

# An Examination of Some Metaphorical Contexts for Biologically Motivated Computing

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## ABSTRACT

Biologically motivated computing seeks to transfer ideas from the biosciences to computer science. In seeking to make transfers it is helpful to be able to appreciate the metaphors which people use. This is because metaphors provide the context through which analogies and similes are made and by which many scientific models are constructed. As such, it is important for any rapidly evolving domain of knowledge to have developments accounted for in these terms. This paper seeks to provide one overview of the process of modelling and shows how it can be used to account for a variety of biologically motivated computational models. Certain key ideas are identified in the subsequent analysis of biological sources, notably, systemic metaphors. Three important aspects of biological thinking are then considered in the light of computer science applications: biological organization, the cell, and models of evolution. The analysis throughout the paper is descriptive rather than formalized so that a large variety of potential applications may be considered.

- 1 *Introduction*
  - 2 *A Conceptual Framework for Characterizing Metaphors and Models*
  - 3 *Systemic Metaphors for Describing Biological Organization*
  - 4 *Computing at the Cellular Level*
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- 

## I INTRODUCTION

Philosophy may be ignored but not escaped; and those who most ignore least escape.

(D. Hawkins, cited by Rosen [1985], p. 45).

Biological motivated computing seeks to transfer ideas from the biosciences to

computer science so that developments in new varieties of hardware and software may be anticipated and issues common to biology and emergent and/or highly parallel computation may be addressed. As such, it can be distinguished from computationally motivated biology which applies computational ideas to the biosciences (see Paton [1991b]).

This paper seeks to provide a descriptive framework for talking about biological applications. A key motivation is the way in which metaphors are involved in the transfer of ideas, how this transferral process may be described and catalogued and how we may anticipate future transfers. In order to do this it will be necessary to develop a model to account for metaphorical transfer between biology and computer science (Section 2) and illustrate its usefulness with a small selection of examples (rest of paper).

We begin the analysis of biologically motivated computing with a look at some contrasting ways of talking about scientific models and the theories which produce them. Hesse [1963] identifies two ways in which a scientific theory (in this case a theory of biologically motivated computing) can affect the production of new models. One way is abstract and systematic, using logical and geometric thinking, and the other relies on imagination and visualisation. The first approach will tend to be narrower and the second much broader in scope. In a similar way, Davis and Hersh [1981] note two approaches to problem-solving in mathematics, analytical and analogical. Rosen [1985] compares a natural system, that is, a referential entity in the real world, with a formal system, that is, a mental construction very often described using the language of mathematics. In each of these cases we may note pairs of contrasting ideas, the abstract and the visualized (iconic), the analytical and the analogue, the formal and the natural, the former providing precision and the latter breadth and explanatory power. This dichotomy is consistent with Levins' comment, that no single model can simultaneously optimize generality, precision, and realism (Levins [1970]). At this point, it is important to note that in formal models definitions close the meaning of elements in the model, whereas in iconic models the use of a natural object (of infinite complexity) as a source allows for openness. The emphasis in this paper is on the breadth and explanatory capabilities of models.

## 2 A CONCEPTUAL FRAMEWORK FOR CHARACTERIZING METAPHORS AND MODELS

The fundamental assumption of the approach developed in this paper is that scientific thinking is characterized by its use of models. In order to manage what we know about the real world we simplify its complexity. We achieve this by constructing models. The construction of a model is dependent upon a theory and an understanding of its theory-dependency can help us anticipate the structure of a research domain.

When scientists developed cybernetic models of the brain (*e.g.* Arbib [1989] and Young [1978]), they used the language of computers (machines) to talk about a neural information processing organ (a part of an organism). As such they used metaphorical language, specifically that of information processing, to articulate a model. Scientific metaphors are not ornamental properties of language that can be replaced by literal description. They play a central role in the conception, maintenance, and development of a scientific theory in a variety of ways, which includes:

- Supplying new terms for the theoretical vocabulary.
- Providing the linguistic context in which explanations can be made.
- Influencing the way(s) we interpret the world
- Affecting the kinds of questions we ask.
- Suggesting new hypothetical entities and/or mechanisms.
- Facilitating communication, for example, between teacher and student.

Metaphor is language-based, but a model need not be. For example, a scale model of an aeroplane is still a model even when nobody talks about it. However, talking about the model as an aeroplane will be metaphorical because we are talking about one thing (the model) in terms of another (an aeroplane). Metaphors and models are very closely linked together. Metaphor provides the linguistic context in which models are described and analogies and similes are made (Harré [1970, 1986] and Soskice [1985]). Put simply, the language of models is metaphorical.

As discussed elsewhere (Paton *et al.* [1991a]), the characterization of metaphors and the ways in which they are applied to biologically motivated computing can provide valuable insights into the development of this area of research. The following discussion attempts to develop a way of interrelating models in biology to those in computer science. Following Harré [1970], a model will be described in terms of:

- its subject, that is, what it is a model for and,
- its source, that is, what the model is based on.

Thus, a model aeroplane has the same subject as its source, that is, the full-scale aeroplane. However, a cybernetic model of the brain has the brain as the subject but a computer as its source. Models which have the same subject and source are called *homeomorphic* and those which have a source which is different from the subject are called *paramorphic* (Harré [1970], Chapter 2).

A homeomorphic model is produced by abstracting or simplifying from a real world object. No other entity is used to provide modelling information. In this case the model is produced by abstracting from what is observable alone. This kind of model lacks explanatory power because it cannot account for the causal relations between its parts. Most scientific models have explanatory power. This is because the descriptive or homeomorphic model (see Figure 1) is

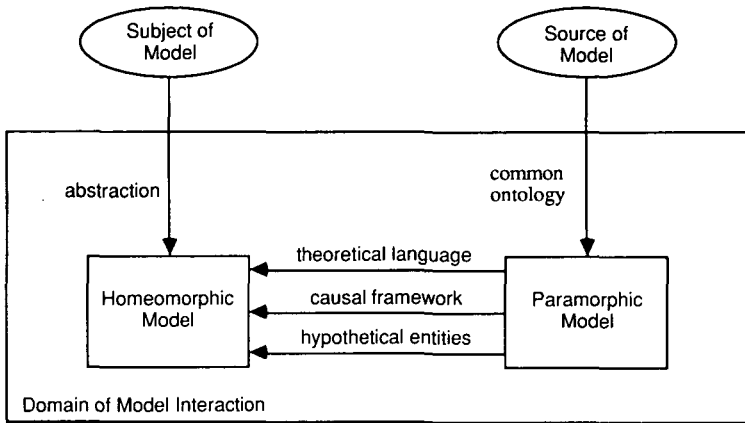


FIGURE 1. The context of biologically motivated computing: computing is the subject and biology is the source.

not only formed by abstraction from observables but is dependent on models of what cannot be observed. These explanatory (paramorphic) models provide the causal framework necessary for explanation as well as theoretical terms and hypothetical entities. Their basis is in interpretations of the unobservable real world which share common kinds of entities. It is metaphors which provide the context for such common ontologies (see Aronson [1984]). For example, Harvey's 'invisible anastomoses' (later called capillaries) were described within the context of a circuit of fluid flow. However, observing these vessels was not possible until developments in light microscopy by Malpighi revealed what was until then unseen.

It is now useful to summarise the three key ideas of metaphor, model and theory:

- Metaphor—the figure of speech that allows us to talk about one thing in terms which are suggestive of another.
- Model—a representation of one thing (either verbal, symbolic, mathematical, or physical) in terms of another.
- Theory—the evolving cognitive complex which provides the conceptual environment by which models can be constructed, predictions and explanations made, and hypotheses generated.

In the approach elaborated in the current paper, biology provides the source for models in computing, and theory maps phenomena (observable states of affairs) on to unobservable states of affairs. As much of the purpose of a theory is about picturing the mechanisms of nature responsible for observable

phenomena, a theory is more than a set of statements, mappings are achieved through statements and pictures. At the core of a theory are various modelling relations (see Figure 1).

Paramorphic models tend to provide iconic and relational details about given phenomena. Many scientific theories can generate paramorphic models because they have cognitive objects with iconic properties that enable the representation of a certain class of unobservable beings. Examples of such theories are the bacterial theory of disease, plate tectonics, and X-ray stars. These theories involve the representation of a physical system and its modes of behaviour, which, at the time of the formulation of the theory, have not yet been observed. The vast majority of scientific theories are of this type. These theories make use of common ontologies whose context is often supplied by key metaphors. For example, the realist notion of a virus as a disease-causing particle was postulated in the mid-nineteenth century but was only confirmed to exist in the mid-twentieth century with the invention of electron microscopes. Its basis in theory existed prior to its confirmation with scientific instruments. The ontologies of these theories are both observable and non-observable.

Another group of scientific theories have cognitive objects with mathematical properties which enable representations of non-picturable systems of beings and of their behaviour and interrelations. The ontology behind ideas such as symmetry, transformation, order, and harmony is a case in point, and we may note the importance of what could be called the relationship between ontology and 'mathematical beauty', from the Pythagoreans to the present time (see Engler [1990]). The ontologies of these theories are both observable and non-observable (as above), but the non-observable referents may never become observable. From the point of view of theoretical computer science, mathematical abstractions, achieved using the language of algebraic automata theory, complexity theory, and category theory, provide general frameworks in which to investigate formal systems.

Some metaphors are based on an ideal mathematical form. For example, the circle has been an important inspiration to the development of the biosciences. There can be little doubt that Harvey's mechanistic approach, together with subsequent investigations of Stephen Hales on vascular systems, had an important influence on the development of physiology. In more recent times we may hypothesize that the discoveries of various biochemical cycles have conceptual associations with the mathematical notion of a circle (*e.g.* the closed loop in a thermodynamic circuit). Circles are not only found in physiological systems but also ecosystems (*e.g.* biochemical cycles) and evolutionary models (*e.g.* the hypercycle) and generally in what may be described as feedback systems. In the current discussion of biologically motivated computing, we may identify several important forms of digraph, such as a chain (as in a linear sequence of vertices), a cluster (a single vertex

TABLE 1. Systemic Metaphors with some Associated Properties

Systemic metaphor	M-properties associated with the systemic metaphor
MACHINE	Input, output, mechanism, efficiency, goal, balance, elasticity, optimal, equilibrium, control, adjustment, design
ORGANISM	Growth, openness, autopoiesis, adaptability, organizational complexity, individuality, life and death
TEXT	Interpretation, context, meaning, code, translation, grammar, theme, language, genre, comprehension

connected to many others), a network and a tree (as the names suggest). These graphs can provide powerful images for conceptualizing a model. Furthermore, they are related to certain pervasive metaphors in theoretical language associated with thinking about systems.

'System' is a very common word in the biosciences and we characterize systemic metaphors by a set of basic properties called systemic M-properties (see Paton *et al.* [1991b]):

- Interacting parts;
- Organization;
- Collective behaviour and whole system functionality.

These M-properties provide important aspects of the common language for comparing biological and computer systems. In order to provide the widest discrimination between biosystems, the systemic M-properties are associated with a set of systemic metaphors which inherit the three basic properties given above and include machine, organism, society, circuit, game, text, and culture. There are further properties which typify particular systemic metaphors in the language used when talking about them (see Table 1) and each type has particular graphical form(s) associated with it. For example, machine is often described in terms of a sequence (*e.g.* input-process-output), whereas organism may be described in terms of a hierarchy (tree). We have called these forms 'metaphorical graphs' (Paton *et al.* [1991d]).

The M-properties of the systemic metaphors listed in Table 1, though not exclusive to a particular metaphorical type, are associated most clearly with that type (see Paton [1991a]).

An approach to the analysis of the sources of paramorphic models is summarized in Figure 2. It is by no means a complete description but hopefully provides a useful framework for probing particular features of a model. A source model can be described in terms of a combination of up to five general

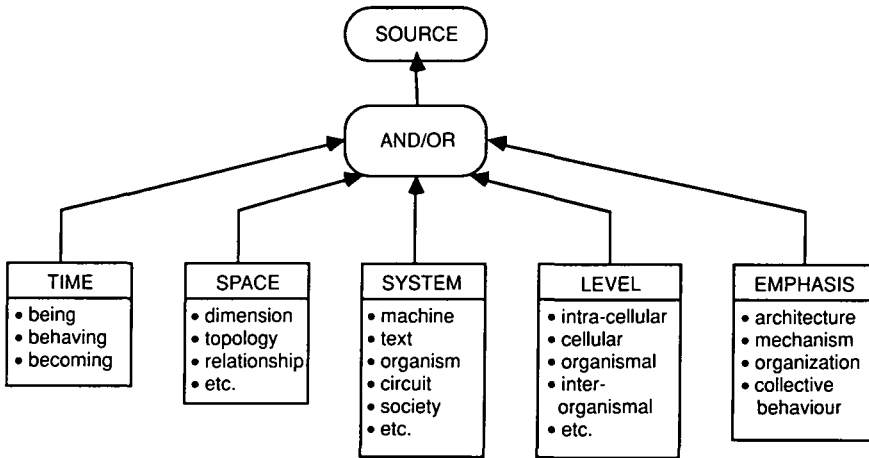


FIGURE 2. Some general features contributing to the source of a model.

features which have been identified as being relevant for biosystem description:

- Time—dealing with instantaneous state ('being'), contiguous states ('behaving'), or history ('becoming').
- Space—language associated with space, dimension, metric, form, etc.
- System—as described above.
- Level—organizational level as defined by classical hierarchy in theoretical biology.
- Emphasis—focus of attention of the model (see Paton *et al.* [1991a]).

Each general feature has particular details associated with it (see Figure 2). The number of ways of combining these details is, potentially, very high.

A simple example is now given to illustrate the point. In an attempt to extend the functionality of an artificial neural network (ANN), it may be helpful to use a paramorphic model from another network such as the immune network (see *e.g.* Weisbuch and Atlan [1989]) or from another systemic source such as an insect society (see *e.g.* Collins and Jefferson [1990]). Examples of concepts that can be transferred to ANNs within the context of each system include:

- Immune system—distributed memory, fault tolerance, pattern recognition, connectivity, non-linear behaviour, learning, selection, and adaptation.
- Insect society—local interaction, common language, division of labour (adaptive specialization), emergent intelligence, and problem solving.

In addition to this, it is possible to consider a particular part at one level of

organization as a whole at another. The variety of combinations of systems and levels is a major contributor to the number of paramorphic sources (Paton [1991a]). Thus, because they can share the same metaphorical context, we may meaningfully talk of genes as neurons, as antibodies, as ants, as enzymes and of cells as ANNs, as colonies, as immune networks. This does not compound a metaphorical fudge so long as the context is understood; especially in terms of level and system.

### 3 SYSTEMIC METAPHORS FOR DESCRIBING BIOLOGICAL ORGANIZATION

The definition and description of biological organization is a non-trivial problem to the biosciences (Weisbuch [1986]) and attempts at clarification have ranged from thermodynamics (*e.g.* Smart [1985]), spatio-temporal integration (Weibel [1977]), self-modifying/self-regulating automata (Kampis and Csanyi [1991]), and emergent computation (Forrest [1990]), to analogues related to the nature of text (see below). Clearly, there is a large literature on this subject which could not be reviewed in this article. Instead, some aspects of the notion of 'organization' will be examined from the point of view of systemic metaphors.

The classification given in Figure 2 can now be applied to a variety of attempts which have been made to describe the concept of organization. For example, it is possible to apply a temporal framework to a definition in which organization is a process (*i.e.* behaving) which brings about order (*i.e.* being). Organization is a dynamic property of a biosystem and the temporal relations between being, behaving, and becoming must be fully appreciated. For example, we may say that, as time elapses, being gives way to behaving, behaving to becoming, and then, at any moment in time, becoming is reflected as being. This cycle of temporal relations is not without significance in a fuller understanding of organization. For example, emergence is a property associated with becoming, which at any moment will be expressed by using such classical ideas as polarity of function, compartmentation, modular design, and hierarchy of levels. Spatial attempts to describe organization usually distinguish the parts of the system (*i.e.* physico-chemical parts) from a non-reducible holistic level using such ideas as 'topological causal inter-relations' (Schaffner [1976] or organizational level (*e.g.* Feibleman [1954])).

A cell is a whole at the cellular level but a part at the organismal level. This distinction is important for systemic metaphors. As Rapoport [1972] noted, certain dichotomies exist in our thinking which have related meanings: analytic-synthetic; atomistic-holistic; local-global; differential-integral. Part-whole is a further example. The first of each of these terms deals with detail or analysis or parts or local conditions whilst the second term deals with wholes or gestalten or configurations. Following Feibleman [1954] we note



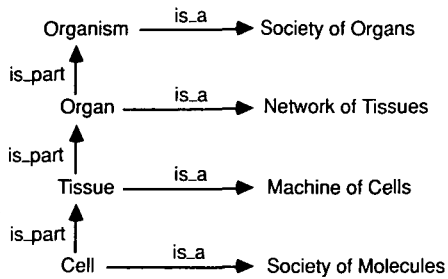


FIGURE 3. One way of interlinking organizational levels using systemic metaphors.

that for any organization, at any given level, its mechanism lies at the level below and its purpose at the level above. We now see how the systemic metaphors provide a variety of metaphorical context for describing organization at different levels. An example is given in Figure 3 (see also Paton [1991a]).

In one approach to the description of cellular organisation, Albrecht-Buehler [1990] suggests that the concept of information is crucial to a non-reductionistic description. He argues that thermodynamic models of information, which talk of negative entropy and physical constraints, are currently inadequate. We may say that the machine view, specifically a thermodynamic machine, is insufficient. Speaking metaphorically, he suggests that information is like 'glue' which holds the cell together. Although he does not fully clarify the nature of cellular information, he argues that the glue is analysable at the level of text rather than letters. Indeed, he points out, 'the more we decompose a cell into molecular letters, the more we destroy its meaning' (p. 192). Here we see how the metaphor of text can be very important when discussing the organizational level of description; hence, cells have meaning. For the purpose of the current analysis, we may say that the language of cell-as-text is being used rather than cell-as-machine; the source of the paramorphic model is text. On a very similar issue, namely the organization of a whole, but in a very different context (that of situation semantics), Barwise [1984] comments on how verbs are like the 'glue' which provides the organizational framework which holds together nouns and provides the organizational structure of a discourse.

Consider another example of text as a source analogue used for modelling and describing a biosystem's behaviour by a computer. In this case, the abstract system representation in a program together with the mode of operation of the computer can be used to model functionality. One attempt to exploit this idea using physiological models has been made (Yamamoto and Wolff [1984]). Concepts describing the compartments of the system digraph,

called 'nouns', are represented by memory locations within the computer and the functional dependencies of the 'nouns', the arcs of the system digraph, are called 'verbs'. The verbal behaviour of the system is only realized when the program is executed. An example of the interrelationships between machine, text, and organism comes from the well-known argument of Polanyi [1968] in which he attempts to demonstrate the non-reducibility of living systems at all levels of organization by using analogues from machines and text. He investigates certain common properties between the three in order to demonstrate non-reducibility:

- Machines, texts, and organisms are under dual control—that is, control that applies to component interactions and control that applies to the emergent behaviour of the whole.
- Machines, texts, and organisms have irreducible boundary conditions—in the case of machines and text this is related to design and in the case of organisms to structure.

The significance to the current argument is the way in which text, machine, and organism can be ascribed common systemic properties. This is very important when we come to appreciate that biologically motivated computational models may have several paramorphic sources.

The relationship between structure and function and the argument for treating them as two types of the same thing has been proposed by many writers. As Young [1978] points out, they both express the language of the machine metaphor and he notes how an alternative description to a functionalist view of machine is a structuralist view in which 'the whole organism can be considered as a coded representation of its environment. We can say the wings of a bird "represent" the air . . . Thom has put it information equals form' (Young [1978], p. 43). It is interesting to note how some workers in *Alife* have made similar suggestions, *e.g.* 'certain aspects of the environment can be "compiled" into the structure of the animal's genome' (Jefferson [1991]). Clearly, equating 'coded representation' with the symbolic level of description might permit the production of an algorithm that could execute a grammar. At this stage we would still be talking in terms of a machine, albeit an automaton. However, the question of the application of such an approach would depend on the computability of a solution. This may not be possible. If 'information equals form', an appreciation of the meaning and context, that is the semantics, will be necessary. Indeed, consideration of M-properties of text, such as style, structure, interpretation (not the same as translation), and context, have a validity in biosystem descriptions. This is because more formal terms lack the expressive potential necessary to provide sufficient meaning.

In concluding this section, we return to one further implication of the machine metaphor, namely the biological ideas of homology and analogy. The ideas of homology and analogy used here pre-date Darwin and are attributable

to Richard Owens (see Barrington [1967], pp. 19–20). The language used is that of structure and function, that is, the language of the machine. Organs from different species are said to be homologous when they are similar in their fundamental structural plan, irrespective of the functions which they carry out. Analogous organs from different species are those which carry out similar functions but are fundamentally different in structure. Given that we are seeking to apply biological source ideas, we must ask if a given artificial entity is homologous or analogous to its biological source (even though they may be classed as different categories in certain ontologies).

A disadvantage of models based on the machine metaphor is whether they can provide sufficient expressive power to deal with the multi-functionality of biological systems. The human liver is a very good illustration of this (Paton *et al.* [1991c]). It has been estimated that this organ has upwards of five hundred different (though many interrelated) functions. As conditions change (*e.g.* stage in life history or certain pathological states), so the functionality of the organ changes. For example, it is haemopoietic in the fetal stage and in certain diseases. It has been argued elsewhere (Paton [1991a]) that a preferred metaphorical context would be to think in terms of niche and ecology rather than structure and dysfunction. The challenge to biologically motivated computing is the development of both homologous and analogous models with sufficient descriptive capability to go beyond machine thinking.

#### 4 COMPUTING AT THE CELLULAR LEVEL

The idea of the cell as a processor of biochemical symbols can be traced back though the work of, for example, Stahl and Goheen [1963] to the notion of cell as a Turing machine. However, it is not only the cell that can be modelled as a Turing machine; biomolecules such as DNA can be contextualized as simple devices (Burks & Farmer [1984]) and it has been suggested that small biomolecular assemblies such as ion pumps behave as non-deterministic machines (*e.g.* Lauger [1987]). In each of these cases machine is used as the source for a biosystem. The implication for biologically motivated computing is that the biological machine can be used as a source model for a computer.

##### 4.1 *The Cell as a Machine (Computer)*

Holcombe [1990] applies Eilenberg's general type of machine, the X-machine, to a model of intracellular biochemical organization. The basic thesis of this approach is that many types of biological activity can be modelled using various types of X-machine at various levels of behavioural description. Each level within the cell has its own variety of X-machine corresponding to:

- 0 Energy transfers for the whole system
- 1 Conformational level (set of states)

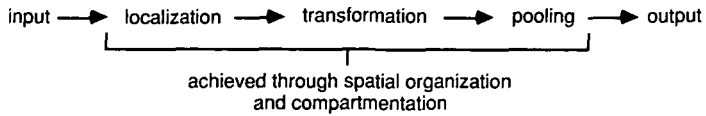


FIGURE 4. The cell as a spatial machine (based on Welch [1977]).

- 2 Metabolic level
- 3 Enzyme control level

In this hierarchy of X-machines the enzyme control machine (level 3) is used to provide variable values (inputs) to the metabolic level machine (level 2), and so forth. This kind of approach is typified mathematically by the language of algebraic automata.

In the former approach modelling is based upon levels of behaviour and can be formalized by the application of abstract structures such as task hierarchies. Other cell-as-machine models have been concerned with the spatial organization of the cell and do not have levels. For example, Welch [1977] models the cell as a machine-with-slots; slots are the inputs and outputs and the machine is a transformation system. However, the functionality of the system is not restricted to a slot transfer function. Welch emphasizes the spatial organization in terms of localization of processes (due to sub-cellular organelles and multi-enzyme complexes) and pooling of transformed materials due to the spatial arrangement of the system (see Figure 4). This emphasis on organization is found in Welch's model of the evolution (becoming) of the system from a homogeneous bulk reaction-diffusion system to that characterized by topographical segregation of individual processes. This transition towards a spatially segregated system is important to the way we understand the cell. Recent research (*e.g.* Welch and Clegg [1987]) indicates that the cell is spatio-temporally highly organized. The cytoplasmic microtrabeculum, together with the membranous surfaces and organelle compartments, indicates that, organizationally, a realistic model would be far removed from any bulk reaction-diffusion system.

Another example of cells-as-machines concerns the development of biologically motivated molecular computers, that is, biomolecular machines. In this case, emphasis is placed on the structural and functional properties of biomolecules and the source models deal with the functionality of parts. For example, Conrad [1990] identifies two key molecular types:

- **Enzymes.** In the context of a switching circuit machine an enzyme is like a transistor because it can act as a switch. However, enzymes are much better switches than their electronic analogues: firstly in terms of their variety and

secondly in terms of the very low dissipative energy required by them to operate.

- Secondary messengers. These play the linking role in cellular information processing, providing the cell with the capability to process patterns.

Some of the technological spin-offs of this kind of computing may be some way off but, as has been noted elsewhere (Paton *et al.* [1991a]), metaphorical transfers in biologically motivated computing that involve developments in biotechnology are valuable. One example in the present context of the machine describes an organism as a bioreactor: specifically, a multi-phase enzyme reactor (Sernetz *et al.* [1985, 1989]). In this case, the source of the model is a bioreactor, a machine, and the subject is an organism. The bioreactor source provides transferable concepts for modelling organisms, in terms of:

- System—both are open, multiphase, and dissipate energy to maintain organization.
- Self-similar scaling—both display allometric relationships with regard to area and volume.
- Kinetics—both exhibit heterogeneous (multiphase) catalysis.
- Fractal organization—maximization of distribution of materials to the tissues is provided by turbulence due to fractal organization.

There are several interrelated problems that emerge from this discussion. A biological ‘machine’ at the cellular level consists of a very large number of different molecular species most of which are in very low concentrations in the cell. A model based on this picture would be very different to any based solely on a random diffusion (*e.g.* Fickian) scheme. The organization is far more complex. Meaning and information will require clarification and the language of the text metaphor is pertinent here for dealing with this level of description.

#### 4.2 The Society/Community of the Cell

The discussion so far has focused on the cell as a molecular processing machine. An alternative to this is that of Albrecht-Buehler [1990] who describes an approach to cell modelling which emphasizes what he calls an information-driven rather than energy-driven approach (see Section 3 for further clarification). This approach may be directly contrasted with the energy-drive (level 0) emphasis of Holcombe. Using sociobiology as the source model he proposes that the idea of a colony (*i.e.* a kind of society) be applied to the description of the behaviour of molecules in cells. He develops this argument by looking at the emergence of colonies of the alga *Chlamydomonas*. In this case, he treats individual organisms as chaotically active goal-driven units, subtly interacting with each other and their environment. The emergent

properties of the system, which provide the source model for describing a cell, are identified as:

- Self-structuring of the colony into vertical columns;
- Problem-solving in terms of circulation of O<sub>2</sub> and CO<sub>2</sub>;
- Catastrophic changes in columns due to accumulation of small effects;
- 'Intelligent' or adaptive collective behaviour.

These are the shared properties of source and subject. The model then treats individual molecules as individual *Chlamydomonas*. Clearly, the organizational details are different with regard to the spatial complexity of the cell (see above), and the very low frequency but very high heterogeneity of molecular species.

Langton [1989] treats biosystems as machines when he notes that they are 'nothing more than complex biochemical machines' and that a living organism is not a single, complicated machine but 'a relatively large population of relatively simple machines' (pp. 4–5). This kind of analysis can attach meaning to the parts (the simple machines) rather than the whole (in this case society of machines). This raises the issue of functionalist versus structuralist differences. If, as noted here, meaning and organizational information is associated with text then it is the whole that is the level for description.

#### 4.3 *The Network in the Cell*

Network models of the cell that involve some form of computational activity can be traced back beyond switching circuit approaches of the 1950s. This kind of approach has been continued in more recent times with the elaboration of, for example, electrical analogue models (Sen [1990]). Another recent approach has been to simulate certain pattern recognition abilities of the cell using a PDP model (note: this has also been applied to the circuit properties of the immune system, see Vertosick and Kelly [1989]). For example, Bray [1990] considers the way in which intracellular signalling can be modelled as a parallel distributed process. In particular, he looks at the response of a hepatocyte to glucagon. The source in this case is a computational model which Bray applies to a model of the performance of intra-cellular signalling pathways (see Figure 5). Of particular interest is the way a PDP unit and the learning algorithm are articulated in terms of signalling pathways.

It should be noted that only a few source transfers are given in Figure 5. It would be valid to consider further ideas as listed as immune system transferable concepts which are given at the end of Section 2. An important feature of circuit thinking is that it can provide the mechanistic details by which machine, text, or organism processes are described.

## 5 SELECTION AND PROCESS MODELS

Two models of evolution, selection and process models, are discussed in this

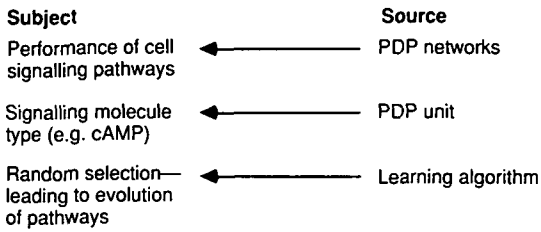


FIGURE 5. Source–subject relations for hepatocyte as a PDP network.

section and ideas associated with machine and text are identified. The purpose is not to debate the biological significance of these evolutionary (becoming) approaches but rather to highlight the importance of the metaphors to the models and to raise some questions about the development of evolutionary algorithms.

We begin with the sources of Darwin's model as originally proposed (see Figure 6). From this, and taking account of the neo-Darwinian position which has a Mendelian model to account for change, we follow Darden and Cain [1989] and describe common characteristics of selection theories in the biosciences, including:

- A set of a given entity type;
- Set members which vary according to a particular property (P);
- An environment in which the entity type is found;
- A factor in the environment to which members react differentially due to their possession/non-possession of the property (P);
- Differential benefits (both short- and long-term) according to the possession/non-possession of the property (P).

The selection metaphor is itself the source for other models, such as the clonal selection theory of immunity. More recently, the selection metaphor has become the source for models of non-linear optimization problems. However, it is not only the idea of selection which has been transferred, but also, in the case of genetic algorithms and evolution strategies, aspects of the Mendelian mechanism underlying a neo-Darwinian approach. Furthermore, classifier systems and the immune system have been shown to share common properties. However, the source metaphors for the biological immune system is not only selection; the idea of a network is also a prime property and this can in part be used to explain the relations between ANNs and the immune system (see Vertosick and Kelly [1989]).

It can be argued that selection is related to a machine because:

- Organisms are considered to be mechanical objects (*i.e.* mechanical).
- Language such as selective forces, selective pressure is used.

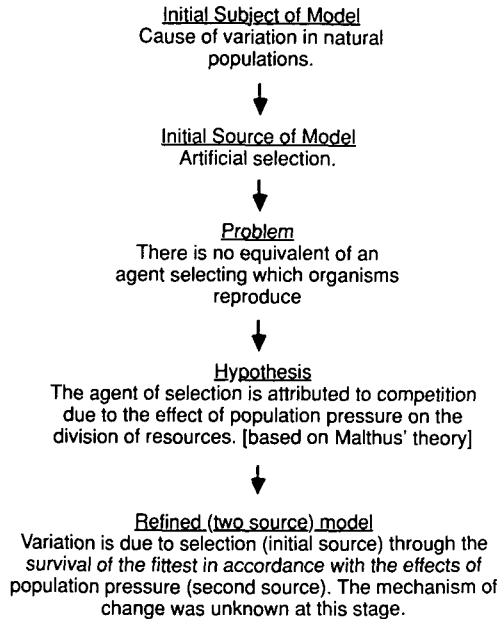


FIGURE 6. Simplified scheme showing the sources of the natural selection model (based on Harré [1970]).

- Change is articulated in relation to parts.
- DNA is not considered as dynamically responsive to the environment.
- Models are functionalistic, in terms of reducible, interrelated parts.

The following discussion is intended to set out the reflective analysis carried out by Ho and others in their characterization of a post neo-Darwinian evolutionary theory (*e.g.* Ho [1988] and Ho & Fox [1988]); we shall call this the process model. Ho argues that the idea of nature as process is related to a structuralist position, namely, that entities are described in terms of relationships or transformations on wholes rather than in terms of the sum of parts. The approach through process challenges the neo-Darwinian perception of evolutionary change in two ways:

- The fluidity of the genome. The genome is not invariant within an individual life history. There is interaction between genome and environment as in the case of gene amplification, transposing effects, and the conversion of DNA sequences.
- Permeability of Weismann's barrier. Ho describes this as the soma 'talking back' to the germline (Ho [1988], p. 134). This includes reverse transcrip-



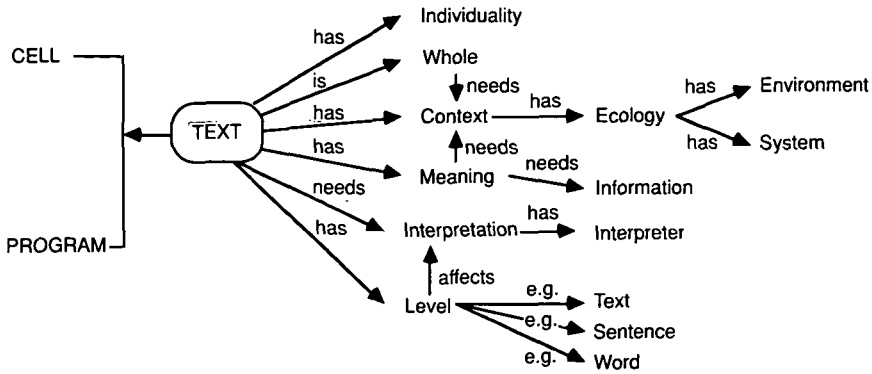


FIGURE 7. A simplified concept map showing how TEXT can be a source for models of a cell as a program.

tion, environmental effects on non-random changes in DNA, and biased gene conversion.

The consequence is that genomic DNA is ‘not immune to change as a result of feedback from the environment and the physiological state of the organism’ (Ho [1988], p. 135). Organism and environment are inter-connected, from genes to the sociocultural domain. The organism is an integrated whole—genotype with phenotype and soma with germline. As a result, there is a non-reducibility of levels. Process is related to text because:

- Organisms are considered to be life histories (*i.e.* history).
- Language such as context, whole (*e.g.* field), is used.
- Change is articulated in relation to the whole organism (*i.e.* meaning is a property of the whole).
- DNA may be just as responsive and flexible to the environment as the rest of the organism.
- Models are structuralistic, in terms of the non-reducible whole and associated transformations.

The subject of these two metaphors is the biological organism. The paramorphic systemic source of the selection metaphor is related to machine and game and the paramorphic systemic source of the process metaphor is related to text and society. This brief analysis hopefully provides some contrast between selection and process metaphors.

So what does this analysis provide? It is suggested that although non-machine thinking may be less formalized, it is necessary in order to take account of certain non-reducible aspects of biosystem being. These may not be codable in quantitative terms but may be described qualitatively. Furthermore, emphasis on text and society currently presents theoretical language that is more ‘sensitive’ to environmental interaction (see Figure 7). This section has

outlined the distinction between selection and process metaphors. Hopefully, the reader will appreciate the need for both mechanical (machine) and interpretative (text) models.

In concluding this section we return briefly to the issue of biological organization and the relation between cell-as-text-as-program. A simple concept map is given in Figure 7 to show how text, as a source, can provide a metaphorical context for describing cells programs. This is presented as a framework for highlighting the shift in language the text metaphor can provide. The ideas associated with text provide a difference in perspective and accommodate new ideas, and ways of thinking and exploring the interactions between non-linear adaptive systems and their environments. The models that are constructed are more interactive with their environment and issues of becoming are not solely dependent on randomness and chance. Further investigation is needed to clarify the scope and applicability of the text metaphor as well as the notion of society-as-text.

## 6 CONCLUDING REMARK

The transfer of biological ideas to new developments in computing presents an exciting challenge to researchers in many branches of science. This paper represents the stage at which new ideas from biology and computing can be accommodated into current thinking and investigations. It is from this informal setting that more formal (though less general) models may be developed. An appreciation of the metaphorical thinking involved may provide workers with a means of accounting for current and future discoveries.

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