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TURING MACHINES AND EVOLUTION. A CRITIQUE OF GREGORY CHAITIN'S METABIOLOGY

Abstract. The aim of the paper is twofold. First, it presents the fundamental ideas and results of the “metabiology” created by Gregory Chaitin. Second, it shows why metabiology ultimately fails as a candidate for being a proper mathematical model for the theory of evolution by natural selection. Because of genocentric reductionism and biological oversimplifications, metabiology should be perceived rather as an expression of the philosophical worldview of its author.

Keywords: Gregory Chaitin, metabiology, genocentrism.

In 2007 the World Scientific published a volume titled *Randomness & Complexity: from Leibniz to Chaitin* including works offered to Gregory Chaitin on the occasion of his sixtieth birthday. An essay by Chaitin ending the volume comprises a list of seven problems which, according to the author, are worth dealing with in the future. First two problems on the list go as follows:

To develop a model of mathematics that is biological, that is, that evolves and develops, that's dynamic, not static.

and:

To understand creativity in mathematics – where do new ideas come from? – and also in biology – how do new, much more complicated organisms develop? Perhaps a life-as-evolving-software model has some merit? (Chaitin 2007a, 440)

The quoted excerpts present the seeds of ideas underlying the project of metabiology developed by Gregory Chaitin in a number of articles from

the years 2007–2012 and summed up by the volume titled *Proving Darwin: Making Biology Mathematical* published in 2012.

On the one hand metabiology is an attempt to create a mathematically advanced form of the theory of evolution by natural selection. On the other hand, it is a pioneering attempt to extend the boundaries of applicability of the concept of life to areas where nobody has used it before. It is also an attempt to indicate hidden similarities between the infinite richness of the world of pure mathematics and the astonishing variety of forms of the living world. Finally, as a whole it is an expression of the unwavering faith of its author, one of the most outstanding modern mathematicians, in the explanatory power of modern mathematics.

This article aims to introduce the main ideas of metabiology (omitting technical details) and then, to present their critical discussion. This goal will be realized in three successive sections. In the first of them I determine what metabiology is, what were the motives behind its creation, and the targets set by its creator. I also present the conceptual apparatus and mathematical core of metabiology. In the second chapter I present the assumptions and results which have been considered debatable by reviewers and critics (from the point of view of computer science and biology). The last chapter contains a discussion of what I consider the most limiting feature of metabiology: its focusing exclusively on genetically understood biological information.

I discuss Chaitin's ideas expressed in scattered texts as well as in those he included in the volume *Proving Darwin*. This book may be considered as the author's attempt to both summarize and popularize metabiology. That's why I refer extensively to the texts contained in it.

1. Presenting metabiology

1.1. Starting point

For many years I have thought that it is a mathematical scandal that we do not have a proof that Darwinian evolution works. (Chaitin 2012, 53) With those words Gregory Chaitin began the lecture which he delivered in the Santa Fe Institute, on 10 January 2011. Given the fact that their author is a mathematician, such an assessment of the situation should not surprise us. However, one should ask: what exactly does Chaitin mean when he talks about “a proof that Darwinian evolution works”? Let us consider another statement by Chaitin: *If Darwin's theory is as fundamental as biologists think, then there ought to be a general, abstract mathematical theory of*

evolution that captures the essence of Darwin's theory and develops it mathematically. (Chaitin 2012, 9) It appears that Chaitin means the absence of a mathematically advanced theory formalizing the central concepts of the biological theory of evolution by means of natural selection. The project of metabiology is an attempt to fill this gap in modern science. Such motivation brings Chaitin's proposal to previously made attempts to formalize the theory of evolution. Among them, population genetics was pioneering, followed by various successive attempts (referring, amongst others, to the theory of stochastic processes and game theory). Unfortunately, in spite of undeniable advantages and usefulness, none of them is the expected mathematical theory of evolution *par excellence*; all of them should be regarded as partial attempts. We are forced to admit that for now, the consistent mathematic language with which the processes of evolution could be described has not been worked out yet. (Kozłowski 2011)

Let us come back to the last quotation. The implication contained in it is taken by Chaitin as true in an obvious way, without having to justify it. Such a position is not an isolated one. The question of the ability to mathematize the theory of Darwinian evolution is considered important also by biologists. It is also assumed that knowledge which cannot be duly mathematized does not deserve to be called true. In other words: the ultimate touchstone of the significance and truthfulness of a scientific statement is its susceptibility to being properly mathematized. In spite of many attempts to make the theory of Darwinian evolution a mathematically advanced theory, it still cannot be ruled out that it cannot be consistently mathematized. (Kozłowski 2011)

This very prospect seems scandalous and deplorable to Gregory Chaitin. To eliminate it he undertook construction of a mathematical model he called metabiology. As he wanted to build such a model, he found it expedient to use the tools of discrete mathematics practiced after the results of Gödel and Turing: mathematics that is not founded in an ultimate axiomatic system, containing an infinite hierarchy of truths, each opening the prospect leading to another one. He considers such mathematics the most suitable for making an attempt to construct the expected formal theory of evolution by means of natural selection.

1.2. What is metabiology?

[It's] *a field parallel to biology and dealing with the random evolution of artificial software (computer programs) instead of natural software (DNA).* (Chaitin 2012, xvi) In many texts published between 2009 and 2012 Chaitin gives similar definitions of his metabiology: *instead of studying randomly*

evolving natural software, DNA, we will develop a parallel theory, a theory of randomly evolving artificial software, randomly evolving computer programs. That's what metabiology is about. (Chaitin 2012, 12) We need to keep in mind, however, that his goal is not working computer simulations. The prospect of rooting metabiology *in silico*, although conceivable, is postponed in time by its creator. The primary objective of Chaitin is not to run a simulation but to build a theory: *we want proofs, not computer simulations!* (Chaitin 2010, 10) This is what distinguishes metabiology from the research on Artificial Life and brings it closer to pure mathematics.

1.3. What is the aim of metabiology?

The answer is: to create a general mathematical model of the processes of evolution, i.e. to construct the simplest possible formal system able to express key concepts and mechanisms of the Darwinian evolution. (Chaitin 2010) Metabiology is meant to be such a system. It appears, however, that the aim so formulated has a more profound meaning. In fact metabiology appears to be for Chaitin his *current best effort to find the Platonic ideal of evolution*. (Chaitin 2012, 66) Creating a mathematical model of Darwinian evolution is not treated here exclusively as constructing a useful tool to fill the gap in the current state of knowledge. It is rather understood as discovering objectively existing, abstract (“Platonic”) mathematical structures. Thus, the entire project of metabiology turns out to achieve philosophical goals. Such recognition is supported by reference to another philosophical tradition made by Chaitin: *metabiology is a kind of Pythagorean biology*. (Chaitin 2012, 12) This gives us a clue to revealing the ultimate goal of Chaitin’s project: a formal proof for the existence of abstract, mathematical forms of life.

The aim of metabiology is twofold then. On the one hand, it is about creating the simplest formal system in which one may implement processes of Darwinian evolution. On the other hand, its aim is *to show life’s hidden mathematical core*. (Chaitin 2012, xv)

1.4. Formal model of Darwinian evolution

The procedure adopted by Chaitin while constructing metabiology is simple. First, key concepts are identified in the dictionary of evolutionary biology. These are: *organism, DNA, mutation, fitness, evolution* (note the absence of such basic terms as *heredity, reproduction, variability, population, genotype, phenotype*). Next, they are expressed using the conceptual apparatus of theoretical computer science. Finally he gets the following list:

Organism = natural (not man-made) software
DNA = natural programming language
Mutation = a program modifying a given organism
Fitness = integer calculated by an organism
Evolution = random walk in space of all possible programs (toward increasing fitness).

Chaitin is not consistent in his understanding of the concept of DNA. In many places he writes about DNA as “natural software”, whereas in others he refers to it as “natural programming language” and even a “universal programming language” (he writes about *entities governed by software (cells)* and treats DNA as a *language for this software*). (Chaitin 2012, 17) He also makes no clear distinction between genotype and phenotype: *My organisms have no metabolism, no bodies, only DNA; no hardware, only software.* (Chaitin 2012, 19) I write more on this in chapter three.

Based on this, Chaitin builds a simplified mathematical model of Darwinian evolution. A hypothetical organism is modelled by a Turing machine (the computer program P of n-bits length). The fitness level of this organism is interpreted as the natural number F (*fitness*) calculated by it. Next this program is subjected to a random mutation, i.e. it becomes input data for the mutation program (M) which returns a descendant program (P') of the same length as the parent program but with higher fitness F. Thus a single step on the evolutionary path in this model is simple: in each generation the ancestor (P) is mutated into the descendant (P') which replaces the ancestor if it:

- a) stops,
- b) prints the natural number (F),
- c) F is greater than the number printed by the ancestor.

If F does not meet condition c), another mutation is applied, to obtain a descendant having F higher than the ancestor has.¹ It appears, however, that this simple procedure generates some insurmountable problems.

To model competition between generations of organisms-programs Chaitin uses the Busy Beaver Function (BB Function). The BB(n) function is defined as the largest natural number returned by n-state, binary (stopping) Turing machine (M), which starts from a clean tape. Each such machine M, for which BB(n) function takes the greatest possible value is called Busy Beaver.²

Let us consider the reasons why Chaitin decides to use the BB Function to model competition between consecutive generations of his organisms. This function turns out to play a double role in metabiology. On the one hand, using it is justified by the need to put a goal in front of organisms,

to give them something difficult to do. (Chaitin 2012, 42) Thus for Chaitin the BB Function serves as a kind of an “engine”, necessary to “start” and then to “drive” the evolutionary process of abstract organisms.³ On the other hand, the BB Function is regarded as the equivalent of the biosphere’s ability to generate new solutions in response to evolutionary pressure (which is the core of Darwinian evolution). The author of *Proving Darwin* calls this feature “creativity” and regards it as inscribed in the very essence of life. He compares the natural creativity of the biosphere to a different type of creativity, namely that inscribed in the essence of mathematics. And the creative potential inherent to mathematics is considered to be well rendered by the BB Function (the fact of its non-computability, to be precise). For the same reason Chaitin regards this function as a good approximation to the phenomenon of creativity of the biosphere. The details of Chaitin’s reasoning are presented in the following steps:

Premises:

- 1) Natural evolution is constant creation
- 2) Continuously achieving higher levels of fitness = natural creativity
- 3) Computing higher values of BB Function is constant creation
- 4) Continuously achieving higher levels on the way toward the Busy Beaver level = mathematical creativity

Conclusion:

- 5) Natural creativity = mathematical creativity.

Chaitin clearly sees an analogy between the potentially immeasurable richness of living forms and the infinite content of pure mathematics. He doesn’t try, however, to explain why he considers this analogy clear or why the reader of his texts should agree to it. He simply recognizes the evolving biosphere as the physical equivalent of mathematical creativity and *vice versa*.

We already know what Chaitin meant by biological creativity and what he equates it to. Another question posed by him is the pace of evolutionary changes. The mathematical tools chosen to build metabiology are hardly suitable for a description of qualitative changes. Consequently, the creativity of the biosphere should be presented in a way allowing for quantitative description. That’s why Chaitin makes a simple equation: *Biological creativity = evolution rate*. (Chaitin 2012, 47) Thus it appears that Chaitin means not so much the creative potential of the Darwinian evolution but rather the pace of emergence of novelties generated by it. The aim is to answer the question: *how fast does fitness increase?* (i.e. how fast does parameter F grow). And to measure this exactly Chaitin decides to use the BB Function. Let us now look at the results obtained by Chaitin in this field.

As for the mutations, Chaitin regards them as the most important element of the mechanism for generating evolutionary novelties. He also tries to describe the relation between the way mutations are applied to an organism and the time needed to achieve the Busy Beaver level. As a result he identifies three different rules for choosing a particular mutation from the pool of all possible mutations available at each step of the evolutionary process. These are:

- a) Purely random choice,
- b) Choice according to the probability distribution (the probability of choosing the mutational program is proportional to its length in bits),
- c) Optimal mutation only (we always choose a mutation which will produce a descendant returning the highest possible value of the parameter F).

The relations between these rules and the rate of evolution are presented in table below:

Rule for choosing a mutation for organism P of length n	Time (T) needed for P to achieve the Busy Beaver level
a) Purely random choice	$T = 2^n$
b) According to the probability distribution	$n^2 \leq T \leq n^3$
c) Optimal mutation only	$T = n$

Answering the question which one of the above scenarios is the best approximation to the actual process of biological evolution, Chaitin points to the second one. Scenarios a) and c) are rejected, but for different reasons. The first one does not convey evolutionary processes well enough, since creating a descendant with a higher fitness would last too long and would not allow the starting of real evolutionary processes. The last scenario requires an assumption that there is a mechanism acting purposely and guided by the previously acquired knowledge about mutations optimal for each step of the evolutionary process. Chaitin picks up scenario b), names it *random cumulative evolution* and states that it is the best possible implementation of Darwinian evolutionary mechanisms within the model he created. He regards the formal proof of the relation presented in this scenario as the single most important achievement of his metabiology. He also claims it is the key argument indicating that Darwinian evolution is able to build objects with continuously higher and higher degrees of fitness. What is more, he thinks the very fact of existence of such proof is sufficient reason for regarding his mathematical model as literally alive: *it is why we claim that*

our model evolves and is therefore alive. (Chaitin 2012, 49) If it behaves analogously to the processes of biological evolution, that is a good reason for attributing the feature of being alive to it. Chaitin sums up his investigations with a triumphant cry: *I have found an evolving life-form in the Pythagorean world of pure mathematics!* (Chaitin 2012, 19)

This is the effect of the specific approach in which the ability to evolve by means of natural selection is regarded as the sufficient condition for “being a living object”. Any given system equipped with mechanisms of such evolution may be regarded as a living object then.⁴ One must remember, however, that in Chaitin’s model we do not deal with any physical system, but with a purely mathematical construct, a formal model of evolution by means of natural selection. Therefore one can hardly speak about any actual change of a system over time in this case. Mathematical objects, as timeless abstracts, do not change or evolve in any biologically acceptable sense of the term. Only physical systems subject to the laws of thermodynamics can evolve. Computer simulation of artificial ecologies studied within the Artificial Life Studies can be certainly considered physically grounded. Chaitin, however, claims that these are of no interest to metabiology, which is a purely mathematical theory (and in a shape that makes impossible any practical application).

2. Problematic aspects of metabiology

The four problems presented below may be divided into two groups. The first ones (problems 1 and 2) are important mainly from the point of view of a mathematician or computer scientist. It’s because Chaitin’s model makes use of the non-standard concept of Oracle and omits the physical constraints essential for possible future computer simulations. The other group (problems 3 and 4) will be important rather for a biologist, as it shows metabiology as a model inconsistent with evolutionary biology and simplified in a way that makes its biological adequacy debatable.

2.1. Use of Oracle

Let us remind briefly: program P simulates a biological organism. The value of fitness of this organism-program $F(P)$ is expressed with the natural number N returned by P at the moment of finishing its work: $F(P) = N_P$. Next, P is subjected to a mutation M and as a result a descendant P' is obtained: $P' = P(M)$. If $N_P < N_{P'}$, P is replaced with P' and the whole procedure is repeated again (this time with P' treated as a starting point).

The problem with the above procedure is that it is **uncomputable**, since its use requires solving the halting problem first. To cope with this problem, Chaitin decides it is necessary to resort to using Oracle twice:

- 1) when we mutate ancestor P using the mutation program M, to obtain descendant P'
- 2) when we check if program P' halts or not.

In point one we must know if the mutation program M ever stops producing descendant P' as a result (mutation that never stops is unwanted for obvious reasons). In point two we must know if the descendant is a program printing a number F higher than the number printed by its ancestor (a descendant with undetermined fitness value would be unwanted as well).

Chaitin is aware the procedure he constructed is uncomputable. Nonetheless, he puts this fact aside not considering it problematic or even uncomfortable. At first glance this may seem nonchalant on the part of the researcher. (Shallit 2013) It ceases to be like that if we keep in mind that Chaitin is operating in the domain of pure mathematics. He does not try to create any model design for implementation in any of the existing programming languages or for execution on real computers. Chaitin knows that his model is a simplification so far reaching that only common terminology and nothing more links it to the world studied by biologists. Therefore he regards it only as a mathematical "landmark", as well as an impetus for further studies. (Chaitin 2012)

2.2. Unlimited resources

Metabiology is problematic also for other reasons. Among them the most important is equipping the evolving organisms-programs (although it would be more appropriate to use the singular, as Chaitin never considers any populations of programs) with infinite computing resources and infinite time. This objection is clearly formulated in the critical paper by Ewert, Dembski and Marks: *Chaitin's model uses [...] limitless resources, things that do not exist in reality, or are unknowable, or are unbounded. [...] With unbounded resources and unbounded time, one can do most anything. One can also quickly exceed the computational resources of the known universe.* (2013, 4) Chaitin is fully aware of this fault of his model and treats this state of affairs as temporary, trying to point out the possible future paths for metabiology: *More realistic models will limit the run time of programs and thus avoid the need for oracles. I expect there to be a trade-off between biological realism and what can be proved: The more realistic the model, the more we will have to rely on computer simulations rather than proofs.* (Chaitin 2012, 89) We shouldn't, however, expect metabiology

to ever become as realistic as theoretical physics or chemistry. And why not? Because *biology is just too messy, too far removed from mathematics*. (Chaitin 2012, 68)

The problems I presented in the last two sub-chapters seem quite serious. Still, they make only the first half of a bigger whole. The other half consists of serious problems of a biological nature.

2.3. Directed evolution

Notice that in Chaitin's model there are no mutations decreasing fitness (**F**), thus negatively affecting the survival of the organism. Here mutations return a descendant with a higher fitness than the ancestor or they do not return it at all. (Kaznatcheev 2012b) Therefore, an evolving program-organism (**P**) is bound to achieve the Busy Beaver level every time, although the time needed for this may be different. In the space of all descendants of a given **P** there are no local adaptive peaks on which evolution could get stuck. This means that there is always a mutation which leads towards a higher value of **F** and up to the Busy Beaver level. In other words: the fitness landscape in Chaitin's model is **extremely smooth** – only a journey from the foot (the first generation) to the very top (Busy Beaver level) is possible. (Alicea 2013, Luskin 2014) Again, as with previously described problems, Chaitin is aware of the fact that the fitness landscape he proposes is unusual (and that it doesn't have much in common with the fitness landscape of actual biological organisms): *The fitness landscape has to be very special for Darwinian evolution to work*. (Chaitin 2012, 68)

As a result the conclusion can be drawn that mutations in the model in question are not random but directed. In other words: Chaitin's model of evolution is **teleological**, which makes it inconsistent with modern evolutionary biology (Kaznatcheev 2012a). That's why metabiology aroused some interest amongst modern creationists. Ewert, Dembski and Marks (2013) argue that Chaitin's model is counterproductive in effect. In spite of trying to prove that the blind mechanism of natural selection is the sole source of the creative power of the biosphere, it rather shows that for this mechanism to be able to work, prior conditions must be satisfied – and these precede any work by natural selection. What is more, they require a source of information external to the whole mechanism (Oracle) and a very special fitness landscape.

2.4. Biological inadequacy

Another striking feature of metabiology is a discrepancy between Chaitin's assumptions and the findings of modern evolutionary biology.

From a biological point of view, Chaitin's model is extremely simplified and unrealistic. Evolution by means of natural selection requires the existence of a population, not a single organism (and that's what we observe in Chaitin's model). Only within populations do we deal with individual variability, competition over limited resources, and environmental adaptation. All these elements are absent from metabiology, a fact emphasized by many critics of Chaitin's proposal. (Kaznatcheev 2012a, Luskin 2014, Shallit 2013)

Also the mechanism of applying mutations is unrealistic in Chaitin's model. It does not distinguish between a mutation itself and its selection by environmental factors. The very act of mutating and its subsequent effect on the survival of the organism have been merged together into one step of the evolutionary process. (Kaznatcheev 2012a) This should not surprise us, since in the considered model there are no phenotypes, no ecologies and no environmental pressure. Because of that, Chaitin's algorithmic mutations cannot have much in common with actual mutation mechanisms known to biologists.

Chaitin's formal approach resulted in a simplified model, which is not inspiring either for computer scientists (because it resorts to Oracle for help, and ignores the physical constraints of hardware as well as the results of 30 years of research in the field of Artificial Life) or for biologists (due to the mentioned simplifications and omission of some fundamental problems). (Shallit 2013, Kaznatcheev 2012a) The present analysis has indicated only the points of incompatibility of metabiology with fundamental findings of the modern theory of evolution. In the next part of my paper I will deal with criticism of Chaitin's proposal from a slightly different perspective.

3. Radical genocentrism of metabiology

Chaitin explicitly makes information the appropriate subject of interest for both biology and metabiology. (Chaitin 2006) Yet the word "information" means for him one, and only one thing – information encoded in the DNA, genetic information. Such an attitude is also present in modern biology, and especially in molecular biology, genetics, and neo-Darwinism. (Downes 2006) Some researchers find this situation beneficial (G. Williams, R. Dawkins, J. Maynard Smith), while others not very much so (B. Goodwin, S. Kauffman, R. Lewontin, D. Noble). One indisputable fact is, however, the common presence of this attitude in popular culture thanks to the constant efforts of famous biologists (particularly of R. Dawkins whose texts Chaitin appreciates). This results in a situation that B. Goodwin sums up like this: *Something very curious and interesting has happened to biology in*

recent years. *Organisms have disappeared as the fundamental units of life. In their place we now have genes, which have taken over all the basic properties that used to characterize living organisms. [...B]ehind the front that we see as the living, behaving, reproducing organism is a gang of genes that is in control. They alone persist from one generation to the next and so evolve.* (Goodwin 1994, 1) Goodwin calls the biology practiced in this perspective “genocentric”. On the next pages we will see this notion fits perfectly with Chaitin’s research attitude.

Chaitin concentrates solely on DNA-stored information, regarding it as the only significant subject worthy of research and reflection. To understand the processes of Darwinian evolution, and life in general, we should focus our research efforts exclusively on the information aspect of life (*software*), regarded as more essential than the energetic aspect (*hardware*). Chaitin confesses that it was R. Dawkins who inspired him to take such a radical position: *I do take from Dawkins his emphasis on genes. Who cares about bodies!?* (Chaitin 2012, 48) The provocativeness of the last sentence is complemented with the self-confidence we can see in Chaitin’s opinion about the thermodynamical aspect of life: *biologists think that every detail counts; they do not distinguish between what is fundamental and what is secondary. [...] the energetics, the metabolism of living organisms is unimportant, all that counts is the information, all that counts is where you get the instructions for doing something. The energy will take care of itself!* (Chaitin 2012, 19) To understand why Chaitin makes such radical statements, we must first capture the logic behind building metabiology. The following procedure is meant to catch its core:

1. build a formal (mathematical) model of evolution by means of natural selection,
 2. find a definition of life that can be implemented in the model,
 3. find an object in the model that meets the definition,
 4. consider it to be alive,
 5. conclude you’ve just proved the existence of life in your model,
- and because your model is purely mathematical (abstract), then:
6. attribute an essential, timeless, absolute, Platonic mode of existence to the model,
- finally:
7. conclude that you have proved the existence of a purely mathematical (thus: essential, timeless, absolute, Platonic) life-form.

To perform the above procedure, certain conditions must be met. First of all, one must build a formal model of Darwinian evolution. To achieve this, however, it is necessary to make far-reaching simplifications (so Chaitin removes

from his model populations, phenotypes, competition over resources, etc.). Next, we must have an appropriate definition of life. We need a definition which can be easily implemented in the model and at the same time, biologically credible (i.e. one with which there is widespread agreement that it aptly captures the very essence of life). Here Chaitin refers to the so-called “Darwinian definition” he borrowed from J. Maynard Smith. The definition of life proposed by him:

- a) [...] *life should be defined by the possession of those properties which are needed to ensure evolution by natural selection. That is, entities with the properties of multiplication, variation and heredity are alive, and entities lacking one or more of those properties are not.* (Maynard Smith 1986, 7)

became the starting point for the definition of life created by Chaitin. Unfortunately, the author of *Proving Darwin* treated it only as a pretext.⁵ He attributes to the British biologist definitions which are imprecise:

- b) *life is a system that has heredity and mutations and evolves by natural selection* (Chaitin 2012, 48)

or just oversimplified:

- c) *life is what evolves.* (Chaitin 2012, 19)

Let us notice how much definitions b) and c) differ from that definition a) proposed by Maynard Smith. Populations have vanished from the original version and so has individual variability (after all, variability is possible only in a population). The ability to reproduce (that is, to give offspring) vanished too, and mutations appeared in its place, which were absent in the original (mutations are the mechanism responsible for genetic variability and that’s why Chaitin needs them). Finally, what is left from the original definition by Maynard Smith, is put into definition c). If we are to consider life as “anything that evolves”, why would not information be such a “thing”? From here it is only a small step to the definition of life that Chaitin needs: *life is evolving software*. And such a version is quoted repeatedly in various texts by Chaitin. Note that this definition is extremely mono-attributive as it deprives the phenomenon of life of any energetic aspects.⁶ In combination with Chaitin’s other assumption – that the *natural software controlling the structure and functioning of organisms is DNA* – it makes a genocentric worldview in which the immense richness and complexity of life are reduced to duplication of nucleic acids. Within its framework the living cell is managed by natural software – DNA. To understand life, one should focus on this software. Evolution is understood as a random path in the space of natural programs, whereas biology is the archaeology of this software.

It should be stressed that what is problematic in Chaitin's approach is not the focus on biological information itself but rather the reduction of this information **exclusively** to information encoded in DNA. Emphasizing the importance of information and its processing for the functioning of living systems is neither new nor controversial.⁷ The problem is, however, that Chaitin's metabiology is blind to the existence of a great domain of **non-genetic information**; that is, the information whose carrier is not the DNA. We know today many epigenetic mechanisms of transferring information whose systematic studies have lasted at least since the middle 1980's. (Holliday 2006) It seems that biological information is not located in any particular place in the living system. It is rather a non-local property, scattered throughout the whole system. It is impossible to point to any isolated physical structure in a cell and state: "biological information is located precisely here" (Walker, Cisneros, Davies 2012; Walker, Davies 2013; Beaverstock 2013). We also need to remember that information stored in the DNA is relevant only in a specific context, i.e. with respect to specific chemical objects present in the cell. Therefore it would be more correct to state that biological information is a property of complex networks of intra- and intercellular relationships (as well as inter-tissue, inter-systemic, inter-organismal and ecological) (Marcos, Arp 2013). Such networks are the object of extensive research in systems biology, which has been developing dynamically in recent years. A growing number of biologists emphasize the importance of thorough study of such networks and the need for going beyond the genocentric point view (Nurse 2008). Following the words by D. Noble: *the book of life is life itself. It cannot be reduced to just one of its databases. For let's be clear that the genome is only one of the databases* (Noble 2006, 10) are a good metaphor for expressing the essence of the system approach in biology which is directly opposite to that of Chaitin.

Despite that, the author of *Proving Darwin* does not try to nuance his understanding of bioinformation, ignoring completely the very existence of non-genetic information. He merely adopts a simplified scheme, according to which DNA is both the **repository of information** about the structure and development of the whole organism, and a universal **programming language**, as well as the software **controlling** all the functions of this organism. In his approach Chaitin literally transfers schemes from theoretical computer science into biology. A scheme like this:

Program → Execution → Output

is translated to:

DNA → Development → Organism

He also makes an unambiguous comment: *I regard life as biochemical software. In particular, I focus on the digital information contained in DNA. In my opinion, DNA is essentially a programming language for building an organism and then running that organism.* (2007b, 305) This is precisely the attitude that R. Lewontin called “DNA doctrine” (Lewontin 1993) and D. Noble “DNA-mania” (Noble 2006). Unfortunately, Chaitin’s proposal seems to be ill-judged from a biological point of view, since DNA is neither the central repository of information about the structure of the whole organism nor the software directly controlling its functions and behaviour (Noble 2006, Davies 2012).

Certainly Chaitin is not an isolated case. A substantial part of modern biology is dominated by what P. Griffiths has called *information talk* – notions and ideas derived straight from the dictionary of information theory and computer science. (Griffiths 2001) The problem is, however, that these concepts are rarely anything more than metaphors, whereas much more often they lead astray, resulting in incorrect recognition of the mechanisms governing the biosphere (Sarkar 1996).

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Setting about the construction of metabiology, Gregory Chaitin faced the necessity of choosing the appropriate ontological categories which he used to conceptualize the phenomenon of life. The choice of such categories and the way they are used are always dependent on commonly adopted theories explaining studied phenomena. Choosing information as the basic ontological category for metabiology was the right decision. The way Chaitin used it seems to be less appropriate. Limiting its range to DNA-stored information only, and completely omitting the thermodynamic aspect of life, resulted in a proposal with a narrow range of application. Objections also appeared from mathematicians and computer scientists arguing that the mathematical core of metabiology, although quite interesting, does not herald a revolution similar to the algorithmic information theory co-founded by Chaitin in the 1960’s (Shallit 2013). In its present form, metabiology is rather an interesting mathematical experiment, but it’s hard to treat it as a serious proposal in the field of theoretical biology (not to mention as a candidate for the fundamental theory of life). Chaitin seems to be aware of the many deficiencies of his model, as he suggests that it will require further work to make it more credible and able to be implemented in the form of computer simulations.

The general mathematical theory of Darwinian evolution still remains a song of the future, and biologists seem to remain moderate pessimists in

the question of the ability to formulate it. Kozłowski (2011) suggests two possible scenarios: 1) it is impossible to build a mathematical theory of evolution at all, 2) it is possible, but such a theory would be useless for any practical purposes due to the hyper-complexity of the evolving biosphere. As for metabiology, I believe it should be regarded rather as an expression of the philosophical views of its creator than a serious attempt at contributing something new and vital into the field of theoretical biology.

N O T E S

¹ What we observe here is random evolution of a **single** program toward increasing fitness. Absence of any population is one of the points making Chaitin's model incompatible with modern biology. More on this in chapter two.

² Busy Beaver can be understood as a program of length **n** which at the moment of finishing the work prints the largest natural number of all programs with the same length. Busy Beaver should not be confused with Busy Beaver Function!

³ In this role Busy Beaver Function might be regarded as a metabiological equivalent of selective pressure responsible for supporting the process of natural evolution. Every living organism has a clearly determined goal: to survive and produce offspring. Evolutionary pressure, however, causes that not every individual manages to achieve this goal. Thus it drives evolution and determines the direction of changes the next generations of organisms are subjected to.

⁴ Let us notice, however, that a set of objects able to evolve by means of natural selection doesn't have to be considered identical with the set of living objects. It is like that e.g. in the definition proposed by T. Gánti, who distinguished between real and potential criteria of life, placing the ability to evolve in the latter. (Gánti 2003)

⁵ It is almost ironic that the Darwinian definition has no sense if it is considered beyond the context of a population. It cannot be applied to a single individual, whereas Chaitin's model does not include populations at all.

⁶ The vast majority of existing definitions of life is poly-attributive; that is, they emphasize both energetic (connected to metabolism) and informational (connected to reproduction and heredity) aspects of life processes. Few mono-attributive definitions (that is those which highlight one of the above aspects at the expense of another) seem to be too radical, since they force us to regard as living, objects we usually do not regard as such (e.g. computer simulations of living processes or biosphere as a whole). (Chodasewicz 2013) The mono-attributive approach of Chaitin ignores the consensus worked out by biologists and manifested by common adopting one of numerous poly-attributive definitions of life. As a result, the definition proposed by Chaitin does not meet the requirements usually expected of a reliable definition of life.

⁷ There are various proposals for explaining mutual relationships between information and evolution that are able to avoid the extremity of Chaitin's metabiology. An excellent example of such a proposal is the theory developed by E. Jablonka and M. J. Lamb. (2005)

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