

Four Analogies Between Biological and Cultural/Linguistic Evolution

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The intricate phenomena of biology on the one hand, and language and culture on the other, have inspired many writers to draw analogies between these two evolutionary systems. These analogies can be divided into four principal types: species/language, organism/concept, genes/culture, and cell/person. Here, it is argued that the last analogy—between cells and persons—is the most profound in several respects, and, more importantly, can be used to generate a number of empirical predictions. In the first half of the paper, the four analogies are each evaluated after briefly describing criteria for a good predictive analogy. In the second half of the paper, the cell/person analogy and predictions deriving from it are explored in detail.

1. Introduction

The origin of life and the origin of human thought constitute two particularly significant turning points in the history of our distinctive planet. The prebiotic world was radically transformed by living, evolving cellular organisms; likewise, the world of prelinguistic animals was profoundly modified by the advent of human-style cognition and cultural evolution. Many have been prompted to compare these two evolutionary systems; both depend on a new form of information-accretion not found in the pre-existing worlds.

Most serious work on this topic has grown out of three focal comparisons: *species/language*, *genes/culture*, and *organism/concept*. These three analogies have been articulated in almost complete isolation from each other. In historical and comparative linguistics, species with similar individuals capable of interbreeding are compared to language communities of mutually comprehensible speakers. In sociobiology and the study of animal behavior, genes coding for physical and behavioral traits are compared to fragments of culture capable of transmission and expression. And in evolutionary epistemology in the history and philosophy of science, interacting organisms in an environment are compared to competing scientific concepts and theories in an “intellectual ecology”.

In the years after the discovery of the structure of DNA in the 1950s and its relation to protein structure in the early 1960s, there was a burst of excitement about a fourth kind of comparison—the *cell/person* analogy. Many authors drew comparisons between cellular and linguistic coding systems (e.g. Gamow, 1954; Crick, 1959; Beadle, 1963; Jakobson, 1970; Masters, 1970; Berlinski, 1972). But a less-than-delicate treatment of the details of the fields involved did not help the project, and it soon became hackneyed, or worse, a refuge for dilettantes and loose-thinkers.

In this paper, it is argued that the first three analogies actually depend implicitly upon relations that can only be satisfactorily stated in terms of the fourth analogy. We think there is a deep and detailed mapping between the processes in living *cells* and the processes in brains of linguistically competent *persons* that was only dimly glimpsed in the earlier enthusiasm about DNA and language. The first part of the paper evaluates the four main analogies in light of criteria for a good predictive analogy, concluding that the cell/person analogy alone is consistent across different levels of organization. An analogy is only finally useful if it helps us make predictions about one or both systems involved. We think that the cell/person analogy provides us with a whole new way of thinking about linguistic processes, and it makes a number of novel, testable predictions. The precise grounds for the cell/person analogy and several predictions about the neural substrates of human language deriving from it are then developed in detail in the second part of the paper (see also Sereno, 1984, 1986, unpublished).

2. Criteria for Evaluating Explanatory Analogy

There has been a long-lived interest in metaphor and analogy in philosophy, literary criticism, and linguistics (e.g. Richards, 1936; Black, 1962; Ortony, 1979; Lakoff & Johnson, 1980). In the philosophy of science, by contrast, analogical reasoning has often been viewed with ambivalence or suspicion. Duhem (1914/54), for example, grants that once a set of very dissimilar phenomena have been reduced to 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); but he was highly critical of the use of concrete analogical models like those employed initially by Maxwell in developing his theory of electromagnetic radiation. Though analogical reasoning was not ignored in logical empiricist philosophy of science—see e.g. Hempel (1965: 433–47)—it nevertheless became something of a side issue (see e.g. Suppe, 1977).

Recently, however, there has been a renewed interest in generative and explanatory analogy and its role in scientific discovery in both the history and philosophy of science and in cognitive psychology (Sellars, 1965; Hesse, 1966; Glucksberg *et al.*, 1982; Darden, 1983; Gentner, 1983; Bobrow, 1985; Hofstadter, 1985; Holland *et al.*, 1986; Indurkha, 1987). Analogical reasoning has been studied in many contexts. The simplest sort of analogy, the minimal four-element problem (see e.g. ABC:ABD:PQRS: ? and many other variations in Hofstadter, 1985), has been extensively studied. More complex is a group of what might be called frozen pedagogical analogies (e.g. the hydraulic analogy for simple DC circuits, the solar system/atom analogy). The most formidable and least well-understood analogies, and those most interesting for the present purposes, however, are active, evolving theoretical frameworks that often inspire years of deliberate study. Many examples come from mathematics and physics (including the historical form of the solar system/atom analogy—the Rutherford and Bohr atoms); others virtually define whole fields of inquiry, including the analogy between artificial and natural selection, the analogy between computation and cognition, and the analogies discussed in the present paper.

Complex generative and explanatory analogy is characterized by four distinct activities: (1) decomposition of the source and target systems, (2) establishment of a map between the two systems, (3) generation of predictions about the target, and (4) testing of the predictions. The treatment here highlights the crucial role part/whole relations (levels of organization) play at every stage in this process†. We will use the solar system/atom analogy as a familiar concrete illustration.

The first activity is to decompose the two systems into "objects" (e.g. stationary central body, orbiting bodies) with attributes (e.g. mass), and "relations" between these objects (e.g. the central body is much more massive than the orbiting bodies), using structural and functional criteria internal to each system (Gentner, 1983). An obvious but important type of relation hardly mentioned in previous discussions of analogy is the part-whole relation (e.g. the sun and planets are part of a solar system; stars and solar systems are parts of a galaxy; the nucleus is composed of protons and neutrons; groups of atoms form molecules). Many subtle failures of mapping involve inconsistent manipulation of the levels of organization defined by such part-whole relations. Typically, an analogy is centred on one or a few particular levels of organization in each system; the decomposition process trails off at levels above and below these levels (e.g. protons and neutrons constitute a level below the focus of the analogy while the arrangement of stars into galaxies is a level above).

An important part of the decomposition process is to specify contextual or *ceteris paribus* conditions (Wimsatt, 1976; Hooker, 1975) involving background relations between the system and the larger domain in which it is embedded (e.g. most of the system consists of empty space; trajectories are not mainly determined by collisions; the orbital system is isolated from inhomogeneous external forces). These contextual considerations do not extend, however, to the other system; the source and target decompositions are performed on the basis of system-internal criteria.

Finally, for a complex source or target system (and these are primarily the ones of interest), our understanding is likely to be incomplete; alongside well-understood, "exposed" regions, there will be areas in both the target and source system in which objects are poorly defined, or even completely "hidden" (consider the state of knowledge of atomic structure in 1900 when the atom/solar system analogy was active). In some cases, we may know little more than that an object probably exists.

The second stage is to arrange a mapping between parallel parts and relations that are "exposed" in both the source and target systems. Usually, analogies are

† It is interesting to compare the process of predictive analogical comparison sketched out here with the heuristics for prediction and explanation by interlevel reduction as developed by Wimsatt (1976, 1980), Darden & Maull (1977), Hooker (1975, 1981a, b), and Churchland (1986). These heuristics apply to the development of interlevel identificatory links between entities in two theories that describe the same phenomena from the vantage point of two different levels of organization (e.g. macroscopic genetics vs. molecular genetics). There are a number of similarities with predictive analogical comparison. The most obvious *difference* is that there is no requirement in analogical comparison that the entities compared actually be identical. This is less of a difference in practice than it may first seem, however, since the diachronic process of attempting to reduce one theory to another almost always involves successive attempts at mapping two rather incommensurate descriptions of the "same" phenomena. This process usually requires reconstruction, and occasionally elimination, of various entities in one or both theories before a coherent map between the upper and lower level descriptions is achieved. Even in the end, with parallel descriptions in hand, the attributes and relations of an object viewed from two different levels may not map at all smoothly—e.g. "color" and "pressure" described at molecular and macroscopic levels. In some cases, analogical comparison may be *more* transparent than interlevel identification.

organized around a focal comparison involving particularly prominent objects or relations (e.g. sun/nucleus and solar system/atom). There must be a core of exposed, parallel structures here to warrant proceeding to the third, predictive stage. Gentner (1983) argues for two rules of mapping. The first is that similar relations (e.g. the central object is more massive than the orbiting objects in both systems) are more important than similar object attributes (e.g. the central object is hot and yellow in both systems). The principle is sound, though the line between an attribute and a relation is often somewhat arbitrary; object attributes with numerous ramifications, for instance, are as important as explicit "relations" (e.g. the contrast between the "attribute", atomic electrical charge, which can be positive or negative, and the single-signed gravitational charge (mass) of celestial bodies, is an important point of disanalogy between the two systems).

Gentner's second rule is that higher order relations among other relations (e.g. Newtonian law of universal gravitation) are especially important in constructing analogical mappings (cf. Duhem, 1914/54; Indurkha, 1987). Interconnected networks of relations take precedence in mapping and prediction over singly connected relations that form structural "appendages". It is important, however, to go beyond Gentner's strictly syntactic specification of a relation (a two-place predicate). Strictly speaking, the moons of a planet, for example, share in much of the same network of relations with the sun as do the planets (including distance, mass, and gravitational relations). Yet, because of their small masses and the small diameters of their orbits around a planet, the moons are essentially appendages to a planet; removing the planets would disrupt things much more than would removing the moons. Since the moons are primarily connected to one planet, they are less important in mapping and prediction[†].

We think the most powerful constraint on constructing a map between two complex, multi-level systems is the conceptually simple requirement that *part-whole relationships be kept parallel across several levels of organization*. This condition is not met at higher levels of organization in the solar system/atom analogy (e.g. solar systems do not "bond" together into stable "molecules" by virtue of their orbiting bodies since binary stars do not support stable planetary orbits; and the gravitational forces holding solar systems together (if there are in fact other ones!) into galaxies are weak, resembling *intermolecular*, not *intramolecular* forces). Most previous essays on biology and language have fallen down on this point. The great complexity of the two domains makes this simple requirement difficult to meet in practice.

The third stage of predictive analogy is to infer things about an object or relation in one system based on what we know about it in the other system. A key distinction

[†] Holland *et al.* (1986) have also criticized the strictly syntactic approach to analogical comparison, arguing that the goals or "context" of analogy may affect decomposition, mapping, and prediction (pp. 300-4). Goals may be important in their simple examples of metaphor ("Sam is an elephant" vs. "induction is an elephant"—in the first example, they suggest we should map clumsiness, while in the second, they want to reference the story of the blind men and the elephant). But we think it is a mistake in complex explanatory analogy to allow the goals of analogy to influence or revise a decomposition that has been performed on the basis of factors internal to the domain from which the system was drawn; this only vitiates the predictive power of an analogy. None of this is to deny the importance of domain-*internal* contextual considerations, or the role of analogical goals in determining which objects on which to focus the analogy.

needs to be made here between objects that are merely "hidden" and objects that are truly "missing" (or, from the point of view of the other system, "superfluous"). In the first case, we have enough indirect information about an object (or relation) to suggest that it exists, and want to extend our knowledge of it via predictive analogy. In the second case, we know that an object or relation in one system probably *does not* exist in the other; there is a point of disanalogy. In order for a predictive analogy to be useful, it must be articulated clearly enough to distinguish between these two cases.

A "missing" or "superfluous" object or relation rarely vitiates an analogy by itself; in fact, it may suggest a new, more general explanation for certain system characteristics (e.g. the "missing", classically-predicted radiation in the context of the Bohr model of the atom led to the hypothesis of "stationary" electron orbits and the first theories of quantum mechanics). But when, in the context of strong upper and lower level parallels, an especially prominent object is found at an intermediate level of organization in one system but not in the other, there is cause for alarm, and for a re-evaluation of the mapping scheme[†]. Such seemingly obvious misalignments in levels of organization are often difficult to spot even after the analogy has been developed at some length, as we shall see presently. The moral is that one must pay strict attention to part-whole relations before splashing around too recklessly in the details.

The fourth activity in predictive analogy is testing the predictions. Informal testing normally accompanies and aids the decomposition and mapping processes. Testing is constructed broadly enough to include things like suggesting an approach to a problem. Analogies are often particularly fruitful in suggesting new ways to explore familiar conceptual terrain.

3. The Species/Language Analogy

The first major field in which biological and linguistic processes have been considered together is historical linguistics. The early founders of Indo-European comparative grammar had consciously tried to draw upon the study of biological development and evolution, just as evolutionists like Darwin and Lyell were fond of discussing the evolution of languages (see e.g. Newmeyer, 1986; Richards, 1987). A late statement of the philologist Schleicher illustrates a clear analogy between a *single organism* and an entire language:

"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: 16).

Analogies between organismal development (and decay) and language evolution engendered hot debate in the later 19th century (see Aarsleff, 1982; Knoll, 1986;

[†] Note the intimate relations between prediction, disanalogy, and outright mapping-failure. More formal criteria for deciding when to predict, when to note differences, and when to reconstruct seem desirable. Existing treatments (e.g. Holland *et al.*, 1986; Indurkha, 1987), however, are still far from helping us with realistically unconstrained contexts.

Wells, 1987; Morpurgo Davies, 1987)†. But by the turn of the century, these ideas had been all but banished from historical linguistics; they make no appearance in the recognizably modern work of Saussure.

Nevertheless, a different analogy between biological and linguistic evolution, introduced by Darwin himself in the *Origin of Species*‡ (1859: 422–3), has persisted around the fringes of modern historical linguistic investigations (Anttila, 1972; Bynon, 1977; Platnick & Cameron, 1977; Wiener, 1987)§. This is the analogy between a *species* of organisms and a language. The population-level alignment of a species with a language implies the individual-level alignment of an organism with a single speaker [see Fig. 1(a), which schematically illustrates the part-whole relations].

A number of specific comparisons flow from the species/language starting point (biological parallels are given in parentheses). An intercommunicating group of people defines a language (cf. gene flow in relation to a species); language abilities develop in each speaker (cf. embryonic development); language must be transmitted to offspring (cf. heritability); there is a low level process of sound and meaning change that continuously generates variation (cf. mutation); languages gradually diverge, especially when spatially separated (cf. allopatric speciation); geographical distributions of dialects (cf. subspecies, clines) gradually give rise to wholesale rearrangements of phonology and syntax (cf. macroevolution); sociolinguistic isolation can lead to language divergence without spatial discontinuity (cf. sympatric speciation). Finally, the technique for adducing language relationships (e.g. see Anttila, 1972: 207–63) shows a remarkable resemblance to the cladistic techniques independently developed by biological systematists (Hennig, 1966).

There are a few obvious disanalogies when using this alignment that have often been noted by linguists. First, languages commonly “borrow” words from neighboring languages, from the language of an invader or colonizer, or from the invaded or colonized, with little regard for the phylogenetic distance of the source language. Such uninhibited lateral transfer of genetic material is much less common in

† The organism/language analogy of Bopp and Schleicher has a superficial resemblance to the cell/person analogy argued for in the last section in that entities within a single organism are implicitly compared to relations between different parts of an evolving language. These writers, however, seemed very little concerned with processes underlying language comprehension and wrote as if the structure of a language was an autonomous thing, somehow separate from the persons using it. It was this point that was most roundly criticized by Bréal, Whitney, and Saussure.

‡ There were several other incommensurate versions of a biology/language analogy current at this time. The philologist Max Müller, for example, though adamantly opposed to the suggestion that capability for human language and thought might have gradually evolved, nevertheless wanted to draw upon ideas about biological evolution to explain the subsequent evolution of different languages. Interestingly, he compared the struggle between organisms to a “struggle” between different words and grammatical forms *within* a language (Knoll, 1986; Richards, 1987). This analogy is closest to the organism/concept analogy discussed in section 5.

§ Darwin went into some detail on this issue, at one point comparing the unpronounced letters in a word with vestigial organs (Darwin, 1859: 455). Rudimentary organs were one of Darwin’s favorite evidences for evolutionary change.

¶ The present “fringe” status of the species/language analogy in linguistics may be attributed to earlier excesses, but also to the perennial need to combat sociolinguistically naive notions of “correct” (read upper-class) and “incorrect” speech, as well as notions of “primitive” and “advanced” languages developed in the absence of any knowledge of comparative phonology, syntax, and semantics of the world’s 5000 or so languages [see, e.g., discussions in Anttila (1972) and Bynon (1977)].

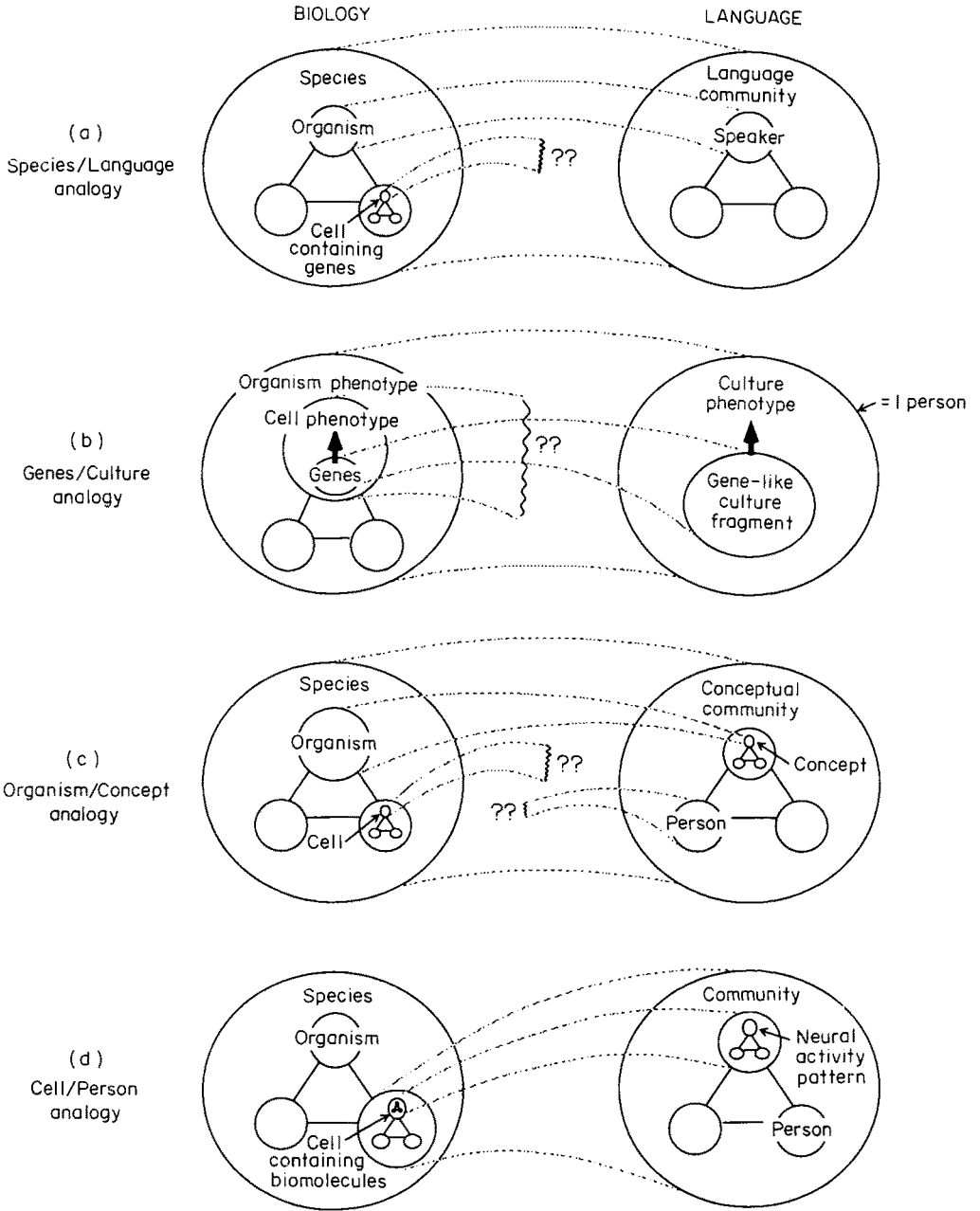


FIG. 1. Schematic comparison of part-whole relationships in four analogies between biology and language. In the species/language analogy (a), objects in one system map to objects of approximately the same size in the other system. In the genes/culture analogy (b), small biological objects (genes) map to large cultural objects (gene-like culture fragments). In the organism/concept analogy (c), large biological objects (organisms) map to small cultural/linguistic objects (individual concepts). In (a), (b) and (c), there are unmapped intermediate-level objects (cells, persons). Finally, in the cell/person analogy (d), small biological objects (cells) map to large cultural/linguistic objects (persons).

biological evolution. Second, spoken natural languages do not apparently become a great deal more "adapted" or "fit" through time (this is less true of scientific languages and notations). For example, all natural languages seem capable of expressing similar ranges of meaning, especially if paraphrasing is allowed; Eskimo may have more words for "snow", but it is not difficult to express their meanings in English.

At first glance, there seem to be an impressive number of parallels between a species and a language (there are more here than any one other author has produced). A closer examination reveals, however, a number of puzzling differences. For instance, there are actually three kinds of local changes or "mutation" in language evolution involving fundamentally different "materials"—changes in the set of possible speech sounds, changes in sound/meaning correspondences, and changes in the meanings themselves. Then, there are the actual sound sequences spoken, which change from day-to-day. It is unclear, given the framework of the species/language analogy outlined above, which subset of these four types of changes should be compared to the changes in gene sequences that constitute biological mutation.

These problems grow out of the vague characterization of lower levels of organization on the language side of the analogy. The mapping does not clearly specify what mutates, and what is transmitted. In trying to be more specific, we uncover a mismatch in part-whole relationships. Since the analogy focuses on genetic processes, which in biology, fundamentally involve *intracellular* entities (DNA and genes), the cell is left as a prominent "missing" intermediate-level object; there seem to be no cell-like compartments in a language speaker that each carry a full complement of gene-like entities.

The different types of sequence changes in biology and language are dealt with more explicitly and productively in the context of the cell/person analogy, where it is argued that new DNA sequences generated by mutation are most similar to new sound sequences perceived from day-to-day. Analogs of the other three types of change in language evolution turn out to have occurred only very rarely in cells (see below).

4. The Genes/Culture Analogy

A second area in which biological genetics and human linguistic and cultural phenomena have been considered together is human sociobiology. Considerable effort has recently been expended in developing a mathematically detailed analogy between genes and culture as parallel systems for transmitting information about phenotypes (e.g. Cavalli-Sforza & Feldman, 1981; Lumsden & Wilson, 1981; Boyd & Richerson, 1985; Rindos, 1986; Brandon & Hornstein, 1986) [see Fig. 1(b)]. These authors have usually not restricted the putative analogs of genes to linguistic phenomena. Boyd & Richerson, for example, state that

"the codification of culture via public symbol systems may have interesting effects on the human evolutionary process . . . but to our minds these effects are less fundamental than the effect of social learning *per se* (Boyd & Richerson, 1985: 36)".

Boyd & Richerson (1985) point out two basic differences between cultural and genetic transmission that make it unrealistic to treat the cultural "system" as a group of additional genetic loci. First, it is not possible to represent cultural evolution as a process that transforms genotypes in generation t into genotypes in generation $t+1$ since we must take the distribution of starting *phenotypes* into account (e.g. the phenotypes of the cultural parents that are capable of transmitting cultural analogs of genes). Second, in cultural transmission, genotype analogs are transmitted to an organism throughout its life rather than as one bolus at fertilization. Once these differences were noted, a so-called "dual inheritance" approach was developed along broadly similar lines by several authors.

This analogy suffers from a mismatch in part-whole relationships. The problem stems from the definition of the phenotype at the cultural level. Boyd & Richerson (and many others) draw an analogy between the "cultural genotype" transmitted by various cultural practices and the cellular genotype transmitted by DNA. But then they essentially *identify* the cultural phenotype with the multicellular biological phenotype. This is not surprising, given that most authors have expressed interest in hypothetical "gene/culture" interactions. It results in an upper level match (biological person/cultural person) and a lower level match (gene/gene-like fragment of culture), but also a prominent "missing" intermediate-level object on the language/culture side of the analogy (cell/??).

The advantage of identifying the cultural phenotype with the biological one is that enculturated humans are clearly localizable units; the drawback is a cluster of disanalogies with respect to the mode of action of cultural and genetic information. The adult biological phenotype of a person is generated from a zygote by ever increasing numbers of interacting cells, each of which contains a complete copy of the genetic information present in the zygote as well as a copy of the decoding apparatus required to derive a primary interpretation of that information. By contrast, 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 any repeated part) of an enculturated person. Likewise, cultural information is not initially interpreted piecemeal by each cell; there is only one interpreting apparatus (sense organs and brain) per person. Another way to say this is that genes generate organismal phenotypes by generating *cell* phenotypes, which then interact to generate the organismal phenotype[†].

The levels-of-organization mismatch can be avoided if we perform a more careful decomposition of the internal architecture of information use at the cellular-genetic and cultural "genetic" levels. We then identify the cultural phenotype as an interacting *group* of people. Each person in the group is capable of providing an independent

[†] We do not mean to deny all direct interactions between the cellular and cultural genotypes in the context of a single person. The most obvious interaction is the incorporation into the human genome of the ability to effortlessly learn a language upon hearing or seeing one; even enthusiasts for ape "language" agree that the difficulty in teaching fragments of language to chimpanzees must have a genetic basis.

initial interpretation of cultural information, which can be thought of as existing in multiple (if approximate) copies. One need not deny that the human cultural phenotype actually "resides" in human biological phenotypes; the point is that there is not a one-to-one relationship between the two. This turns out to be one of several routes to a cell/person analogy.

5. The Organism/Concept Analogy

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 at many junctures (see the many interesting examples exhumed by Campbell, 1974, and overview by Bradie, 1986). We shall concentrate on the more recent and lengthy treatments of Campbell (1974, 1977), Toulmin (1972), and separately, that of Hull (1982, 1983, 1988). Compared to the Procrustean generalizations about human culture of some sociobiologists, the claims of evolutionary epistemologists appear muted. Toulmin, for example, does not want to get involved with "specifically biological details" or get "drawn into discussions about genetics, predators, or water supply" (Toulmin, 1972: 39). Some of the debates in evolutionary epistemology, however, would benefit from clearer statements of the objects of analogy, uncomfortable as this may be. Such an analysis serves to distinguish "classical" evolutionary epistemology as a distinct kind of alignment—that of *organism/concept*—alongside the species/language and genes/culture analogies discussed above, and the cell/person analogy discussed last.

With Campbell and Toulmin, the primary comparison is between an organism in an evolving species, and a concept in the "evolving" (i.e. learning) brain [see Fig. 1(c)]. They would like to apply a selective retention paradigm to all "knowledge processes" but especially those of humans and scientists. A "concept" is usually taken to be word-sized or larger (e.g. a theory), but decidedly smaller than the entire conceptual contents of a learner's brain. Thus, the focal comparison of evolutionary epistemology actually inverts the size relationships between (multi-cellular) biological and linguistic-cultural objects found in the genes/culture analogy. In evolutionary epistemology, the evolution of (large) multi-cellular organisms belonging to a species is compared to the evolution of a class of (small) things—concepts—many of which can reside in a dormant or active form within a single scientist's brain. By contrast, the genes/culture analogy compares (small) genes contained within a single cell to (large) gene-like fragments of culture perceived by whole brains [compare Fig. 1(b) and (c)].

Like the genes/culture analogy, the organism/concept analogy suffers from a mismatch in part-whole relationships that derives from an inadequate treatment of the linguistic-cultural phenotype. Since evolutionary epistemologists often want to compare a biological species with a scientific discipline thought of as an "interbreeding" intellectual community, there is no convenient entity left on the biological side to analogize with a single person or scientist—clearly a prominent "missing" object. And on the linguistic-cultural side, there is nothing to compare with a cell.

The main culprit appears to be the focal organism/concept comparison itself. By starting with this alignment, one is led to neglect the genotype/phenotype distinction, since presumably, this would have to correspond to something *within* a concept or theory. Kary (1982) has also criticized this aspect of evolutionary epistemology. Using somewhat different terms, we agree that a generalized theory of biological evolution must include an analog of the genotype/phenotype distinction. Otherwise, there is little to distinguish the theory from other deterministic theories of change—e.g. the “evolution” of a dynamical system in six-dimensional momentum space—that are clearly not “evolutionary” in the biological information-accreting sense of the word. In fact, the cell-based architecture summarized by the “genotype/phenotype” distinction is precisely a means for getting beyond the simpler deterministic evolution of physical systems, based on storing symbolic information about how to make certain otherwise unlikely chemical events occur more readily. As in the previous cases, we think it is difficult to argue for particular higher level alignments (e.g. analog of selection and adaptation) when there are no analogs of cells and genes, nor good reasons for the absence of this most basic instantiation of the genotype/phenotype distinction.

Hull (1982, 1983) applies his concept of species as spatiotemporal “individuals” (as opposed to classes with members) to conceptual evolution. Hull’s main point is that the only things that count are the actual lines of descent. Thus, as Olby (1979) has quipped, Mendel might not have been as much of a Mendelian as his later “rediscoverers”, who were instrumental in transmitting his work to the general scientific community. In developing this insight with respect to conceptual evolution, Hull sees that it would not do to have the nodes in the genealogical framework be concepts (e.g. Mendelian laws), grouped into similarity classes. He suggests that we individuate scientific communities as biologists define species in practice—by using a “type specimen”. As a particular organism marks a species that includes it (regardless of how the including species may be subsequently redefined), a particular *scientist* can be used to mark a conceptual community (Hull, 1982: 297).

Clearly, this aligns one organism with the entire conceptual system of a scientist, in contrast to the organism/concept focal comparison of “classical” evolutionary epistemology. Notice that this is closest to the mapping previously described for language evolution (i.e. species/language, and especially, organism/speaker); and it shares the former analogy’s disregard of the cellular level of organization. Hull claims that his cultural gene-analogs (memes, following Dawkins) only reproduce, but do not generate a phenotype (Hull, 1982: 307). Taken at face value, the lack of a cultural phenotype would seem to greatly weaken the analogy (surely the phenotype is a prominent part of a biological organism); but we think the implication is instead that the biological phenotype also serves as the cultural phenotype, though modified by cultural gene-analogs. Hull’s analogy thus also recalls the human sociobiologist’s collapsing of the genetic and cultural phenotypes; and it generates a similar cluster of disanalogies with regard to the mode of action of genetic and cultural genetic information (multiple vs. single copies of information and interpreting apparatus).

Recently, Hull has emphasized the distinction between conceptual replicators and interactors. Even on the biological side, however, both DNA and cells are treated as replicators or interactors (Hull, 1988: 135, 148), depending on one's perspective. On the conceptual side, it is not clear what should correspond to replicating genotype and interacting phenotype; he labels scientists replicators (Hull, 1988: 140), but elsewhere hints that the genotype/phenotype distinction might be analogous to the observation/theory dichotomy (Hull, 1988: 148). Hull also extends his type-specimen method to *parts* of a scientist's conceptual system—e.g. terms (single words). This ostensibly is a return to an organism/concept analogy. However, since he regards a cell as the canonical organism, and compares DNA bases to letters (Hull, 1988: 142), his analogy could also be classified as cell/person. The enrichment of the biological and conceptual sides of the analogy is commendable, but the analysis into only replicators and interactors is not sufficient to specify a unique analogical mapping scheme, and hence, lacks predictive power.

6. The Cell/Person Analogy—Previous Work

The final source of analogies between biology and language is molecular biology. An implicit analogy between cellular processes and human language dates at least to Schrödinger (1944), who suggested in a widely read book that cells must contain a "hereditary code script" stored in an "aperiodic crystal". As a preface to my treatment of the cell/person analogy, several previous attempts to compare cellular and linguistic processes are discussed (Gamow, 1954; Crick, 1959; Hofstadter, 1979; Pattee, 1980, 1982).

6.1. THE GENE AS WORD IN EARLY MOLECULAR BIOLOGY

The first concrete proposals for protein coding following the discovery of the DNA structure by Watson & Crick in 1952 used linguistic analogies. Interestingly, language initially served as the source system and cellular processes as the target system of the analogy, inverting the polarity of the previous mappings. An early scheme for protein coding due to the cosmologist Gamow (1954) had proteins being polymerized directly from cavities in the DNA template (the cavities are not actually the right shape). It was introduced in the following manner:

"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"."

In a similar vein, Crick described the coding problem as one of "translating from one language to another: that is, from the four-letter language of the nucleic acids to the 20-letter language of the protein" (Crick, 1959: 35). The analogical use of "language", "translation", and "letters", so stimulating and controversial at the time, now seems casual, and even a bit quaint. A few linguistic terms, however, were permanently adopted by molecular biologists—e.g. protein synthesis is still formally called "translation" today.

This initial form of the cell/person analogy, in fact, violates the maxim that parallels be maintained across levels of organization. In Crick's analogy, for example, the DNA bases are compared to letters; but then three-base codons are each "translated" into *single* amino acid "letters" that make up the giant, hundred-letter-long protein "words" originally mentioned by Gamow. Thus, we have a (degenerate) lower level match (DNA bases/letters *and* amino acids/letters), an upper level match (proteins/words), and a prominent "missing" intermediate-level object (codon triplets/??)†. Waters (1981, unpublished manuscript) in an otherwise clear-headed review essentially repeats this move. It seems, despite the use of linguistic terms, that the source system for the initial cell/person analogy was actually something more like a coding process relating two sets of uninterpreted symbols—e.g. the Morse code—than like human language or translation between languages. Interested linguists have surprisingly followed this lead‡. Jakobson (1970), for instance, equates DNA bases with phonemes, codons with words, and codon sequences with syntactic units, but then accepts without comment, a "translation" into a "peptidic language", where—given his previous parallels—we might expect to find a "measuring extraction" step.

6.2. THE GENETIC CODE AND GÖDEL NUMBERING

Hofstadter (1979) presents a detailed comparison of the genetic code and the structure of Gödel's Incompleteness proof that qualifies as a cell/person analogy since it compares cellular coding and human mathematical codes closely related to language. Gödel's proof involved constructing an undecidable sentence within number theory meaning approximately "there is no formula that is the proof of the formula we are in now". To do this, Gödel invented an elegant numbering scheme to map the formulae of any possible number theory proof to a unique integer. Hofstadter's starting point is an intuitively attractive comparison between the self-referential aspects of Gödel's sentence (i.e. a single number within it refers to the whole sentence) and self-referential phenomena in cells supported by the genetic code (a stretch of DNA may code for a protein that can then interact with or "refer to" the same stretch of DNA).

On closer examination, this analogy exhibits both contextual as well as focal mismatches (see Fig. 2 for schematic summary of his analogy). On a broad view, the primary function of the two systems being compared is very different. The

† Actually, the unmarked use of "word" refer to a codon in other texts (e.g. Watson, 1976) suggests that modern molecular biologists intuitively draw a different parallel than the one outlined here—namely, that DNA bases resemble letters, and codons, as opposed to whole genes or proteins, resemble words. This, of course, is more in line with my development of the cell/person analogy.

‡ See also the review by Masters (1970). Notably, the linguist Lees avoids this inconsistency—"a word (in most cases) has a meaning, a triplet specifies a particular amino acid" (Lees, 1980: 222). And Lees has 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 (Lees, 1980: 225)". But these intriguing ideas are not developed.

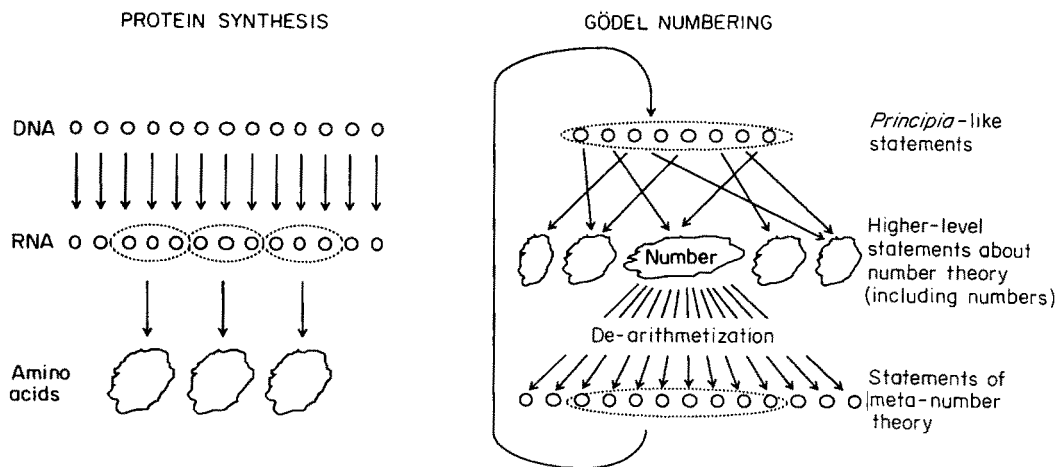


FIG. 2. Schematic diagram of mismatches in the mapping between protein synthesis and the version of Gödel numbering presented in Hofstadter (1979). The simple part-whole relations in protein synthesis are not found amongst the putatively similar parts of the Gödel numbering scheme.

mechanism of the genetic code figures centrally in any explanation of how cells work—transactions between DNA, RNA, and protein are explicitly involved in the minute-to-minute operation of every cell. Gödel numbering plays no similarly explicit role in most mathematical inquiry. Now a contextual mismatch does not automatically vitiate an analogy if counterbalanced by strong focal comparisons. But Hofstadter's focal comparisons are also weak. For example, a DNA strand is compared to a *Principia Mathematica*-like string, but then the complementary messenger RNA strand, which is equal in length to the DNA strand, is compared to a string of higher order constructs such as might appear in a number theory proof. A higher order string of that kind is typically a great deal shorter than its *Principia Mathematica* equivalent† and as a rule, never consists of a sequence of symbols that could be construed as “complementary”.

Further difficulties arise in the details of the comparison between Gödel numbering and the genetic code. Hofstadter draws up a modified Gödel numbering scheme to look like the genetic code (Hofstadter, 1979: 535) made up of triplets (cf. RNA codons) of four possible numbers (cf. RNA bases) standing for *Principia*-like symbols (cf. amino acids). Thus, “de-arithmetization” is compared to protein synthesis. Certain “informal statements about number theory” (cf. RNA strands) in addition

† For example, Hofstadter shows (1979: 204, 212) that “5 is prime” (a putative messenger RNA-like string) can be decomposed rather opaquely into more explicit, lower level language (a putative DNA-like string) as:

$$\forall d: \exists e: \sim \exists b: \exists c: (d + Se) = (SSb * SSc), \tag{1}$$

where small letters are variables, *S* is successor, and * is multiplication. Clearly, (1) is not a complementary one-to-one mapping from “5 is prime” in any obvious sense. Because of this, the pair of number theory sentences are remarkably different from their intended analogs at the cellular level, which are equal in length.

to being the "interpretation" of formal *Principia*-like statements (cf. DNA strands) as described above, can be partially reinterpreted by decoding the strings of numerals in them via the "Gödel code" to get a different set of *meta*-mathematical *Principia*-like statements (cf. proteins) about other *Principia*-like statements. We end up, after de-arithmetization, with the same sort of stuff that we started with; each symbol has the same meaning as before, but the de-arithmetization step has generated a new, predictable logical string from a string of numerals in one of the starting statements. Of course, this is exactly what Gödel needed to construct his undecidable, self-referential sentence. The situation in cells, however, is quite different. The decoded product—an amino acid string—is made up of fundamentally different stuff than the DNA and RNA strings, and its units follow entirely different "syntactic" and "semantic" rules of self-assembly and chemical interaction.

Hofstadter's alignment leads to an obvious disanalogy between the two systems in the way information is transmitted across the three main strings in the analogy. In the genetic code, we can find the same piece of information in all three strings (DNA triplet, mRNA triplet, amino acid). The lack of a one-to-one map between Hofstadter's DNA and RNA analogs was already mentioned. But there is a similarly opaque mapping between his RNA and protein analogs; only part of the putative RNA analog—i.e. the numerical part—can be de-arithmetized. By contrast, any RNA can potentially be turned into a protein. In sum, then, Hofstadter's comparison between Gödel's proof and the genetic code is not drawn carefully enough to be useful as a predictive analogy.

6.2. PROTEIN FOLDING AND SEMANTICS

Pattee (1980, 1982) has recently invited psychologists to examine the "primitive embodiment of a symbol-matter system" in cells as an exercise in "mental hygiene", and as an alternative to the study of artificial symbol systems. In its basic outlook, Pattee's approach is closest to mine. He writes with great insight about the biological side of the analogy:

"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 *not* related to their referent action in any detailed or explicit form, but only through an implicit harnessing of natural laws and structures which need 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. 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" (Pattee, 1980: 266).

There are fundamental issues at stake here of great relevance to the study of language, but Pattee is less incisive as he turns to consider psychology and language explicitly.

His analogy rests on a comparison between *genes*, *enzymes*, and *substrates*, on one hand, and *word-strings*, *meanings*, and *objects*, on the other (see Fig. 3 for schematic summary). The middle object in each trio (enzymes, meanings) has what

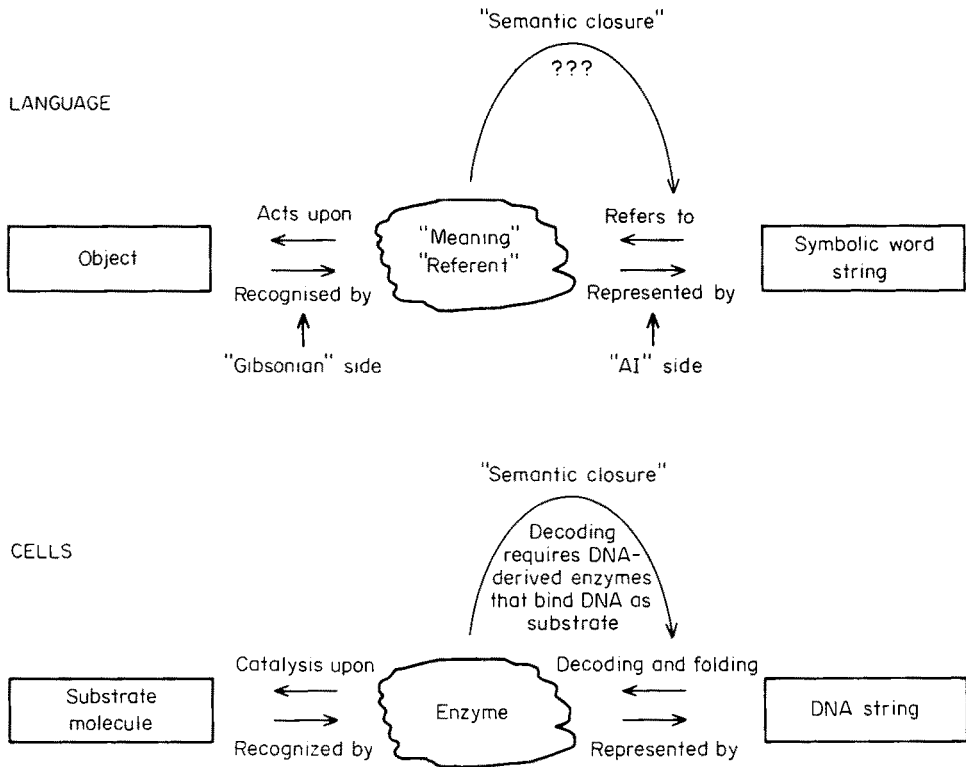


FIG. 3. Schematic diagram of the analogy presented in Pattee (1980, 1982). This analogy is closest to the cell/person analogy presented in the second half of the paper.

Pattee calls an “artificial intelligence”-style relation with the first object, and a “Gibsonian”-style relation with the third object. The meaning is “represented” by symbolic word strings as an enzyme is “represented” by a DNA symbol string (the AI relation). The meaning is also taken to “recognize” its object by resonating in a non-symbol-like manner, just as an enzyme is shaped so as to bind and alter a particular substrate molecule (the Gibsonian relation).

The problem with Pattee’s analogy is that it is difficult to tell exactly what he is referring to at the linguistic level. For example, it is unclear whether “word” and “word string” refer to actual sounds, marks on paper, neural patterns underlying speech sound perception, motor system neurobiology, an activated word concept, or some combination of these. Perception, production, and comprehension have very different implications for this predictive analogy. Although Pattee does not specify it, the all-important “folding” process (by which a chain of amino acids assembles itself into a unique three-dimensional structure) seems to be intended to apply (correctly, I think) to the *comprehension* of word sound sequences. A similar problem with lack of specificity arises in the discussion of the “meaning/object” relation and “semantic closure”. These relations could refer to early visual perception

(a favorite subject for many Gibsonians), sentence-like meanings constructed as a result of seeing actions and objects, the effect of language-generated meanings on the perceptual processing of an object, motor patterns underlying behavior toward an object, and others.

The root of these problems is the stated intent of Pattee “not to model cognition or language at the brain level” (Pattee, 1982: 325). Of course, that is not intrinsically objectionable. However, his analogy is set up so that brain states are just what it makes predictions about, as Pattee himself has pointed out in other contexts: “We may compare the role of these . . . constraints [on possible secondary and tertiary structures in proteins] to the postulated deep structures of the brain” (Pattee, 1980: 271). To conclude, I think Pattee has found the correct starting point for a productive analogy between biology and language, in spite of the strong criticisms I have given.

7. The Cell/Person Analogy—Present Treatment

The present treatment of the cell/person analogy draws many detailed links between biology and language across three main levels of organization: organism/community, cell/person, and biomolecules/neural activity patterns (see Fig. 4)†. I will focus here on comparisons at the last two levels. The analogy is introduced by first considering the common problem “solved” by life and language-based thought, and then considering three parallel constraints that suggest why the solutions should have been similar. Second, the basic common scheme is presented with a summary of the proposed primary correspondences between the two systems. Third, I give

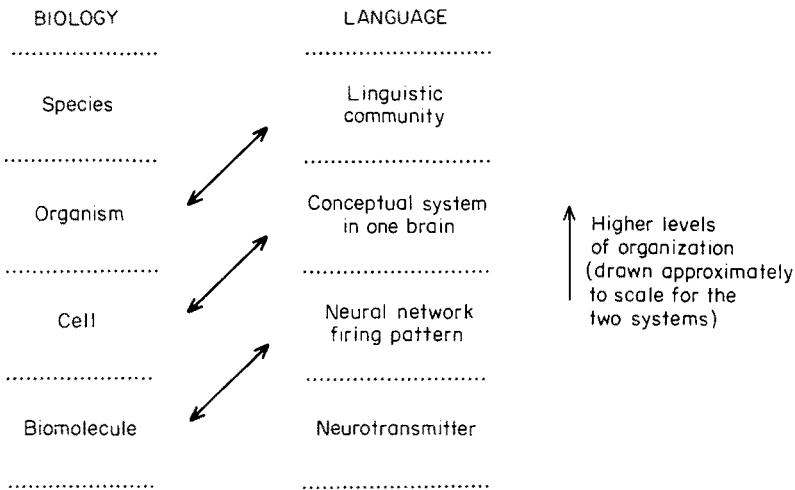


FIG. 4. Levels of organization in the cell/person analogy.

† The cell/person analogy is developed in more detail in Sereno (1984, unpublished). Those presentations also emphasize the relation between the symbolic-representational system in cells and persons, on one hand, and the artificial symbol systems presently in use in computers and proposed for neural networks, on the other.

several exposed comparisons to establish the analogical mapping scheme. Finally, three predictive comparisons are explored.

7.1. MOTIVATION

7.1.1. *Defining the common problem*

This thesis is that a unique single-celled symbolic-representational system first arose from a prebiotic chemical substrate at the origin of life, permitting Darwinian evolution to occur. Subsequently, multicellular organisms evolved and they developed more and more elaborate humoral and neural control mechanisms. But I claim that a similar, autonomous symbolic-representational system did not re-emerge on any intermediate level until the origin of thought and language from the substrate of prelinguistic neural activity patterns in the brains of Pleistocene hominids. I would first like to try to define the common problem that was, so to speak, solved by the origin of life and the origin of thought.

Put crudely, the apparatus involved in cellular protein synthesis, and the neural patterns underlying human language comprehension are both mechanisms for escaping "determinism". This does not imply that these systems create mysterious, irreducible holistic forces. But it is a natural way of characterizing the "solution" to a straightforward "problem" common to the pre-existing states. The pre-existing (prebiotic, prelinguistic) states can be described as complex, highly interactive, but deterministically evolving, "soups" containing a number of different types of dynamically stable units (prebiotic molecules, prelinguistic neural activity patterns). The problem is simply to encode, use, and reproduce information about how to make certain "reactions" (chemical reactions, alteration and recombination of neural activity patterns) in this soup happen. The tricky part is that the information, as well as all the interpreting apparatus has to be *in* soup, and thus, is subject to its deterministic buffetings. Some of the reactions can already happen a little by themselves without the system's help; the system, however, speeds some reactions, slows or prevents others, invents many new ones, and orders them—in short, controls phenomena in the soup. A way had to be found to "camouflage" information from the dissipative attack of the soup, but the information could not be hidden so well as to be 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 exploiting partially hidden, partially arbitrary information that the soup has trouble seeing and thus destroying, the system is able to evolve in a new, symbol-based manner very far away from its initial state into configurations that are exceedingly improbable from the soup's viewpoint. In this sense, the resulting system is "intentional".

7.1.2. *Three parallel constraints*

So far, we have only suggested a similar *raison d'être* for the two systems. Here are three specific constraints on constructing such a system, common to both levels of organization, that may account for thoroughgoing similarities in structure as well

as function. The first constraint arises because many distinct reactions must be controlled simultaneously at close range. A large number of units of various kinds (reactants, special purpose devices to run each of the many reactions, code-like material, and so on) 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 reaction-controlling devices used by the system must have a great deal of *specificity of action*; they must operate only on their intended target in the highly interactive milieu of the cytoplasm or the language-proficient brain.

The second constraint arises because the system did not originate in a vacuum, but from a “soup” containing a variety of pre-existing units. Structures in the two systems had to be built up partly out of these units. By itself, the necessity of “using what was at hand” would not be expected to lead to structural parallels. However, for various reasons, only certain types of units, with certain pre-existing relations to entities in the “soup” can be used (e.g. only some of the pre-existing units are stable enough to accumulate in reasonable quantities; only some can form chains that fold up into determinate structures). A second constraint leading to similarities, thus, is the *nature of the pre-existing units* that make up some of the devices needed to operate the system.

Finally, a third important constraint has to do with the assembly of units into reaction-controlling devices. The reaction-controlling devices are large and complicated compared to the pre-existing units. Also, this assembly process must be directed by coded information. Consequently, the device-assembling reactions are inherently more complex than any of the other reactions in the network which result in smaller, simpler end products. The result is that the reaction-controlling devices must be *assembled locally, one unit at a time*. This goes beyond the often noted requirement for modular subassemblies (cf. Simon, 1969; Pattee, 1980); the more subtle need for serial assembly was, in fact, overlooked in the early treatments of the cellular coding problem discussed above (see Gamow, 1954; Crick, 1958, who envisioned the assembly of many units simultaneously). Local, serial assembly breaks down what would be an impossibly complex reaction into a series of reactions, each of which is nearer in complexity to the numerous other controlled reactions in the “metabolic” network. This is probably the most important reason why the overall architectures of the two symbolic-representational systems are similar.

7.1.3. *Lack of “language production” in cells and the purpose of human language*

All previous attempts to compare cellular and linguistic phenomena have failed to recognize a clear difference between the cell- and person-level symbolic-representational systems. This is the utter lack of explicit “language production” at the cellular level. Cells have no mechanism for turning the three-dimensional structural “meanings” in proteins back into coded DNA messages for the purpose of directly communicating with other cells. Rather, each cell “listens to” and “comprehends” only its own internal coded DNA “speech stream”. Instead of mediating communication, the long code sequences in cells mainly direct the construction of thousands of reaction-controlling enzymes that interact to maintain a complex, self-reproducing *metabolic network*.

I think the main purpose of human language might similarly be to generate and maintain a stable network of “mental reactions” (i.e. modifications of neural activity patterns)—a mental metabolism as it were—by directing the construction of special purpose “reaction-controlling” devices (i.e. other neural activity patterns). From this perspective, the ability to communicate some of these internal reaction-controlling patterns into other people’s brains by turning them *back into code* is an added bonus (with far-reaching consequences, to be sure), but something that might be conceptually distinct from a common core of similarities having to do with the “perceptual” processes of constructing and maintaining the internal network in the first place. The idea that communication is the *sine qua non* of language has been challenged before, though perhaps not on these grounds. The linguist Edward Sapir, for example, wrote:

“The primary function of language is generally said to be communication . . . [büt] 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 that renders it a fit instrument for communication . . .” (Sapir, 1921: 159).

Perhaps, the advent of such a mental metabolism has allowed hominids to take control of the highly patterned, but nevertheless, prelinguistic “soup” of mental patterns in their brains in a way that is qualitatively different from the way that apes or other animals do it. This new system has quite apparently allowed an entirely new mode of evolution of mental patterns to occur.

To see more graphically the differences between the systems that can be traced to the lack of production, it helps to envision human language without production, or cells with it. 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 would be internal, like DNA; each person would store hundreds of thousands of messages inside his or her brain in a permanent magnetic tape-like format. These independent libraries would be inherited from one’s parents. During daily activities and interactions, messages appropriate to various situations could be accessed and meanings generated from them internally. Communication would be restricted to pantomime and onomatopoeic vocalizations. No new internal messages could arise during a person’s life time, except as a result of random deterioration (“mutations”) of his or her permanent store. Cultural evolution would be 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 person-like cells *with* production. In the first place, it would be possible for cells to synthesize proteins *de novo* without the need for a coded DNA message, 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 some effort. So far, cells have just started to “think to themselves”. Full-fledged human-style production of the DNA language would require a brand new chunk of molecular machinery for

unfolding a protein and turning the unfolded chain back into a coded DNA strand. Then the cell would be able to communicate directly with other cells by injecting the new, re-coded DNA strand into them so that they could generate a protein from it. This constitutes a more thoroughgoing, minute-to-minute Lamarckianism than has ever been conceived for biological organisms.

Organisms would evolve at a faster pace, adapting in a directed, Protean manner to environmental and social conditions, constantly passing on acquired knowledge to cells and organisms unrelated by descent.

Notice that the productive aspects of human language make it doubly different from the genetic code; humans not only produce new internal meanings by directed changes of the (mental) phenotype, but then they communicate them promiscuously. Cultural or conceptual evolution has often been characterized as “Lamarckian” but it could presumably be so without the communicative function of language. To emphasize this, if whole animal phenotypes evolved the way human mental “phenotypes” do, not only would a giraffe’s neck elongate as it tried to reach the higher branches, but then 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 simply by “lecturing” to them. From the view of the present analogy, mere conversation or even a few moments of thought to oneself results in immediate evolutionary change in the mental phenotype potentially capable of transmission to any person.

The unilateral provision for language production (or, from our view, its lack in cells) has many ramifications. The multitude of differences traceable to it have quite effectively deflected attention from the very deep similarities in architectural principles on the comprehension side—concerning especially the way in which specific sequences of meaningful units are assembled. If it were not for this stumbling block, the present analogy would have been recognized much sooner.

7.2. A COMMON SCHEME

7.2.1. *The abstract scheme*

A general scheme for a symbolic-representational system is now given, at first omitting system-specific details. The simplest self-contained symbol structure has, from the perspective of one time-slice, five main parts—the external *symbol*, the internal *symbol-representation*, the “*three-dimensional*” *connector*, the internal “*thing*”-*representation*, and the external “*thing*” (see Fig. 5). This describes a comprehension-only system; production of symbol streams requires additional internal entities, not illustrated here.

We start with the external symbol. It has a *non-arbitrary* causal relation with the internal symbol-representation. That is, this relation is not defined by the symbol system itself but depends on deterministic, pre-systemic processes. By contrast, the internal symbol-representation has an *arbitrary* causal relation with the internal “*thing*”-*representation*. That is, there is no deterministic, pre-systemic reason why a particular symbol-representation should be preferentially connected to any one of the various “*thing*”-*representations*. What determines which pairs get connected

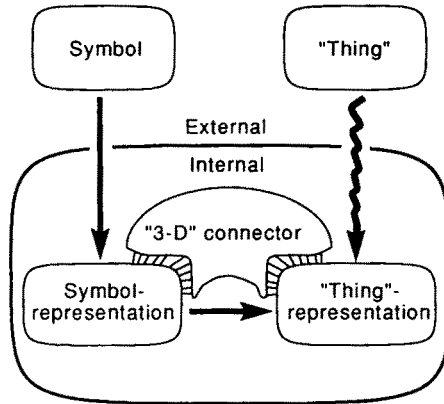


FIG. 5. A basic scheme for a symbolic-representational system. The main relations are shown by bold straight lines. The bold wavy line indicates a pre-systemic relationship.

is an entity capable of recognizing in a non-arbitrary way, the “three-dimensional” structure of those two members. “Three-dimensional” recognition (short lines) is defined as a between-part connection that involves large, non-standard regions, in contrast to an arbitrary bond which involves smaller, standardized connecting regions. The “thing”-representations have more variegated “three-dimensional” structures than the symbol-representations. The “thing”-representations also have a non-arbitrary relation with external “things”. Again, the relation is not defined by the symbol system but depends on pre-systemic transformations. This relation (indicated by the wavy line) is not causal in a systemic context because the “things” are often not present; the “thing”-representation is causally called up in normal operation only by the symbol-representation.

In a static view just presented, the scheme is reminiscent of a Peircean triad (symbol, object, apparatus that “perceives” the relation between the two—see (Peirce, 1931–58: vol, 2, para. 250–274) except that the internal interpreting apparatus has been subdivided; but the present scheme diverges considerably from other treatments of symbol-processing systems in diachronic view. Figure 6 illustrates the same parts shown in Fig. 5 but fills in more detail (names of five main parts from Fig. 5 are in boldface). The proximal purpose of the system is to assemble long chains of “thing”-representations based on the ordering of long symbol chains. The symbol chains consist of segments concatenated by arbitrary₂ bonds. Each segment has a constant backbone and a variable sidechain, and there are several segments per symbol. Arbitrary₂ bonds form chains (i.e. each unit bonds to *two* other units; bond connects units from same class); the bond is arbitrary in the sense that its stability is independent of identities of the two bound symbol segments. There are nearest-neighbor interactions between sidechains as well as backbones in the symbol chain (short lines).

The symbol chain is first sequentially and non-arbitrarily perceived, generating an *internal message*, which consists of a chain of symbol-representation segments. *Word-recognition devices*, also made of symbol-representation segments (these are

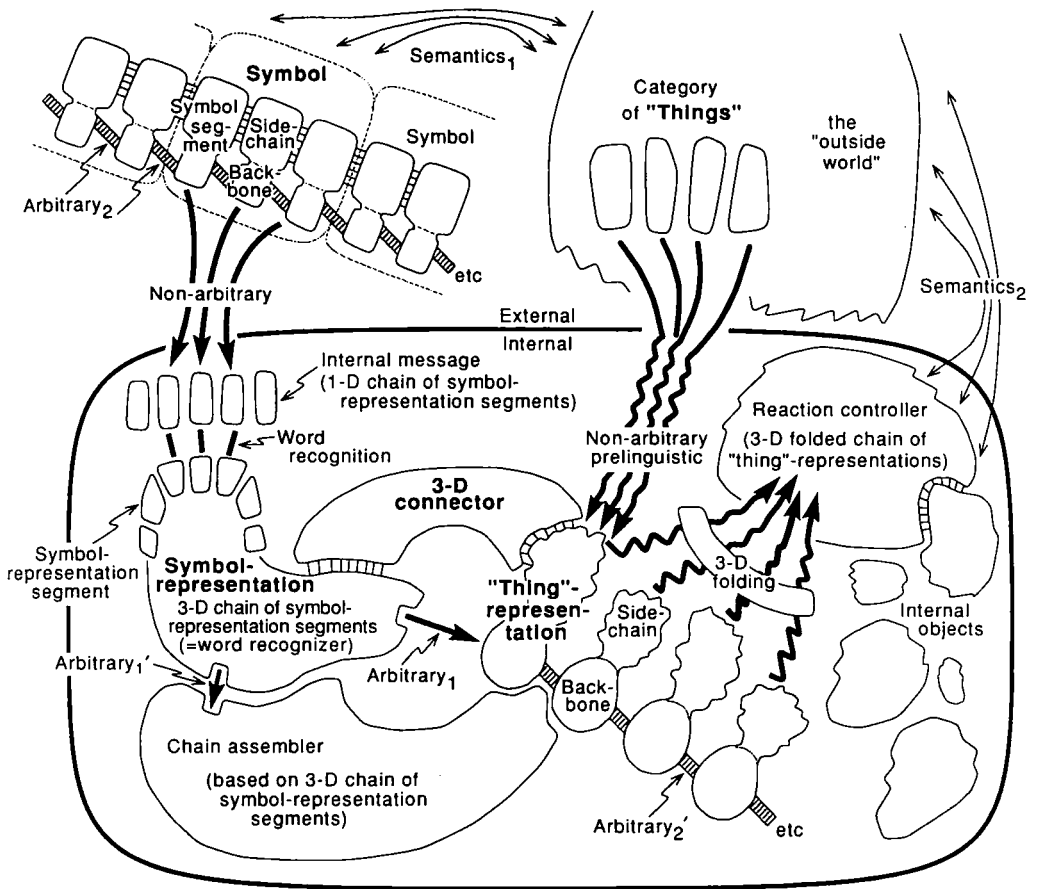


FIG. 6. A scheme for a symbolic-representational system in action. The five basic parts of a symbolic-representational scheme illustrated in Fig. 5 are in boldface. The three main functions of chains of symbol-representation segments are now illustrated (internal message, symbol-representation, chain assembler). The diagram illustrates in more detail the dynamic process by which chains of symbol segments (upper left, connected by one kind of arbitrary bond) are non-arbitrarily recognized in small groups by the symbol-representation (lower left), which then presents its connected "thing"-representation (lower right, connected to the symbol-representation with a different kind of arbitrary bond) to the chain-assembler. A parallel string of "thing"-representations is constructed, which then folds upon itself (sharply wavy lines), forming reaction-controlling devices, which operate upon internal objects (middle right). The gently wavy lines (upper right) signify a pre-systemic relationship.

symbol-representations proper), recognize the symbols in this message and present particular "thing"-representations to the *chain assembler* which is also based on symbol-representation segment). The 3-D connector has previously attached the "thing"-representation to its appropriate symbol-representation by an arbitrary₁ bond (i.e. between pairs of units—each unit bonds to only *one* other unit; bond connects units from different classes). During chain assembly, temporary arbitrary₁

bonds are made between the chain assembler and various symbol-representations (similar to arbitrary₁ bonds except that one member of the bonded pair is always the same—i.e. there is only one chain assembler to which all symbol-representations bind).

The chain assembler generates arbitrary'₂ bonds between the backbone parts of pairs of "thing"-representations (similar to arbitrary₂ bonds—each unit bonds to *two* other units; units from same class—except that the sidechains of adjacent units do not interact). The chain of "thing"-representations then folds into a particular configuration as a consequence of interaction among the local semantic functions of the sidechains. Folding is a process by which *non*-adjacent units in a chain are brought into close contact. The main function of the folded "thing"-representation chains is to control reactions—i.e. to modify the 3-D structure of internal objects by making and breaking bonds within and between them. The overall purpose of the system is to generate a homeostatic internal world that mediates interactions with the external world.

7.2.2. Primary correspondences

The primary correspondences between the two systems, both exposed and predicted, are listed in Table 1. Starting with the static five-part scheme in Fig. 5, the corresponding entities are as follows. The *symbol* at the cellular level is the DNA triplet, and at the person level is the group of sounds in a word. The *symbol-representation* in cells is transfer RNA, and in persons, an auditory cortex word-recognizer pattern mediating the on-line connection between internal speech sound representations and meanings. The "*thing*"-*representation* in cells is the amino acid, and in persons, a higher visual cortical areas activity pattern constituting a category representation of a thing, action, event, path, place, property, or manner. The 3-D *connectors* in cells are aminoacyl-tRNA synthases, enzymes that attach particular tRNAs to particular amino acids prior to protein synthesis, and in people, an activity pattern that attaches auditory cortex word-recognizer patterns to visual cortex word meaning patterns off-line. Finally, "*things*" at the cellular level are substances in the pre-biotic soup like water, hydrogen cyanide, formaldehyde, and amino acids, while linguistic things are prelinguistic activity patterns in the primate brain that arise in the course of the organism learning to interact with objects and events in the world.

Turning again to the more detailed scheme in Fig. 6, the initial perceptual processing of the symbol chain generates an *internal message* consisting of messenger RNA in cells and a chain of speech sound representations in auditory cortex in persons. Word-sized chunks of segments in the internal message are recognized by the *word-recognizer* (=symbol-representation), which with the help of the *chain assembler*, constructs a parallel chain of "thing"-representations based on the word sequence. The internal message, word-recognizer, and the chain assembler are all made from symbol-representation segments—RNA nucleotides in cells, and auditory cortex activity patterns representing single speech sounds in persons. The chain of

TABLE 1
Summary of the cell/person analogy

General term	Cell	Person
Symbol	DNA triplet	Sounds in a word
Symbol segment	DNA nucleotide	Single phonetic segment
Symbol-representation segment	RNA nucleotide	Secondary auditory cortex (Wernicke's area) activity pattern representing one phonetic segment
Internal message (chain of symbol-representation segments)	Messenger RNA (mRNA)	Secondary auditory cortex activity pattern representing the sounds in several sentences
Word recognizer—same as symbol-representation (chain of symbol-representation segments)	Transfer RNA (tRNA)	Secondary auditory cortex activity "adaptor" pattern that recognizes particular phoneme groups and activates appropriate meaning
Chain assembler (chain of symbol-representation segments)	Ribosome (rRNA plus protein)	Secondary auditory cortex activity pattern that assembles unit meaning-patterns into a chain
3-D connector (chain of "thing"-representations)	Aminoacyl-tRNA synthases	Secondary visual cortex areas activity pattern for attaching meaning patterns onto "adaptor" patterns prior to word recognition
"Thing"-representation	Amino acid	Secondary visual cortex areas category representation activity pattern lasting several hundred milliseconds; a word meaning
Reaction controller (chain of "thing"-representations)	Enzyme (4-20 sections of secondary structure per domain, each of which may contain several hundred amino acids)	"Bonded-together" structure generated in short term working memory upon hearing a discourse (four to 20 clauses, hundreds of words)
Objects (heterogeneous intermediate 'substrates')	Enzyme substrates (including amino acids, proteins, carbohydrates, lipids, small molecules, and so on)	Mental "objects" including single word meanings, assembled discourse meanings, emotional meanings, images, and many intermediate-sized units all construed as activity patterns
"Things"	Substances in the prebiotic soup (e.g. water, hydrogen cyanide, formaldehyde, amino acids)	Prelinguistic firing patterns in the primate brain arising the course of cognitive development; may be integrated into larger units in adult

"thing"-representations—a chain of amino acids (polypeptide) in cells, and a composite activity pattern constructed by concatenating single visual category activity patterns in persons—then folds and develops the ability to specifically modify *internal objects*. These objects are quite various, including amino acids, whole proteins, carbohydrates, lipids, and small molecules (e.g. constituents of the Krebs

cycle) in cells, and single word meanings, whole discourse meanings, emotional meanings, images, and many intermediate-sized units, all taken as neural activity patterns, in persons.

A helpful summary of the person side of the analogy is that language comprehension may be thought of as a kind of *code-directed scene perception*. Upon first looking around a new place, a viewer must assemble a temporarily persisting representation, in higher level visual areas, of the immediately surrounding environment for the purpose of navigation, recognition, food-finding, social interactions, and so on. The raw material for this representation is a series of quarter-second glances, which aim the high-resolution part the retina, the fovea, at a sequence of locations, generating bursts of activity in primary visual cortex. Language comprehension may build upon these mechanisms (see Sereno, 1991); the main extension is that human primates (as opposed to apes and other animals) also freely construct such higher level visual cortex patterns using strings of *auditory cortex* patterns, in the absence of direct, lower level visual input.

7.2.3. *Symbolic-representational systems may have a minimum "size" or complexity*

The cellular level symbolic-representational system is characterized by a clear minimum "size" or level of complexity. The smallest free-living cells—the mycoplasmas (bacteria-like organisms, but without cell walls)—have genomes only 1/5 the size of *Escherichia coli* (for review see, Neimark, 1979). These minimal genomes contain under a million DNA bases (symbol segments) and code for slightly less than a thousand different 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. Mammalian cells have three orders of magnitude more DNA bases (e.g. 3 billion in human cells), though much of this appears not to code for proteins.

It is harder to define the minimum "size" of a person-level language; human 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 discussing the number of sentences of discourse meanings "in" a language, insisting that there are infinitely many possible. Set against this, however, is the obvious fact that any one person can only experience a finite, though rather large, number of sentences while learning, using, and thinking a language. The total number of symbol-segments is actually not as large as one might at first think. For example, it would take 10 years to experience a billion segments at the rate of 300 000/day (=8 hr continuous speech/day). By analogy with cells, it may be that a *self-reproducing, independent* (i.e. "free-living") symbolic-representational system at the person level minimally requires the perception of at least hundreds of millions of ordered segments, and thus the comprehension of hundreds of thousands of connected discourses. [In a similar vein, Anderson (1983: 132) has estimated that human-style cognition requires about 1 million paragraph-sized "productions".] Below this size, it may not be possible to support a human-style "mental meta-

bolism”†. The large gap between symbol use by animals and human language lends support to this notion.

7.3. EXPOSED COMPARISONS

7.3.1. *The prominence of cellular and human symbol chains*

The enormous covalently bonded DNA molecules that characterize even the simplest organisms are quite distinct in a prebiotic milieu. The isolatable DNA molecule in each *E. coli* is nearly 4 million nucleotide bases long. There are, of course, isolatable prebiotic molecules—amino acids, for instance. And there are, amongst the great variety of substances in the prebiological natural world, a bewildering variety of rocks and minerals consisting of regular, bonded networks of atoms (crystals), as well as many complex and less regular gel-like, colloidal, or “cryptocrystalline” substances (see Cairns-Smith, 1982, for a summary from an origin-of-life perspective). The key point is that when the bonded network of a mineral—the layered silicate sheets of a clay mineral, or the framework structure characteristic of a metal oxide, for example—is exposed to water, it typically breaks up into small, heterogeneous, individually-solvated pieces, each containing only handfuls of atoms, instead of forming a uniform species of macromolecular, isolatable, solvated chains. Non-biotic macromolecular gels exist (e.g. Al^{3+} solutions), but are rather hard to study because, in contrast to biotic polymers, their covalent structures in solution are labile, forming and disassembling in response to slight changes in ionic concentrations, pH, and so on. In this respect, the molecular structure of minerals is much less suitable for constructing stable code chains that could serve as templates for constructing other self-folding structural chains. This is not to deny that mineral-based proto-living systems may have provided a scaffold, now stripped away, for the evolution of organic life (Cairns-Smith, 1982).

Crystals typically grow in sedimentary environments under nearly the same conditions that result in their degradation—dilute solutions of ions or small charged molecules. Crystallization of many minerals requires the exclusion of water (e.g. some of the water of hydration of a metal ion), but in general, this water is rather easy to remove. Long biological polymers do not form “naturally” in aqueous solutions because the strong covalent bonds between each unit require the removal of strongly bound water-forming groups. Exactly how enormous biopolymers came to be generated and incorporated in homeostatic, self-reproducing cells has therefore long been a mystery.

In turning to human language related activity, we find its long symbol chains similarly distinctive in a pre-linguistic context. While immersed in language, it is easy to forget how odd an animated, hour-long conversation consisting of a sequence of perhaps 30 000 closely connected speech symbol segments must appear to a

† From this point of view, an artificial intelligence program designed to interact with the world (e.g. to read a menu and order in a restaurant, to use a task studied by several AI groups) 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 clear that LISP is the language of thought, whereas viruses have the same type of DNA (or RNA) and proteins as their hosts do.

contemplative non-linguistic animal. The only examples of serial vocal behavior in present-day animals that even remotely resembles this in scale are from songbirds; wrens, for instance, typically sing hundreds of distinct songs, each consisting of a small group of "syllables" with a few sound segments per syllable (for review see, Konishi, 1985). It is easy to tell the human and avian behaviors apart, though, since in humans, the ordering of the sequence at intermediate scales (as reflected in word and sentence order, spanning hundreds to thousands of segments) is essential in coding for a meaning, while the songbird's intermediate range ordering (as reflected in song order) does not appear to be determinate, or to code for, or mean anything. The analogy is imperfect at this point since truly DNA-like "speech sounds" would be permanent, encyclopedia-length *internal* code-like activity patterns constituting an enormous verbatim memory. Nevertheless, the internal avian neural activity patterns that generate and are elicited by song-sequences are undoubtedly much less "stably bound" and less isolatable as distinct species than the human neural activity patterns that generate and are generated by word sequences.

That cellular and human symbol chains are especially prominent is not really controversial. The point here is that they are unique; there are no other naturally-occurring systems independent of those two that use long, one-dimensional sequences to stand for meanings. Even a casual inspection of intermediate levels of organization suffices. Chains of cells do not systematically code for anything, any more than chains of tissue types, organs, or whole animals do. There are, of course, many examples of segmented activity patterns in brains—for example, the patterns underlying the generation of complex movement sequences. These patterns, however, do not code for movements in the present usage of the word since there is no sense in which the resulting movement is *arbitrarily* related to those patterns. The parallel uniqueness of long symbol chains is thus one of the primary exposed comparisons used to motivate the cell/person analogy.

7.3.2. *Word recognition*

Cells and persons routinely "perceive" and "comprehend" their code chains. One stage in this process is *word recognition*. Word recognition is a process by which a continuous chain of symbol segments lacking word delimiters is recognized to contain a series of multi-segment words. A key requirement is that the end of one word must be actively recognized in order to locate the beginning of the next word. The mechanistic details of word recognition are better understood at the molecular level than they are with respect to neurophysiology of language comprehension. Nevertheless, what is already known makes word recognition an unambiguous exposed comparison.

In cells, the smallest meaningful group of symbol segments (DNA nucleotides) is the *codon* (or *word*)—a triplet of DNA nucleotides that stands for one of the 20 different amino acid meanings. Thus, all words in cellular symbol chains are the same length. Four different types of nucleotides taken three at a time make 64 possible codons, of which 61 are used to code for amino acids. There are no systematic chemical differences amongst the 16 internucleotide linkages *within* and *between* codons in both DNA (chain of symbol segments) and RNA (chain of

symbol-representation segments); that is, there are no explicit markers indicating where one codon ends and another begins. Therefore, each triplet codon in a messenger RNA strand has to be recognized sequentially in order to determine the start of the next codon. This is done by a set of 40 tRNAs, each of which binds, in the context of the ribosome, to a particular mRNA codon (or in some cases, a few different codons). As soon as the currently bound tRNA adds the amino acid it is carrying onto the growing chain of bound amino acids, it is released from the ribosome. The mRNA is then pulled through the ribosome, exposing the next codon. When by chance, the correct tRNA diffuses into place, the process is repeated. The ribosome actually binds two tRNAs at once; when the second site is vacated, the tRNA in the first site moves into the second site, opening up the first site for a new tRNA. This allows the amino acid chain to remain attached to a tRNA at all times (for review, see Watson *et al.*, 1987).

In persons, an easy demonstration of the lack of explicit word-boundaries can be gotten by listening to an unfamiliar foreign language; it in general is quite impossible to tell where one word ends and another starts. Now human language is considerably more complex than cellular protein synthesis. There are more symbol segments in human languages (typically 30–40 different speech sounds or phonemes vs. four nucleotides in cells); there are many different human languages (with few exceptions, all cells use the same codons for the 20 amino acid meanings); word length is variable in human language (one to ten or more symbol segments vs. three in cells); and finally, there are more word meanings (10 000 or more vs. 20). Nevertheless, there is still a strong requirement in spoken language that each word be recognized in turn, so that the beginning of the next word can be identified[†]. The process of word recognition has been studied in great detail by psycholinguists (e.g. Frauenfelder & Tyler, 1987). Many theories recognize an automatic component that operates one word at a time in a rather context-insensitive manner, and several other processes that are sensitive to syntactic and semantic context. It is known that initial stations in the auditory pathways carry a sequence of activity patterns that closely parallel the rapid spectral changes in speech sounds (Delgutte, 1982). The early process of auditory word recognition mentioned above must commence within tens of milliseconds after this stream of activity arrives in secondary and tertiary cortical auditory areas. In spite of our current ignorance of the low level details,

[†] The ratio between the number of mathematically possible symbol segment combinations (i.e. possible symbols) and the number that are actually used is much larger in human language than in cells. There are billions of possible word-sized speech sound combinations but only tens of thousands are used to code for word meanings in human languages, while there are 64 possible nucleotide triplet combinations and almost all of them (i.e. 61) are used to code for 20 word meanings in cells. Thus, the code in cells is almost entirely overlapping—it makes sense if one starts reading from any nucleotide. Of course, the cell virtually always uses only one of the three possible interpretations of a piece of DNA; the others are only accessed in the event of a frameshift error produced when a nucleotide is somehow skipped or lost. Since there are so many more combinations to work with in human language, it can afford to be less overlapping. Though the probability of an ongoing “frameshift error” in human language is low, there are often many alternate parsings on a short term basis (see Cole & Jakimik, 1980). Interestingly, the perceived stringency of sequential word recognition prompted early molecular biologists to look for ways to get around it. The ingenious but ultimately incorrect “comma-less” code proposed by Crick *et al.* (1957), for instance, could only be read in one frame. Human language is certainly not completely overlapping, but neither is it comma-less.

the process of word recognition already constitutes a unique exposed parallel between the cellular and human symbolic-representational systems†. In the following sections the cell/person analogy is used to make preliminary predictions about some of presently hidden mechanisms underlying word recognition and its goal of meaning assembly.

7.4. PREDICTIVE COMPARISONS

7.4.1. *Message and structure—implications of structural RNA*

One of the most striking aspects of the molecular organization of cells is the fundamental involvement of RNA strands (symbol-representation segment chains) 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 (mRNA) 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 (tRNA, rRNA) that serve architectural, recognition, and catalytic functions. The intermingling of roles is very ancient, probably having changed little since soon after the origin of life (Woese, 1983).

The great majority of the thousands of catalytic functions in the cell, of course, are performed by proteins, not RNA strands. There are more possible units in protein chains than nucleotide chains (20 vs. four) and the protein subunits, amino acids, are much more structurally various than nucleotides. Because of this, it came as something of a surprise when it was discovered several years ago that certain RNAs actually show enzyme-like binding site specificity and reaction rate acceleration (Cech, 1983; Zaug & Cech, 1986). This discovery prompted renewed speculation on the implications for the origin of life of the role of RNA as both message and structure (Orgel, 1986). The important point here is that out of the thousands of reactions run by a cell, the few reactions that crucially involve RNA in a three-dimensional, structural capacity are precisely those reactions that are most closely involved with the *transformation of one-dimensional message to folded three-dimensional structure*—that is, the reactions of protein synthesis. Three important functions are: generating an active internal message, word recognition, and chain assembly.

The fundamental and ancient bridging roles of symbol-representation segment chains at the cellular level suggests that we look for similar bridging roles for chains of symbol-representation segments at the level of human language. The first of these functions for symbol-representation segments—as *internal messages*—is rather uncontroversial. A number of models of speech perception have postulated that external sound sequences (symbol segment chains) are initially processed to give

† The process of word recognition plays a prominent role in the primitive concept of a computer. The main difference between human and cellular word recognition, on one hand, and word recognition in computers, on the other, is the use to which the recognized word is put—in cells and humans, a chain of “thing”-representations is constructed for the purpose of constructing and maintaining an internal “metabolism”, while in computers, a particular word stands for an operation *back on the chain of symbol segments*. This distinction is discussed in detail in Sereno (unpublished manuscript).

at some level, a parallel, internal, one-for-one chain of standardized units (roughly a continuous sequence of phoneme representations). The need for the second and third of these functions—*word recognition* and *chain assembly*—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—that is, neural activity patterns closely resembling internal message (phoneme) streams, different from them only in that they are more “stably folded”, and hence, persistent as a result of their particular sequence. The analogy suggests that the processes of the interactive recognition of words in a 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—the symbol-representation segment, which is nothing more than what happens in the auditory cortex upon hearing (and categorizing) a particular speech sound, but *without* understanding it to stand for anything else.

The enlarged portion of secondary auditory cortex in the posterior part of the superior temporal gyrus of the left hemisphere (Wernicke’s area—Braak, 1978; Galaburda & Sanides, 1980) may be the site of many of these functions†. This may partly explain the curious importance of secondary auditory cortex in language *comprehension* (for review see, Damasio & Geschwind, 1984; Caplan, 1987; Ellis & Young, 1988). One might expect damage to the auditory perceptual apparatus to be expressed as a deficit in perceiving spoken language. But the deficit in Wernicke’s aphasics seems to extend far beyond perception—to the integration and semantic interpretation of linguistic symbol strings. Analytic thought itself seems disarranged. By the present analogy, a Wernicke’s aphasic may lack the means to assemble word meanings into chains, in addition to having deficits in phoneme perception and word recognition.

† Discussions of the localization of language functions (e.g. Caplan, 1987) typically ignore the last 20 years of research into the anatomy and physiology of the (non-human) primate cortex. This is unfortunate, because this research has challenged long held views about the general layout of the cortex. In brief, “primary” and “secondary” cortical areas had long been distinguished in each of the main sensory modalities—vision, audition, and somatosensation. In between, there was a large area, much prized by philosophers, psychologists, as well as neurologists, where sensations from various modalities could come together to generate or interact with abstract, relational, modality-free representations (see e.g. Fodor, 1983; Garfield, 1987). Recent investigations in primates have uncovered an unexpectedly large number of cortical areas in each modality (over 25 in the visual system) each defined by a more or less topographic map of the receptor sheet in that modality (see Sereno, 1988; Sereno & Allman, 1991, for review of visual areas). The problem for the old view is that these modality specific maps have consumed virtually all of the remaining posterior cortex.

The significance of this for human neuropsychology has yet to be recognized. Of course, it is not entirely implausible that the increased area of cortex in humans (relative to monkeys) between the primary sensory areas (which are more nearly monkey-sized) contains a large polymodal area for which no analog exists in all other primates. But a more likely hypothesis, I think, is that the multitude of secondary visual, auditory, and somatosensory areas are simply larger and perhaps slightly more numerous in human brains (see Sereno *et al.*, 1988). Thus, the main character of the processing underlying peculiarly human abilities like language comprehension may be determined in large part by cortical areas whose main truck was—and probably still is—in visual, auditory, and somatosensory activity patterns, as opposed to the abstract, modality-free “representations” more commonly invoked (see Sereno, 1991).

7.4.2. *Pre-systemic origin of multi-functional “thing”-representations*

At the cellular level, many of the “thing”-representations—i.e. amino acids, the units composing proteins—can be easily generated prebiotically from chemical interactions that occur in primordial gas or “soup” mixtures (Miller & Orgel, 1974; Schlesinger & Miller, 1983). 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”. 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. Nucleotides, for example, do not readily arise under similar conditions (Shapiro, 1984; Joyce *et al.*, 1987). Since amino acids are category representations of what are actually complex quantum mechanical transitions, I have called them “thing”-representations with quotes. The implication is that the major advance of cellular 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 in isolation, are quite unremarkable in this regard.

A given amino acid will appear to have many different molecular “meanings” in the context of different protein chains, forming, for example, a part of the protein interior in one instance, while strongly interacting with a substrate molecule bond in the active site in another. In isolation, however, amino acids appear to have little specific “meaning”. They are small molecules (average 19 atoms) with rather undistinguished chemical properties; many are quite stable and unreactive (e.g. alanine has a billion year half-life in aqueous solution, which explains how it might have accumulated prebiotically). Chemical specificity and catalytic properties emerge only in the context of a chain. Of course, a bound amino acid in a protein is still perfectly identifiable as the same group of atomic nuclei (minus one water molecule). And none of this implies that the functions of the folded chain result from anything else than the very complicated sum of the interactions among the amino acids in the chain and the molecules in the surrounding solvent.

These observations suggest a novel reinterpretation of the linguistic notion of polysemy. Polysemous words like “line”, “put”, “sweet”, and “make” are useful, high frequency words in any language. Yet they appear to have a large number of different meanings—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) (an example from Miller, 1978). The present analogy suggests that if we could isolate the experience of a single word meaning (with thoughtlessness before and after!), it would have the *same* small non-specific-appearing content (e.g. a minimal visual representation of a line), no matter what the context. At the molecular level, we can clearly distinguish the amino acid unit itself, either isolated or concatenated, from its very different functions in those two cases. With language, by contrast, the relevant neural phenomena are still mostly hidden. Hence, it is much more difficult to sort out what might be the bare, constant units from their

various functions in context. It would be easy to mistakenly attribute the modified, more specific functions of a unit in a particular context to the unit itself—e.g. as “different” word meanings. The molecular system shows us instead that we can get quite different, but very *specific* meanings out of the same well-defined unit when it is placed in different contexts, but also, that if we isolate the unit, we find it to be almost meaningless. The implication at the level of human language is that there might be similarly *well-defined, singular* units that, in the context of a chain of words, take on much more specific and varied functions or meanings than they have in isolated form.

In particular, the analogy suggests that a subset of these unit word meanings in human language are *prelinguistic*—that is, they can arise in the course of the primate visual system non-linguistically learning to categorize activity patterns caused by things, actions, events, directions, places, manners, and so forth in the world. The unit meaning might be a brief, stable activity pattern in higher level visual areas specifically elicited by the presentation of a particular type of visual thing. It seems quite clear, especially from the carefully controlled experiments of Savage-Rumbaugh *et al.* (Savage-Rumbaugh *et al.*, 1983, 1986; Weiskrantz, 1985; Savage-Rumbaugh, 1987), that chimpanzees can acquire quite a number (hundreds) of such unitary concepts referring to classes of real world objects, actions, locations, and manners. This was tested using clever paradigms (e.g. sharing games with two animals) that require an animal to activate one of these concepts internally (bring one to mind even when a real world example of the concept is not initially present) upon viewing a non-iconic symbol for it that had been previously learned. The concepts include not only concrete categories like “banana”, “sweet potato”, and “wrench”, but also a few more abstract like “same”, “on (top of)”, “toy”, “food”, and “tool”. I think the labeling phenomena exhibited in these experiments point to the acquisition of unit concepts resembling human concepts, especially in the concrete examples. However, pigeons can also rapidly learn to categorize certain classes of natural stimuli (e.g. photographs of scenes with trees vs. scenes without trees), and parrots have learned auditory-vocal symbol sets for objects, properties, actions, and number similar to those studied in the ape experiments (Pepperberg, 1990).

The most striking ape “language” finding, however, has so far been negative. There is presently little convincing evidence that words are being productively combined into long sequences whose meaning depends on interactions between the unit concepts, either in production or in comprehension. Selective reportage combined with random word combination and imitation of the human interlocutor are now thought to explain away much of the data suggesting manipulation of sequences beyond one or two words. Thus, apes (and surely other animals not tested) seem to be able to acquire human-like concepts, but seem almost entirely unable to bond them together to form linguistic sequences. Pygmy chimpanzees (as opposed to common chimpanzees) seem to be more skilled at forming meaningful two- and three-word utterances; but this ability does not generalize to longer sequences as it eventually does in humans (Greenfield & Savage-Rumbaugh, 1990). As with cellular life, the major advance of language may therefore have been mainly to *control the*

ordered assembly of pre-existing meaning units rather than to invent those units themselves.

It is suggested above that we might think of many concepts as primarily visual in nature (in sighted people). This is because of the very large size of visual cortex in primates (more than 50% of the total neocortex), but also the ease of representing many concrete concepts using simple pictures (and the greater difficulty in using onomatopoeic sounds, and tactile objects). Most philosophers, linguists, psychologists, and neurobiologists, by contrast, have been uncomfortable with the idea of having basic word meanings tied to a particular modality (like vision). Recent mapping studies in the cortex, however, have shrunk the traditional site for concepts and meanings—so-called “polymodal” association cortex—to a few diminutive strips in between large expanses of unimodal visual, auditory, and somatosensory areas (for reviews see, Merzenich & Kaas, 1980; Van Essen, 1985; Sereno, 1988; Sereno & Allman, 1991; Felleman & Van Essen, 1991). We presently have no evidence to suggest that humans are any different in this respect (Sereno, 1991). In fact, there is now good evidence that unilateral lesions or stimulation of inferotemporal visual cortex in humans cause severe deficits in language comprehension while preserving auditory word perception and repetition (Rubens & Kertesz, 1983; Burnstine *et al.*, 1990). Concepts, semantics, and other abstract things may therefore primarily reside in visual (and secondarily, in auditory, somatosensory, motor, and limbic) neocortex†.

7.4.3. *Self-assembly and levels of organization of reaction-controlling devices*

Proteins are extremely complex molecules, each containing thousands of atoms in a precise 3-D arrangement (see Schulz & Schirmer, 1979; Cantor & Schimmel, 1980; Richardson, 1981, 1984; Creighton, 1983). The DNA sequences in the genome, however, constitute only a trivial portion of what would be required to explicitly specify the 3-D structure of a protein (Pattee, 1980); a single gene typically contains only a few hundred bytes of information‡. This information goes such a long way because it depends for its interpretation on the existence of elaborate geometrical constraints due to covalent chemical bonding, weak electronic interactions, the hydrophobic effect, the structural details of the 20 amino acids, and so on—a large set of “hard-wired” effects that the cell harnesses, but cannot change. Once the amino acid chain has been synthesized, its self-assembly (folding) is directed entirely by these prebiotic chemical constraints (i.e. a chain of prebiotic units folding by prebiotic rules). Although we know the detailed 3-D structure of many proteins (by X-ray crystallography), the dynamics of the folding process is so complex that it is

† Recent psycholinguistic experiments on picture-word priming (e.g. Vanderwart, 1984) and comprehension of rebus sentences (sentences in which a pictured object replaced a word) (Potter *et al.*, 1986), as well as some theories of linguistic semantics (Jackendoff, 1983, 1987) have independently suggested that visual and conceptual (or semantic) representations may be similar or identical.

‡ Each DNA base can be either long or short (purine or pyrimidine), and make either weak or strong base pairs (two or three hydrogen bonds); thus, each base carries a maximum of 2 bits of information, and each three-base word, 6 bits. Word recognition in the genetic code is somewhat redundant; only 20 of the 64 ($=2^6$) available words would in principle be needed (i.e. 5 bits/word would more than suffice). The entire genome of *E. coli* is less than a megabyte in length; the genome of a human is several orders of magnitude larger.

not presently possible to predict the 3-D structure of a protein given only the sequence.

There is a similar compactness to human linguistic symbols. The minimal amount of code in a paragraph can convey a large amount of information to the reader; it generates an elaborate neural activity pattern across billions of neurons the brain of the attentive reader that interacts with his or her previously stored knowledge in an extremely specific way. As in the case of genes and proteins, a little code goes such a long way because it depends for its interpretation on the existence of complex constraints on the interaction between neural activity patterns. By analogy with cells, many of these may be hard-wired rules of pattern interaction in primate visual, auditory, and somatosensory cortex that the advent of language did little to change, but that are crucially important for language comprehension (i.e. prelinguistic meanings self-assembling by prelinguistic network rules). This suggests that many processes in language comprehension are not autonomous from, say, visual processing (see e.g. Potter *et al.*, 1986; Fauconnier, 1985; Lakoff, 1987; Langacker, 1987; Jackendoff, 1987). One popular strategy has been to guess at these constraints on the basis of externally visible ordering patterns. For example, one might try to construct rules for generating well-formed sentences (Chomsky, 1957). If our experience with the analogous problem in cells—the much simpler (!) protein-folding problem—may be taken as a guide, however, the connection between abstract rules generating external ordering patterns and the underlying neural constraints is likely to be quite an entangled one.

We now return to protein structure to extract some general constraints on folding that might help in the search for neural rules of concept assembly in language comprehension. The structure of a protein is first conditioned by local constraints arising from the nature of the bond between amino acid “thing”-representations. A protein chain tends to fold locally into short stretches (cf. phrases) of either α -helix (3.6 units per turn) or β -sheet (2 units per turn)—the two main types of *secondary* structure. This occurs because the interunit bonds between the constant backbone parts of amino acids (both covalent and hydrogen bonding interactions) essentially restrict the angles of rotation between pairs of units to two values. Interunit bonds that allow freer rotation generate floppy, indeterminate secondary structures; DNA strands, for example are quite flexible (RNA strands, however, are stiffer). A stiff secondary structure seems to be a prerequisite for a stable, determinate *tertiary* structure—i.e. a particular configuration of secondary structure elements.

There are two main amino acid “word classes” in cells—the hydrophilic and hydrophobic amino acids. The distribution of these two classes in a chain strongly affects the final folding pattern of the secondary structure elements—the tertiary structure—since hydrophobic residues group together in the interior of the protein, avoiding water, while hydrophilic residues prefer the water-exposed surface of the protein. For example, an approximate alternation in these two amino acid classes in a protein chain has the effect of causing a strand of helical secondary structure to lie on the water-exposed protein surface with its hydrophobic side facing inward. Tertiary structure is also affected by packing constraints (the inside of a protein

contains no holes) and by occasional strong bonds between non-adjacent units (e.g. disulfide linkage between a pair of cysteines).

The first prediction for language is that there is a standardized way to bond together two word meaning patterns (e.g. higher level visual cortex category representations) such that the composite two-unit pattern is only allowed to adopt a small number of different configurations; bonds allowing too many configurations will generate composite patterns that interact only non-specifically with other patterns. To make sense of these ideas, we first need to construct a network that allows a *single* pattern in it to move in a configuration space while retaining its identity. An extremely simplified though suggestive example of this is the "glider" pattern in Conway's Game of Life—a simple cellular automaton [see Langton (1986) and Toffoli & Margolus (1987) for additional examples]. A glider maintains its identity as it propagates, despite the fact that the update rule for each cell in the Game of Life only refers to nearest neighboring cells. The Game of Life cellular automaton is formally equivalent to a very simple neural net. Needless to say, it is likely to be a rather more difficult task to describe and model glider-like patterns in the immensely more complex networks in inferotemporal cortex of humans. Given such a theory, however, bonding would then be defined as a method of modifying two such stable patterns with respect to an axis between them such that they are subsequently constrained to propagate as a single (possibly flexible) unit.

Word order typology (Greenberg, 1966; Hawkins, 1984; Givón, 1984) provides indirect evidence that something like restricted secondary structures are generated at the level of a phrase. Languages like English tend to place the "head" (predicate) before the "modifier" (argument) across many different local constructions. For example, verbs, prepositions, and genitives precede their objects (*hit* the ball; *into* the house; *John's* car). The adjective-noun construction (brown *chair*) is anomalous (cf. French). Languages like Japanese have the opposite tendency—*post*posing heads of preposing them. This suggests that there may be a small number of initial foldings of the chain of word meaning patterns at the several-unit level of constituent structures in a phrase.

Tertiary structure in language develops as the sentences in a coherent discourse (e.g. a paragraph) begin to interact with each other to constrain the more unspecified, general meanings each sentence has in isolation. There are many effects that extend beyond the sentence boundary in a discourse. Perhaps the simplest is a pronoun, which refers specifically to another word or group of words. Pronominalization in language has many elaborate forms; but its roles in discourse still resemble the tying together of the protein chain by disulfide linkages. The analogy predicts that local word class orderings (e.g. approximate alternation of modifiers and heads) may have an important role in causing the internally generated discourse meaning to adopt a particular configuration. There are, of course, many more word classes in human language than in proteins (5-15 vs. 2); thus, there are probably several different kinds of word-class-dependent organizing principles like the hydrophobic effect in proteins.

If a short sequence of a protein is excised, it will more often than not fold up approximately into its native form. Similarly, we can understand a sentence in

isolation. Nevertheless, an isolated peptide fragment rarely exhibits normal function in the context of a cell. Isolated sentences are similarly underdetermined when compared to the ability of a complete discourse to modify other activity patterns in the brain. The concentration of linguists, especially generatively-minded linguists ones, on *sentences* as opposed to *discourse* structure has tended to obscure the robust interactions that occur across sentences (see de Beaugrande & Dressler, 1981; van Dijk & Kintsch, 1983; Givón, 1983; Fauconnier, 1985).

A neural theory of concept assembly in working memory (language comprehension) will require an explicit mechanism for building up a composite pattern from simpler unit patterns, and a theory for how the composite patterns subsequently fold according to the dynamics of networks of visual cortical areas. I have given no more or less than an inspiration for such a theory here. We might look to the study of scene comprehension for initial models of this constructive process; scene comprehension is another activity that likely involves concatenation or bonding together of units (higher visual cortical areas activity elicited by a single glance) and folding (rearrangement of the persisting composite pattern) (Serenó, 1991).

8. Conclusions

Each of the three analogies summarized at the beginning, I think, are really about different aspects of the generative capacity most fundamentally stated by the cell/person analogy. For much of human history, the homeostatic properties of living organisms were simply mysterious. By the 19th century, many of these peculiar properties had been traced to a special "protoplasm" in cells. But before a satisfactorily detailed explanation for the remarkable properties of cells became available in the later 20th century, one had to choose between thinly supported claims that cellular metabolism and reproduction involved nothing more than organic chemistry with a few twists, and a more respectful but despairing vitalism, constantly reaching for explanations far beyond everyday chemistry. The advent of molecular biology revealed a chemistry that was strikingly frugal in its choice of subunits, yet fantastically baroque in its development, specificity, and function.

In several respects, our position with respect to the neurobiology of mind resembles the position of the 19th century biologist with respect to the cell. We are caught between thinly supported claims that mind arises from network patterns like the simple ones we can now study, while most philosophers and linguists, and many psychologists and neuropsychologists, more aware of the magnitude of the problem, are presently content to ignore the "chemistry" of networks, confident that satisfactory explanations will go far beyond these simple demonstrations. The argument of this paper is that the architecture of the stripped-down symbolic-representational system in living cells may help in bridging the large gap between our casual personal experience of mind and the strange, tangled forest of mental "chemistry" that underlies it.

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