Evolutionary processes in nature, technology and society –a few common trends[a]

Yekaterina Myasnikova[1]*, and *Aleksandr* Spirov[2]

[1] Peter the Great Saint Petersburg Polytechnic University, Centre for Advanced Studies, 195251, Politechnicheskaya st., 29, Russian Federation
[2] Sechenov Institute of Evolutionary Physiology and Biochemistry of the Russian Academy of Sciences (IEPhB RAS), 194223, Toreza av., 44, Russian Federation

Abstract. The diversity of branches of knowledge, within which evolutionary approaches are applied to significantly different objects and processes, includes those branches which are especially interesting due to the implementation of the Darwin's concepts of variation, heredity and selection. This is what is interpreted by some authors as universal selectionism. In this case, objects of evolution may be represented as sequences of symbols, code lines or graphs. This is a method to record heredity of an individual. The recording format allows for mutation (substitution, addition or deletion of certain elements of an individual) and crossing-over during production of offspring from a pair of parent individuals. The approach also allows for a quantitative assessment of the "value" of an individual for evolutionary selection. Such evolution includes, first of all, evolutionary computation, computer-aided modelling of evolution, directed evolution of biomolecules, biological evolution, evolution of technology etc. If we consider the above mentioned examples successively, from computer-based examples to humanitarian one, we can observe definite trends. Firstly, we can see a trend of using "languages" of higher levels to implement an evolutionary problem. Secondly, we can observe a trend of forming "building blocks" in heredity structures as well as a crossing-over mechanism which retains the said blocks. Thirdly, "variation" of an individual is carried out by increasingly high-intelligent methods. Studying of main trends and mutually enriching interchange of experience between such different branches of knowledge may enable to make more reasonable and exact predictions of the results of evolutionary processes and to achieve higher effectiveness of evolutionary search in application areas.

1 Introduction

In modern scientific literature, the term "evolution" is applied to a very wide range of processes and phenomena. Studying of the basic principles of evolution allows explaining

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* Corresponding author: myasnikova_em@spbstu.ru

development of various processes and making well-grounded predictions in such different branches of knowledge as Natural and Life Sciences, Technology, and Human Sciences. Some examples are software evolution [1], social (sociocultural) evolution [2], evolutionary linguistics [3], evolutionary economics [4] etc. From a biological point of view, evolution is a natural process of development of life on Earth. Inspired by evolutionary biology, an attempt to develop a new constructive trend of research often allows obtaining such results and making such conclusions which cannot be achieved by other approaches.

Table 1. Evolutions which the concept of selectionism may be applied to.

Evolutionary Computations (genetic algorithms and genetic programming)
Computer-based Evolution Modelling (evolution of "digital" and virtual organisms and gene network models)
Directed evolution of biomolecules (SELEX)
Biological micro- and macroevolution
Evolution of equipment/technologies

We focus on those cases of evolution which the main concepts of Darwin's theory may be applied to. Table 1 lists such branches where similar features may be found between such different evolutionary processes and biological evolution.

The types of evolution in question are characterized by Darwin's variation, heredity and selection. Heredity is determined so that it is possible to represent an individual in the population as a sequence of symbols, code fragments, sentences of (formalized) language or, e.g., as a graph. Such records are often called "chromosomes". These objects are understood as a method to record heredity of an individual. Consistently, variation is understood as changing such representation. The format of the record allows mutating it (by substituting, adding or deleting its certain elements). Moreover, the possibility of crossing-over of parental chromosomes is implemented during production of offspring from a pair of parent individuals.

For selection, it is important to have a possibility of quantitative assessment (fitness) of desired properties of the individual for the evolutionary process (selection), i.e. "value" of the individual. Then, high-value individuals and/or their offspring substitute low-value individual in the population and this corresponds to selectionism.

Key features of evolutions listed in Table 1 are considered in the comparative aspect in the main section of this paper below.

2 Unity and diversity of "Darwinian" evolutions

In this paper, we attempt to track general trends in the evolutions listed in Table 1. The above mentioned trends are differently expressed in various evolutionary branches and the depth of their study also varies.

2.1 Evolutionary computations and computer-based evolution

Our analysis starts with the first two evolutions from the list which are probably the simplest cases. This is a set of evolutions implemented using a computer. These are branches where the problems and approaches significant for developing and understanding other more complex cases of non-biological evolutions are formulated.

Computer evolution is a very large branch which includes both strictly academic (biological evolution modelling) and strictly application fields (techniques of evolutionary computation in real applied problems) [5-6].

Computer evolution has been considerably strictly and mathematically formalized [7]. As a large branch called evolutionary computation or evolutionary algorithms, it includes such well-known subdisciplines as genetic algorithms, genetic programming, evolutionary programming, evolution strategies, learning classifier systems and many others.

Evolutionary computations are a kind of schematized and simplified representation of selectionism. Evolutionary algorithms solve problems working with a population of a plurality of randomly taken solutions. Individuals/solutions in the population undergo mutations and then are assessed based on pre-defined criteria (fitness of individuals). One part of them is selected to produce an offspring population; the other part is eliminated so that the number of individuals in the population remains unchanged after reproduction. During reproduction, a crossing-over, i.e. recombination of parent chromosomes in offspring, is carried out to qualitatively increase diversity of offspring of the given pair. Then, the renewed population undergoes mutagenesis, and the cycle repeats until a satisfactory solution is found (i.e. an individual with the required fitness level).

2.1.1 Genetic algorithms and genetic programming

Genetic algorithms (GA) [8] are the most well-developed branch of evolutionary computations. As a rule, individuals/solutions represent a line of symbols or figures which is called a "chromosome", and this is just one of the common features of GA and biological molecular evolution. Changes in symbols/figures in the line are mutations. Since chromosomes are sequences of "elements" here, just as in DNA, the crossing-over is implemented similar to the biological one in the form of a "crossing" of parent chromosomes in one or two points (sometimes in many points) to allow offspring to receive recombined copies of the parent chromosomes. The significance of crossing-over for effective evolutionary search has been specifically assessed in GA [5].

In GA, almost any optimization problem (i.e. seeking and arriving to a best solution) may be solved by formalizing it in such a way that it is reduced to manipulations with sequences of figures, numbers or symbols [8]. In this case, computer-based evolutionary search is (often easily) feasible.

Schema theorem and building blocks. As a rather simple and intensively researched branch, GA has its theoretical justifications. The schema theorem [5] suggested by John Holland (one of the GA founders) in 1975 influenced much not only GA itself but also other evolutions. The definitions of schemata and building blocks follow from the above mentioned Holland's considerations (which are omitted here).

Building blocks as fragments of the desired solutions. The building-block (BB) hypothesis states that evolutionary search is carried out in GA though finding individual blocks, i.e. parts of solutions [9]. (Despite that not all problems may be properly decomposed into individual blocks for the given problem implementation, it will work for many cases).

Crossing-over combines BBs, crossing-over destroys BBs. Holland's theorem implies that crossing-over plays a critical role in the evolutionary search in GA [10-11]. Crossing-over is first necessary to combine various parent BBs in offspring, thereby increasing the fitness level of the offspring. However, (common) crossing-over tends to destroy (break) BBs, thereby slowing the evolutionary search down [8]. The gist of it is that the crossing over points in a routine crossing-over algorithm are either fixed or arbitrary. Hence, if parent chromosomes are separated and shuffled in offspring during crossing-over so that parental BBs remain unbroken and are received integral by offspring, the fitness level of the offspring will increase. But if crossing over is carried out through a parent BB and such block is not received by any offspring in its integral state, the fitness level of the offspring will not increase (as compared with that one of the parents), and the said BB will be lost in the

evolutionary search. A problem arises that the evolutionary process must be such that BB appearance, multiplication and recombination are maintained.

2.1.2 Crossing-over operators retaining building blocks

The demand for crossing-over operators retaining BBs (as well as the hopes put on them) has been recognized in evolutionary computations in the course of development of the theory and practice of GA and GP application. In parallel with and independently from them, molecular engineering approaches has been developed to manipulate domains (BB) in directed evolution of biological macromolecules ([12], see Section 2.2). Moreover, modern biological engineering has adopted the idea of modular design (presence of BBs) in many respects from common engineering ([13], see Section 2.3).

Crossing-over retaining BBs is required in GA and GP, evolutionary design of gene network models, directed evolution of macromolecules and some other fields. Many special crossing-over operators retaining BBs are being developed in evolutionary computations [14-18]. There is a chance that such operators will be applied in other evolutions.

Thus, the cross-cutting issue of our analysis is the demand for such crossing-over operator which would retain BBs in the evolution.

2.1.3 Evolution of virtual organisms

Now, let us consider the evolution of virtual and "digital" organisms (Table 1) as they are a good illustration of the statements set forth in the previous paragraphs.

Evolution of virtual creatures and virtual robots: Let us consider the evolution of virtual creatures by the example of Karl Sims's work [19-20]. The approach suggested by Sims is similar to GA and GP, and the issue of modularity (BB) found its expression in this field as well.

These creatures are a kind of virtual robots which move on the plane or swim in a virtual water environment. They have a modular body and modular (block) limbs. They also have sets of sensors, simple signal-processing systems and decision-making systems to decide where to move. They are able to walk, hop, or swim; they can even follow their "targets" and compete with each other for loot (in a virtual environment). Evolving virtual robots is an intensively developing branch of evolutions where approaches to designing real evolving robots are being tried out [21].

From building blocks to modular design. Sims's creatures are implemented as modular ones. Genetically, a creature is an oriented graph, i.e. the design of a creature is represented by a graph. In particular, the segmented body and limbs are represented by points and the links between the segments are determined by arrows (oriented verges). Similarly to GP, crossing-over of genotypes is implemented here in the form of an exchange of graph parts. The assembly of a virtual creature is carried out according to the graph as a block design, and this is what can be defined as single-value mapping from a genotype into a phenotype.

Genotype modularity and corresponding phenotype modularity allow to promptly find series of designs of (virtual) robots becoming more complicated. Thus, if the evolutionary problem is implemented in such a way that BBs appear in the genotype and are retained during crossing-over (and mapping from a genotype into a phenotype determines and maintains modularity), this may provide essential advantages e.g. in evolutionary robotics.

2.2 Directed evolution of biomolecules and biological evolution

The following branch of evolution important for us is popularly called evolution in vitro. Evolution in vitro is also known as SELEX (Systematic Evolution of Ligands by Exponential

Enrichment), or directed evolution [22]. Evolution in vitro is also a very large branch which includes both strictly academic fields (as it is directly connected to the range of problems of biological molecular evolution) and strictly applied problems (obtaining chimeric proteins and enzymes with new properties).

Modular structure of RNA and proteins. Modularity of biological macromolecules of proteins and nucleic acids is studied extensively by biologists. Evolutionary significance of modularity of macromolecules is also the subject of wide speculation. In particular, special crossing-over mechanisms are required to maintain modularity. Such mechanisms have been developed, for example, in directed evolution of macromolecules.

Real crossing-over to retain modules. Experimental molecular biological procedures have been developed for sexual methods in protein engineering [23]. These biotechnological approaches imply exon shuffling similar to that is supposed to have occurred in biological evolution.

As is known, an eukaryotic gene consists of exons and introns. Exons code protein parts, and introns are "service" inserts (sequences) between them. Exon often but not always corresponds to a domain (module, as the BB is called in this branch). These blocks may be cut out of different genes and shuffled as desired. As a result, chimeric proteins that do not exist in nature are obtained. Some of them have new properties. The said approaches use ferments and the peculiarities of gene structure. May be it is the way of evolution of proteins and RNA in living nature.

Thus, the idea of BBs is a mainstream of modern biology, and the mechanisms of genetic material recombination to retain and propagate BBs in evolutions have been the subject of active discussions over recent decades.

2.3 Evolution of technology

Modular design in engineering. The module principle is being actively developed in modern engineering (a modular air plane may be even represented). Modular design of a smartphone is a good example for the man or woman in the street, and the expectations are that smartphones will become modular soon. An important thing for us within the said branch of evolution is the modularity principle which is systematically tracked in our evolutions [24].

Building blocks and design modularity. The idea of BB may be illustrated by the example of the results of computer evolution. So, design modularity allows to easily upgrading a computer by adding new blocks.

It should be noted that the modularity principle in engineering is discussed much in modern literature in the context of a number of branches where the modularity of engineering developments is of importance, and has been repeatedly compared to the ideas of modularity in modern biology [13].

From BASIC to English. The trend of developing high-level programming languages is also being observed in computer sciences. High and very high level programming languages are becoming more like human languages. For example, program codes written in the Inform programming language are read almost just as a text written in the English language which significantly simplifies the work of users not being experts in programming [25]. We arrive to a conclusion that the higher the level of evolutionary process in the direction of "humanitarity" is, the higher the level of languages generally used for implementation of individuals in the evolving population is.

3 Findings and conclusions

The brief analysis of evolutionary processes and phenomena allows arriving to the following conclusions. The following trends are observed in branches of knowledge where "Darwinian"

evolutionary processes may be formulated, formalized and applied; the branches being ranked from their lowest to highest levels of "humanitarity".

In the simplest case, heredity of "individuals" is implemented as a sequence of symbols. In more complex forms, it is represented as programs (e.g., trees) and structures (e.g. graphs). The exception is biology where, in spite of the complexity of evolutionary processes, the hereditary apparatus is based on sequences of symbols.

Mutations of "genes"/ "chromosomes" of individuals are implemented by increasingly high-intelligent approaches: in standard GA, mutation means substituting the binary number in a random position; a lot of examples of non-random mutations may be given in biology; in computer-based evolutions, both mutations and crossing-over become increasingly intelligent and make functional substitutions, extensions and complications rather than random (often senseless) changes. Finally, a human plays the role of an intelligent mutator in "humanitarian" branches. As a result, "languages" of an increasingly high level are used to implement the evolutionary problem: from binary codes in GA to human languages.

Heredity of "building blocks" observed in the evolving material requires using crossing-over mechanisms which retain the blocks during the production of offspring from parent pairs. The more complex evolutionary problems become, the more complex crossing-over operators are; they are, for example, complex algorithms, evolving algorithms.

During selection, the individual fitness assessment in evolving populations demonstrates the trend for implementation by increasingly high-intelligent approaches (artificial intellect or human experts).

It should be noted in conclusion that the exchange of experience between various evolutions may be mutually enriching. In particular, "simple" computer-based evolutions are well-formalized and provide mathematical and software tools for complex, more humanitarian branches. And vice versa, more complex evolutionary processes may be the source of ideas of particular mechanisms in evolution which may be formalized into new computational algorithms and approaches.

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