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Informational Darwinism

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The Theory of Evolution has, since Darwin, been sustained by contributions from many sciences, most especially from molecular biology. Philosophers, like biologists and the man in the street, have accepted the idea that the contemporary form of evolutionary theory has arrived at a convincing and final structure. As it now stands, natural selection is thought to work through the information-handling mechanism of the DNA molecule. Variation in the genome's constructive message is achieved through random errors of processing called mutations. How that mechanism and its revision works, and how much information it can hold are fundamental questions for the Neo-Darwinian theory to face. It is argued here that neither the operation nor the data content of the genome, as science understand them, can underpin the role Darwinism assigns to natural selection. It follows that we cannot put our confidence in the explanatory force of Darwinian reasoning, but neither is there an alternative to it.

Like two powerful jet aircraft thundering down parallel runways, biology and computer science took off at just about the same historical moment fifty years ago; they haven't stopped climbing yet. It was a fortuitous schedule because each has in one way or another informed the other. Research suggests that one day there may be computers based on biological components, and these days we have come to think of organisms as products of their own computation. We know a lot about information processing and a lot about the DNA processor hidden deep within the cell. We do not yet know much about the relationship between one kind of knowledge and the other, but many scientists have high hopes that one day soon the two fields will get together to form a theory that will explain why and how an organism comes to be what it is and consequently how species of organisms change with time. The first giant steps were taken when the structure of DNA's double helix was discovered by Watson and Crick in 1953, and when its method of coding for amino acids was subsequently understood.

All Darwin could do was to observe that heredity and variation were natural and in no need of explanation. 'No one', he said, 'supposes that all individuals of the same species are cast from the same mould. These individual differences are of the highest importance to us, for they are often inherited, as must be familiar to every one; and they thus afford materials for natural selection to act upon' (1872, p. 39). His unavoidable complacency with the source of heredity and variation here contrasts dramatically with what contemporary Darwinians wish to rest evolution on. John Maynard

Smith and Eörs Szathmáry attempt to explain not only the origin of life, but every important transition along the way in terms of the three-and-a-half billion year history of a molecule. It is the history of information stored, retrieved, and revised in DNA. In *The Origins of Life* (1999), they explain their basic assumption this way: 'Information theorists use the phrase "information is data plus meaning". In biology, the base sequence of nucleic acids provides the data, the meaning is the structure and function of proteins' (1999, p. 11).

It should not be thought that everything is going swimmingly. I have spoken of hopes and expectations, not of reality. We should not think that saying the genome contains information in the base sequence of nucleic acids is unproblematical. The application of the term 'information' is in some ways so apt that one is likely to forget that it is metaphorical. The metaphor is sometimes grotesquely inappropriate. The first message to have appeared on earth would have to have been in its simplest form something akin to a baby's pointless gurgle, 'ga-ga-ga'. Over the succeeding billions of years countless messages have developed shaping everything that lives from bacteria to mammals, including us. Those messages are not pointless gurgles but hugely informative programs, each akin to subject holdings in the Library of Congress. How did the barely audible and minimally useful initial utterance turn into the elaborate and eloquent archives we see around us? By mistake! By countless mistakes. And these are quite wonderful mistakes because they are not merely substitution errors, they are errors by addition: the first replicative molecule might have been, like small viruses, a few hundred nucleotides in length, whereas the mammalian haploid is three billion long; moreover, the first molecule, by definition, had only one formula and since then there have been billions, one for each species that has ever lived. It is an odd and remarkable message that gets better and better as mistakes are added to and compounded in it.

Messages that we know of are not like that for the obvious reason that the concept of information is not like that. Shannon's law of progressive information loss, from a well-known mathematical work by Claude Shannon done around the end of World War II, says that if a message (he meant only a set of symbols) is processed in a computer or a communication system, any possible source of error will invariably have a cumulative corruptive effect. Repetition will eventually corrupt the message completely. The effect is irreversible as well as invariable. Shannon's law would apply to information in the genome just as it applies to other information-handling systems. It is because the DNA is *not* an information system, which implies exactitude of copying and implementation, that Shannon's law does not apply. It is obvious. If the message going into the telephone is, 'Hello, Charlie', it is not the same message if it comes out the other end as a Shakespearean sonnet; it is not an improvement on it either.

Metaphors are not expected to stand up to every implication of the idea they illustrate. The facts remain. On the one hand, the facts are that life has existed on earth for billions of years, in that time many species have appeared and gone extinct, and that later forms of life have derived from earlier forms. On the other hand, the facts of molecular biology show us that the DNA, an otherwise uninteresting molecule, codes for the proteins of the body, and that the machinery in the cell completes those proteins so that they can be sent to and take up their stations in the organism. These are the facts, but they do not make sense when you think about it. It is a matter of logic once more.

The logic is easy enough to take in. The conclusion is, there is no account by means of which what is known about the genome can explain what there is to explain. This is not a way of saying the innocent thing, that we are presently ignorant; rather it is our present knowledge that forces upon us this dismal conclusion. Cryptic? Yes, the generalization needs clarification. Evolution is a theory of how natural selection disciplines a random assortment of errors called 'mutations' so that beneficial genes are retained in the gene pool, and injurious or useless ones expelled from it. What is a gene? It is some sort of cause; it causes the structural parts, arrangements, and processes, all of them, which constitute an organism. What sort of cause is this? There are different answers to this question; none of them adequate.

I. The Molecular Gene

In molecular biology what is called a gene is a stretch of the DNA molecule that is read out by an RNA molecule, and after some further treatment expresses a protein. This is known as the central dogma. The molecular gene is a physical object, namely, the bit of DNA that codes for a protein. And the molecular gene is a functional gene, too; it makes a protein whose function is to do something, call it *x*; so we can say that the function of the gene is to *x*. That there are two ways of speaking of genes, as physical objects and as function producers, reflects two interests science has in them: the interest in what they are and in what they do. Before the high-powered techniques of the last fifty years came into existence, only the second interest could be pursued. However, there is an intimate relationship between the two ways of studying a gene. What a gene can *do* is going to be limited by what it *is*. A car has the function of getting us from one point to another, but it cannot do so by taking to the air when the roads are blocked, even though under those circumstances flying would be the only way to get from one point to another. It cannot because it is not that kind of thing.

What kind of thing is a gene? It is a segment of DNA that codes for a protein which, in turn, does something. Are there any limitations on what genes can do similar to the limitations on what a car can do? There are; but the

precedent question is, even if there were no such limitations, what is the probability of finding one to perform a given function? Assume for the moment that genes can, in principle, code for any protein that might exist, and therefore accomplish any organic function that might be useful. If there is a function, we are assuming, there is a potential gene for it. How is that gene found? If you need to fly, what are the chances of getting a machine to take you into the air?

Airplanes have been designed to do this. Now the parallel breaks down. Genes are not designed, they are come upon. What are the odds of finding the gene to do a certain thing by searching randomly through the possible genes that will express the protein to perform the function? Everyone, including the staunchest advocate of Evolution, agrees that the odds are so poor that it is virtually impossible to find the right gene for the job in a random search. 'Virtually impossible' is justified because the number of possible combinations of amino acids in even a smallish protein is a devilishly large number, one equal to the number of all the protons in this universe multiplied by an equal number of universes. It is captured in the exponential expression, 10^{140}, for the benefit of anyone acquainted with such expressions.

The Evolutionist will accept the virtual impossibility, but count on a suppressed clause beginning with *unless*. It is impossible unless the search is not random. Since the search cannot be intelligent or purposeful – they are forbidden in science – the proponent must have another style in mind. The usual one given to the task is a search which is itself monitored by natural selection.

Richard Dawkins proffered the solution in *The Blind Watchmaker* (1986), and proudly cited back to it in his *Unweaving the Rainbow* (1999) as he did in other books. The argument begins with the premise that the informational units in genes are themselves subject to natural selection, and therefore their place in the protein is quickly established by a process which fixes any one of them as soon as it shows up. As an illustration, and one he could program into a computer, Dawkins chose a sentence from *Hamlet*, METHINKS IT IS LIKE A WEASEL, and made it the target of a rule-guided, not an intelligent, search. His program found the target within 11 seconds and in only 64 tries. This is astonishing. To start as he did with a perfectly random group of letters and spaces, and then set the computer to winnow down the alternatives to just those in the target sentence, staggers the mind. There are 26 letters of the alphabet plus a space to go through 28 times, the total number of letters and spaces in the sentence. Again, for those interested, the exponential number is 27^{28}. A very large number, one that IBM's Deep Blue hooked up to a million Deep Blues would not be able to sort through for the single target in a lifetime. How did Dawkins do it on a computer he owned in 1986?

The mathematical answer is built into the premise that informational units are subject to natural selection. The procedure follows two commands: (1)

when the right letters in the right positions come up, retain them; (2) in each subsequent generation, do the same thing. The trick is in keeping the letters that fit and not have to lose them with the next go-round. What are the odds of a thousand pennies coming up heads? The answer is 2^{-1000}; very long odds. But if you keep the first 500 heads, then you only have to flip the remaining 500. Of those, 250 will be heads, so now you only have to flip 250. Carried on to the final flip, you will get 1,000 heads in 12 generations. Not bad; very fast.

It is, of course, just another case of GIGO: garbage in, garbage out. You get out of a computer what you put into it. Still, what is wrong with Dawkins's search? First, the success is too good. If nature followed the same instructions, it would not have taken three-and-a-half billion years to get where we are today, but maybe something like two weeks.

Second, it is a matter of definition, or I should say, common agreement (one Dawkins began with) that genes are subject to natural selection, not parts of genes. A single nucleotide and the 'letter' called a codon of which it is a member (a set of three nucleotides, no more no less, code for an amino acid and constitute a 'letter' in the code) are smaller than a gene; ergo, neither is subject to natural selection. One might suppose that the contest for nucleotide position is conducted in another environment, one inside the nucleus where a form of natural selection is at work. However, there is no rationale for the proposition that a competitive struggle for position exists within the DNA's collection of nucleotides. Neither is there any reason to think that such a struggle for position, if it existed, within the micro-environment would play itself out so agreeably that the gene would get functionally better in the organism.

Third, the example is misused. The gene's function is like the meaning of a sentence. If the Dawkins example were stated correctly, the generations of approximation would be guided not by the shape of the target sentence but by its function, its meaning. The sentence, 'I lied' is not approximated by the sentence 'I died'. I doubt if it makes much sense to speak of approximating functions, but one can see immediately that the approximation to 'I lied' is more like 'I deliberately said something that was not true', than is 'I died'. The number and placement of letters does not come into it.

The argument I wish to make not only in this connection but throughout the succeeding commentary has two parts. First, evolutionary biologists *assume* that the space of proteins and the space of the functions that they might perform are somehow in alignment, a small change in one leads to a small change in the other. This is an enormously strong assumption, one that must be justified particularly when the genome is regarded as a coded message. A comparison with telephone numbers will show why. A small change, the change in a single digit, in dialing a friend's telephone number will not reach the person next door to him. It may not reach someone in the same business, in the same city, or the same country *unless* the telephone system were

prearranged to some such end. If gene-protein-function combinations are coordinated in some fortunate way, then a solid scientific explanation is required for a congruence with such an apparent purposefulness built into it.

The second part of the argument has to do with something we might call psychological. If we think of two spaces, the space of proteins and the space of functions, and grant that they are somehow connected, we will think that the connection has a direction. The discoveries in molecular biology give a sense to one direction only, from the protein to the function. The DNA combination that unlocks the suitable protein must first be encountered before a function is made available; it stands to reason that the physical object comes first, not the functional one. However, be it noted that historically Evolutionary Theory has only tracked the emergence of refined and new functions, or rather functional parts, not proteins. It seems to be a psychological truth that Darwinians, despite their training in biology, still think that the function comes first. The space of functions is comparatively small; it is circumscribed by the practical. It makes no sense to think of a bit of a nursing instinct attaching itself to the elbow or a bit of the mating call attaching to the shoulder; those are practical impossibilities. However, in so far as each, the instinct, the elbow, the call, and the shoulder, are prescribed in arrays of nucleotides, their conjunction in the DNA molecule is perfectly intelligible. The restriction of the search problem to the practical, the function, is psychologically compelling. Yet there is nothing in the possible structuring of the DNA that coordinates with the practical such that the practical restricts the possible; it does so, of course, once a functional modification is achieved, but the functional opportunity does not constrict the possible solutions beforehand. If the possible is not restricted beforehand, then the scope of the search, at the level of the DNA, remains as broad as our impossibly large exponential numbers indicate; and it is this impossible search that comes first.

II. The Elementary Functional Gene

Assuming that genes can be found regularly and in good order, say, by an as yet unknown but natural restriction on possible proteins, there remains the problem of construction. How does the genome work so as to produce an organism? The problem, of course, is that an elucidation, to be scientific, must avoid magic or pre-defined goals creeping subtly into the explanation. 'Regulatory' genes seem to fill the bill at first glance.

Neither constructing nor maintaining an organism could be accomplished by proteins acting by themselves. Hemoglobin is a single protein acting by itself, but the circulatory system is a construction of various tissues, heart, blood vessels, and so on, which are not mere assemblies of individual

proteins; so, too, are all the organs, bones, muscles, etc. Genes have been discovered that seem to connect up just those proteins that are associated in *structures*. They possess a remarkable quality of discrimination. They are the regulatory genes.

Molecular biology began to find regulatory genes some years ago. Among the important kinds is the homeotic selector genes, discovered in 1983. One textbook says these genes 'are involved in orchestrating the development of a wide range of organisms'. The implication of this definition is, to put it politely, exaggerated. Homeobox genes, the ones that exercise the 'control' over the set of genes they turn on, do not themselves *do* anything. They trigger other genes to come to life. Homeobox genes, and hundreds of them have been found so far, express a protein a part of which (60 amino acids, the *homeodomain*, is all) returns to the DNA molecule and there attaches itself, by means of little zinc legs it picked up along the way, to many different locations. At each location a gene is triggered which contributes to the position and formation of a something. In the fruit fly homeotic selector genes may flip the switches on sets of genes which somehow make a leg or an antenna, or control some other part of the body. By fooling around with the homeobox gene, experimenters have made bodies with two rear ends, and put legs where eyes belong, thus proving the power of these short genes. Interestingly, a gene in the mouse related to one which 'orchestrates' the parasegments of the fruit fly's body is involved in the orderly arrangement of its hind brain's development (the *rhombomeres*). Sometimes a homeobox gene will switch on other homeobox genes together with somatic genes and so bring about what biologists call a 'cascade effect'. Genes homologous to these exist as well in the human genome.

The homeobox gene is not incidentally part of the body's structure; it is, quite plainly, one whose role is exclusively a functional one. It might seem, then, that mutations only in the homeobox gene would bring about effects which preclude the need for randomly finding and modifying each of the genes belonging to the coordinated set whose function is to construct a part of the body. A random search for *coordinated sets* of genes is a formidable undertaking because the field to search becomes an exponent of the exponential number which described the field of molecular genes. The number 20^{200} describes the field of proteins with 200 amino acids; if that number is raised by a set of, say, 20 genes in a functional complex, it becomes $(20^{200})^{20}$, and that is the number 20^{4000}. To scan a field with this many alternatives to find just one is quite, quite improbable, vanishingly improbable . . . impossible.

Will the homeobox do the trick? Will a change in the homeobox gene build a different body part, perhaps, bit by bit, turning a leg into a flipper? The answer is unquestionably no. The reason I can answer with such confidence is already buried in the account of what a homeobox gene does. It triggers other

genes to turn on (sometimes off). The information necessary for building the body part is distributed amongst the genes which are turned on; it is not conveyed to them by information packed in the homeobox. An organism is rather like a great temple whose undesigned architecture is scattered in its stones which on a signal shape themselves up and fly to their proper places. The homeobox gene makes its contribution as a mechanism by timing and releasing the stones of an arch or a buttress to do their stuff. It follows that the field to be searched is not one whit abbreviated by the ministrations of the homeobox or any other regulatory gene. Each gene must be informed.

Why do I mention the regulatory gene only to shoot down (so easily?) the contribution it has been envisioned to make? I do so because biologists who have wanted to protect Evolutionary Theory from the challenge of exponential analysis have frequently insisted that reference to the 'cascade' is the proper and sufficient defense. I do not want to leave this stone unturned.

III. Major Traits

Competition for survival by the organism in its environment and its success in contributing to the gene pool of the species is explained by the Theory of Evolution mainly in terms of major traits. Only rarely is success attributed to proteins, individual parasegments, or rhombomere order. It is legs into flippers, down feathers into flight feathers, patches of light-sensitive skin into eyes, those are the sorts of thing that evolve. These major traits are most often ascribed to genes. Advocates of Evolution not uncommonly speak of there being genes for such accommodations as the single toe bone facilitating the horse's swift escape, or genes for the display feathers of a peacock. It is no doubt meant to be a short-hand way of speaking of clusters of genes which go together in constructing the larger features which enable them to analyze evolutionary development.

Permit me an ancillary comment. Darwinians are inclined to concentrate on single traits without taking into consideration the problems of integration. A horse lucky enough to have developed a single toe and so lightened his foot and so got a speed advantage over his confrères, must also *want* to run faster than his herd. Take another example. Evolutionists depict the progress from a protocetus, a land animal with tiny legs, to the modern whale by tracing the morphing of legs into fins. Consider the problem. The sperm whale will dive to a depth of three kilometers, about five times below the crush depth of the best submarine, and remain submerged for up to two hours. To get started, a sperm whale has in its head four tons of oil (spermacetti) which when crystallized shrinks and enables the creature to descend like a stone. The temperature of the oil when fluid is 33 °C and when solidified 31 °C. In order to change the state so as to facilitate a dive, the whale shunts blood circulation

away from the sac holding the oil and it recycles cold sea water through blow holes (two of them); to ascend, blood is restored warming and expanding the oil. Countless other inventions must add to this one; the eyes must not collapse, the ears must be changed, handling oxygen and its deprivation have to be altered – whales' muscles will work anaerobically for long periods of time. The accommodations for the accomplishment of this diving feat are not only many, they are very different, not the least of which is the capacity to form the intention to dive and possess the apparatus of voluntary control to pull it off. To sketch the changes from protocetus to cetus faithfully, the kind and degree of information that needs to be modified and completed more or less at the same time has to be drawn into the account. It is irresponsible for anyone to represent the evolution of the whale as a problem embracing just a little skeletal information. It is not a paragraph but a book that has to be rewritten.

When we consider major traits from an informational standpoint, two questions arise that seem obligatory on the Darwinian to confront. One is a repetition of the questions raised above. What is the probability of a successful stochastic search for the coalitions of mutually supportive genes which are entrained in the trait's production? If what has been said so far is correct, then little more must be added than to mention that a clustering of this magnitude will greatly enlarge the field to be scanned. The enlargement will invoke another level of exponentiality, a third magnitude. This should be clear from what has already been said.

The second question, however, is no less difficult to resolve in Evolutionary Theory, but it is also a question that seems to confound a fundamental conviction in molecular biology itself. The question is: Is there enough information in the genome to construct an organism?

The late Walter Elsasser, a renowned quantum physicist and colleague of Schrödinger and Bohr, turned to biology late in his career (as did his colleagues), producing four books on the subject. One of those, *Reflections of a Theory of Organisms*, was reissued in 1999 with an introduction by the Berkeley biologist, Professor Harry Rubin. In his books, Elsasser makes the point in several ways that the informational requirement for the construction of an organism far outreaches the informational capacity of the genome. It is a shocking claim which deserves to be met, yet few biologists have taken any note of it at all. None has met its challenge.

It is an article of faith in biology that the genome contains information and all the information needed to direct the development of an organism. Environmental factors are acknowledged to play a part in directing and stimulating development, but the programs that are stimulated and directed must be informationally prepared to respond. In that sense *all* construction and maintenance of an organism is instructed by the DNA molecules that it inherited from its forebears. Where else could it be? The only physical object

transferred from immediate ancestor to offspring is DNA and some proteins in the egg which provide the mechanisms of its subsequent translation. There is no informational source other than the DNA. (There is a little extra DNA in the mitochondria that comes with the egg, but this fact does not affect the point here.) The conclusion seems inescapable that whatever information is needed for the new organism is there in the germ cell or in each of the newly divided bacterial cells. If the information is not there, it is nowhere. Nowhere is not a place, and magic is not an alternative. Therefore the information is in the genome.

Let's talk about mammals. Three billion nucleotides comprise the mammalian DNA, of which about 90 percent is regarded as junk. Three hundred million base pairs – that is the way the nucleotides are arranged, in pairs – code for genes. All mammals have about the same number of genes in their DNA divided up in sets of chromosomes. The numbers of chromosomes differ, but the total amount of nucleotides does not. Much is made of the enormous informational capacity of three billion nucleotides. If each base pair were a character in English, then the mammalian genome could carry the information of 100,000 essays the length of this one.

But how these base pairs are used suggests that the carrying capacity is not really so great as it would seem. The base pairs divide up into about 100,000 genes in the set of chromosomes a mammalian organism possesses. (Some estimates have recently raised the possible number of genes to 140,000.) These are the genes which express proteins, not larger functional genes. This fact, and others, led Elsasser to conclude that the genome is insufficient to contain the constructive information needed. It is not a matter of our ignorance, he said, but of our knowledge. It is not that we do not yet know enough about the way the DNA molecule works, but rather that we do know how it works and therefore we know that its informational capacity falls short of its ascribed cargo requirements.

(There is a point I do not want to develop, but one I find odd. There is not a direct correlation between genome size and the complexity of the corresponding organism. Salamanders and flowering plants have ten times more DNA than do whales and human beings. Nor is the number of chromosomes indicative of anything informationally important: the crab has 256 chromosomes to our 46. The number of genes may be significant, but how many genes the Tiger Lily carries or a Dungeness crab is unknown; they have not been sequenced. Nor, by the way, has the chimpanzee DNA been sequenced. Nobody knows for sure what the similarity actually is between its genome and the human, in spite of the oft made claim of 95 percent similarity that seems to have entered the biological lexicon many years ago as an established fact.)

Those who advance the Theory of Evolution regularly tell us how quite amazing adaptations have come about over the eons during which natural

selection has imposed its will on aleatory variations. They do not tell us how the formidable amount of information for these adaptations is stored and fleshed out. Once one reflects on the constructional needs to produce a mammal, the sort of animal we know best and the sort we are, it seems obvious that 100,000 instructions is far, far short of what is needed. It is worth reminding ourselves, however, of what is involved.

It is tempting to illustrate the contrast between the quantity of information in the genome and the measure wanted by mentioning the human brain. The brain is an organ of about one billion cells, of which 100 million are neurons that fall into several general types and must be hooked up together in highly elaborate and precise ways. Those ways are elaborate because they can involve 10,000 and more dendritic ties which must be very exactly connected with other neurons, some of which are similar in type and some are not. The brain's architecture achieves innumerable different functions, such as regulation, metering, monitoring, timing, sensing, coordinating movements of many kinds, instinctual reacting, remembering, believing, *thinking*; and, if evolutionary psychologists have it right, a fairly large sophisticated repertory of penchants (jealousy, maternal loyalty, status acquisitiveness), and so on. Each of the functions breaks down into sub-functions, of course, which may not always be performed in the same parts of the brain (seeing, for instance, is implemented in at least three parts of the brain) further complicating the task of brain-building. Were a computer to be designed to see, assuming we had the faintest idea how to do it, the lines of code prescribed would surely be in the billions. How a device whose structure allows for only 100,000 instructions (and those of an entirely inappropriate kind) could make a brain is quite beyond our best scientific comprehension.

I have succumbed to the temptation to talk about the brain but only superficially. I have not touched on the chemistry of the synapse or the propagation of action potential, for instance. An adequate description of what the brain does or is credited with doing is the subject of a very large and technical textbook. The foregoing paragraph was meant merely to remind you of what you already know and, if for no other reason than that you have a brain and use it, you are able to extend the example without further help. There are other systems the genome constructs that are almost as complicated as the brain: the autonomic nervous system, the immune system, the lymphatic system, digestion, blood cell production and differentiation. It is silly to have started on a list of this sort; it can go on and on without adding anything to the point. The DNA of the genome holds nothing like the amount of information for constructing any one of these systems or functions much less for all of them. Moreover, they must all be coordinated with one another, which one might be forgiven in thinking is a design accomplishment over and above the manufacturing of the parts and physically present in molecular sets of plans.

Can I be so sure that the genome holds too little information? No, of course not. There may be a method of ciphering the information that no one yet conceives. One possibility that comes to almost everyone's mind who contemplates the problem is the multiple use of genes in varying assemblages. In this way a small number of elements could be reread in different ways, just as the active vocabulary of a few thousand words can be used to communicate everything we wish to say in our entire lifetime. The genes ruled over by homeobox genes could very well, in different arrangements and numbers, conjoin with others in virtually infinite numbers of statements.

There are two discouraging reasons to doubt the correctness of this supposition. One is that, except for the limited number of homeotic collections (whose role so far seems to be limited to sequential fabrications), no one has found any experimental support for a biological technique like the one suggested. A reason exists for the experimental failure. There is no known method for interpreting a supercode, that is, a code on a code, other than by intelligence. The only analogy to the supposition of multiple gene arrays is human language, but we have no idea at all of how human beings use a language. There is no key to this code. If Nature speaks in a language of genes, we have no model in mathematics, computer technology, linguistics, or philosophy to show us the way to understand it. Researchers cannot look for what no one is able to see.

A word of clarification. Researchers *do* see multiple uses of genetic elements. Different homeobox genes will trigger overlapping gene collections. And recently an unexpected phenomenon called 'alternate splicing' has been found. The same gene in the DNA, that is, the same string of nucleotides, will be cut up and spliced back together one way on one occasion and in a different way on another; the consequence is that there will be two or more template designs (mRNA) to express two or more different proteins. What researchers do not see is the overall controlling design. Logically, were another control step identified, a second controlling would be called for. A mechanism capable of stopping such a potentially infinite regress is what I had in mind as that whose technique is as yet unimagined; it is a mechanism which, like the intelligence it mocks, cannot be fathomed. Therefore, one cannot see it, not because it is not in plain sight, but because it cannot be discerned.

The other reason is that it makes the evolutionary search infinitely more difficult. With the idea of multiple use, testing a gene by natural selection entails its proving itself not in one function but in many unrelated functional roles. A gene that works well in one role may be disastrous or useless in another. Finding a gene that works well in each of several roles leads us to another exponential level of improbability. Why say the roles are unrelated? Because the whole point of invoking the coding of codes was to explain how so many different functions characteristic of living organisms could be

created from the manipulation of so few elements as the known number of molecular genes.

Where do we end? Is Vitalism or Creationism vindicated? There is no reason to think so. The supernatural is not calculable. What I suspect is that there is a natural solution to the problems sketched above, but we are a long way from finding it. How biology works is likely to be far more counter-intuitive than quantum mechanics. It may be a thousand years before genius penetrates the mysteries we are just now able to perceive, mysteries that the marvelous achievements of modern biology have only recently enabled us to recognize. Biology is a great science, getting greater every day by the incredible imagination and hard work of thousands of biologists working today. Nothing I have said can diminish their breath-taking accomplishments. My only appeal is that Evolutionists cool it. Glib explanations based on imaginative quasi-teleological reasoning make it seem as though biological science and its subject-matter are fundamentally mastered. False. Facts proliferate, but theoretical understanding lags. Science is just beginning to discern faint outlines in our backyard lying just outside the illumination from the porch. There exists, we may think – and hope – a vast *terra incognita* lying beyond. What could be better than to have the greatest mysteries of nature still lying before us to be unraveled, perhaps even yet to be defined?

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