their nuclear-cytoplasmic counterparts. The autonomy of the second system is emphasized by the recent discovery that the genetic code in organelles is slightly different from the nuclear-cytoplasmic code and varies as well from organelle type to organelle type (review: Kroon and Saccone, 1983). Also, the organelles divide throughout the cell cycle as if they were autonomous cells. It is thought that the organelles were initially symbiotic bacteria and blue-green algae (review: Margulis, 1981). The subdominant system (mitochondria, chloroplasts, possibly cilia) is particularly associated with the production of "generalized" energy rich molecules (e.g., ATP, NADPH) which are used by the main system to carry out more specific tasks.

Left and Right Hemishpere

At first, the existence of a second, 'symbiotic' symbolic-representational system in the brain might seem unlikely. Certainly, it is perverse to think that one could have entered the brain from without. If one puts aside differences in geometry, however, it can be seen that the left/right hemisphere dichotomy parallels in a number of key ways the nucleus/organelle dichotomy just outlined. As with organelles, the right hemisphere seems to have its own, somewhat reduced symbolic-representational system that under normal conditions, could be said to have a 'symbiotic' relationship with the more developed system in the left hemisphere. The non-dominant system in human brains is if anything, more autonomous than that in cells; in fact, the right hemisphere appears to be able to understand language on its own, even when disconnected from the normally dominant left hemisphere (Zaidel, 1983; Gazzaniga and Smylie, 1984). In parallel with the molecular system, the subdominant system (operating on its own) has a smaller symbolic repertoire. A strong, functional analogy can be drawn in the right hemishpere's close ties with the "limbic system"-- a somewhat poorly defined collection of brain regions that are responsible for "generalized" neural activity patterns (e.g., drives like hunger) that are subsequently turned into more specific patterns (e.g., food foraging behavior appropriate to detailed aspects of the specific environmental situation in which the hungry animal finds itself).

Community-Level Organization

So far I have concentrated almost exclusively on <u>intracellular</u> organization on the one hand and <u>brain-internal</u> organization on the other. As emphasized in Chapter I, there is a particularly salient level of organization that is defined by cell communities (multicellular organisms) and linguistic communities. Compared to the topics treated previously, the organism/community analogy has probably attracted more sustained (and notorious) attention over the years than any other, engaging writers as disparate in other ways as Herbert Spencer, Teilhard de Chardin and Lewis Thomas. My contribution to this tradition shall therefore be brief.

Modes of Communication Between Cells

Two basic coexisting, complementary modes of intercellular communication are often distinguished. The first is subsumed under the term humoral. This includes not only coordinating mechanisms based on hormones and other diffusible small-molecule signals *per se*, but also mechanisms involving a heterogeneous collection of cell-surface signals, receptors, and effectors. The second basic mode of intercellular communication is neural. This, of course, involves complex distributed patterns of activity in specialized cells called neurons.

The two systems are by no means completely independent; for example, neural communication depends directly on hormone-like signals at the synaptic junction, while release of hormonal signals is often quite directly controlled by neural elements. Nevertheless, in broad functional senses, the two systems are distinct enough. First, neural systems are capable of supporting much faster communication, allowing coordination of cellular activity at large distances with millisecond accuracy. Second, neural systems have a much larger "memory capacity" for events taking place in the life of a single organism. The humoral system is also capable of "remembering" particular events (e.g., a period of a lack or surfeit of food, loss of a limb) but its specificity and capacity are quite limited in comparison with the brain, especially in more complex organisms.

Modes of Coordination at the Linguistic Level

Two broad, complementary modes of language-based coordination and communication have long been distinguished in the same form by anthropologists, sociologists, and historians of science, among others. The first, which parallels in several ways humoral coordination is 'myth'. Myth binds together and coordinates the activities of groups of people; myth provides a working explanation of things and events in the world. The second broad, language-based coordinating mechanism--'science' --has parallels with the neural systems. Science obviously also describes and explains the world.

As with the humoral and neural systems at the cellular level, myth and science are interdependent, and have indispensible functions in present-day social 'organisms'. But, also like the two cellular systems, the two linguistic level systems are distinct in terms of 'speed' and 'memory capacity'. Science, of course, has brought with it fast, long distance communication and coordination. Just as importantly, science has a much larger and more specific memory (e.g., in the course of an experiment) when compared to myth and allows mountains of detailed information about worldly events in the life of a particular social 'organism' to be remembered. Myth, by contrast, has a much poorer 'memory' and makes slower progress in finding out new things about the world.

Conclusion

The community level analogy suggested by the present analogy-- i.e., humoral and neural systems compared to myth and science --if nothing else, offers a fresh starting point. It differs markedly from a number of previous suggestions in the same tradition-- for example, the notion that one might be able to develop an "intellectual ecology" of scientific ideas. Whether it proves to be as productive remains to be seen. It would first have to be articulated in much more detail than in the preceding sketch.

CHAPTER VI

CONCLUSION

It is time now to assess progress toward the three goals laid out in Chapter I. These were: 1) to develop scale-independent criteria for a symbolic-representational system, 2) to point toward a preliminary model of language perception, and 3) to more specifically define what is required for an "evolutionary system". In the course of answering all three, the aim was also to articulate a certain philosophical perspective on meaning. It might seem a bit quixotic to propose to discuss all of these in place since each of the topics with the possible exception of the first have occupied many people for many years. Two points, however, need to be emphasized. First, the "answers" that I want to give to each of these inquiries are all closely related. Second, the answers are in each case presently still quite partial and preliminary. The main thrust here is really to bring out some of the implications of setting up the particular analogy between cellular biology and language described in Chapters II through V. A more extensive treatment of these issues is eventually foreseen.

Scale-Independent Criteria and a Preliminary Motivation

The existence of a structure common to life and language seems to indicate that there are quite determinate, scale-independent constraints on the origin and development of a symbolic-representational system. Most fundamentally, this process results in formation of a distinct relationship or "cut" between the system and the "world" that is lacking in non-living or non-linguistic entities (e.g., those studied by geologists-- igneous intrusions, meandering streams, tectonic plates). In more traditional philosophical terminology, such a cut could be identified as the subject/object relation, though most philosophers would probably object to cell-sized subjects and objects. In fact, I have argued that the relation is in some ways conceptually more transparent at the cellular level (see also Pattee, 1982), where a symbolic-representational system arose from a completely "pre-systemic" state, than at the linguistic level, where such a system arose "within" or on top of an already existing biotic one. Figure 12 was an attempt to summarize the major features of the common structure in more or less scale-neutral terms-- i.e., to give scale-independent criteria for recognizing a symbolic-representational system. Table 1 gives a parallel list summary of the comparable entities in the two systems.

Roughly, the claim was made that there are no other naturally occurring examples of such a system on Earth at any intermediate level between the almost independent cellular and linguistic instantiations (there is of course a weak connection in the genetic propensity for humans to develop a language). Neither is there presently any evidence for a distinct, third parallel system at subcellular levels, or at levels beyond persons. These claims are actually not as metaphysical as they at first might appear. First, consider the rather large number of parts and relations specified by Figure 12. One process illustrated is "word-recognition"-- by which small, contiguous groups of meaningless segments from a long chain are actively recognized one after another to stand for minimal meaning units. Even if there was a putative non-biotic, non-linguistic analogue of this process, it would have to meet many other criteria before we would want to call it a

TABLE 1

SUMMARY OF THE ANALOGY

General Term	Molecular Biology	Language
symbol (S)	DNA triplet	sounds in a word
symbol segment	DNA nucleotide	single phonetic segment
symbol-representation segment	RNA nucleotide	secondary auditory cortex areas (i.e., "Wernicke's area") representation of a phonetic segment
internal message (chain of SR segments)	messenger RNA (mRNA)	phoneme-like activity patterns in secondary auditory cortex areas
word recognizer, same as symbol-representation (chain of SR segments)	transfer RNA (tRNA)	secondary auditory cortex areas "adaptor" pattern that recognizes phoneme groups and activates its 'attached' meaning
chain assembler (chain of SR segments)	ribosome (contains rRNA)	secondary auditory cortex areas patterns that assembles unit meaning patterns into a chain
3-D connector (chain of TR's)	aminoacyl-tRNA synthetases	secondary visual cortex areas neural firing pattern to "attach" meaning patterns onto "adaptor" patterns prior to word recognition
"thing"-representation (TR)	amino acid (AA)	secondary visual cortex areas category representation; a firing patttern lasting for several hundred milliseconds; a word meaning
reaction controller (chain of TR's)	enzyme (4-20 sections of secondary structure per domain, each containing a hundred or more amino acids)	bonded-together "structure" generated in short term working memory upon hearing a discourse (4-20 clauses, a hundred or more words)
substrates (heterogeneous intermediate objects)	enzyme substrates (including, AA's, proteins, carbohydrates, lipids, small molecules, etc.)	mental "substrates", the "objects" of the mind (including single word meanings, discourse meanings emotional meanings, images, and many intermediate sized units
"things" (T)	substances in the prebiotic soup (e.g., water, HCN, formaldehyde, amino acids)	prelinguistic firing patterns in the primate brain arising in the course of development but mostly integrated into larger units in adult (less complex than a word meaning)

symbolic-representational system (e.g., the meaning units would themselves have to be initially assembled into a linear chain, and so on). Second, there is the great prominence of the two attested systems.

Both systems, for example, minimally require very long symbol chains (DNA, speech sounds or print), measured in millions of segments. It is sometimes easy to forget how peculiar an animated, hour-long conversation consisting of perhaps 30,000 closely connected segments in largely non-repetitive sequences must appear to a contemplative non-linguistic primate. The immense, mostly non-repetitive strands of DNA segments in cells are equally distinctive in the (prebiotic) molecular milieu. In fact, I think the existence of an <u>independent</u>, intermediate system is ruled out by even a rather casual inspection of presently known intermediate level phenomena. The situation is nearly as clear at larger and smaller scales. In the remainder of this section, the structural and functional criteria are summarized and then the motivations for similarities that were introduced at the end of Chapter I are developed in a little more detail.

Scale-Independent Criteria

Instead of redescribing Figure 12, I would like to explicitly summarize the primary distinctions on which it is based in light of the analysis presented in Chapters III, IV, and V. The task of coming up with truly scale-independent descriptions is obviously hampered by the minimal 'sample'-- i.e., only two different symbolic-representational systems. This task, of course, is a version of the venerable problem of giving a definition of life, which has a long and intriguing history. A prescient and influential treatment of the problem was the short book by Schrodinger (1944). Four decades later, a great mountain of detailed information about the molecular configuration of living things has accumulated. It seems to me, nevertheless, that the more general philosophical question of how to define life has remained fallow. Most biologists would deem it solved-- i.e., living things are cells or groups of cells containing nucleotides and proteins arranged in the way described in a molecular biology textbook. One advantage of the present project is that although it treats only one more example of a symbolic-representational system-- in a sense, a second kind of "life" --the second example is on a different enough level that we can begin to pick apart the scale-dependent features from the scale-independent ones. Though a few more examples would help greatly, it is possible that there are non reasonably close by.[1] From the point of view of the present project, it is rather ironic that conscious attempts to produce a general, scale- and substance-independent definition of life (e.g., Feinberg and Shapiro, 1980, pp. 141-179), though peppered with speculation about exotic creatures possibly living in the mantle, in the interior of the Sun, in the deep atmosphere of Jupiter (which probably has no true surface) as large "balloons", or in the hypothetical cold

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[1] The enthusiasm about life on other worlds has been dampened somewhat by the recent planetary probes, which revealed surprizingly inert and dismal (at least by Earth standards) conditions on Mars, Venus, and most of the moons of Jupiter and Saturn. Craters from the "Great Bombardment" (4.0-3.6 billion years BP) eroded and subducted away long ago on Earth are still visible on most of the terrestrial bodies. Current hopes remain pinned mostly on cloud-covered Titan. The larger question of the existence of Earth-like planets outside the solar system is more difficult since at present, they cannot be directly or indirectly observed. The fact that the majority of nearby stars appear to be binary taken together with the Sun-like composition of the Jovian planets has been used to argue that some other single stars might at least have gaseous planets (subequal binaries do not support stable planet orbits) (see summary in Shu, 1982). Terrestrial planets on nearby stars cannot be ruled out, but it is difficult to estimate how probable they might be. One recent estimate is that there might be between one and a hundred Earth-like terrestrial planets within 1000 light-years (Pollard, 1979).

A common argument against "intelligent" life nearby begins by noting the unlikelihood that the other life would be at exactly the same stage of development as us. It is much more probable that the other world would be, say, a billion or so years ahead or behind (in a 10 or 20 billion year old universe). A billion years ago the Earth was populated mostly by bacteria, while a billion years hence, it is conceivable that we might have checked out or signalled all the reasonably nearby methane sea on Titan, have failed to even mention the most observable "new life form" of all-- namely, language.

Complexity

Symbolic-representational systems seem to be characterized by a minimum level of complexity. This is most clearly defined at the molecular level by the smallest free-living cells-- the mycoplasmas (bacteria-like organisms, but without cell walls) --some of which have a genome 1/5 the size of E. coli (review: Neimark, 1979). These minimal genomes contain under a million DNA bases (symbol segments) and code for less that a thousand proteins ("thing"-representation chains). Viruses contain about one (e.g., T4) or two (e.g., M13) orders of magnitude less DNA, but, of course, require a host cell to grow and reproduce. It is harder to define the minimum "size" of a language; linguistic systems seem so much more open ended. In fact, most linguists (especially generatively minded ones) and philosophers (e.g., Davidson, 1976) would balk at the idea of setting a limit to the number of sentences or discourse meanings "in" a language, insisting instead that there are infinitely many possible. Set against this, however, is the obvious fact that any one

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possible worlds. By analogy, the present lack of obvious extra-terrestrial signals or contacts suggests perhaps that there might only be "bacteria" or nothing at all on nearby worlds.

Notice that the "intelligent" life scenario above more or less assumes the existence of a secondary symbolic-representational system past life itself, and probably language production as well. On Earth at least, it seems somewhat unlikely that the comparatively leisurely rate of evolution allowed by the organic system without production would give, say, insects, fish, or even New World monkeys enough time to have evolved a non-language-based interest in exploring the universe. The recent suggestion that many of the major bursts of speciation in the fossil record have resulted from recurring catastrophic meteorite impacts disturbing a globally rather static ecosystems (Raup and Sepkoski, 1984) could point to an even slower "intrinsic" or "natural" rate of evolution for a "perception"-only system, again, at least on Earth. We have clearly reached, however, the point of untamed speculation.

person can only experience a finite, though rather large number of sentences while learning and using a language. The total number of symbol-segments involved is actually not as large as one might as first think. For example, it would take 10 years to experience a billion segments at the rate of 300,000 per day (approximately equal to 8 hours of continuous speech per day). A billion symbol segments is only about two orders of magnitude more symbol segments than there are all at once in 'normal' cells. Such a number is not out of line with other crude numerical "size" comparisons between the two systems (e.g., two or three orders of magnitude more word meanings in language than in cells, an order of magnitude more kinds of symbol segments than in cells). By analogy with comparative cytology, it is possible that a <u>self-reproducing</u>, <u>independent</u> (i.e., "free-living") symbolic-representational system (in contrast, for example, to a language understanding computer program) at the linguistic level minimally requires the perception of at least millions or perhaps even a billion ordered segments.[2]

There are some problems with the direct comparison given above. First, cells "perceive" many of their DNA messages simultaneously. Second, they reprocess some over and over as verbatim repeats throughout their lives. People, by contrast, under normal conditions only actively comprehend one message at a time and verbatim repeats seem to be less common. The first difference is a real architectural one-- there is only one chain assembly apparatus per person, but many per cell

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[2] From this point of view, an artificial intelligence program designed to interact with the world (e.g., read a menu and order in a restaurant, to use a task chosen by R. Schank) is a little like a virus in its dependence on the machinery and real world knowledge in its designer's brain. This analogy breaks down, however, in that it is not at all clear, to me at least, that LISP is the language of thought, whereas, viruses have the same type of DNA and proteins as their hosts do.

(ribosomes); in light of the fact that many different types of assembled "meaning chains" build up in both cases, however, this difference seems less profound in the end. The second difference having to do with lack of verbatim repeat perception seems to be yet another of many examples of increased flexibility made possible by the presence of linguistic production. The main point not to lose sight of is that the minimum number of actual "meaning chains" (proteins, discourse meanings) is large relative to the number of basic meaning units (amino acids, word meanings). In cells, the difference is about two orders of magnitude (20 amino acids, thousands of proteins). A similar ratio extended to the linguistic level would suggest that the minimum number of discourse meanings needed to support a linguistic system might be on the order of a million (a similar estimate has been made by J.R. Anderson, 1983, p. 132).

The numbers given here are, of course, quite rough. Nevertheless, there are clear implications about absolute levels of complexity necessary to support a symbolic-representational system. Even 10,000 ordered symbol segments is not enough. In addition, there must be many more different types of meaning chains than there are types of meaning units. This does not absolutely rule out "reduced" systems, but it is unclear, especially at the biological level, what one would look like. Also, it seems perfectly possible that the primordial life forms (or language forms) "crystallized" out of a highly complex, interactive (but still prebiotic) matrix, as opposed to being built up piece by piece out of simpler isolated parts. From this perspective, the requirement of a minimum level of complexity need not imply saltationism; rather, some prebiotic or prelinguistic situations might have been 'preadapted' to develop a symbolic-representational system (though strictly speaking, "preadaptation" implies adaptation to something else, which would not have been possible prebiotically).

Units

Most of the detailed arguments given in Chapters III, IV, and V depend on the recognition of stable, objective units of different kinds. Even at the biological level, the recognition of hierarchical units for certain purposes is quite controversial. This is the case, for example, with units of biological selection (see Brandon and Burian, 1984). The units of biological structure important for the present project (see Figure 12 and Table 1)-- e.g., nucleotides, amino acids, enzymes --are in fact accepted as real, objective, structural units by all parties in spite of the fact that they are probably rarely units of selection. (this situation contrasts with some of the higher level population structure units that may very well be important units of selection, but whose existence as objective structural units is harder to document). The phenomena underlying linguistic behavior are presently less well defined than their biological counterparts and one of the main strategies was to use the better defined biological units as a guide to theorizing about some of the underlying units there.

One main criterium used for recognizing units (in a larger structure) is that they must be able to exist stably in an "unbound" or "free" form (as well as in a bound form). Amino acids, for example, are especially good units in this sense; many are extremely stable and regularly appear as isolated molecules in prebiotic synthesis experiments. The linguistic implication is that a core set of "word meaning" firing patterns (analogous to amino acids) might be prelinguistically generated in primate brains as stable, "unbound" firing patterns (i.e., not built into an interactive structure in short term working memory, but only appearing in "isolated" form-- see below on "bonding").

A complementary way of finding units described in Chapter II is to start with an already assembled structure, and then break it down using various pre-systemic "reagents". This was successful in defining the basic units of molecular symbol chains (nucleotides) by hydrolysis even before the stereochemical structure was known (from which the units can be determined by mere inspection). A linguistic analogue of this can be found in experiments where speech sound streams are presented to the 'reagents' in the brains of prelinguistic animals to see how they are 'broken down'. Preliminary results suggest that animal perceptual systems may have a strong tendency to divide the stream between what we know to be the linguistic symbol segments.[3]

The three major types of units described in Chapters III, IV, and V-- symbol segments, symbol-representation segments, and "thing"-representations --could each be further analyzed into a constant backbone part and a variable sidechain part. At the biological level, the backbone-sidechain connection can be identified in some cases as the next least stable bond after the interunit bond (this is so, for example, in the hydrolysis of nucleotides); this is not possible in other cases (e.g., some amino acids lose a carboxyl, a part of the backbone, rather than the sidechain upon hydrolysis) and the distinction must then be made on structural grounds. At the linguistic level, a backbone (FO, the fundamental frequency) and a sidechain (formant

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[3] Proteins too, can be prebiotically analyzed to give amino acids units (e.g., by simple hydrolysis). The corresponding experiment with prelinguistic animals, however, would be quite difficult. One would have to somehow cause a pattern of activation corresponding to a discourse meaning to appear in a non-linguistic primate brain, and then see what happened subsequently.

frequencies) can be distinguished in many speech sounds (though a few lack the backbone). The backbone-sidechain distinction is presently less obvious from a functional viewpoint with other linguistic units (e.g., with the proposed analogues of amino acids) and may only become apparent when the underlying "structures" of the neural firing patterns are finally revealed.

Bonding

The three major types of units listed above are each capable of "bonding" to each other to form linear chains. "Bonds" in the present usage have several distinguishing features-- they occur between pairs of units, their configuration depends mostly on local factors involving the bonded pair, the bond modifies both units with respect to an axis or a plane between them, and a bonded pair has different properties than a pair of juxtaposed but "free" units. Higher order, non-local effects, if they occur, are due to "transitive", order-dependent interactions; in general they do not involve strong local bonds of the sort that occur between units.

At the biological level, the notion of covalent bonding is well developed in quantum chemistry, and the modifications in electronic structure that constitute a chemical bond can be very accurately calculated in some cases (see e.g., summary in Flurry, 1983). The interunit bonds described above (internucleotide bond, peptide linkage) are a subset of chemical bonds. They occur between pairs of nucleotides or peptides, their configuration depends to a large extent on the particular pair (though non-local factors can choose among a few possible configurations), and the bond modifies both units with respect to an axis or plane between them (e.g., a plane in the case of the peptide bond, which has double-bond (pi) character). There is in practice a clear distinction in electronic structure between a covalently bonded pair of units and a pair of free units simply juxtaposed (e.g., during an unreactive collision), or stuck together by simple Coulombic forces ("ionic bonds).[4]

At the linguistic level, a preliminary model (really an idea for a model) of "bonding" was developed in which two stable firing pattern units (represented as vectors in a firing pattern state space) would be modified with respect to an axis between them (by by changing the neural connectivity matrix-- approximately, short term working memory). As with a chemical bond, this process would be "local" in the sense that the modifications involved depend only on the two temporally adjacent units and would be little affected by temporally separated units (this does not imply that the linguistic level units involved in a bond are local in a <u>spatial</u> sense-- i.e., they could each be distributed across much of the network). Higher-order interactions (e.g., "folding") between temporally non-adjacent units would usually be conditioned by weaker interactions, spread over more units, and involving the simultaneous satisfaction of a large number of constraints (see "1-D and 3-D" below).

The notion of covalent bonding at the chemical level is very general and applies to many other connections besides those between amino acids or nucleotides. For example, covalent bonds are made and broken in substrate molecules at enzymes active sites. they can also exist between non-adjacent units in a chain (e.g., the disulfide linkage in

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[4] There is a continuum of bond types from "pure covalent" to "pure ionic"; nevertheless, the local interunit bonds in polynucleotide and polypeptide backbones are obviously covalent bonds, while the non-local interunit interactions are, for the most part, clearly non-covalent.

proteins), and of course, the units (e.g., amino acids) themselves are built up from subunit atoms held together by covalent bonds. It is interesting to contemplate a generalized "bonding" at the neural network level. By analogy, it may be that a major purpose of a perceived linguistic discourse is to generate an internal structure capable of manipulating "bonds" (i.e., moving "locations" of stable firing pattern states) between parts of "substrate" firing patterns. Similarly, there may be at times some strong "bonding" of this type between the units in the linguistic level chains (such a process may be involved in anaphora), and the various firing pattern units in an adult human brain may themselves have originally been built up by "bonding together" in the same sense, groups of sub-word or "atomic" firing patterns early in development (by analogy, even prelinguistic animal brains would probably be capable of this).

1-D and 3-D

A major distinction developed in Chapters III, IV, and V involved "one-dimensional" and "three-dimensional" chains. Symbol segment chains were described as "one-dimensional", symbol-representation segment chains as an intermediate case, and "thing"-representation chains as fully "three-dimensional". In one-dimensional chains, the constituent units interact only with their nearest neighbors; there is no tendency for particular, stable associations between non-adjoining units to arise. In three-dimensional chains, by contrast, though the nearest neighbor interactions are still by far the most vigorous, a repeatable set of less vigorous interactions arise between pairs or triples of non-adjacent units, defining a unique "folded" structure.

On the subject of dimensions, George Temple states in his (1981) overview of the last century of mathematics that

> There are at least half a dozen different theories of dimensions, and dimension theory consists essentially of the construction of the various different definitions of dimension and the investigation of their equivalence. In each case it is of crucial importance to examine the topological invariance of dimension, i.e. to prove that two spaces which are respectively of dimensions m and n cannot by 'homeomorphic' unless m equals n (p. 130).

I do not intend to (and would hardly be capable of) furthering this cause. The notions of "one-" or "three-dimensionality" developed previously are much less abstract and general than the topological ideas referred to by Temple. The "one-dimensional" symbol segment chains described above are by no means composed of point-like units (though, perhaps, one might attempt to map them onto points in a more abstract space) and there is no particular interest here in rigorously determining the properties of a biomolecule that are preserved under continuous transformations (deformations). Now a topologist in effect transforms or analogizes a protein with a great many more types of things than we have done here. In fact, a useful heuristic for predictive analogy (<u>pace</u> Duhem) might be paradoxically, to keep the analysis <u>un</u>abstract and system-specific enough (at least to start with) to be able to make concrete predictions about unknown or "hidden" phenomena.

At the biochemical level, the difference between "one-dimensional" DNA and "three-dimensional" RNA was traced to the increased local stiffness afforded by an extra oxygen in the RNA backbone; the resulting stiffer RNA helix can then somewhat counterintuitively force the appearance of determinate, <u>folded</u> structures. The more flexible DNA helix folds too easily to fold as determinately. Categorical perception-- in which variable exemplars of sounds are funnelled into the same percept --is analogous to increased stiffness. The analogy then predicts that "stiff", standardized patterns (like those thought to underlie categorical perception at some level) might be required to build up a determinate, "three-dimensionally folded" firing pattern in secondary auditory cortical areas. More "flexible" patterns-- i.e., that follow the stimulus closer --would not be expected to result in determinate, temporally non-local interactions between firing patterns in the neural network.

When proteins fold, compact structures called "domains" arise in which there is little free space. There are two main levels of three-dimensional structure beyond the "primary" one-dimensional sequence structure within a domain-- namely, "secondary" structure elements (lengths of alpha-helix and beta strand, beta turns), and "tertiary" structure (pattern of association of secondary structure elements). A sentence (or more precisely, the interaction between firing pattern units-- presumably in secondary visual cortex --resulting from the comprehension of a sentence) was suggested to be the analogue of a secondary structure element, while a 'paragraph' or a connected discourse (again thought of as interacting neural firing patterns) was suggested to be the analogue of a protein domain. The sizes of each of these two types of three-dimensional units measured in terms of "thing"-representation units are approximately comparable in the two systems (often ranging between 5 and 15 units). Small proteins contain only a few secondary structure "sentences" while large domains may contain as many as 20. Quite similar estimates of the range of lengths of a cohesive discourse have been given for language (using, for example, the number of sentences over which a pronoun rather than a full referent may be used) (see e.g., Beaugrande and Dressler, 1981; Givon, ed., 1983).

In folded proteins, there is a clear distinction between secondary and tertiary structure. Secondary structure tends to be determined by local sequence and local packing effects involving only one or two nearby units while tertiary structure is based on larger numbers of interactions with units at a considerable distance in the linear, unfolded chainn. Tertiary structure is more "three-dimensional" than secondary structure. The implication for the connectivity (along temporal dimensions) of a lingusistic discourse is that each of activiated word meanings may end up interacting with 5 or 10 other meanings at non-adjacent locations in the chain. It would be possible only to illustrate a small fraction of such an irreducibly "three-dimensional" structure, especially if one was determined to use a "tree" diagram (in fact, it is not even possible to indicate the connectivity of an isolated alpha helix in this way!). There has been, of course, a perennial enthusiam for using these diagrams or their formal equivalents; the present analogy suggests at the very least that other conectivities be tried out (cf. McNeill, 1979).

Rates

The rate at which "thing"-representations are assembled into functional chains is surprizingly similar in absolute terms for the two very different sized systems-- the rate of protein synthesis in eukaryotes and of speech perception or reading averages between 2 and 4 units per second (prokaryotic protein synthesis is 6 times faster, however-- Lewin, 1983). I can see no obvious reason why this should be so, especially considering the greatly differing rates of other processes at the two levels; many molecular processes (e.g., protein fluctuations) are almost instantaneous when measured on a time scale appropriate for observing the evolution of neural activity in a neural network. An interesting possibility is that a very profound scale-independent constraint on absolute rate of chain assembly exists. But whatever the case may turn out to be, the fact that the rate of the most fundamental and most complex process in a symbolic-representational system _is_ equivalent for the two systems allows interesting direct comparisons of other processes to be made. Thus, the vastly different rates of evolution observed in the two systems probably cannot be attributed to scaling; instead, it was suggested that the presence of language _production_ at the linguistic level might be mainly responsible for the differences.

A Second System on the Substrate of the First

A clear difference between the two symbolic-representational systems discussed briefly in Chapter I is that while the first arose from a substrate containing no other symbolic-representational systems, the second system actually arose within the context of the first. Heretofore, a number of significant similarities between the pre-systemic states at the biological and linguistic levels were emphasized, and it was argued that the two systems are in many ways uncoupled from each other, especially with regard to what we might roughly call their "information content". In this section, I would like to point up a few differences.

One of the most basic differences is that the second symbolic-representational system developed within already defined enclosures (hominid brains) in contrast to the first system, which among other things, defined its own enclosures (cells); the prelinguistic "soup" came in predefined packages. The need for control and coordination of "reactions" in such a partitioned soup, however, was nearly as great as in the prebiotic case, where it is often assumed that a more homogeneous situation initially prevailed.

A second difference has to do with the hypothetical independence of the two systems. There is a fundamental asymmetry here. It is difficult to imagine a linguistic level system originating <u>de novo</u> and existing by itself, while a biological system did just that and existed by itself for a great majority of the Earth's history. One gets the feeling that the boost in complexity, if that is the best word for it, given to the Earth by life was virtually a prerequisite for a linguistic level system to have arisen.

Finally, the fact that the second system arose on a substrate of the first probably partially accounts for the existence of production at the linguistic level. Human language arose within primates, which as a group have evolved some of the most complex social behavior seen in the animal world, and in particular, a variety of visual, vocal and tactile gestures. These gestures initially evolved for other reasons than to support a symbolic-representational system; but when such a system did arise at the linguistic level, the pre-existing communicative systems must have predisposed early hominids to develop an ability to produce as well as to perceive the language. The structure of the biological system, nevertheless, seems to indicate that a perception-only system is perfectly capable of maintaining a homeostatic network of reactions, and probably, that the perception-only system is more basic.

Motivations for Observed Similarities

In Chapter I, several preliminary motivations for similarities were sketched. In the following sections, I would like to restate those points in light of the discussions just given.

Specificity

As previously noted, the need for specificity arises because so many distinct reactions must be run in close proximity. Some of the assumptions behind that statement should now be clearer. First, the need for many reactions-- a minimum level of complexity --appears to be an inherent property of a symbolic-representational system. It seems quite likely that even 100 reactions is not enough; the minimum is probably nearer 1,000. Second, the need for proximity (and hence specificity) reflects the requirement that the system, roughly put, has to be self-assembling. This is brought out by comparing a cell to an organic chemist, another entity clearly capable of controlling chemical reactions. Typically, an organic chemist can get away with (or must use) much less specific reagents and catalysts than a cell uses and yet still come up with specific end results. The chemist does this by completely isolating long sequences of reaction mixtures and products in space and time. Cells, too (especially eukaryotic ones), capitalize when possible on spatial and temporal isolation of enzyme mediated reactions; but compared to a chemist's reaction vessel containing a few reagents, the crowded phenomenology of the cytoplasm or an organelle demands highly specific devices. It would not be possible to 'uncrowd' the cytoplasm into thousands of separate containers and still have the whole system operate in real time. In the same vein, an organic chemist's approximation of the Krebs cycle using standard laboratory techniques would be amazingly energy intensive compared to the real thing, and not suited to incorporation into a self-maintaining system (i.e., without a chemist!). The serious conclusion to be drawn is that the specificity-demanding conditions under which the biological reaction controllers must operate are quite probably impossible to avoid in the design of a symbolic-representational system. At the linguistic level, the implication is that a similar minimum level of complexity of interacting neural firing patterns demands similarly specific devices to control "reactions" between them.

Pre-existing Units

A second constraint producing similarities is the use of certain types of pre-existing units to build up devices in a symbolic-representational system. Each system arose from a complexly patterned substrate containing several different types of self-assembling, stable units. In chapter III and IV, it was argued that a stable unit in a highly interactive "soup" could be seen as a category representation-- i.e., a single entity standing for a class of reactants and collisions that could potentially have given rise to it. By itself, such a definition is circular since everything represents everything else. In reality, however, the chemical and neurobiological constraints of the prebiotic and prelinguistic situation give rise to a reproduceable and surprizingly limited set of units quite distinct from the starting materials of primordial gases or equally 'primordial' innate firing patterns in developing neural circuits. In addition, only a subset of these pre-existing units are suitable for incorporation into a symbolic-representational system. First, some of the units do not possess a suitable backbone and sidechain structure for constructing a chain with variable unit properties but also with standardized interunit bonds (e.g., some aromatic bases are relatively easily available prebiotically yet unsuitable in this way for concatenation into a chain). Second, even some of the units with a proper backbone and sidechain are not usable for the reason that they do not develop a determinate enough three-dimensional structure when assembled into a chain (e.g., beta amino acids as well as the biotic alpha amino acids appear in electric discharge experiments, but the additional "joint" in each beta amino acid monomer probably leads to more floppy, metastable, and hence less desirable three-dimensional structures).

Local Assembly

A third important constraint producing similarities involves the method of building up complex three-dimensional structures. The end product of chain assembly-- the completed protein or the firing pattern built up in short term memory upon comprehending a coherent discourse --is a very complex "device" compared to primordial subunits, pre-systemic units, or many "metabolic" intermediates. Just as the overall reaction network describing a symbolic-representational system appeared to be characterized by an irreducible or minimum level or complexity, the separate reaction controlling devices involved are quite probably unavoidably rather complicated things.[5] An additional difficulty in

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[5] There have been various concrete suggestions at the molecular level why this should be so-- e.g., why enzymes apparently need to be so large (reviews: Richardson, 1981, 1984; Welch et al., 1982; Bajaj and Blundell, 1984). One controversial suggestion is that enzymes need to be large because they act as "energy funnels", dynamically coupling thermal fluctuations of the ambient medium to catalytic events. Other authors have emphasized the reoccurrence of complex, highly symmetrical structures in structurally and evolutionarily unrelated proteins (e.g., the 16-piece alpha-beta barrel seen in triose phosphate isomerase and pyruvate kinase domain 1-- see Richardson, 1981, p. 264) that appear to reflect general constraints on foldable structures rather than adaptations for particular functions at the active site, which often

assembling the "thing"-representation chains in question, of course, is that it must be done by recognizing particular groups of symbol segments in a coded chain (which have an essentially pseudo-random order) to stand for particular "thing"-representations. Doing all this at once with a low error rate probably mandates that it be done locally, one unit at a time, rather than simultaneously across the coded template (e.g., as originally proposed in the late 1950's). Notice that this is a somewhat more specific argument that the one often given (e.g., Simon, 1973; Pattee, 1980)-- i.e., that proteins are complex systems and hence must be assembled from stable substructures --since a simultaneous template process also builds up a complex system from stable substructures. Taken together, however, these arguments might account for why chain assembly in a symbolic-representational system is such a profoundly local process involving 'dumb', context-free bonds. This is not to say that contextual effects are unimportant, but simply that they occur only after a series of fundamentally local interactions has defined the arena of possible non-local contacts.

Toward a Neurobiology of Language Comprehension

Other Perspectives on Language and the Brain

The question of how language relates to the brain is an old one, dating in its modern form to the end of the last century. In spite of this, frustratingly little progress has been made since those early formulations (the excerpts from the earlier literature given in Morton, 1984 are particularly revealing). Several recently fashionable schools

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seems tacked on somewhat haphazardly. In a few cases, however, sizeable supersecondary structures may be loosely associated with particular functions (e.g., the so-called "Rossman fold" for binding nucleotides). Other factors might be the need to have a large enough surface area at the active site to allow the weak, non-covalent, "stickiness" there to overcome the loss in entropy involved in immobilizing the substrate.

of linguistics and psychology have even sought to return to ideas about the brain and language relationship that predate the mid-nineteenth century (see e.g., Chomsky, 1980; Fodor, 1983; Pylyshyn, 1984; Morton, 1984).

This has provoked surprizingly little protest from neuropsychologists. Geschwind is an exception; in his (1984), he expresses considerable exasperation at rehearsals of arguments against functional localization based on car repair (as in "a broken starter gear tooth is not a starter noise suppressor") instead of the now quite substantial collections of human brain lesion data. As an instance of this practice, Morton (1984) in the same volume argues vigorously against localization but cites not even one CAT scan or blood flow study in support of his contentions. I do not want to impugn the value of psychological argument, but I do agree with Geschwind that the best available data at each level should be considered.

Other psychologists and philosophers have been equally adamant about protecting psychology from the brain. Fodor (1983) begins by granting that there are specific input regions in cortex whose connections and architecture might condition the processing that goes on there (see also Pylyshyn, 1984); thus, according to Fodor, primary visual cortex at least is mostly involved with visual processing. The jaundiced observer might point out that this has been known for a long time on the basis of rather unphilosophical investigations into its anatomical connections, neurophysiology, and the effects of lesions there (especially in humans). Nevertheless, when it comes to more important functions (symbolic processing) Fodor holds out for something like a common sensorium-- a flexible, unstructured central processing unit (a sort of programmable pineal gland that would have made Descartes proud) whose program content is entirely unconstrained by the brain tissue in which it happens to reside (by implication, in hypothetical polymodal "association" corticies localized somewhere in the parietal and temporal lobes).

Chomsky (e.g., 1980) has adopted a slightly different tack; instead of trying to keep special parts of his theory brain-free, he would ostensibly annex the whole of neurobiology and pyschology. In essence, he claims that linguistics, psychology, and neurobiology are all isomorphic-- to generative linguistics, that is. Practitioners of these three disciplines have often granted albeit grudgingly that one should eventually be able to give a linguistic, psychological, and a neurobiological explanation of a particular phenomenon in language comprehension and then, understandably gone on to argue that the level at which he or she has chosen to work is really the most important or interesting. Rarely, however, has it been suggested that the three levels of explanation might divide the phenomena of language comprehension up in such similar ways that one could, in effect, study all three levels by explicitly treating only one. This is essentially what Chomsky implies with respect to neurobiology in his discussions of the "language organ"[6] and what he explicitly says with respect to psychology--

> I don't see any useful distinction between 'linguistics' and 'psychology',... [and] I am uneasy with J. Morton's proposal that '...linguistics is more abstract than psychology... [and] is better to be considered at a different level' (1980, pp. 48-49).

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[6] It is intriguing to note that the early architectonicists of the cerebral cortex at the turn of this century often treated the areas they described in the cortex as if they were organs. Brodmann (1909), in fact explicitly claimed to be constructing a "cortical organology"; one of his well known brain maps shows over 40 areas or more literally, "organs", each presumed to be subserving a different function.

Wimsatt (1980a) has identified a number of "reductionistic research biases" that arise when following the (often successful) strategy of concentrating on lower levels of organization at the expense of higher levels in the study of a particular multi-level phenomenon. The strategy of Chomsky, Fodor, and Pylyshyn in many ways is just the opposite of this, and is accompanied by an interesting catalog of complementary "top-down research biases" that need more explication that there is space for here. The recent critique of computational psychology by Stabler (1984) moves in that direction.

Two Suggestions Arising From the Present Analogy

In contrast with the treatments briefly summarized above, the present treatment of language and the brain is a self-conscious attempt at a preliminary reductionist account. This does not imply that higher levels are to be ignored, eliminated, or in any way denigrated, but merely that the goal is to establish interlevel relations (Wimsatt, 1976, 1980a). The analogy developed in Chapters III, IV, and V has many parts and gives rise to a number of predictions about relations between neurobiology, psychology, and linguistics, not all of them novel. I would like to highlight two major predictions about the language-level symbolic-representational system based on the analogy that I think are original here.

The Uses of Symbol-Representation Segment Chains

Three basic kinds of units were defined-- symbol segments, symbol-representation segments, and "thing"-representations. the first kind forms a "one-dimensional" chain carrying coded sequence information and it does not "fold"-- i.e., generate repeatable, stable interactions between non-neighboring units. The third kind, by contrast, forms a chain that invariably "folds" up into a complex "three-dimensional" structure; folded chains such as this control most of the reactions in the system. The second kind of unit, the symbol-representation segment, occupies an intermediate position-- it forms a chain that carries usable "one-dimensional" sequence information but is also capable of some "folding". The striking observation about cells is that out of the thousands of reactions that are controlled by three-dimensional devices, the few controlled by RNA-based (symbol-representation segments) as opposed to protein-based ("thing"-representations) devices are precisely those reactions that are most closely involved in the transformation from one-dimensional message to folded three-dimensional structure-- i.e., the reactions involved in protein synthesis. Three such transitional roles were identified-- internal message, word recognizer, and chain assembler (corresponding to mRNA, tRNA, and rRNA).

The fundamental bridging roles of symbol-representation segment chains at the cellular level are universal in currently existing cells and undoubtedly quite ancient (see also Schuster, 1981; Barbieri, 1981); this suggests that we look for similar bridging roles for chains of symbol-representation segments at the linguistic level. The first of these functions for symbol-representation segments-- as <u>internal messages</u> --is actually rather uncontroversial. A number of models of speech perception have postulated that external sound sequences (symbol segment chains) are initially processed to give at some level, a parallel, internal, one-for-one chain of standardized units (symbol-representation segment chain-- roughly a continuous stream of phoneme representations). The need for the second and third of these functions-- <u>word recognition</u> and <u>chain assembly</u> --is not itself in dispute; they are required in some form by almost any theory of language comprehension. The unorthodox suggestion arising from the present analogy, which I believe is original here, is that these two functions may be carried out in large part by nothing more than chains of symbol-representation segments-- i.e., by neural activity patterns closely resembling internal message ('phoneme') streams, different from them only in that they are more stably "folded" as a result of their particular sequence. Thus, the analogy suggests that rather complex processes like interactive recognition of words in the continuous internal phoneme stream and the concatenation of the sequentially activated word meanings may be carried out by neural activity patterns built up out of a quite unexotic unit-- namely, the symbol-representation segment, which is nothing more than what happens in the auditory system upon hearing (and categorizing) a speech sound but *without* understanding it to stand for anything else.

Pre-Systemic "Thing"-Representations and Self-Assembly

The second proposal about the neurobiology of language has already been discussed from several different angles above. At the cellular level we saw that the "thing"-representations (i.e., amino acids-- the units composing proteins), in contrast to the other parts of the system, are easily generated prebiotically from chemical interactions that occur in primordial gas or "soup" mixtures; in essence, they can be viewed as naturally occurring representations (or better, embodiments) of the different categories of reactive chemical collisions that occur in such a "soup". The implication is that the major advance of life was not to invent the basic amino acid "word meanings" but rather to find a reliable, standardized way to attach together pairs of pre-existing word meanings. Once this was done, self-assembling reaction controlling devices with extreme functional specificity could be built out of units that by themselves, are quite unremarkable in this regard.

The first implication for the neurobiology of language is that there might be a core group of word meanings (instantiated as a group of stable firing pattern states in secondary visual cortical areas) that are prelinguistic-- i.e., they arise in the course of the primate visual system interacting with and learning to categorize things, actions, events, directions, places, manners, and so forth, in the real world. The issue of how language on the one hand and nonlinguistic or prelinguistic perception and cognition on the other are related has been a durable one over the years and is unlikely to go away at once. Nevertheless, the present analogy suggests a partial resolution-- that the nature of a core group of word meaning firing pattern units is strictly attributable to nonlinguistic or prelinguistic perceptual and cognitive factors (see Jackendoff, 1983 for different arguments but similar conclusions). It seems probable, in fact, that word-meaning-like units are generated 'naturally' in the prelinguistic "soup" of firing patterns in the cortex of other primate species and perhaps to a lesser extent in the cortex of all mammals.

Thus, as in the case of the origin of life, the major advance in the origin of language might not have been to invent the basic word meaning firing pattern units; rather, it was to find a standardized way to "bond" together there pre-existing units into long chains, one pair at a time. Once a chain assembly apparatus become established, self-assembling neural "reaction controlling devices"-- i.e., stored patterns in the network designed to alter other stored patterns --of great specificity (quite out of necessity in a network containing many superimposed stored patterns) could be built out of units in the network that by themselves, show little specificity of "reaction".

It is important to emphasize how different the 'self-assembly' model of language comprehension suggested by protein synthesis is from many currently popular models based on computer software/hardware analogies. One way of stating the difference is that the basic level category representations ("thing"-representations) in the present model interact directly with each other on the basis of their prelinguistic properties (which arise from constraints in the architecture of the brain and the world) rather than via a set of rules insulated from the system-specific details. For concreteness, one might imagine the pre-existing basic level units as a set of complex, irregularly shaped objects with many protrusions. In the present analogy, the strategy is simply to stick these objects together into chains, let them interact directly with each other, and then pick out the resulting contraptions that work best for the task at hand. By contrast, the computer software/hardware analogy suggests that we first attach onto each object, a convenient "handle" that summarizes important properties of the object in a more 'logical' way-- say, by a pattern of notches --and then set up a system of rules isolated from the real (lumpy) world that manipulates the meaningless (i.e., from the world's point of view) notch patterns in a functionally interesting way.[7]

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[7] Notice that the symbolic-representational system in cells uses a related strategy to assemble the chains in the first place-- tRNA's are essentially standardized handles for amino acids. The crucial point is that once the word-meaning chains have been made, they fold by themselves, without the help of "handles". The "handles" allow the cell to take advantage of the subtle non-local interactions involved in folding but would be quite unsuited to directly mediating those interactions.

The hope that one might be able to stick with the "notch patterns" has sprung up repeatedly in twentieth century philosophy and psychology, ranging from the early attempts of the logical atomists and company to replace messy real world semantics with neat, logical syntax, to the recent pronouncements of Fodor or Pylyshyn that all the interesting functions are, to use their cleverly misleading code-word, "cognitively penetrable"-- i.e., insulated from the world as well as the system architecture. The present analogy suggests that we give up this strategy once and for all in modeling meaning comprehension in human language and use it precisely where it does work-- namely, in programming von Neumann machines to do useful things with linguistic input.

The Preliminary Nature of the Model

The proposals given about how various sorts of firing patterns might interact are no more (and no less) than preliminary ideas for an explicit working model. At the risk of severe disillusionment, I would like to make an explicit comparison between a currently existing model (Hopfield, 1982, 1984) and the structure of visual cortex as it is currently understood in cats and primates (Merzenich and Kaas, 1980; Schmitt et al., 1981; Woolsey, ed., 1981; Gilbert, 1983; Symonds and Rosenquist, 1984a, 1984b). First, there is the simple question of numbers of neurons-- the model has 30 while the visual cortex has on the order of a billion. Second, the model has only one "area" while both cat and primate visual corticies have 15 to 20 areas. Third, the model has only one type of neuron while each cortical area has a distinctive mix of at least 10 or 20 different neuronal types each differing in its dendritic architecture and axonal projections. Fourth, the neurons in the one "area" of the model are completely interconnected, while within-area connections in many visual areas are restricted in a variety of ways both parallel and perpendicular to the cortical surface. Finally, there is a second level of connectivity between areas (each cortical area has a different mix of extrinsic inputs) not present in the model.

The gap between this quite typical model and real visual cortex is obviously rather large. Now it appears likely that newer parallel computer architectures will begin to allow some of the idealizations in current models to be relaxed. It will be, nevertheless, some time before a working model capable of interesting a neuroanatomist becomes available. Lastly, it is worth pointing out that even the daunting complexity of the cat and primate map-networks does not support the language-level symbolic-representational system that we have been attempting to model. The point here is simply to emphasize the preliminary nature of the proposals given previously. This is not to devalue them; in fact, I think that the analogical method employed can be especially useful in directing research at a time when brute force techniques are not practical. In any case, we can look forward to great insights into the presently completely unknown dynamics of map-networks.

Definition of a Natural System Capable of Evolution

"Evolution" is used in several different technical senses that partially overlap. What I would like to do in this section is pick out one of them-- roughly, organic evolution --and then argue that such a process is only well-defined in the presence of a symbolic-representational system.

Different Types of Evolution

One type of evolution is the "time evolution" of the physicist. For particular types of systems, there are well known mathematical techniques for describing the deterministic time evolution as a trajectory through a multi-dimensional phase space. There seems to be a clear enough distinction between this sort of evolution and biological evolution (Bowler, 1984); for example, one might envisage deterministic descriptions (though perhaps not Hamiltonians !) of all the molecules in a barren as well as life-filled solar system, yet somehow we would want to contenance organic evolution only in the second case; thus, organic (i.e., cell-based) evolution seems to be something that can be "added on" to a deterministically 'evolving' system. Since there appears to be only one major type of life in light of the universality of the genetic code, organic evolution seems to have been successfully initiated ("added on") only once.

Biologists, somewhat suprisingly, have often been nebulous on this point. In fact, there is a commonly held hunch among evolutionary biologists that a variety of systems-- some perhaps not biotic --are capable of "evolution" in the biological sense. R.A. Fisher, one of the acclaimed architects of the New Evolutionary Synthesis, for example, states in an early paper:

> One of the most interesting things about Darwin's explanation of the origin of species is that scarcely anything need be assumed about the actual nature of species, as evidence that natural selection occurs; the same process is in progress with respect to languages, religions, habits, customs, rocks, beliefs, chemical elements, nations, and everything else to which the terms stable and unstable may be applied (1912, p.58).

This tendency to overgeneralize organic evolution has been reinforced recently by the notion that living and hence evolving organisms are partly characterized by the presence of dissipative, far-from-equilibrium structures (See Prigogine, 1980), since such structures are also generated within clearly non-living systems (e.g., the waves in the Zhabotinzky reagent, meandering streams, and so on).

A commonly quoted definition of organic evolution is the three-piece motto of Lewontin (1970)-- that evolution requires 'heritable variations in fitness'. This serves well-enough in many cases, distinguishing the dynamical evolution in a box of perfectly elastic point particles from the evolution of pesticide resistance in fruit flies. Without more specificity though, it seems that one could too easily produce an artificially-rigged case. Thus, one might imagine that a group of streams are competing to empty a periodically filled resevoir-- each new "generation" of streams inherits its parents stochastically generated variations in course and the fittest streams (i.e., the ones that transport the most water) become the most enlarged or give rise to the most new branches and thus are at an evolutionary advantage (actually, just such a model inspired the original stochastic evolutionary simulations of Raup et al., 1973). The problem is that the particular system in living things that clearly separates their sort of evolution from that of streams does not explicitly appear in Lewontin's rules; but it is just that system (the genetic apparatus-- the cellular symbolic-representational system) that most clearly demarcates the biotic from the non-biotic case. In the absence of such a system-- e.g., in streams --the application of evolutionary terms seems artificial or arbitrary. This is because streams cannot, so to speak, "define" themselves or the base level of organization at which they should be analyzed; though, they exhibit definite morphological patterns (e.g., meandering _versus_ braided) and have distinct boundaries. There is no internal specification, either direct or indirect, of those things. The symbolic-representational system in a living thing, by contrast, "defines its own levels" (e.g., a prominent, lowest genic level of selection). It has often been pointed out that the intertwined functional organization of living things leads to many alternate decompositions; nevertheless, I think just the opposite is true in a sense-- i.e., the existence of a symbolic-representational system in living things actually forces us to analyze their evolution with reference to a particular level of organization.

The detailed definition of symbolic-representational systems presented in Chapter II has many parts. The implication throughout this work has been that all of these parts would be required for such a system to exist at any level; and a preliminary motivation was developed to explain some of them. However, there are presently not as many empirically unequivocal parallels (especially with regard to internal parts of the language system) as would be needed to strongly argue that all of the parts in Figure 12 are, in general, absolutely necessary to make a symbolic-representational system. If some of the more speculative proposals for parallels between the two systems come to be established, we will have to return to the task of trying to provide detailed motivations. Perhaps then we will be able to explain why symbolic-representational systems have such a curious, asymmetrical architecture.

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