The importance of molecular hierarchy in information processing

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In this note I would like to confront some conventional concepts of information processing (selective dissipation) with the facts of molecular biophysics.

There are a number of theoretical computers which provide formalizations of the intuitive notion of effective (or algorithmic) information processing. The best known of these is the Turing machine. This is a finite automaton along with a memory space. The memory space consists of units whose states can be changed by the Turing machine—for example, it can write or erase symbols held by these units. The Turing machine can exert some control over which unit it accesses at a given time—for example, it may be able to move the units to the right or left. The way in which the Turing machine acts on its memory space is determined by the transition functions which characterize its finite automaton, for example, the tables which determine the next state and output given the present state and input.

The following facts about Turing machines are important.

1. There is a definite procedure for translating the transition tables of the Turing machine into networks of physical elements which give the desired behavior (for example, neural networks).

2. It is possible to program a universal Turing machine, that is, a Turing machine which can accept the transition tables of any special Turing machine as input (from its memory space) along with the original input data of this special machine, and transform this input data in the same way as the special machine. Any general purpose computer is universal in this sense.

3. The universal Turing machine can be translated into an actual machine according to the definite procedure in 1.

The definite procedure in 1 depends on two features of the components from which the actual machine is built. (a) The components are elementary units with definite transition functions or linkages of these. (b) The transition functions of linkages of elementary units can be derived from the individual transition function and the pattern of linkage, assuming that the inputs to each unit belong to its input set.

Each memory unit is also an elementary device—it receives input from the

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automaton (or its reading head) and its state is a possible input to this automaton.

Now I would like to consider some notions about self-reproducing automata. Von Neumann had the idea that universal constructors could be developed which correspond to universal computers. Such a constructor may produce any machine with whose description it is provided. If it is provided with a description of itself it is self-reproducing—except that it does not construct another description. This would lead to an infinite regress since in this case the description would have to provide a description of itself. The system achieves complete self-reproduction by xeroxing the description. Von Neumann exhibited a set of elementary devices which in fact realizes this capability.

I should emphasize that in order to demonstrate the existence of such self-reproducing systems it is necessary that the description serve as a program (transition function) which prescribes the behavior of the system. This means that the dynamics of the components which are being manipulated must be suppressed—their behavior must be so constrained that they are completely subject to a prescriptive computation process.

In sum, the existence of self-reproducing systems can be demonstrated. The demonstration is based on the idea of a universal constructor which is provided with a description. This description is a program, or a prescription for the behavior of the constructor.

There is some resemblance between the overall process of self-reproduction in such classical systems—involving transcription of and construction from a description—and the biological processes of transcription and translation of D NA. The resemblance, however, is superficial and does not confront the facts of molecular biophysics.

The D NA is not a program or sequentially accessed control over the behavior of the cell. This is because the biological process of translation does not correspond to the construction process. Translation just amounts to breaking the energy degeneracy of D NA by coding it into the primary structure of protein. This undergoes a spontaneous, energy dependent folding process. The function of the enzyme (as regards catalysis or the control over energy transformations and therefore the selectivity of dissipation in the cell) is determined by the three-dimensional shape and charge distribution assumed in this folding process. Naturally, there is some sequential accessing of different blocks of D NA during different phases of the cell cycle. However, this sequential action is not comparable to the sequential action of the manipulable elements in a computer program.

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The manipulable elements in the D N A are accessed on a global basis, at least after they are translated to the primary structure of protein.

I shall call this mode of operation of the biological cell the hierarchical mode of information processing, as opposed to the single level mode characteristic of conventional computers and proposed constructors. Single level systems obey assumptions A and B—each unit in such a system reacts to defined outputs of other units, not to the global properties of collections of these units. In particular, they respond to (or access) distinct units in the memory space. This is because their interaction with different memory units is temporally distinct.

These features of single level systems are in sharp contrast to those of hierarchical systems. Hierarchical systems do not satisfy assumptions A and B since their mode of operation is based on the fact of hierarchy in molecular structure. It is not possible to program such systems in the conventional sense because the action of the program units in the description is not sequential and therefore cannot be combined according to a definite rule. Nor is it possible to manipulate the units in such a system directly in order to tailor its behavior or make it realize a given transition function. It is not a linked device whose transition function can be derived from the transition functions of its units, that is, it is not a device whose selectivity is increased simply by imposing certain initial conditions on given, unmodified subunits. It is really an elementary device with a complicated transition function.

These facts of molecular biophysics have implications for information processing in biological systems.

The forfeiture of prescriptive control means that a certain amount of information processing can be eliminated. This is possible to the extent that the information processing is not inherently sequential, that is, in so far as it can be realized by processes which really run parallel to one another. As a consequence, hierarchical self-reproducing systems may process information faster than general purpose single level systems which simulate them. This follows because the sequentially controlled single level device must execute a large number of temporally distinct (but perhaps very rapid) steps in order to reproduce itself. In contrast the hierarchical system acts on an energy basis. Essentially the process of self-reproduction in such a system is a constrained minimization of free energy. The main constraint—at least the most manipulable one—is the D N A description. By and large this is not a sequential constraint and as a consequence many fewer (although perhaps not such rapid) steps are required for self-reproduction.

The hierarchical system may also be simpler than a special purpose single level

device which simulates it. (Of course no special purpose device has been proposed which is capable of producing more complex offspring.) Again this is associated with forfeiture of the capacity to design such systems to realize given transition functions—in this case by prescribing the appropriate pattern of linkages according to a definite procedure. Such prescription is always possible in the case of single level systems whose elementary units execute definite, usually simple functions. The rigidity of this function—the fact that selectivity of the system is modified by appropriate restriction of the possible inputs to the subunits and not by modification of the subunits themselves—often imposes significant topological complexity on the network which realizes the desired behavior. In contrast the hierarchical system is itself an elementary device with complicated behavior. The device is not built out of subunits with simple, definite functions ; rather manipulation of these subunits (at the primary level of structure) directly modifies the dissipative properties of the system. Again this is possible because the hierarchical system acts on an energy basis.

I want to underline an important point apropos this discussion of simulation. The use of a computer (single level system) to solve the equations of motion which describe a system is not the same as its use to simulate the system. Thus we might suppose that we can describe some system by certain state-to-state transition tables. Then the single level machine (tessellation automata, neural network, and so on) which realizes these transition tables simulates the system —at the cost, perhaps, of much more hardware. Alternatively, the single level machine may be designed to realize the input-ouput behavior of the original system by providing it with some transition table. This is an even looser notion of simulation, especially as the system may operate on an incommensurable time scale.

It should also be clear that the hierarchical mode of information processing is not the same as analog information processing. This is true even if the analog computer acts on an energy basis. In this case the choice and linking of components prescribes the physical law which the system will obey—the problem which the system must solve is communicated to it in this way. Such systems may communicate with digital devices or may be controlled by discrete information. However, they are never controlled by molecular folding and aggregation processes, that is, by the manipulation of a discrete substratum.

It is evident that the hierarchical system cannot be programmed like an ordinary computer—in order to plan its behavior we would have to consult physical laws and, of course, this plays no role in ordinary programming. Clearly such systems

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can only be 'programmed' on a trial and error basis—essentially through evolution by variation and natural selection.

In general such evolution processes are much more effective in hierarchical than in single-level systems. This is also a consequence of the absence of prescriptive control, for example, the fact that the DNA is a description of the primary structure of important molecules in the cell, not a prescription for the behavior of the cell. Ordinarily slight modifications in a computer program produce radically different behavior. This is because the modified program prescribes new behavior and there is no necessary relationship between this and the original behavior. This is not true in the case of the hierarchical system. This is based on energy primarily, and a modification of the description (constraint) will often produce only a slight perturbation to the behavior of the system. This increases the likelihood that single genetic changes will produce functional systems. This is unusual in the case of conventional computer programs.

The significance of this fact for the rate of evolution follows from fairly simple probabilistic considerations—essentially it is very much (astronomically) more probable for an evolutionary change to take place through a series of small steps each one of which is associated with objects (enzymes) which are to some extent functional or multifunctional than for it to take place in one jump. If the system as a whole is functional or has slightly increased fitness at each step the change may be amplified by population growth, thus increasing the likelihood of the appearance of the next step in the evolutionary sequence. In this case the evolution process is facilitated by transfer of function.

It is important that the effectiveness of this evolution process is itself an evolutionary property. This is because the extent to which a single genetic change perturbs the function of the enzyme depends on the extent to which it modifies its three-dimensional shape and charge distribution. If the enzyme is larger, that is, supports greater redundancy of weak bonding, the effect of a typical mutation may be attenuated. In this sense the topography of what has been called the adaptive landscape is itself an adaptive property.

Now I should like to consider some of the consequences of these molecular biological facts for concepts of information processing in general. According to the Turing–Church thesis any effectively computable function (function computable by some recipe) is computable by a Turing machine or by any of the machines which can simulate Turing machines. (All such machines compute the same class of functions—the partial recursive functions.) At least no algorithms have been found which cannot be expressed in this way.

Certainly the Turing–Church thesis would not be so interesting if we could not communicate algorithms (or definite recipes) to actual machines, either through programs (in the case of universal machines) or by manipulating subunits directly. The question arises as to what happens when we deal with systems — systems such as the biological cell — to which we cannot communicate algorithms. Do such systems have properties which are essentially unattainable by systems with which we can communicate in this sense ?

The fact of such systems is evident. All physical systems undergo some definite (but perhaps noisy) behavior. But this behavior is prescribed if and only if the transition function of the system can be communicated to it in a definite way. This is not true in most cases — most mechanical (physical) processes are not algorithmic processes. Nevertheless such processes may involve selective control over transformations of energy-selective dissipation. This is true, for example, apropos the elementary units of an ordinary computer (resets, 'or' devices, and so on). The information processing in such devices does not proceed according to a recipe that can be communicated to them. Rather, recipes prescribe the way these devices are linked together.

In the case of the biological cell these elementary processes are much more complicated ; furthermore, novel processes are often built by modifying the elementary processes directly rather than by combining them in different ways. Essentially the most important information processing in biological systems does not proceed according to definite recipes. Some rule (Turing program, for example) may generate the behavior of a biological system, but this does not mean that the biological system follows (embodies) this or any other rule (as opposed to obeying a physical law).

According to the Turing hypothesis, at least in so far as it has been interpreted as a link to psychological (or more broadly biological) processes, this distinction is of no fundamental significance — it is always possible to recapture the behavior of a system which processes information in the hierarchical mode by a system which processes information in the single level mode. However, this sense of recapturing or simulation is completely formal — it ignores entirely the spatial and temporal aspects of information processing.

I think, in view of the preceding considerations, that it is reasonable to conjecture that it is impossible to simulate a hierarchical system by a machine to which we can communicate algorithms (single level machine) without distorting its rate of operation or the amount of hardware which it requires. This tradeoff arises from the fact that it is necessary to pay for the constraints which make it

possible to prescribe a system's behavior. It is important that the sacrifice of this feature is compensated by the adiabatic modifiability of function which facilitates evolution processes.

This conjecture is evidently significant apropos the molecular processes under-lying cellular self-reproduction and evolution. Does it have ramifications for higher-level biological processes, processes possibly based on similar underlying mechanisms ? I think that our approach to such processes ought not to be overly restricted by concepts of information processing which derive from the single level devices with which we are familiar.