IS THERE A PURPOSE IN NATURE?

HOW TO NAVIGATE BETWEEN
THE SCYLLA OF MECHANISM
AND THE CHARYBDIS
OF TELEOLOGY

edited by Ivan M. Havel and Anton Markoš

phenomena. Professor Ho is a good example for me that living organisms can be studied and admired, and that an understanding of holistic nature around us may create a background for a deeper understanding of the wisdom of interrelations in our world, where teleological and other relations are also considered, and a kind of holistic unity of all individual phenomena, whose parts they ultimately are, is respected.

THE DARWINIAN PURPOSE ENTERS
THE POST-GENOME ERA (A CASE STUDY)
_____*FATIMA CVRČKOVÁ*

Summary

The contemporary scientific worldview provides a supposedly objective and therefore universal projection of reality. This projection (or map) has been purged of anything individual, deliberate, metaphysical or anthropocentric, at least as far as possible (which may not be very far - see e.g. Mahner and Bunge, 1997; Neubauer, this volume). The world of science is as free of purpose as it is of any other man-made values, although the word "purpose" can be used as a metaphor (see Driesch, 1905). For instance, a modern biologist may occasionally feel obliged to remind that talking about "animals having legs for running" only means that "those animals who acquired legs (presumably by a random process) could run and survived, while those who did not were eliminated by natural selection". However, an initiated reader does not have to be reminded: "purpose" in biology is just a figure of speech, commonly understood as a metaphor for the (neo) Darwinian paradigm.

The above-summarized metaphor of biological purpose, which would be considered scientific by most readers, contains a number of tacit presuppositions. While these presuppositions have possibly fostered major progress in biology (particularly molecular genetics), they appear to be paradoxical in the light of recent data, reminding us of the inherent incompleteness of maps in general, including the one we call "the scientific universe".

The background: Purpose as fitness acquired by mutation and selection

One of the central assumptions of modern biology is the notion that organisms evolve by natural selection. If *a population of animals or plants exhibits some degree of variability, some individuals can cope with environmental challenges better than others, and the fittest ones are likely to produce most offspring and therefore possibly pass on the corresponding part of the population's variability to the next generation.* While this core of Darwinism is apparently true beyond reasonable doubt and generally accepted by the scientific community, a number of open questions exist with regard to related aspects:

• The role of direct inter-organism competition. The standard formulation of the natural selection argument is based on macroscopic, sexual organisms, but the situation may be quite different when we consider microbes (see Markoš, this volume) or communities as individuals.

• The origins of (and possible limits to) population variability. In the absence of known causes, chance is a legitimate approximation of an uncertain number of complex and uncharacterized factors. However, this line of thought has often led to conclusions that there is no other source of variability besides random errors (mutations) and that if pigs needed to fly, they would have evolved wings solely by a trial-and-error mechanism (e.g. Dawkins, 1982).

• The explanatory power of the natural selection argument in situations other than the origin of varieties or speciation (i.e. generation of a reproductive barrier between two populations of organisms which thereby become two species), in particular its usefulness regarding the origin of higher taxa.

• The problem of heritability. Not all variability is heritable and not all heritable variability can be efficiently passed on to the next generation even under selection (Flegr, 1998). The question of what actually represents heritable variability will be dealt with in more detail.

• The existence of open problems is a sign of the viability of a scientific theory, not the reverse. However, people whose only experience with science comes from high school textbooks do not always appreciate this fact. Newtonian mechanics offers better exam

topics than quantum physics, and the reasons go deeper than just requirements for mathematical background. It is easier to explain things that are well understood than those where even the teacher experiences uncertainty, and the average non-biologist often leaves school feeling that "evolution has been scientifically explained by the law of natural selection". Combined with everyday experience and common European tradition, this produces a familiar pattern of thought many of us grew with, which could be formulated as follows:

Living beings are no worse adapted to their environment than any man-made machine is adapted to its task. Indeed, organisms have been constructed to be adapted to their environment by the wise hands of Natural Selection (which the pre-Darwinists called God for lack of relevant knowledge), which could have done anything that a human engineer could do: a blind watchmaker who nevertheless produces clocks of supreme beauty and perfection.

Shouldn't one ask why we would rather accept the idea of a blind watchmaker than renounce the belief that living beings are just very complicated clocks?

The Genome as a compact description of an organism

Comparing the eye to a camera, the heart to a pump or the leg to a system of levers may perhaps bring about a somewhat nostalgic feeling in a reader who did not personally experience the technological enchantment of the Cartesian era. However, this kind of mechanical metaphor has produced the whole field of molecular biology. A contemporary textbook author does not hesitate to use similar imagery when describing the internal workings of a bacterium - the simplest model organism capable of life independent from an external supply of information:

> *The bacterial cell is a precisionally fine-tuned machine. The day has long passed when the question should be asked whether there is more than the laws of chemistry behind the functioning of the bacterial cell. We now see the bacterium as an extraordinarily sophisticated set of interrelated molecules that harmoniously work together in highly predictable ways to ensure the growth and selective survival of more of its kind. At the heart of these remarkable, at most clockwork-type, machines are the DNA molecules that encode, with total precision, sets of commands that bring into action*

molecules needed to cope with ever-changing nutritional potentials. What is equally important is that DNA has the capacity to incorporate within its structure new changes that will permit further evolution of the cell into forms needed to prosper successfully upon the Earth's continuously changing face.
(Watson et al., 1987)

The "common-or-school" variant of Darwinism, presented above, has acquired a new flavor. The discovery of the biological role of DNA and the universality of life's molecular machinery provided a plausible solution for one of the great questions of the natural selection theory. Some part of organisms' variability subjected to selection *(phenotype)* can be explained by undirected, random mistakes (mutations) arising upon replication of its DNA *(genome)*. We can focus our attention on this part of variability and ignore the rest, together with all variability that is not encoded in DNA and therefore presumably not transferred to the next generation. The genome is being viewed as a recipe containing all the information that organisms require to construct themselves. This "self-construction" is often likened to execution of a program by a computer. The program would, of course, have to be of a very special kind, since no man-made programs specify the structure of their own hardware. However, one obviously has to assume either self-construction or a designer to get the "machine" working.

An oversimplified version of this view, which has more or less taken root among the lay public, could be summarized as follows. *Assuming that the program (genome) contains a complete set of instructions for building an organism, we should be able to reconstruct the organism's structure (or even behavior) if we know the complete program and the rules for its execution, which are supposed to be shared by bacteria and elephants alike.*

And not only bacteria and elephants: we human beings are no exception.

Entering the post-genome era

As humbling as this idea may be, it is at the same time equally wonderful (or terrifying) for the appropriately prepared mind. A lot of paper and emotions have been used (and wasted) in endless discussion of the possible benefits and dangers of knowing the complete human

genetic makeup. Although we are far from knowing how much of the human diversity is actually DNA-based (see e.g. Michel and Moore, 1995), the possible outcome of the ongoing project of determining human genome sequence tends to be somewhat overstated by those who seek funds for this noble effort. Doubts have no place if one has to justify spending money:

> *For all the diversity of the world's five and a half billion people, full of creativity and contradictions, the machinery of every human mind and body is built and run with fewer than 100,000 kinds of protein molecules. [...] In a material sense, then, all of the subtlety of our species, all of our art and science, is ultimately accounted for by a surprisingly small set of discrete genetic instructions. More surprising still, the differences between two unrelated individuals, between the man next door and Mozart, may reflect a mere handful of differences in their genomic recipes – perhaps one altered word in five hundred..* (Anonymous. 1996)

It is not surprising that non-biologists in particular expect that knowing our complete genome sequence will bring an immediate, revolutionary turn in the development of biological sciences. Biologists often anticipate something similar, with the remarkable difference of being aware that there is no reason to single out the *human* genome sequence. *Homo sapiens* is, after all, a rather bad model organism, given the unavailability of experiment and the long generation time. The "post-genome era", whatsoever it brings, begins with completion of the *first* genome sequence - which means that we already entered it 5 years ago, when the genome sequence of the bacterium *Haemophilus influenzae* was published (Fleischmann et al., 1995). Many more bacterial and archaeal species and several eukaryotes followed since, including common model organisms - the bacterium *Escherichia coli*, the budding yeast *Saccharomyces cerevisiae*, the nematode (worm) *Caenorhabditis elegans* and the fruit fly *Drosophila melanogaster* (see e.g. http://www.tigr.org for a current list of sequenced genomes).

Yet the world does not seem to have changed. Or has it?

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THE PARADOXES
C-value paradox

As genome projects progress, paradoxes begin to surface. The first signs of the coming "revolution" have been around already for some time. If a genome represents a more or less complete description of an organism, the complexity of the organism and its genome should be correlated - more complex organisms should have larger genomes. However, already the results of relatively early experiments (some dating to the 1960s) have shown that this correlation is far from straightforward. It may appear surprising that the common view of the genome as a "recipe" for an organism has survived the finding that a humble amoeba has 200x more DNA *per cell* than ourselves (see Blom and Rapacki, 1997 for more such remarkable observations, including a bibliography).

The size of a haploid set of chromosomes (i.e. the organism's unique DNA sequence size) is often referred to as the organism's species-specific *C-value* (C stands for complexity). *"The C-value paradox" expresses the observed lack of correlation among an organism's genome size, genomic complexity and phylogenetic status.* While an organism's phenotypic complexity may be a matter of opinion (especially if we compare protists, plants and vertebrates), its phylogenetic status is easier to define, and we intuitively feel that it *does* reflect the phenotypic complexity, whatsoever it may be - closely related organisms are supposed to be comparably complex. Indeed, the most irritating examples of the C-value paradox are not those mentioned above but those where related organisms radically differ in their genome sizes. Why does the housefly *(Musca domestica)* have a five times larger genome than the fruit fly, and why do various rodent genomes differ in size up to double (Blom and Rapacki, 1997)?

Given these observations, can we still maintain that the genome exclusively determines the organism's structure? Answering this question by a straight-out "no" seems to be the most obvious way out of the C-value paradox, and it may appear strange that textbooks usually do not mention this possibility. However, as genome sequencing reveals surprising similarities in the molecular composition of phylogenetically distant organisms, it may be time to start taking this option seriously:

Given an entire genome sequence, can you predict computationally the systems behavior of a biological organism? [...] [A] traditional view is that the genome is a blueprint of life containing all the necessary information to make up a biological organism. If you replace a nucleus, then you get a clone. So, this might be called Dolly's cloning principle. However, I think an alternative view can be taken where the genome is a warehouse of parts, or building blocks of life, and all the regulatory signals in the genome are simply bar codes to retrieve them. (Kanehisa, 1997)

If we accept this view, a whole new realm opens up for biology. We know nearly nothing about the complex network of interactions joining all the gene products and small molecules that make up a cell, and the information specifying the organism's structure may, to a substantial extent, reside in this network. Indeed, the need to focus on interactions rather than on the "building blocks" seems to be gaining general acceptance in the mainstream of molecular biology (Hartwell et al., 1999), though not universally, and the lay public seems to be more or less untouched by it. A good example was provided the public debate that arose when Craig Venter of The Institute of Genome research announced identification of the "minimal genome" a bacterium needs to maintain itself alive (Hutchison et al., 1999), and suggested an exciting experiment:

... some specific experiments ... could be carried out to engineer a cell with the minimal genome required for survival in the laboratory environment. The researchers suggest that one way to do this would be to synthesize, and test in the laboratory, a chromosome specifically designed to identify a minimal gene set. TIGR scientists decided that prior to proceeding with the chromosome synthesis experiments, it would seek ethical review from an outside advisory panel.
The Institute of Genome Research (TIGR) Press Release, December 8, 1999

The resulting debate in the press appears to be almost entirely focused on the possible disastrous consequences of an experiment based on synthesizing a chromosome in vitro, enclosing it in an artificial membrane and letting the "bacteriunculus" live and grow. The very likely possibility that such an experiment will fail is rarely ever mentioned ... (see Harris, 2000 and http://www.tigr.org for an up-to-date list of references).

However, this exciting field reaches far beyond the scope of our current interest. Another question becomes rather pressing: *If the genome is just a warehouse, can we assign a "purpose" to each of its components?*

Gene number paradox
The "traditional" view of molecular biology is that we can.

> *A living cell is a delicate, interconnected assemblage of molecular machines and processes. There is not a great deal of room for error. If a necessary vitamin is not available, the cell dies. If a virus injects a malignant piece of nucleic acid, the cell dies. If a poison destroys one key enzyme, the cell dies.* (Goodsell, 1993).

Is this view justified by data and observation, or do we only reiterate a common belief that Nature is purposeful and nothing useless can survive Darwinian selection?

The results of many genetic experiments seem to support the "clock-like organism" model. Before large-scale genome mapping and sequencing was possible, only those genes whose perturbation (mutation) caused an observable change in the organism's phenotype could be studied. *Much of the framework of our current understanding of cellular structure and function is extrapolated from studying specific model situations – a selected group of cellular processes (mostly reactions of bacterial and fungal intermediary metabolism) which are dispensable under the laboratory conditions and which can therefore be perturbed by mutation.* However, it became soon obvious that such an extrapolation may not bee always legitimate. Only a fraction of yeast genes found by sequencing a large chromosomal fragment could have been identified on the basis of a mutation. This led to the formulation of the *"gene number paradox": the number of genes found by molecular methods is always larger than the number of genes accessible to classical genetic analysis.*

One reason could be that genes truly essential for life cannot be mutated since mutants would not survive. However, not all of the hidden genes can be explained away in this elegant way while leaving the clock-like organism model intact. Quite a substantial part of eukaryotic genes can be mutated not only without a major deleterious effect on the organism level, but without *any* detectable phenotype, at least under laboratory conditions. Upon closer analysis, such genes

often appear to be duplicated (or multiplied) within the genome with minor modification, and *all* copies would have to be mutated in order to perturb function (which often appears to be critically important for life – e.g. required for DNA replication). How does this phenomenon of *gene redundancy* (Brookfield, 1997) fit into the general model of a machine-like organism molded by merciless natural selection?

One could argue that "redundant" is not the same as "useless"; even sequences without a clear present function can be useful as a possible source of material for future mutational experiments producing new functions. (As Sydney Brenner noted in one of his lectures, there is a substantial difference between junk and garbage; natural selection eliminates "garbage DNA", while keeping a certain level of "junk DNA" which is advantageous in a constantly changing environment.) Redundant functional genes can be, moreover, viewed as finely-tuned alternatives whose minor structural differences may have important functional consequences under specific conditions (Nasmyth et al., 1991). Either of these two possibilities, although fully consistent with the neo-Darwinian paradigm, appears to be at odds with the tacit assumption that the "mechanical machine" model represents a valid approximation of living organisms: clocks, as a rule, have no redundant parts.

Do we have to abandon the machine metaphor entirely – which would mean undermining the foundations of the majority of modern biological theories – or is there any other alternative? I believe so; maybe all we have to do is broaden the concept of the "machine model" so that it would include the Turing machine as well. If we accept that cells can be likened to computers rather than to clocks, gene redundancy and the non-trivial relationship between program (genome) length and performance suddenly appear predictable and logical, not paradoxical. However, we should not believe that we are therefore rid of paradoxes once and forever. We have only replaced one metaphor by another, perhaps broader and more powerful. Any metaphor is only a caricature of the reality, not the reality itself; and as useful as the computer metaphor may be as a tool for description and prediction of organism properties and behavior, we should never make the mistake of identifying the organisms with computers.

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Conclusion: Life-as-it-is vs. Life-as-we-describe-it

`..to lidé jsou z masa a krve, stvoření světa dědicové věční
kteří své krásné sny zabíjejí tím, že je uskuteční...

...the people of flesh and blood, eternal heirs of Creation
who kill their beautiful dreams by making them true...

Jiří Wolker: Balada o snu (The Ballad of the Dream)

As scientifically literate people of our time, we have learned to live in two worlds. One of them, the real world, we make our home in a way dependent on a number of "metaphysical and anthropomorphic" terms and speculations forbidden in the other - the rigorous, precise, but rather uninhabitable world of science. We can dream of expanding the "scientific universe" so that it would encompass even meaning, symbol and beauty (see Ho, this volume; Sermonti, this volume). However, what should we do if this noble task turns out to be as unachievable as walking to the horizon?

Instead of delegating the (possibly unreachable) answer to the next generations, we may take a lesson from science itself. We can accept the "objective scientific universe" not as a world in its own right but as a necessarily incomplete, reduced, flattened model, a caricature of the complex reality of life. Such a model may (and will) contain gaps and paradoxes which could indicate not only weaknesses in our theory and methodology, but also limitations inherent to the varying ways and viewpoints science uses to produce maps of the rich, multidimensional reality (see e.g. Prusinkiewicz, 1999; Cvrčková, 1998).

While we may perceive paradoxes as disturbing threats to the universality of the scientific worldview, they may be as well taken as welcome reminders of its incompleteness. We, the self-domesticated part of humanity living in a world of global television, Internet and standardized sausages, have perhaps become too well used to the image of scientists as professional problem-solvers. But science is here not only to kill dreams by making them true. I believe that keeping questions alive is an even more important task.

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