Is it Really so Easy to Model Biological Evolution in Terms of Design-free Cumulative Selection?

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Abstract: Without directly taking sides in the design/anti-design debate, this paper defends the following position: the assertion that biological evolution "*is*" design-free presupposes the possibility to model biological evolution in a design-free way.

Certainly, there are design-free *models* of evolution based on *cumulative selection*. But "to model" is a *verb* denoting "*modeling*" as the *process* leading to a model. So *any* modeling – *trivially* – needs "previous human design."

Nevertheless, *contrary* to other scientific activities which *legitimately* consider models while *ignoring* the process leading to them, evolution theory must take into account the *human activity* of *modeling* required by its corresponding models.

0. Introduction

Having stirred up passions, the debate around ID is a false debate where people are not talking about the same thing.

As long as sharing faith in God is not definitively assimilated to a psychiatric symptom, it is legitimate that believers do not wish to reduce their faith to some kind of surrealism just tolerated, provided that it is not taken seriously. So, in the eyes of believers, the belief in God's Creation can imply several conceptions of a biological evolution previously designed by the Creator.

I would be the last to deny the sound principle saying that faith and rational science are not to be confused (comp. Collins 2006, pp. 5 ff.). Or, more precisely, going perfectly together with scientific knowledge, faith should not enter within scientific argumentation.

However, the sound principle of non-confusion between science and faith *does also operate in the opposite sense*. Scientific knowledge should not be used as an argument *against* faith. Indeed, it seems reasonable to consider faith as a special case of metaphysics, knowing that the potential negations of metaphysical approaches are in turn metaphysical approaches.

Nonetheless, does science – here, the synthetic theory of biological evolution – systematically respect the principle of non-confusion between science and faith? This is not sure. Richard Dawkins represents a living example of a scientist who really feels able to prove "scientifically" the "nonsense" of faith and so of the faith in ID *assumed as faith* and nothing but faith. (Dawkins, 2006, p. 50)

The unique way to call into question the faith in ID without veering towards a mixture of science and metaphysics *perhaps* would be to show that scientific understanding of biological evolution *does not need* ID to remain consistent. Yes, but in order to do so, defenders of such an approach should be certain that they really understand what could be an ID-free biological evolution.

Now, there is a heuristic principle to be taken into account: being able to *model* what we are supposed to understand does not ensure our real understanding. By contrast, if we are *not* able to *model* what we are supposed to understand, then that we are supposed to understand is certainly *not* understood. So, *before asking whether biological evolution* as such *is design-free or not*, are we able to *model* evolution in a design-free way?

The present paper shows that a *design-free modeling of biological evolution* is *merely unimaginable*.

According to the current synthetic theory, real biological evolution is "motorized" by an interaction between pure chance and randomly configured constraints, an interaction we will elucidate in terms of "*cumulative selection.*" From the standpoint of the synthetic theory, this "motorization" can function without previous design emanating from God or any other intelligent entity. So, to correspond to a design-free biological evolution, a *human-made model* of evolution necessarily must operate without any design previously *emanating from humans*. But is this possible?

Certainly, there are *models* where something – perhaps – comparable to biological evolution evolves "blindly." We will come back to this point. But recall that "a model" and "modeling" are not the same thing. "Modeling" denotes the *process* leading to a model. So, to consider a modeling in a complete manner, we have to take into account (i) the human intelligence required by the modeling in question, as well as (ii) the *resources* implemented in this process according to a *previously conceived* strategy.

Of course, the foregoing will meet predictable objections. First, *scientific work exclusively considers models* as such*, and not the elaboration of these models, nor the resources implemented in the elaboration process. So, all that should concern us is the design-free functioning of the model of evolution. By contrast, the* trivial *fact that any* modeling *as a human-conceived process by definition presupposes human design is to ignore.*

Another probable objection may be that *the essentially human-conceived and subsequently non-design-free aspect of modeling as a process concerns the elaboration of models not only of biological evolution, but of any other phenomenon to be investigated.*

Yes, the foregoing objections – please pay attention to the conditional – would be right in most

scientific areas beginning by physics.

But this paper will show that biological evolution represents an exception, and more precisely that in the area of biological evolution, considering a model of biological evolution without taking into account the required modeling resources *would deprive the model of the essential*.

0.1 Some short precisions concerning models and modeling

Let us say that in our context a *theoretical description TD is a model M* of a system Σ if there are (i) a one-to-one-relation Φ between the items belonging to *TD* and certain characteristics *attributed* to the given system Σ to be described by *TD*, and (ii) appropriated means to test the adequacy of the one-to-one-relation $TD \leftarrow \Phi \rightarrow \Sigma$ in an experimental or experimentation-like way. In our context, we consider as "experimentation-like" *computer simulations* replacing experimentation *stricto sensu* where the latter is not possible. Here, these a bit reducing proposals are sufficient; for a less reducing view, see Peschard, 2010, p.20.

Recall that "modeling", in our context, denotes the global process dedicated simultaneously (i) to the construction of the model *M* as a special case of a theoretical description *TD* and (ii) to the implementation of the resources required by the experimentation-like approach specifying certain aspects of *TD* as a model *M*.

0.2 Overview

In section 1 we will see why contrary to other scientific areas legitimately ignoring the *modeling process* leading to the considered *models*, an evolution theory wishing to carry adequate models is not authorized to separate the latter from the corresponding modeling.

Section 2 is dedicated to the meaning of "cumulative selection" and to the fact that cumulative selection is easy to model as long as there is *given* selection device. However, since according to synthetic theories nothing is previously given in evolution, the necessity of given devices within modeling of cumulative selection leads to insurmountable problems.

Section 3 approaches several simulations of biological evolution, more or less convincing thanks to *given* selection devices. Subsequently, section 3. also evokes the – utopian – idea of simulations of biological evolution where the implemented selection devices instead of being given, are in turn configured by cumulative selection.

Finally section 4 shows that even the *virtual* realization of such *de facto* unrealizable simulations would not be adequate with biological evolution insofar we know it, while recalling that contrary to other scientific disciplines, evolution theory must take into account the resources required by the realization of a model.

1. Why can we consider physical models without taking into account the corresponding modeling? Why is this not the case for models of biological evolution?

1. Models and modeling in physics

Consider a model of an astrophysical process, say the formation of a new star from a a large gas cloud. To test the model under at least experimentation-like conditions, we need a computer simulation as is for example proposed by Tegmark in an accessible way (see Tegmark, 2014 pp. 38 ff.). Now, the simulation, in order not to be reduced to a kind of computer game, necessarily must be programmed according to the concerned physical laws as we know them. Of course, *writing the corresponding program belongs to human design*, whereas the *computer resources required by any program are in turn designed by humans*. Nevertheless, in physics, a model which – as usual – does not take into account this form of "human design" remains adequate with regard to the phenomenon to be modeled. Indeed, we can do physics – i.e. explain physical phenomena according to known

physical laws and/or discover new physical laws – *without* asking *where these laws are coming from, or who programmed them in which way*. So, conversely, it is legitimate to consider just the simulation as such, *without* asking *by whom* the simulation had been *programmed*. Analogously, we can legitimately *neglect the resources* the "designer" of the simulation program had needed to execute her/his task.

Now, there is a question: why just physics can ignore the modeling resources behind its models? The relatively simple answer consists of the following three closely related points. (i) Physical laws remain identical through the history of our universe. (ii) Although nowadays physical law generally require advanced mathematics, the structure of these laws is astonishingly simple. (iii) For group-theoretic reasons we cannot explore here (see Punin, 2016, pp. 6 ff. 11), the specific investigation field of physics allows a *distortion-free* approach of physical systems taken out of their wider context. Since physical laws are easy to identify because of their structural simplicity while remaining unchanged under time as well as through the passage from any context to another one, we can consider them as *given*.

Finally, add that – unless we accept the genuine *circularity* approaches conceiving physical laws emerging "with" the physical phenomena expressing these laws – physical laws must precede *ontologically* the physical phenomena occurring all along the history of our universe. However, since it is possible to make physics without taking into account ontology, a simulation of the history of the physical universe remains adequate without taking into account the resources behind the simulation and, subsequently, the fact that these resources require "intelligent human design."

1.2 Models and modeling in theory of evolution

In this subsection, we will see that contrary to physical simulations, *honest* simulations of biological evolution *should not neglect their resources issued from human design*.

Physical laws recognizable as such and remaining identical over time impact biological evolution. But, *by definition*, biological evolution is not reducible to the sole physical laws intervening in it. The occurrence of more and more sophisticated organisms – whether the "motorization" of the process may be "cumulative selection" (see below) or something else – necessarily *goes together* with more and more complex configurations of physical laws CPL_i. Concerned by physical laws but, obviously, without belonging to the investigation field of physics as such, biological evolution enters into the domain science just is beginning to identify in terms of "*inter-theory relations*", a domain undermined by controversies about – among others – "[the] hierarchy of levels (levels of organization/levels of description), part/whole relations, the fact of emergence)(...), the relevance of scales (...)" (Castellani, 2012, p.6), while asking "whether the relation of the units on level L_{i+1} (coarser) to the units on level L_i (finer) [are] better described in terms of: reduction to, supervenience on, emergence from?" (Castellani, 2012, p.7). Under these conditions, all we can say is that within a design-free biological evolution there are – once again by definition – no *given* "meta-laws" governing the transitions from some configuration of physical laws CPL_i to a more complex one CPL_{i+1}.

Since there are no *given* "meta-laws" governing the transitions from some configuration of physical laws CPL_i to a more complex one CPL_{i+1}, this time we *necessarily have to ask* where the CPL_i, CPL_{i+1}, … … come from.

Of course, the synthetic theory of evolution *asserts* that there is an answer to this issue, an answer in terms of design-free cumulative selection.

Nevertheless, recall that especially in the context of biological evolution where experimentation *stricto sensu* is not possible, modeling is the only way to test theoretical approaches of biological evolution under *experimentation-like conditions*. (see subsection 0.1) The assertion that (i) biological evolution is exclusively driven by an entirely design-free cumulative selection, and that (ii) among all the factors acting on evolution, we find no one related to any form of previous design, this assertion belongs until further notice to the theoretical approaches of biological evolution, and, for this reason, remains to be tested. Concerning point (i), it may be acceptable to consider just a

design-free simulation of cumulative selection, without asking whether all the resources required by the simulation are in turn design-free. But concerning point (ii), the things are essentially different. To test under *experimentation-like conditions* the assertion that *no* factor *acting on* biological evolution as such is related to any previous design, we should *at least* be able to conceive a design-free simulation of cumulative selection whose required resources in turn occur in a design-free way. *So, in the very special context of biological evolution, the notions* "design-free modeling" *and* "design-free mode*ling*" *cannot be separated*.

By contrast, if we *decree* that in nature, *there are* "some" design-free factors replacing the design-related resources required by a simulation of evolution, then we merely forget the *raison d'être* of the simulation being a *test*. In other words, we confuse the *demonstrandum* with a departure hypothesis formulated *ad hoc*.

2. Single-step selection and cumulative selection by small steps

According to the current "synthetic theory" of biological evolution, the latter is "motorized" by design-free "cumulative selection." So we have to ask whether design-free modeling of cumulative selection is possible. Section 2. opens an inference showing that design-free *modeling* of cumulative selection, *de facto* not possible, could be envisaged only in virtual way, and that even *if* this virtual *modeling* were realizable, it would not lead to a *relevant model* of real biological evolution.

2.1 The meaning of "cumulative selection"

Biological evolution is characterized by the occurring of quasi-infinitely high improbabilities which cannot be issued from pure chance. It would be hopeless to expect that a monkey typing randomly on a keyboard would produce the small sentence "I am a monkey.", (Misra, 2015, p.1) whereas the occurrence by chance of just a cell is infinitely more improbable than such a random monkey performance.

So, according to synthetic theories of biological evolution, the latter results not from pure chance, but from "cumulative small-step selection."

Personally, I have never found a real *definition* of "cumulative selection", only more or less compact/clear *descriptions*. Indeed, to be possible, cumulative selection implies several non-self-evident presuppositions which may vary from case to case.

So, at least let us try to encompass the possibility of cumulative selection. First there must be a constraint C and a system Σ_C supposed to approach as well as possible the state $S^*(\Sigma_C)$ the constraint C tends to *impose* to Σ_C. On the other hand, occupying any possible state $S_i(\Sigma_C)$, the system Σ_C must be able to express for each $S_i(\Sigma_C)$ *random fluctuations* $\Delta^+S_i(\Sigma_C)$ and $\Delta^-S_i(\Sigma_C)$, where the $\Delta^+S_i(\Sigma_C)$ and $\Delta^-S_i(\Sigma_C)$ respectively approach Σ_C to $S^*(\Sigma_C)$ and moves Σ_C away from $S^*(\Sigma_C)$. Finally, for Σ_C to support *cumulative small-step selection*, there must be a selection device associated to Σ_C – let us note it $ASD(\Sigma_C)$ – which, recognizing both $\Delta^+S_i(\Sigma_C)$ and $\Delta^-S_i(\Sigma_C)$, allows only the $\Delta^+S_i(\Sigma_C)$ while forbidding the $\Delta^-S_i(\Sigma_C)$.

Under these conditions, Σ_C initially occupying *any* state $S_i(\Sigma_C)$ necessarily tends to $S^*(\Sigma_C)$.

Now, two closely related important remark remain to be formulated. (i) The *tendency* of Σ_C to *approach* $S^*(\Sigma_C)$ does not not necessarily mean that $S^*(\Sigma_C)$ is *reached*. (see subsection 3.123). (ii) $S^*(\Sigma_C)$ is not necessarily known. (see 3.12) So, *as such*, cumulative selection can be conceived without any previous design.

However, there are at least two things which, instead of being treated with an incredible flimsiness, must be seriously underlined. (i) For cumulative selection to be possible for Σ_C, C and Σ_C must go together. Far from being self-evident, the compatibility between C and Σ_C encounters higher and higher improbabilities as Σ_C becomes more and more complex. (ii) Since for cumulative selection to be possible for Σ_C, there must be a selection system $ASD(\Sigma_C)$ associated to Σ_C, going together with C and Σ_C, *without belonging* to Σ_C, we *at least potentially* have to ask *where* the necessarily improbable $ASD(\Sigma_C)$ *comes from*. Now, in fact, most often (see subsection 1.2), this question can

be neglected, but (see subsection 1.2) it is easy to prove that just within any attempt to explain biological evolution by cumulative selection, neglecting this question means neglecting *the* essential.

The following parts of the paper will be directly or indirectly centered on the foregoing points (i) and (ii).

2.2 An intuitive modeling of cumulative selection; Maxwell's Demon as an associated selection device ASD(Σ_C)

Although having been conceived for a different purpose – to show that the Second Law of Thermodynamics, far from being a law of nature *stricto sensu*, just denotes the human inability of generating work by entropy reduction (comp. Myrvold, 2011, pp. 2, 5 ff.) – the thought experiment well-known as "Maxwell's Demon" represents a good example of modeling of cumulative selection.

Here a very simplified version of the Demon is sufficient. Imagine a box divided into two parts A and B by by a partition comprising a microscopic open hole. The box contains a gas whose molecules initially are located in say the half A. But over time, the molecules tend to be equally distributed in the two halves A and B of the box. Now it would be quasi-infinitely improbable to see the system spontaneously return to its initial state. Indeed, the concentration of all molecules in the half A is just one among a quasi-infinity of possible configurations. It would be hopeless to expect the return of the system to its initial state *under single-step selection conditions*.

Now, let Maxwell's Demon operate. As a mathematical *limit*, the most probable state of the molecule system consists of the exactly equal number of molecules in both halves A and B, but in fact, the system describes very slight fluctuations around its most probable state. Sometimes a molecule coming from A passes through the hole and enters into B. Sometimes it is the same in the opposite sense. Now admit that a microscopic ultra-intelligent entity – "Maxwell's Demon" – after having installed a little gate at the hole, opens the gate when a molecule randomly passes from B to A, while closing the gate when a molecule randomly passes from A to B. Under these *cumulative selection* conditions the system actually tends to its quasi-infinitely improbable initial state, which would be unimaginable under these *single-step selection* conditions.

Concerning the original vocation of the Demon: to show that entities performing better than simple humans can violate the Second Law, a large majority of theoreticians thinks – for diverging reasons; you can find a exhaustive overview in Gijsbers, 2004 – that the Demon cannot do its job. By contrast, consuming energy and subsequently respecting the Second Law, the Demon represents an *adequate model* of a particular case of cumulative selection leading to higher and higher organization. Note that the development of living organisms requires factors we can qualify as "Maxwellian-Demon-like." (Kurzynski and Chelminiak, 2016, pp. 9f.)

However, simultaneously the Demon as a *model* of cumulative selection expresses the principal difficulties striking any attempt of design-free *modeling*. Obviously, Maxwell had conceived his thought experiment according to his "previous design", whereas the Demon works " consciously" according to a previously defined project, but for the moment, we leave this issue aside. (see subsection 3.1) Here we just have to recall and to underline that, for cumulative selection to be possible for a random system Σ_C, there must be a selection system ASD(Σ_c) associated to Σ_c, *going together* with the constraint *C and* Σ_c, *without belonging* to Σ_c. Now, it is clear that Maxwell's model requires an entity not only extraordinarily capable, but above all "*made for*" the task it is supposed to execute over a system as such limited to a molecule box and its molecules, knowing that the Demon does not belong to the system as such. Denying this point would resemble the not very adequate assertion that a given software *made for* a specific task also could do any task. Of course, synthetic theories of biological evolution notoriously claim that natural selection as a special case of cumulative selection "has" a design-free solution for this problem. Well, but if instead of *asserting* what allegedly *does* happen within evolution "motorized" by design-free cumulative selection, we first try *to model* all this assertion in a *globally* design-free way, we

manifestly have to expect great difficulties.

The coming pages are dedicated to a more detailed approach of the foregoing. Meanwhile, we have to point out that what for the moment is just a simple observation we nevertheless later will have to generalize. Operating as an associated cumulative selection device, the Demon certainly makes the molecule system tend to a final state whose actual occurrence under single-step selection conditions would be unimaginably improbable. Yes, but the actual occurrence under single-step selection conditions of the Demon itself would be even more improbable than the unimaginably improbable final state of the molecule system. So, within Maxwell's thought experiment, the cumulative selection process allowing the considered system to reach has a "cost": *the single-step improbability affecting the required associated selection device is unimaginably higher than the single-step improbability affecting the target of the thought experiment.*

2.21 The hypothesis of external improbability associated to cumulative selection

Let us try to generalize the foregoing in the following way:

Hypothesis (H2.21) For a given random system Σ_c to reach through a cumulative selection process $CSP(\Sigma_c)$ the target $S^*(\Sigma_c)$ whose occurrence by single-step selection would be affected by an improbability $Imp(S^*(\Sigma_c))$, there must be an associated selection device $ASD(\Sigma_c)$ whose occurrence by single-step selection is affected by an improbability $Imp(ASD(\Sigma_c))$, so that $Imp(ASD(\Sigma_c))$ is higher than $Imp(S^*(\Sigma_c))$.

2.22 About the status of the hypothesis (H2.21)

Certainly I have not invented the hypothesis (H2.21). Quite the contrary, common sense could suggest that the patent evidence of (H2.21) makes its qualification as a "hypothesis" rather pompous. And yet, (H2.21) *is* a hypothesis, and above all a hypothesis of a very special kind. (H2.21) *apparently* is obvious, but this appearance is deceptive. More precisely, the apparent evidence of (H2.21) is a special case of the *false evidence* of *irreversibility.* Of course, living at the macroscopic scale, we are *familiar* with all the irreversibility around us, but being familiar with something does not mean knowing the thing in question. Indeed, the philosophical controversy over whether irreversibility is *law-like* or just *fact-like* goes back to Boltzmann himself, even if the *formulation* in terms of *law-like/fact-like* irreversibility as such was introduced by Mehlberg in 1961. (Mehlberg, 1961, pp. 126, 128). Maxwell's Demon playing a relatively important role in this paper is a typical product of the *law-like* v/s *fact-like* irreversibility debate which, engaging great and the greatest physicists and/or philosophers, still continues today. As long as the debate is not decided, the principle of scientific cautious orders us to opt for *fact-like* irreversibility. So (H2.21) which, as a special case of irreversibility, is embedded in an area where nothing can be obvious. Subsequently (H2.21) has to be treated as a *hypothesis*. But on the other hand, as long as we consider irreversibility as a *fact* – and it would be very hard to do otherwise – (H2.21) also must be considered as a *fact*, and this *despite its status of a hypothesis.*

The strange nature of (H2.21) – sharing the strangeness of irreversibility – necessarily has good chances to complicate any modeling of biological evolution "motorized" by cumulative selection. We will necessarily come back to this point. (see subsection 4.3)

3. Current computer simulations related to biological evolution

In this section 3. we approach some simulations of cumulative selection: Richard Dawkins' famous weasel and biomorph programs as well as "evolutionary algorithms" developed by Dave Thomas and Suzanne Sadedin. As a first step, we will consider the computer programs and the computer resources required by these programs as "*given*", in order to examine to what extent the corresponding simulations – under such necessarily reducing conditions – (i) effectively model

biological evolution as it is supposed to manifest itself and (ii) remain design-free. But thereafter (see subsections 3.2n; section 4), we will be obliged to ask whether in the area of biological evolution, modeling presupposing "*given*" resources really can be adequate. It is at this level that the hypothesis (H2.21) and its consequences generate substantial complications.

3.1 Simulations from the perspective of *given* Maxwellian Demon-like devices

In subsection we 2.2 we saw that Maxwell's thought experiment represents an absolutely plausible model of a simple case of cumulative selection, remaining consistent as long as we do not (need to) ask where the Demon is coming from. *From this perspective*, the following simulations of cumulative selection represent significant analogies with Maxwell's Demon. Concerning the latter, as we saw in subsection 2.2, the thought experiment is not design-free, neither as a model, nor at the level of modeling. Maintaining provisionally the reducing approach ignoring the issue where (i) the required selection systems and (ii) the actually implemented modeling resources are come from, we now will examine whether the scenarios expressed by following simulations are *as such* really design-free. The answer is rather complex.

3.11 Dawkins' weasel-simulation

Referring to the famous Borelian typist monkeys supposed to reproduce randomly Shakespeare's work, Dawkins rightly says that it would already be hopeless to expect the purely random reproduction of Hamlet's short reply "Methinks it is like a weasel." (Dawkins 1996, pp. 46 ff.) By contrast, it is astonishingly easy to reach the target "Methinks it is like a weasel" by *cumulative selection*. Dawkins considers a computer program initially displaying on the screen a senseless combination of 28 characters or spaces, say WDLMNLT DTJBKWIRZREZLMQCO P. This combination is *repeatedly duplicated* by the program, but with very slight random errors Dawkins calls "mutations." However, the actually occurring sequence is subjected to a constraint: the computer compares each new item and its predecessor to determine which one resembles more – even *very slightly* – the target METHINKS IT IS LIKE A WEASEL, conserving only the relatively better solution and eliminating the other one. Launching his program, Dawkins obtains as a first "mutation" to be conserved WDLTMNLT   DTJBSWIRZREZLMQCO   P, then, 10 "generations" later, MDLDMNLS   ITJISWHRZREZ   MECS P, and after 20 "generations" MELDINLS IT ISWPRKE Z WECSEL. By 30 "generations", Dawkins already obtains METHINGS IT ISWLIKE B WECSEL, by 40 "generations" METHINKS IT IS LIKE I WEASEL, whereas the target METHINKS IT IS LIKE A WEASEL is fully reached in the 43th "generation." Starting from two different initial combinations,   the simulation reaches the same target respectively through 64 and 41 "generations." (Dawkins 1996, pp. 47 f.; for more technical details, see Khomenko, 2004, pp. 1f.)
As well as Maxwell's Demon, the weasel simulation considered as a part of a *model*, is *not* design-free. In *both* cases, the cumulative selection system could not reach the target if the latter was not *previously designed*. Dawkins himself qualifies his "monkey/Shakespeare model" as "misleading in important ways." (Dawkins 1996, p. 50). Indeed, the cumulative small-step selection characterizing the weasel-simulation operates according to something Dawkins calls a "*distant ideal* target" (*ibid*.; Dawkins's emphasizing), or, if you prefer, to something virtual *previously* projected into the future, whereas natural selection according to synthetic theories defended by Dawkins precisely "has no long-term goal." (*ibid*., comp. Khomenko, 2004, p.2)
Now, in fact, the foregoing, *in its context*, is *not* a real problem. The weasel-simulation does not pretend to model biological evolution , nor its "motorization" by "blind" natural selection. The weasel-simulation is conceived in order to demonstrate the extraordinary power of cumulative selection *as such*, or, if you prefer, in order to show that cumulative selection easily can do things which under single-step selection conditions would be unimaginable.

3.12 Dawkins' biomorph-simulations

Aware that his weasel-simulations are not design-free – even in the very restrictive sense he attributes to "design-freeness" – Dawkins, in order to show that design-free – "*blind*" – but meaningful increasing complexity is possible, also conceives a second computer simulation with "biomorphs", i.e. *initially* very simple computer images in fact reduced to some strokes. (Dawkins 1996, p. 55). These biomorphs have "genes" conferring them their initial configuration while transmitting the latter – but sometimes with slight random "mutations" – to the next "generation" and so on. In other words, the "genes" have two functions: the "development" of given individuals and the "evolution" of their "progeny." The randomness of the "mutations" makes "evolution" in turn aleatory. On the other hand, the survival of these "evolving" biomorphs is submitted to selection. This time, the selection modalities are a bit more complicated than in the weasel-simulation. The survival of a mutated biomorph depends on its its relative degree of resemblance to a given "object" (see below) humans can recognize as such through its essential qualities. (Dawkins 1996, p. 57) If a mutated biomorph is more performing with regard to this criterion, then it is selected whereas its predecessor is eliminated. The opposite case implies the conservation of the predecessor and the elimination of the mutated biomorph. We still have to specify the nature of the given "object" that biomorphs, to survive, are supposed to resemble as well as possible. Dawkins evokes as an initial constraint the "resemblance to a weeping willow", adding nevertheless that the selection is programmed to be *capricious*, passing from the weeping willow reference to a different one and so on, and this for the simple reason that natural selection operates through environmental pressure which changes over time. (Dawkins 1996, p. 57)

Once again, the simulation *as such* leads to impressive results. Starting from trees just schematized in the most simple way, and hoping to reach "weeping willows, cedars of Lebanon, Lombardy poplars, seaweeds, perhaps deer antlers" (Dawkins 1996, p. 57), Dawkins in fact obtains incredibly complex and meaningful images – spiders, bees, bats, men, men with hats and even with decorated hats – spread over numerous of pages of his Blind-Watchmaker book. (Dawkins 1996, pp. 57 ff.)

Nevertheless, independently of the fact that the biomorph-simulations, unlike weasel-simulations, operate without any "*distant ideal* target", *both* types of simulation encounter the same serious problem which will be analyzed in the following subsection 3.130.

3.13 Genetic algorithms

3.130 Structural complexity and functional complexity

Indeed, both approaches – weasel- and biomorph-simulations – *first* encounter the following difficulty: motivated by the attempt to show *in the context of biological evolution* that design-free increasing complexity is possible, neither the weasel- nor the biomorph-simulations imply the *specific kind* of increasing complexity concerned by *biological evolution*.

Strictly speaking, the weasel-simulations do not treat *any* kind of increasing complexity. They illustrate the possibility of reaching, by cumulative selection, quasi-infinitely improbable targets single-step selection *de facto* never would reach. But *as such*, the target METHINKS IT IS LIKE A WEASEL is neither more, nor less complex than the initial configuration WDLMNLT DTJBKWIRZREZLMQCO P, and we can say the same for any other equivalent target or initial configuration. The fact that unlike say "KLZCO BLIPWAQNBV NFCERTWPAWP", "METHINKS IT IS LIKE A WEASEL" has a sense is without any importance since it is a *social*/*cultural* fact having nothing to do with *biological* evolution. On the other hand, the challenge of weasel-simulations exclusively is to reach previously given quasi-infinitely improbable targets, knowing that the respective improbabilities to reach KLZCO BLIPWAQNBV NFCERTWPAWP and METHINKS IT IS LIKE A WEASEL are equal.

Concerning biomorph-simulations, there is certainly a kind of increasing complexity: even if each item occurring all along a biomorph-simulation is ultimately a configuration of simple strokes, men

wearing hats decorated by flowers are more complex than the just-suggested trees being the start items of the simulation. But obviously, biological evolution cannot be reduced to *this kind* of increasing complexity. Living matter is characterized by *functional complexity*. So, a simulation of biological evolution operating exclusively with the increasing *structural* complexity of pictures consisting of stroke configurations *ignores the essential*.

Now, are simulations of increasing *functional complexity* possible, and if so, to what extent?

This issue leads us to Dave Thomas' and Suzanne Sadedin's genetic algorithms.

3.131 Dave Thomas' genetic algorithm

3.131-a Motivation

Recall that according to Michael Behe, functional complexity – Behe calls it "irreducible complexity" – is incompatible with the synthetic theory of biological evolution, pointing out that for a system characterized by functional complexity, the failure of a sole function would stop the functioning of the entire system. So, *simplifying*, for Behe, the idea of a less performing precursor of a system characterized by functional complexity has no sense. (Behe, 1996, p. 36) Standard arguments against Behe's view generally evoke the essential difference between mechanical systems and biological ones expressing among others plasticity. (comp. Brigandt, 2012, pp. 3 ff.)

Anyway, in order to show that Behe's argument cannot hold, Dave Thomas tries to simulate a system (i) characterized by *functional complexity*, which (ii) is supposed to *evolve in a design-free way*.

3.131-b Description

The aim of the simulation is to determine a solution to the *Steiner problem*: "(…) given a two-dimensional set of points, find the most compact network of straight-line segments that connects the points." (Thomas, 2010, pp. 43 f.)

Simplifying a bit – for technical details, see (Thomas, 2010, pp. 43 f.) – the simulation operates on "organisms", here different potentially given networks characterized by their respective "DNA", i.e. alphanumeric combinations which "when read by the transcription routine, supply three types of information about the network represented by each organism: the number of Steiner points, the numerical locations of these points, and a true/false connection map that dictates which points are to be connected by segments." (Thomas, 2010, p. 44) The selection criterion striking these organisms is their degree of fitness with regard to the Steiner requirement. "The fitness function used tests for two things: Are the fixed points all connected? What is the total length of all "expressed" segments?" (*ibid*.)

3.131-c Discussion

Now let us examine (i) whether the Steiner simulation really generates an evolution of functional complexity and (ii) whether this evolution is simulated in a design-free way.

Concerning point (i), I think that simulation *does* generate the evolution of authentically functional complexity. Indeed, on the one hand, the degree of compactness characterizing a given configuration simultaneously takes into account all the characteristics of the configuration in question. On the other hand, for every path P_g leading to the *relatively* (see below) optimal solution, the precursor S_{gh-1} of each selected S_{gh} step by definition is less adequate than S_{gh}.

However, concerning point (ii), personally I am not so sure that the simulated functional complexity really evolves without human design. Recognizing that the "ID community" denies the validity of the simulation, qualifying the latter as target-oriented (Thomas, 2010, p. 44), Thomas first advances as a counterargument that the simulation reaches only occasionally the exact Steiner solution, while converging most of the time on imperfect solutions. (*ibid*.) This argument is at least disputable.

Consider an artist who, far from making "random art", tries to realize a work corresponding as well as possible to her/his previous intentions. Now, even if the realized work does not exactly correspond to the intention of the artist, would-it be relevant to evoke a "human design-free" realization?

On the other hand, Thomas points out "(...) that the fitness function need not have any descriptions of the actual Steiner solution for any given set of points. Fitness, here, is not based on any specific future function but only on present function." (*ibid*.) and that that "(...) the specific details of complex solutions are *not* explicitly embedded in the overall design goals." (*ibid*., Thomas' emphasizing) A detailed analysis of the foregoing would take us too far. However, I think that the *allegorical* argumentation Thomas advances with regard to this point turns *against him*. Indeed, Thomas' proposals "Stating the objective 'Build a vehicle that can carry men to the Moon and back' does not result in the spontaneous appearance of the complete plans for an Apollo spacecraft (with separate command, service, and lunar modules), along with a Saturn V launch vehicle." (*ibid*.) are right as such. And yet, proposals like "Build a vehicle that can carry men to the Moon and back" do express human design with a potentially tangible impact. Simply speaking, for to reach the moon, saying "Build a vehicle that can carry men to the Moon and back" obviously is not sufficient. But without saying "Build a vehicle that can carry men to the Moon and back", humans never would have reached the moon. And, in order to go a little further, note that there are significant analogies between the moon vehicle-story and Dawkins' weasel-simulation. Concerning the moon-story, there is a target: "Build a vehicle that can carry men to the Moon and back." In order to reach the target, humans conceive solutions. A *de facto* given cumulative selection retains what is to be retained, eliminating that what is to be eliminated. So, contrary to a hopeless junkyard tornado strategy where just the Boeing liner is replacing the moon vehicle (Hoyle, 1983, p. 19), the project reaches its target. The logical structure of the weasel-simulation is not very different. Now, since Dawkins himself recognizes that the weasel-simulation *does* respond to a "*distant ideal* target", any denial, with regard to the moon project, of a "*distant ideal* target" would not be relevant. So there is no reason to say that Thomas' Steiner-simulation does not respond to a "*distant ideal* target", even if – *as well as within the weasel-simulation* – the "*distant ideal* target" can be reached by an *infinity of unpredictable paths*.

3.132 Some words about Suzanne Sadedin's simulation

Sadedin proposes another simulation showing that – *contra* Behe (Sadedin, 2006, p.1) – an evolution of functional complexity is possible. (Sadedin, 2006, pp.2ff.) Because of space constraints, I cannot advance a detailed analysis. Here, I just would summarize the following points: (i) Sadedin's approach actually simulates evolving functional complexity; (ii) contrary to Thomas' simulation, Sadedin's approach indisputably simulates a design-free evolution with unpredictable results; (iii) nevertheless, contrary to Thomas' simulation whose "complexities" are "really complex" – behind its apparent simplicity, the Steiner problem represents a highly challenging issue – Sadedin's approach just engages really simple structures: her simulation goes from relatively less to relatively more complex configurations, but *absolutely speaking*, there never is high complexity.

3.14 Maxwell's Demon-like device stocktaking

A global overview on all simulations related to biological evolution we analyzed can give the following impression. As long as the simulation in questions focuses on the power of cumulative selection while neglecting *simultaneously* the issues of *design-freeness* and *complexity*, very impressive results can be obtained. But for *design-free* evolution of complexity to be simulated, our task seems easier as long as we exclude really functional complexity. Indeed, concerning simulations of design-freely evolving functional complexity, limiting constrains appear. Either, we consider "'really complex' functional complexity": then the simulated evolution is not really design-

free. Or, we want to simulate really design-free evolving functional complexity: then the implemented evolving functional complexity must be restricted to a non-significant minimum. Certainly, the foregoing does not repose on a formal proof. *But anyway, the essential problem remains before us*.

3.2 Going *beyond* the Demon-like device horizon?

3.21 Maxwell's Demon-like functions issued from cumulative selection?

Retake Maxwell's Demon. First, recall the motivation of the thought experiment. In order to qualify the Second "Law" of Thermodynamics as a *fact-like* phenomenon not to be considered as law of nature, Maxwell tries to show that beings or entities more capable than humans could be able to violate the Second "Law." In the context of this issue and regardless of the relevance or non-relevance we attribute to the thought experiment, *there is no* constraining *reason to ask where the Demon comes from*. On the other hand, Maxwell's Demon, even if probably it does not do the job for which its author had conceived it, seems to model biological functions within living beings allowing the latter to increase their internal organization in a manner single-step selection never would allow (Kurzynski and Chelminiak, 2016, pp. 9f., see subsection 2.2). Anyway, studying a living being equipped with Maxwellian Demon-like functions, there is in turn *no* constraining *reason to ask where these Demon-like functions are comes from*, in the same way as we are not *obliged* to be interested in the evolutionary origins of the other biological functions of a living being we are studying *as such*.

But now suppose that we consider biological evolution as – among others – a process leading to living beings equipped with more and more sophisticated (configurations of) Demon-like functions. In this case, *we obviously have to ask* in terms of evolution theory *where these Demon-like functions come from*. Certainly, in terms of *standard* evolution theory, this question has its *standard* answer: the more and more sophisticated Demon-like functions characterizing living beings appearing all along biological evolution "motorized" by natural selection originate in turn from biological evolution "motorized" by natural selection as a special case of cumulative selection (comp. van Hateren, 2015, pp. 4 ff.).

Well, but regardless of our choice to accept this explication or not, *would we be able to model it in a design-free way*?

This is not so sure. As long as we just use the Demon in order to model cumulative selection, say to bring a gas into a quasi-infinitely improbable configuration, the fact that the Demon is a given, and more precisely a *human-designed* device executing a task in turn *previously designed* does *not represent a problem*. But now try to pass from this human-designed model to a design-free one. In this case, the Demon in turn must occur in a design-free way. But how?

3.22 Return to modeling as a minimal experimentation-like approach

Let us formulate otherwise the problem to be discussed. Current computer simulations of biological evolution based on cumulative selection need a *fitness function* which selects or eliminates with regard to a given criterion aleatory occurrences generated by the simulation. Obviously, this criterion, as well as its corresponding fitness function are conceived by human design.

Now, the standard view claims that real biological evolution, contrary to its simulations, does not need specifically programmed fitness functions responding to in turn specifically programmed criteria. Aleatory given constraints – say the pressure of environment comprising factors like predators, preys rather able to escape, climatic conditions and so on – would operate the selection among aleatory mutations making the concerned organisms less or more fit with regard to theses constraints. Briefly speaking, "nature" would have its own resources analogous to *resources* required by programmed simulations.

Well, but now recall that in our context, the role of a *model* is not limited to illustrate the above

mentioned standard conception dogmatically considered as an obvious truth. Quite the contrary, in our context, a model is supposed to test, in experimentation-like conditions, whether the standard conception is at least conceivable (see subsection 1.2) Since the standard conception *postulates* a "nature" having design-free resources allowing a design-free evolution, it is indispensable to test the *possibility* of simulating a design-free evolution so that the *resources* required by this simulation are in turn design-free. Unless we decree the *demonstrandum* to be a previously given obvious truth, we have to examine whether beyond – more or less design-free – *models* of cumulative selection, design-free model*ing* of biological evolution is possible.

4. Trying design-free model*ing* of biological evolution

4.1 Identifying the challenge

Until further notice, simulations of biological evolution require computer programs and computers able to execute them. Now, perhaps "nature" is a "great computer" which, having occurred in a design-free way, is able to write and to execute – always in design-free way – biological evolution in the form of a "computer program" whose processes are "motorized" like a computer. The latter point seems rather hypothetical and even a bit contradictory, knowing however that we can not categorically assert its non-possibility.

Anyway, recall that, before asserting the possibility of a design-free biological evolution, we at least have to be able to model biological evolution while respecting a very restrictive constraint: neither the *model* as such, nor the resources required by the corresponding *modeling* (see subsection 1.) can comprise something resembling human or other previous design. Obviously, the program expressing biological evolution and the computer supporting the program are issued from human design. From the perspective of present day knowledge – same remark as for "until further notice" – there is no tangible solution. All we can do is to envisage a purely *virtual* approach.

In subsections 2.2 and 2.21, we had recalled that any random system, to reach under cumulative selection conditions a target $S^*(\Sigma_c)$ whose occurrence by single-step selection would be affected by an improbability $Imp(S^*(\Sigma_c))$, requires an associated selection device $ASD(\Sigma_c)$, knowing that the improbability $Imp(ASD(\Sigma_c))$ affecting the occurrence by single-step selection of $ASD(\Sigma_c)$ is strictly higher than $Imp(S^*(\Sigma_c))$. Intuitively speaking, a *given* Maxwellian Demon, independently of any issue of energy degradation, allows a gas in equilibrium to reach a highly improbable order state it would not reach under conditions of single-step selection. But obviously, the occurrence, under single-step selection conditions, of the Demon itself would be *unimaginably more improbable* than the return of a gas in equilibrium to its ordered initial state. So, if for one reason or another we want a design-free occurrence of the Demon, then the unique – virtual – solution, a supplementary cumulative selection process, would require the help of a supplementary associated selection device, say a "super-Demon" SD, assuming that the single-step-improbability $Imp(SD)$ is in turn *unimaginably higher* than the improbability $Imp(D)$ affecting the single-step occurrence of the Maxwellian Demon in question.

Subsequently, if we wish to see our Maxwellian gas returning to an unimaginably improbable initial state, and this thanks to a globally design-free process entirely operated by cumulative selection, we have to assume an *infinite* chain of "more and more superior" Demons SD_i so that for any i, $Imp(SD_{i+1}) > Imp(SD_i)$.

4.2 An extension of the hypothesis H2.21

In a more general way, we have to reformulate the hypothesis H2.21 for entirely design-free cumulative selection processes where *no* associated selection device ASD can be considered as *given*, or, if you prefer, where any implemented ASD must be generated exclusively by cumulative selection.

Hypothesis (H4.2) For a given random system Σ_c to reach through a globally design-free cumulative selection process $CSP(\Sigma_c)$ the target $S^*(\Sigma_c)$ whose occurrence by single-step selection would be affected by an improbability $Imp(S^*(\Sigma_c))$, $CSP(\Sigma_c)$ must be supported by a chain of associated selection devices ASD_i, $i = 1, 2, \ldots \ldots \infty$, so that $Imp(ASD_1) > Imp(S^*(\Sigma_c))$, whereas for any i, $Imp(ASD_{i+1}) > Imp(ASD_i)$.

4.3 The status of the hypothesis H4.2

Like H2.21 (see subsection 2.21), its globally design-free extension H4.2 *is trivial* while not being specific to the modeling of biological evolution.

Nevertheless, concerning our issue whether evolution as it is seen by the synthetic theory can be modeled in a design-free way, an explicit extension of H2.21 to H4.2 is necessary.

H2.21 is a particular expression of *generalized irreversibility*: if a system Σ_i which apparently violates irreversibility, then Σ_i *must* be included in a wider system Σ_{i+1} so that irreversibility is globally reestablished at the level of Σ_{i+1}.

H4.2 is a particular expression of the following – obviously virtual – principle. *If* within a series of systems $\ldots \Sigma_i, \Sigma_{i+1}, \ldots, \Sigma_i \subset \Sigma_{i+1}$, *any* system Σ_i belonging to this series apparently violates irreversibility, *then* this series must be an *infinite* one.

So H2.21 and H4.2 have not the same epistemic status. Whereas H2.21 until further notice is confirmed by observable – natural as well as artificial – phenomena, H4.2 implementing an *infinite* series of systems Σ_i is more than problematic. *And yet*, H4.2 *directly concerns the possibility of modeling evolution in a globally design-free way.*

Certainly, there is a potential objection: H4.2 is just a hypothesis; so the here above-mentioned problem is not an absolute one. Yes, but at this level, we can identically retake an important point already advanced with regard to H2.21. As well as the latter, H4.2 is and remains a hypothesis because of the *fact*-like and not law-like status of irreversibility (see subsection 2.22). Nevertheless, as long as we accept irreversibility as a *fact*, we also must take seriously H4.2 as well as H2.21.

Concerning cumulative selection, H2.21 implies the following consequence: far from circumventing irreversibility, cumulative selection *confirms* its generalized diktat, whereas H4.2 emanates from the insurmountable difficulties encountered by any attempt of circumventing irreversibility "despite all."

4.4 Back to a globally design-free modeling of evolution

H4.2 implies that *any* cumulative selection process CSP functioning thanks to an associated selection device ASD, to be *globally* design-free, requires an infinite chain $\ldots ASD_i, \ldots$, $i = 1, 2, \ldots \ldots \infty$, allowing the design-free occurrence of ASD which within a globally design-free CSP cannot be considered as "given." Since reasonably the occurrence of each ASD_i takes a time-period different from zero, we may think at the first glance that our model would correspond to a biological evolution taking an infinite time-period, contradicting the finite age of our universe.

But in fact there is a much more serious problem.

Evolution is characterized by the occurrence of more and more sophisticated organisms. So, modeling the passages from given stages of evolution to the following ones necessitates more and more sophisticated devices ASD, and not just an *unique* ASD as is the case for Dawkins', Thomas' or Sadedin's simulations.

Now choose any passage from the stage Σ_i of evolution to the stage Σ_{i+1}. Call "ASD_u" the associated selection device we have to integrate into our model of evolution in order to run by cumulative selection the transition $\Sigma_i \rightarrow \Sigma_{i+1}$. As we saw above, the occurrence by cumulative selection of requires a series of associated selection devices $ASD_{u1}, ASD_{u2}, \ldots ASD_{ur}, \ldots$, where $r \rightarrow \infty$. Obviously, it is the same for any *other* transition $\Sigma_j \rightarrow \Sigma_{j+1}$ and its required ASD_v.

Subsequently, a model "explaining" biological evolution *exclusively* by design-free cumulative selection would correspond to a biological evolution where *each* passage from a given stage to the

following one takes an infinite time-period.

4.5 A dichotomy

Now, the time period globally taken by the real biological evolution is *finite*. So, any *even virtual* attempt to model biological evolution exclusively on the basis of cumulative selection encounters the following dichotomy. Either the sole cumulative selection is not sufficient to explain biological evolution. Or biological evolution is entirely explained by cumulative selection which nevertheless comprises factors we do not know until further notice. In both cases, the present day state of knowledge excludes an entirely design-free *and* adequate modeling of biological evolution in terms of cumulative selection.

5. Conclusion

Of course, the foregoing does not prove scientifically that there must be previous design within biological evolution. But *until further notice*, the assertion that biological evolution "*is* design-free" belongs to speculation, and not more than speculation.

Now, independently of the personal position with regard to the faith or non-faith in God behind His Creation everyone among us is free to defend, the sole *scientific honesty* suggests us to wonder which option, scientifically speaking, is more honest.

(i) To assume that the faith in God, *by definition*, is a belief?

(ii) Or to claim the possibility to "refute scientifically" ID while referring to "arguments" which, being not more than beliefs, nonetheless are represented as "science"?

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