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**THE MAIN EVOLUTIONARY IDEAS OF MODERN
BIOLOGICAL KNOWLEDGE**
An outline of the historical and methodological analysis¹

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ABSTRACT

The aim of this article is to show the methodological principles that govern the interrelationship of the main ideas, concepts, and theories of modern biology. In recent years, several prominent biological researchers attempted to offer insights into the development of biological knowledge. However, a critical examination of these attempts indicates that a methodological analysis is a more fitting approach for achieving this goal. Indeed, the challenge of establishing inter-theoretical connections between biological theories and discoveries falls not within the purview of biology itself but rather within the methodology of biology. This paper explores the key research findings that determine the vertical order of biological knowledge, thereby deepening our cognitive understanding of this field. It also explores the theoretical advancements that expand the horizontal scope of this knowledge. The conceptual framework is illustrated through two diagrams Map I and Map II, which illustrate the methodological structure of biological ideas, concepts, and theories from the era of Linnaeus to the early 21st century. Map II further demonstrates how complex explanatory narratives can be constructed based on contemporary biological and evolutionary knowledge.

Keywords: Aggregation, evolutionary biology, disaggregation, history and levels of biological knowledge, map of biological ideas and theories, methodological relationships.

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INTRODUCTION

The central theme is situated within a field delineated by two research areas. The first is a reflection on the concepts and theories of evolutionary biology, and the second—general methodology. In the first of these areas, the starting point includes the concepts initiating modern ideas of biological knowledge: the concepts of Carl Linnaeus and Jean Baptiste Lamarck, Charles Darwin's theory and subsequent ones resulting from a development or deepening of Darwin's ideas. The initial concepts are also clearly philosophical: Linnaeus's concept, crafted between 1735 and 1768, belongs to the philosophical reflection on studying plant organisms. Lamarck's concept, published in 1809 in the work *Zoological Philosophy* (1914), attempts to speculatively present the mechanisms of evolution of animal organisms, including humans. Linnaeus' ideas are non-evolutionary in nature; they only reflect the order of the living world, while in Lamarck's concept, the most important thing is to seek answers to the question: How do organisms change during their lives and on what factors do these changes depend? In this thematic area² Darwin's theory is revolutionary because it answers questions: How and why do biological species evolve? The answer to this question turned out to be the foundation of modern achievements in the theory of evolutionary biology.

The second of the indicated research areas is general methodology, which provides tools to show the connections, i.e., methodological relationships between scientific concepts and theories. As a part of this study, methodological relations between selected theories of evolutionary biology will be presented with appropriate conceptual tools. What is essential in the proposed approach is that analyzing the content of scientific theories and discovering methodological connections between them are fundamentally different research tasks. This is because the theories of evolutionary biology adjudicate the mechanisms of transformation and evolution of organisms, species, and gene pools. At the same time, methodological reflection aims to present the implicit methodological relationships through which the given theoretical approaches correspond with each other. The objective of this preliminary exposition is to precisely delineate the latter.

² In the tradition of Anglo-Saxon research, this kind of knowledge belonged to natural history; Darwin's theory of evolution is, in this tradition, a theory of the natural history of species. However, on the European continent, these issues belonged to biological knowledge. According to Ernst Mayr, it is from Lamarck and Treviranus (in 1800–1802) that the name "biology" originated and applied to the reflection on living organisms and their transformations. See also: E. Mayr, *To jest biologia* [This Is Biology: The Science of the Living World], J. Szacki (trans.), Prószyński i S-ka, Warszawa 2002.

1. IDEAS OF MODERN BIOLOGICAL KNOWLEDGE FROM A HISTORICAL PERSPECTIVE

The dynamic development of biological knowledge that we have observed since the beginning of the second half of the 20th century has led to the creation of over fifty different specialist fields within biological knowledge, differing significantly in research. The differentiation and specialization of biological research began to be noticed in the 1970s. The pioneering figures who endeavoured to engage with this phenomenon in the context of biological knowledge's evolution during the latter half of the 20th century included, among others, Ernst Mayr (1904–2005) and François Jacob (1920–2013). Nevertheless, their focus was indeed on philosophical and scientific contemplation on the history of developing biological and evolutionary knowledge.

The indicated approaches can be described as attempts to synthetically organize the history of the development of biological knowledge, including evolutionary knowledge. It should be noted, however, that the concepts of the development of biological and evolutionary knowledge proposed by these researchers significantly differ from the approach accompanying the vision of the development of biology (including evolutionary biology) outlined here.

Mayr's proposal focuses mainly on showing the historical development of biological and evolutionary ideas.³ This comprehensive, three-volume study of the history of biology, presenting biological research in various cultural traditions and regions of the world, accounts for the interplay of research ideas and the results to which the guiding idea of evolution leads. Mayr also shows the cognitive and non-biological consequences of the impact of the idea of evolution on other fields of science, including philosophy and social sciences.

Jacob's approach is entirely different. In the book titled *La logique du vivant. Une histoire de l'hérédité* he focuses on presenting a certain general methodological concept of the development of biological ideas—from the Middle Ages to the first half of the 20th century.⁴

This wide-ranging subject matter is included in four main thought paradigms, which Jacob refers to as “integrans.” It seems that these mental wholes, i.e. integrans, consist of two basic content layers: the ontological

³ E. Mayr, *Growth of Biological Thought: Diversity, Evolution and Inheritance*, Harvard University Press, Cambridge, Mass.–London 1982. The “noteworthy” for this work is the title of the Introduction itself, which is: “Introduction: How to write history of biology.” This work thoroughly discusses the historical conditions for the development of various biological and evolutionary ideas.

⁴ Although its author is quite clearly inspired by the concept of the structure of scientific revolutions by Thomas S. Kuhn (1962), he does so based on rich biological thought material, showing discoveries, ideas and research hypotheses that appeared from the late Middle Ages to the second half of the 20th century.

layer, which characterizes the subject of research in a given era of the development of biological knowledge and the epistemological layer, which describes conceptual, experimental and technological tools (e.g. the development of computer technology and progress in experimental research methodology). These tools make the basic research subject accessible to human cognition. The first integron, in historical terms, is a “visible structure,” followed by the others: integron II (already available to scientific knowledge) is an “organization,” integron III is “time,” and integron IV is a “gene.” Jacob’s proposal indicates that the development of biological knowledge took place in a revolutionary way, similar to the way Thomas S. Kuhn understands the development of science. This also means that the overarching conceptual frameworks of conceiving the animate world are not significantly interconnected.

However, such an approach to the development of biological knowledge raises serious doubts because it is difficult to imagine a situation in which creative—even historically understood—ideas of biological knowledge would not encounter critical reflection. An example of this type of research reaction is Darwin’s critical (but at the same time somewhat approving) reference to Lamarck’s evolutionary approach, which Darwin expresses in the Introduction to his work *On the Origin of Species* (1859). However, a significant difference is made by the modern methodological approach, which breaks away from a simple critical reference to the analysis of the content of the idea of evolution.

The intensive development of the idea of evolution in the 20th century prompts researchers to consider the regularities of the development of evolutionary and biological knowledge. This issue, however, goes beyond the scope of simple theoretical consideration of the structure of evolutionary biology.

The approach of evolutionary biologists, inclined to historical reflection, usually refers to the reconstruction of the chronology of subsequent cognitive achievements that make up the body of biological knowledge. Below, I will present an inventory of the most important ideas in biological knowledge and the cognitive achievements in this field.

I will begin this historical reconstruction by presenting the ideas of Linnaeus, who, already in the 18th century, drew attention to the rule that organized existing biological species. This order was established by adopting the Aristotelian principle of reasoning about similarities and differences between complex animate objects, i.e. the “higher-lower” principle. The higher ones are always complex objects called genera, while the lower ones are those we call species. The simplest diagram showing Linnaeus’s main idea is given below. Species arise and exist by the creator’s will, but they reproduce and regenerate according to a given pattern. That is why individuals of a given species are so similar to each other, and the observable dif-

ferences between them are only hereditary “deviations” from a given pattern.⁵



The most important ideas of this approach are the following: (1) evolution does not occur, and the will of the creator creates species; their nature is unchangeable, and therefore, the features they have are constant; (2) intraspecific diversity is the result of errors in the reproduction of individuals in subsequent generations in the process of inheritance; (3) the species' nature is expressed in a standard set of properties and their intensities. The hierarchy of genera and species constitutes a systematic order of the world of biological species. In Linnaeus' concept, we do not receive an explanation as to why this order is like this and not another—it is not possible to answer this question based on this view. However, this question also turned out to be fundamental because one of the first answers was provided by the outstanding French biologist Jean Baptiste Lamarck (1744–1829).

It was an attempt to understand the evolutionary process of shaping order in the living world. Lamarck focused his research mainly on botany and zoology. Already in 1800, he tried to combine knowledge about plants and animals, proposing a common name for them, “biology.” Lamarck's particular area of interest was the behaviour of animals and plants. In 1809, he published *Zoological Philosophy*, in which as much as 2/3 of the content is devoted to animal behaviour. In this work, he presents a psychological concept of the evolution of behaviour, although more speculatively. He also presents the theoretical foundations of his concept of evolution, also referred to as a “transmutation.” According to this concept, the basic object of evolution is the organism, and its changes result from the influence of living conditions and inheritance processes in which organisms participate.

In this approach, organisms evolve because more complex entities, such as species, are not real objects. The process of evolution, therefore, applies only to organisms. On this point, Lamarck writes as follows: “... among its

⁵ The most important components of the concepts discussed are marked in bold. It should be remembered that the idea of species as a hereditary pattern was borrowed from Plato. Therefore, according to Linnaeus, the taxonomic order is determined using the Platonic species pattern, and the systematic order is determined using the Aristotelian “higher-lower” principle.

creations, nature has in fact produced neither clusters, nor orders, nor families, nor genera, nor fixed species, but has only created individuals who succeed one another and resemble those from which they sprung.”⁶

The objects subject to evolution are organisms that interbreed pangenetically. For then: “individuals belong to infinitely diversified races which transform into each other [...] in all forms and in all degrees of organization, and each of which behaves without mutation [i.e. is not subject to change—K.Ł.] so long as no cause of change acts upon it.”⁷

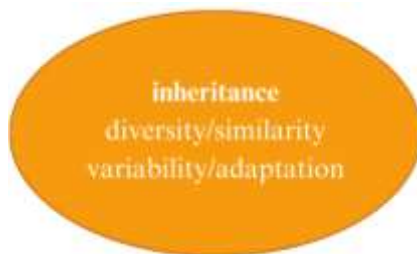
The essence of the process of pangenetic inheritance is—let us define it for convenience as the P principle—is a rule that says:

P: in the process of inheritance, in subsequent generations, the similarity of organisms increases, and their diversity decreases.

It determines the course of the inheritance process, which involves a relative balance between the similarity and diversity of organisms. In fact, it is the principle of Lamarck’s understanding of the inheritance process. However, Lamarck is aware that organisms live in changing conditions, so they are often forced to adapt to them; sometimes, it succeeds (adaptation), and sometimes—it fails (selection, i.e. death). Given the phenomenon of evolution (transmutation), the principle P requires reformulation into P#. When organisms respond effectively to changes in environmental conditions and, therefore, change their behaviour to be more conducive to survive, taking this circumstance into account transforms the principle P to P#. This principle dictates that

P#: in the inheritance process in subsequent generations, the similarity of organisms decreases and their diversity increases.

The diagram below shows this concept’s most important conceptual components.



⁶ This is an important philosophical assumption (of nominalist provenance), i.e. a theoretical assumption regarding the object of evolution, which turns out to be an individually understood organism. Lamarck allows the use of the name “species” but only for the convenience of naming the multitude of organisms very similar to each other, and in fact indistinguishable (J. B. Lamarck, *Filozofia zoologii* [*Zoological Philosophy*, p. 21], p. 57, own translation).

⁷ J. B. Lamarck, *Filozofia zoologii* [*Zoological Philosophy*], op. cit., own translation.

According to the **P#** principle, we also know that: (1) organisms evolve according to changes in conditions, and by keeping up with their unfavourable changes, they modify their structures and functions; (2) the result of these changes is adaptation. If this is not done, the organism is selected and dies. In other words, the source of diversity is both evolution and selection; (3) inheritance is the main mechanism in maintaining variability in organisms; (4) environmental conditions and their changes (transmutations) that accompany the existence of organisms are a side factor; (5) the survival of organisms is possible thanks to evolution leading to adaptation. On this point, Lamarck argues as follows:

“The races themselves undergo changes in their parts, in proportion to any considerable change in the circumstances which affect them. [...] These changes only take place with an extreme slowness, which makes them always imperceptible, the proportions and relations of the parts always appear the same to the observer, who does not really see them change. Hence, when he comes across any species which have undergone these changes, he imagines that the differences which he perceives have always existed.”⁸

Lamarck's concept was the first to exhibit the idea of the evolution of organisms. However, the fundamental answer to the question of where the diversity of biological beings comes from (simultaneously, however, clearly similar to each other) required consideration of the question of species similarity. Therefore, the evolutionary view of the living world is the issue of variability and the emergence of new species, not just organisms. The answer to this question in the history of biological knowledge (especially in natural history) was provided only by Charles Darwin (1809–1882). His work titled *On the Origins of Species* turned out to be a breakthrough in understanding the processes of evolution of organisms and biological species. Its title clearly indicates what the author is interested in: (1) the fact of the existence of species (i.e. the thesis: thanks to the struggle for existence, species/races stay alive) and the fact that (2) species arise from each other, and are the driving force of the process of evolution is natural selection. Darwin qualified his research into the field of knowledge about life, which was then called “natural history,” and his research achievements caused it to be separated from natural theology. The most critical theoretical findings of Darwin's theory include: (1) the thesis about the actual existence of species; (2) the existence of a species in subsequent generations depends on the course of the inheritance process and the environmental conditions in which they live, as well as on changes in these conditions; (3) in subsequent generations, adaptation takes place, to which a part of it is usually subject (the population with a favourable endow, i.e. the optimally adapted fraction),

⁸ *Ibidem*, p. 30.

and natural selection decides what part it is and what belongs to it. This means that the mechanism of natural selection is the cause of evolution, and its effect over generations is the process of evolution. The essence of this mechanism is the relationship between the endowment of a biological species and the conditions in which the species lives. It works by selecting an adaptively optimal fraction from a given species that survives in a given generation; it includes those individuals of a species that maximize their adaptive value to the conditions in which they live. These values determine the degree to which the adaptation criterion of organisms is met in subsequent generations. The sequence of adaptively optimal fractions in subsequent generations is the process of species evolution. The diagram below shows the essence of Darwin's theory of species evolution.⁹

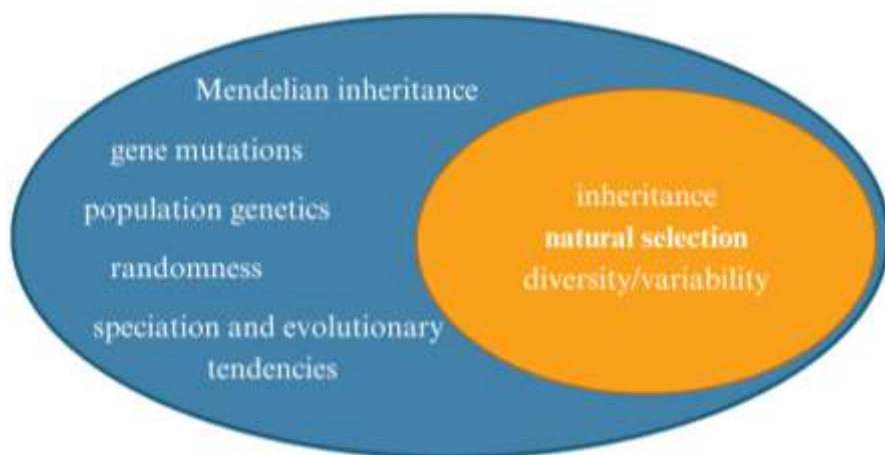


Darwin's achievement led to ongoing discussion about the evidence for evolution during the second half of the 19th century, in the field of research on the evolution of species, there was still debate about the evidence for the existence of evolution. Various categories of evidence were considered, from anatomical-comparative to genetic. The development of biological knowledge in the 20th century emphasized the importance of grounding our understanding of evolutionary processes in a realistic view of the inheritance process, both on an individual scale (organismal—which was addressed by experimental genetics like Thomas H. Morgan and Theodosius Dobzhansky) and on population scale (which was explored by population geneticists: Sewall Wright, Ronald Fisher and others). Ultimately, the formal form of the synthetic theory of evolution (also called Modern Synthesis) was given by Dobzhansky (1900–1975), who in 1937 published a work entitled *Genetics and the Origin of Species*.¹⁰ In this way, he fulfilled Charles Darwin's will because, while maintaining an important component of Darwin's project, i.e. the mechanism of natural selection, he incorporated the mechanisms of inheritance into the theory of evolution, or more precisely, he explained the sources of genetic variability (mutation) and genetic diversity (recombination) in the process of inheritance.

⁹ The primary mechanism of the process of species evolution is marked in bold.

¹⁰ T. Dobzhansky, *Genetics and the Origin of Species*, Columbia University Press, New York–London 1951.

Dobzhansky, therefore, assumed that there are two foundations of the theory of species evolution: inheritance and natural selection. The first one is a source of changes, while the second one tests these changes. According to modern studies, the synthetic theory of evolution (*Modern Synthesis*—MS) includes: (1) the Darwinian core of the theory of evolution, i.e. the theory of natural selection, (2) elements extending this theory with a hereditary component, e.g. gene mutations, Mendelian inheritance, population genetics, speciation along with elements allowing us to understand the processes preceding it and isolation as well as accidental phenomena inherent in the course of evolution. This understanding of the synthetic theory of evolution is advocated by Massimo Pigliucci and Gerd B. Müller.¹¹ According to them, a schematic image of the content of this approach is as follows:

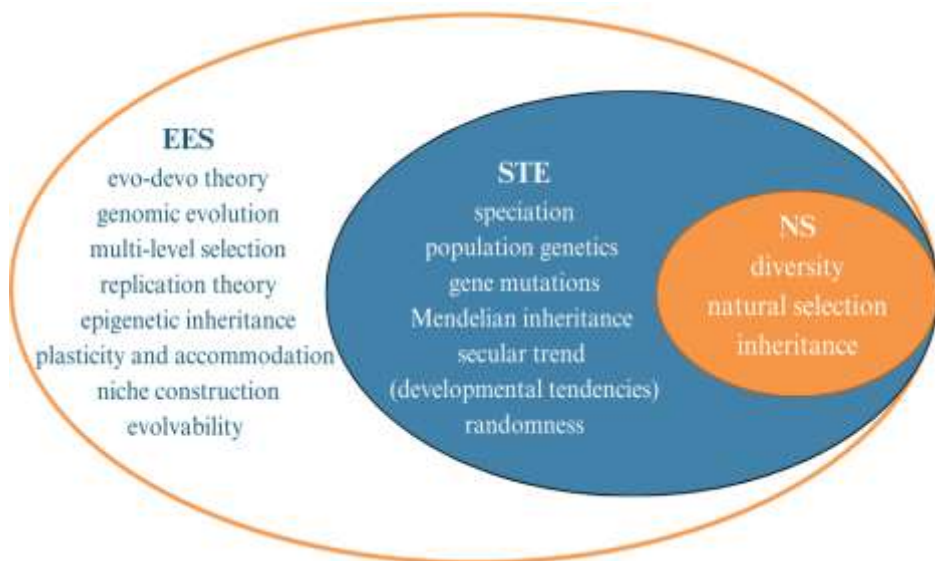


As it can be seen, the synthetic theory of evolution (STE) includes: (1) natural selection theory [NST], i.e. the hardcore (theory of natural selection, in a slightly modified, modernized 20th-century approach, e.g. in the sense of Dobzhansky); (2) new scientific phenomena and facts discovered after Darwin, which include the achievements of: Dobzhansky, Huxley, Mayr, Simpson, Stebbins; and Schmalhausen; (3) gene mutations (discoveries of Morgan and Dobzhansky); (4) Mendelian inheritance; (5) population genetics (Fisher, Wright, Haldane, Li); (6) randomness; (7) speciation and evolutionary tendencies (Dobzhansky), also studied by paleontology and natural history. Pigliucci, in pointing out the above components of the synthetic theory of evolution, supports the opinion of Douglas J. Futuyma (2005, p. 14), when he writes:

¹¹ M. Pigliucci, G. B. Müller, *Evolution—The Extended Synthesis*, The MIT Press, Cambridge, Mass.—London 2010.

“The evolutionary theory developed during and since the evolutionary synthesis consists of a body of principles that explain evolutionary change. Among these principles are (a) that genetic variation in phenotypic characters arises by random mutation and recombination; (b) that changes in the proportions of alleles and genotypes within a population may result in replacement of genotypes over generations; (c) that such changes in the proportions of genotypes may occur either by random fluctuations (genetic drift) or by non-random, consistent differences among genotypes in survival or reproduction rates (natural selection); and (d) that due to different histories of genetic drift and natural selection, populations of a species may diverge and become reproductively isolated species.”

However, these authors go further. They write that in the last few decades, evolutionary biology, particularly the theory of evolution, which explains the course of evolutionary changes in species and changes in organisms, has been enriched with new content and theoretical approaches. In their opinion, the synthetic theory of evolution has, in recent years, transformed into a new theoretical form, which they propose to call *Extended Evolutionary Synthesis* (EES). The presentation of this proposal is an extended synthesis scheme.¹²



As the diagram shows, in addition to the classic components of evolutionary biology: the theory of natural selection. NST (inner ellipse), synthetic theory of evolution MS] (central ellipse), for extended synthesis EES]

¹² Por. M. Pigliucci, G.B. Müller, *Evolution ...*, op. cit., p. 19.

(outer ellipse) include: (1) complexity theory (i.e. levels of selection action); (2) the phenomenon of epigenetic inheritance (the achievements of Ewa Jablonka and Marion J. Lamb should be taken into account here)¹³; (3) evolvability (including: how natural mechanisms change themselves, e.g. how natural selection evolves); as well as relatively unified areas of research, such as: (4) genomics (studying the distribution and possible combinations of genes); (5) evo-devo theory (developmental and evolutionary shaping of the organism, i.e. answers to the question of how the mechanisms of evolution control the development of the organism); (6) “potential” ecology (i.e. niche construction and inheritance, discussed by authors such as John Odling-Smee, Kevin N. Laland and Kim Sterelny and others)¹⁴.

A separate issue of interest to philosophers, theoretical biologists and methodologists is whether the approach to the development of evolutionary biology proposed by Pigliucci and Müller is subject to any methodological concept already known in the philosophy of science.

The simplest way to explain the emergence of the extended evolutionary synthesis seems to be Kuhn’s concept of scientific revolutions. However, Pigliucci is critical of this view. He believes that the creation of an extended evolutionary synthesis is not subject to Kuhn’s concept of paradigms—almost universally held by most philosophers and theoreticians of the development of science. Pigliucci gives the following argument—he says that the paradigmatic change would consist in the fact that if we were dealing with a revolutionary change in biology (including evolutionary biology), it would have to be a change in the type of rejection of Paley’s creationism or the idea of “intelligent design” rather than a transition from Darwinian theory to STE (Pigliucci, 2009). In his opinion, the transition from the theory of natural selection (NST) through the synthetic theory of evolution (MS) to the extended synthesis (EES) is rather closer to the approach of Stephen J. Gould (2002). The trend in the development of evolutionary biology is clear—the explanatory importance of natural selection is decreasing, while the importance of other components, including genetic elements, is increasing as they explain the diversity, variability, principles of organism development (e.g. epigenesis) and inheritance (as well as ecological elements).

According to Pigliucci, the success in popularizing extended synthesis is seen primarily in three categories (as indicated by Gould): (1) action, (2) effectiveness and (3) its scale of reference. Following Gould, he maintains that in these three orders (principles), inherent in the logic of Darwin’s

¹³ E. Jablonka, M. J. Lamb, *Evolution in Four Dimensions: Genetic, Epigenetic, Behavioral and Symbolic Variation in the History of Life*, A Bradford Book, The MIT Press, Cambridge, Mass.—London 2005.

¹⁴ Cf. K. Laland, T. Uller, M. W. Feldman, K. Sterelny, G. B. Mueller, A. Moczek, E. Jablonka, J. Odling-Smee, *The Extended Evolutionary Synthesis: Its Structure, Assumptions and Predictions*, Proceedings of the Royal Society B, 2015 (1813), 282: 29151019; <http://dx.doi.org/10.1098/rspb.2015.1019>

theory, the phenomenon of the development of the synthetic theory and, consequently, the theory of extended synthesis can be exemplified. These rules concern:

- (1) actions (Gould refers to Adam Smith's metaphor)—“the unconscious hands of nature” manage the struggle for existence so that some organisms survive, others die;
- (2) effectiveness—Darwin discovered that natural selection is a mechanism of evolution that preserves favourable evolutionary changes and eliminates unfavourable ones while accumulating the positive effects of these changes in subsequent generations;
- (3) scale—Darwin's theory can be used to understand not only microscale processes (evolution of species) but also macroscale processes (emergence of higher categories and taxonomic orders). It is also possible to extrapolate the action of selection in the history of life on Earth (e.g. explaining phylogenetic events).

It seems that Pigliucci, in turn, can be criticized for saying that his attempt to explain the emergence of EES is an *ad hoc* explanation because it refers to a view that does not take into account the immanent connections of theoretical and evolutionary ideas, i.e. internal contents related to the mutual conditioning of the development of biological and evolutionary knowledge. This means that in order to explain the development of science, in this case, the theory of evolutionary biology, it would be necessary to refer to the internal conditions of the theoretical content that accompany the creation of new theoretical syntheses. These conditions are rather methodological (intra-theoretical) rather than extra-theoretical. As such, they are subject to entirely different conditions for developing scientific knowledge than those indicated by Pigliucci in his reference to Gould.

2. IDEAS OF MODERN BIOLOGICAL KNOWLEDGE FROM A METHODOLOGICAL PERSPECTIVE

One of the leading Polish evolutionary biologists, Professor Adam Urbanek (1928–2014), in 1973 published a work entitled *Revolucja naukowa w biologii* [Scientific Revolution in Biology]. It contains a pioneering idea: Its author shows that biological ideas and concepts could be systematized in two orders: reductionist, running from the level of the organism “down,” and compositionist, running from the organism “up.” The first path leads us to genetic knowledge and molecular research, and the second—to evolutionary and ecological knowledge. The synthesis of these orders means that researchers consider the phenomena of the “evolution” of a species and the “development” of an organism always in one of the indicated aspects.

However, the scheme of an extended synthesis of the theory of evolution, presented by Pigliucci and Müller, clearly shows that the reconstruction of biological and evolutionary knowledge (already in the 21st century) is based mainly on the definition of selected research areas, understood as a simple synthesis, which is the sum of the areas and problems that biologists undertake in their research tasks. At the same time, they probably omitted the most crucial question: according to what methodological principles were these tasks, problems and areas combined? It seems that this list shows the need to ask specific questions concerning the emergence of new ideas, conceptual connections between distinguished theoretical components, and establishing an order for explaining evolutionary phenomena due to the complexity of animate evolving objects. This methodological analysis has been attempted before (Łastowski, 1987).

The main idea of the project presented in 1987, showing the connections of evolutionary theories, is to point out the methodological consequences that appear in biological knowledge when the disaggregation of complex structures of research on living matter is carried out.¹⁵ In biologists' research practice, for example, we talk about evolution both when dealing with a species and when considering changes taking place from generation to generation in the gene pool. So, the question arises: How do we reconcile the indicated understanding types? There is one answer: a biologist reasonably uses the term "evolution" when examining the transformation of species and when analyzing the evolution of the gene pool. However, at the same time, due to the different levels of complexity of a biological phenomenon, it must be understood differently. The evolution of species is described differently—in a different conceptual framework—and the evolution of the gene pool taking place at the genetic level is described differently. Therefore, the phenomenon of evolution may be understood differently by researchers, depending on what is being studied. If we talk about evolution in general, we talk about it in an aggregated form. If we talk about the evolution of a single, relatively well-defined biological object, we assume that this phenomenon is disaggregated.

I will now refer to this historical approach to show a "first approximation" of the proposed order of biological and evolutionary concepts. I refer to them here as a diagram of biological-evolutionary theories—Map I, whose relatively simple form is shown below.

¹⁵ This procedure enables the researcher (and, above all, the methodologist) to theoretically "break down" the complex structure of a biological phenomenon in order to obtain a less complex, simpler structure and, consequently, to make a more precise description or explanation of the phenomenon under study. This is not the only procedure used by researchers, but it seems to be one of the most important from the point of view of research tasks in biology. A detailed discussion of this and other methodological deformations and the relations between the relevant concepts adopted in biological research; see (Łastowski, 1987).

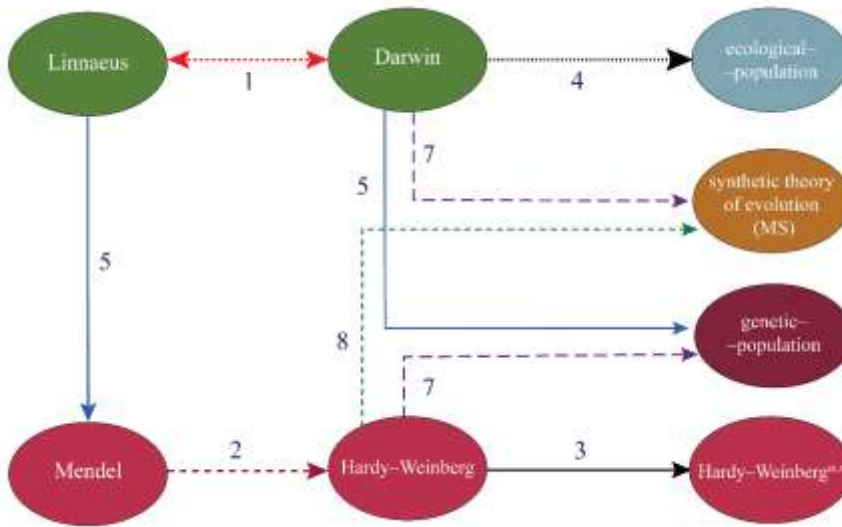


Diagram of biological-evolutionary theories Map I

The diagram above presents a proposal of eight concepts, which are an illustration of the methodological connections that exist between the most important components of the ideas and theories of evolutionary biology reconstructed at that time.¹⁶ The biological concepts/theories distinguished therein determine two main levels: (1) species, initiated by Linnaeus, and (2) genetic, initiated by Mendel. At the same time, they define the main trends in biological research because it is to them that subsequent derivative theories refer (and in some, although rare cases, theories different from the original ones). At level (1), there are Darwin's theory and the ecological-population theory of evolution, represented on the map by the Verhulst-Pearl law and the so-called Lotka-Volterra law. Level (2), next to Mendel's concept, is the Hardy-Weinberg law, along with its specification.¹⁷ In addition to the concepts mentioned above, two more theories are located cross-level: the synthetic theory of evolution and the population-genetic theory of evolution. Moreover, the concepts shown on this map have been organized by appropriate relations connecting the presented ideas. These relations are the following (the markings on the map above correspond to the indicated subsequent methodological relations—there are seven of them):

¹⁶ (Łastowski, 1987, chapter X). The numbers in the diagram and the following explanations correspond to the subsequent relations between important biological ideas and theories.

¹⁷ For a broader description of the components determining these two levels; see (Łastowski, 1987, part 1).

- relation 1: Dialectical Refutation,
- relation 2: Intra-level paraphrase,
- relation 3: Concretization,
- relation 4: Dialectical Intra-level Correspondence,¹⁸
- relation 5: Deaggregating Paraphrase,
- relation 7: Paraphrased Dialectical Concretization-Deaggregation
Correspondence
- relation 8: Aggregating Paraphrase.

However, the map of biological ideas Map I presented in 1987 has severe limitations, e.g. it does not consider the individual level and, consequently, those ideas that could be indicated as significant theoretical extensions at this level. Due to the intensive development of biological knowledge, this scheme requires appropriate broadening and deepening. Nevertheless, this type of methodological correction should take into account not only the internal complexity of intra-theoretical and inter-level connections but also indicate the extension of biological-evolutionary theories to areas that have not been methodologically analyzed so far, despite the conceptual penetration of the thought material accumulated in them.

2.1. Theoretical and methodological extensions to the biological ideas map

The proposal by Pigliucci and Müller analyzed above is interesting, but it ignores the methodological relations in which the relevant ideas, concepts or biological concepts interfere with each other. However, it seems that the map of methodological relations Map I is a good starting point for a broader and more detailed presentation of the complexity of the idea that can be associated with the idea of extended synthesis, i.e. EES. For this purpose, I will significantly modify the map of biological theories from 1987 Map I, building on its basis Map II, in which I will distinguish new component levels and intra—and inter-level connections.¹⁹ The rule of conduct will remain the same, but the consequences of its application reveal new relations, previously unexplored.²⁰

However, the modified form of the map of biological ideas Map II requires comment because it is a proposal for extending Map I. First of all, it distinguishes—by disaggregation—two further levels of research. In addition

¹⁸ Detailed characteristics and courses of the mentioned relationships; see (Łastowski, 1987, chapter VII).

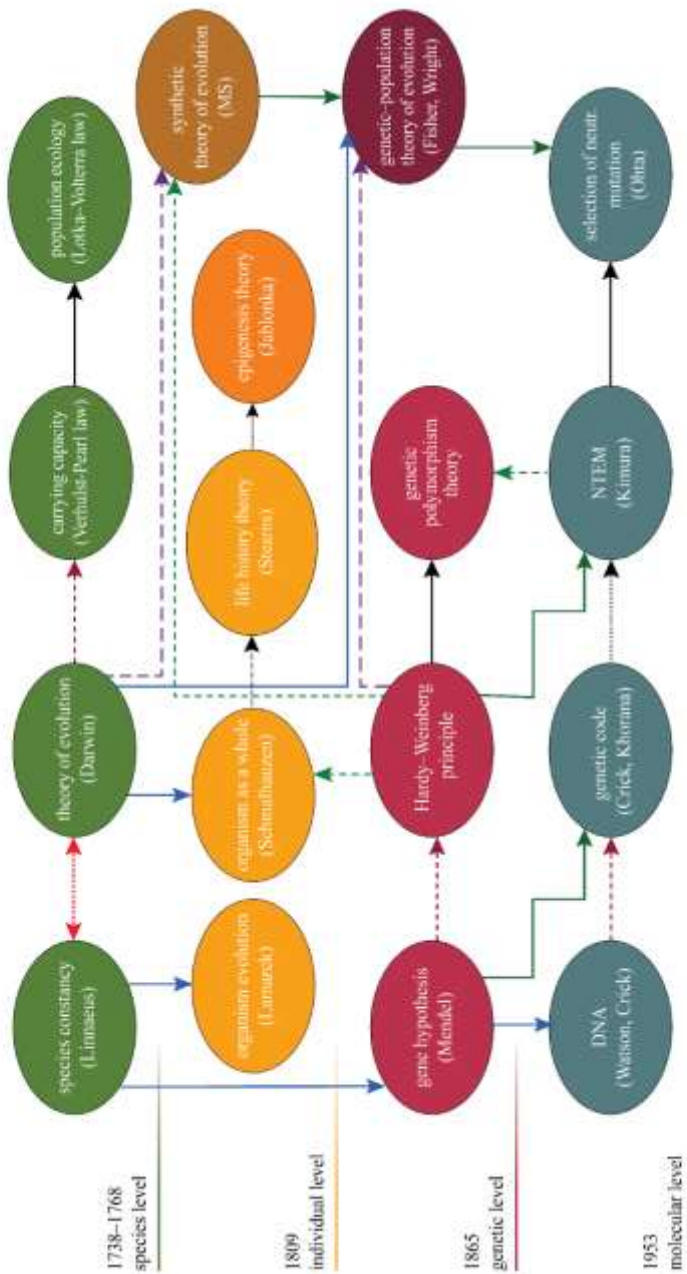
¹⁹ On this matter, I share the view of Chrisantha Fernando and Eörs Szathmáry that MS can be “expanded horizontally and vertically” (Pigliucci, Müller, 2010, p. 209). However, this proposal covers a much broader range of biological ideas than MS.

²⁰ The consistency of the definitions of the relations linking the relevant concepts with Map I is also maintained.

to the previously mentioned ones, i.e. the species and gene levels, we also have the individual and molecular levels. In this form, the order of biological ideas is adjusted to show, on the one hand, the development of biological ideas and theories (including, of course, evolutionary ones) over time and, on the other hand, the cognitive progress that occurs when new hypotheses appear, inspiring researchers in the implementation of the most important research tasks. Starting from the top, on the left side of the diagram, four gradational levels are indicated: species (initiated by Linnaeus' idea; green), individual (distinguished due to Lamarck's idea; orange), gene (designated by Mendel's hypothesis and discoveries; burgundy) and molecular (which was initiated by Watson and Crick with the discovery of the structure of DNA; blue). Depending on the research needs, if the research object is determined, the appropriate conceptual apparatus needed to describe and explain the phenomenon under consideration will also be selected. Intra- and inter-level connections were also highlighted, which "conduct" the content of concepts and the meanings of laws and theories due to the cognitive needs of the biologist researcher. Going down the map, dates are given, indicating that disaggregation was performed based on biological discoveries; there are three such steps in the diagram: descent from the species level to the individual level (due to Lamarck, 1809), descent from the individual level to the gene level (due to Mendel, 1865) and descent from the gene level to the molecular level (due to the discovery by Watson and Crick of the DNA double helix, 1953). Thus, through subsequent gradual steps (as a consequence of the disaggregation procedure), cognitive progress was taking place, involving a deep exploration of the structures of living organisms. It also took place intra-level, when researchers described the studied phenomena more and more precisely at a given level of complexity of living structures.

The numerous connections between ideas, concepts, laws and biological theories indicated in Map II have the status of methodological relations (there are 24 of them). However, a more thorough analysis of these connections allows them to be categorized because some of them have an analogous methodological status. These 24 relationships can be grouped into eight categories of relationships, the characteristics of which are given with reference to the appropriate examples.

Presented relational connections are not the subject of biological reflection because the biologist's research goals are directed at biological phenomena and not at the hidden connections between ideas and research findings. This reflection is a methodological task because recognizing this type of relationships is a specific task and requires a special conceptual apparatus, irreducible to the content and concepts of biological knowledge.



Extended diagram of biological-evolutionary theories Map II

The diagram shown consists of 17 theoretical elements and 24 relationships connecting them. I will explain them rather briefly due to space limitations in this article.²¹

The order of explanation of the relationships selected in the presented diagram is as follows: I will start by showing the horizontal dimension of the map, i.e. the intra-level connections (looking from the upper left side)—in the order: the first level is the species level, the second—the individual level, the next—the gene level and the lowest—the molecular level. Then, I will show²² the vertical dimension of the map, i.e. inter-level connections, reconstructing the basic conceptual connections between them. The most important theoretical connections between the concepts presented in the diagram include: (1) the relationship of dialectical refutation, (2) the relationship of intra-level paraphrase, (3) specification relation, (4) intra-level correspondence relation, (5) disaggregating paraphrase relation, (6) inter-level disaggregation relation, (7) paraphrased inter-level correspondence relation, (8) aggregating paraphrase relation.

HORIZONTAL DIMENSION OF THE MAP

At the species level, there are: Linnaeus's concept, Darwin's theory, the Verhulst-Pearl law and the so-called Lotka-Volterra laws. At the individual level, there are Lamarck's concept, Schmalhauzen's concept of the organism understood as a whole, Stearns' theory of life histories and the theory of epigenesis proposed by Eva Jablonka. At the gene level, we have: the Mendel hypothesis, the Hardy-Weinberg law, the genetic-population theory of evolution and the theory of genetic polymorphism. However, at the molecular level, we should include: Watson and Crick's discovery of the structure of DNA, Crick and Khorane's idea of the genetic code, M. Kimura's neutralistic theory of evolution and the so-called Ohta extension.

Species level

There is a relation of (1) *intra-level dialectical refutation* between Linnaeus's concept and Darwin's theory. Its essence is refutation, i.e. the rejection of the Linnean view about the stability of the biological species. Apart from explaining the existence of species (struggle for existence and natural selection), Darwin also explains the mechanism of evolutionary changes. In

²¹ A more complete study of the issue discussed here should also include justifications for at least some of the concepts highlighted in Map II. However, due to the limitations of the article, it is not possible at this point.

²² Explaining all of them, as there are approximately 24 schematically depicted relationships between theoretical concepts, is beyond the scope of this text, so I have to make a selection, pointing to the most important of them.

other words, based on Darwin's theory, Linnaeus' reasons can be treated as the existence of a species in constant living conditions.²³ In turn, the Darwinian theory is associated with Verhulst-Pearle's (V-P) law because it determines the so-called safe carrying capacity of the species, which corresponds to the Darwinian idea of the adaptively optimal fraction that remains alive. This relation is (2) *an intra-level paraphrase* because the V-P law is the quantitative equivalent of Darwin's qualitatively understood idea of the adaptively optimal fraction. The V-P law at this level is related to the so-called I. and II. Lotka-Volterra law (L-V); this connection is an example of (3) *the relation of concretization* of the V-P law because they also quantitatively determine the safe capacity of various biological populations in two specific evolutionary (and at the same time ecological) situations: competition for food (I. L-V law) and in a situation of predation (II. V-L law).²⁴

Individual (organismal) level

At the individual level, we have the following connections: Lamarck's idea, which initiated the idea of individual evolution, has some—but quite unclear—reference to the idea of Schmalhauzen, who, in continuous experiments on rats, tried to discover the rules of their intergenerational individual variability. The actual continuation of this research appears to be Steven Stearns's concept of life histories (Stearns, 1992). Schmalhauzen's ideas are linked to Stearns' concept by (4) *the relation of intra-level correspondence* because both researchers consider individual variability both in the generational and intergenerational dimensions. Another concept at this level is E. Jablonka's understanding of the body's epigenesis process as a developmental change in which two forces significantly impact the body: heredity and, modifying the former, the influence of life circumstances that the body encounters during its life. Given this relationship of intra-level correspondence, it can be assumed that in further research development, it will turn out that Jablonka's idea is also a form of the (5) *relation of concretization* of Stearns' theory. However, there is no doubt that more advanced concepts within this realm of biological knowledge are aimed at examining epigenetic relationships with evolutionary conditions. This idea guided Lamarck already at the beginning of the 19th century.

²³ This form of refutation can be described as dialectical because, based on Darwin's theory, Linnaeus's idea of the permanence of the species is preserved. An excellent example of this in the conceptual apparatus of the theory of evolution is the concept of stasis, when a species does not evolve despite the passage of time. An example of this is given by Darwin when, in the "tree of life" sketched in *The Origin of Species by Means of Natural Selection*, he indicates species "F" as being in evolutionary stasis.

²⁴ The methodological relations presented at this level also justify that the V-P theorem and the so-called related L-V laws should be referred to as the neo-Darwinist position. This is supported by methodological relations.

Genetic level

This level of biological research was initiated by the discoveries made by Gregor Mendel (1865). His achievements consist essentially of two important ideas: the gene hypothesis (as a material factor of inheritance) and the formulation of principles according to which the proportions of traits passed on to the next generation can be quantitatively determined in the population. The first concept sparked research in experimental genetics, while the second led to population (quantitative) genetics investigations. Another element of the diagram at this level is the Hardy-Weinberg law (1908), which—assuming the real mediation of genes in the inheritance process, but with some significant theoretical simplifications—quantitatively determines the genetic structure of the population and, consequently, also the frequency of occurrence of traits, which these genes determine. In the simplest terms, due to the specific methodological properties of this theorem, the Hardy-Weinberg law (H-W) has two extensions:²⁵ (i) evolutionary, showing the evolutionary consequences of selection (i.e. the genetic-population theory of evolution) and (ii) showing the sources of genetic diversity, i.e. the impact of migration and mutations on changes in the genetic structure of the population (i.e. the theory of genetic polymorphism).

There are methodological relations of the following type between the mentioned theories: (1) between Mendel's gene hypothesis and the H-W law, there is a relation of (2) intra-level *paraphrase* because it transforms the description of inheritance in terms of a fixed frequency of genes determining traits into a quantitative description of the frequency of genotypes determining the state of equilibrium in the gene pool (genetic structure of the population). It is a paraphrase because this relationship transforms the description of a specific object (i.e. a feature in Mendel's hypothesis) into a description of the gene pool that co-determines the frequency of a given feature in the population (H-W law). Therefore, it is a change in the language of describing a genetic phenomenon. Between the H-W law and the theory of genetic polymorphism, there is a (3) *concretization relation*, which brings the content of the H-W law closer to reality by including corrections due to migration and mutation.

²⁵ What I have in mind here is the idealistic nature of the H-W law. It consists of adopting counterfactual simplifying assumptions to theoretically eliminate the influences of selection, migration and mutation and then determining a theoretical, simplified form of the genetic structure of the population. The application of this theorem consists in the fact that, based on empirical data, the actual influence of the above-mentioned factors is estimated, and then appropriate corrections are made to the initial form of the H-W law, thus determining the scale of changes in the genetic structure of the studied population.

Molecular level

The next step in cognitive advancement in biological research was achieved by descending from the gene level (Mendel) to the molecular level. This was due to the discovery of the double helix structure in DNA in 1953 by James Watson and Francis Crick. This discovery then enabled Crick and Khorana to develop the principles of the genetic code, i.e. to determine the order in which the nucleotide bases are arranged when they reflect the correct structure of the DNA helix so that the process of protein biosynthesis proceeds without disruption. These two theoretical structures, i.e. the structure of the DNA helix and the bases of the genetic code, are linked by the (2) *intra-level paraphrase relation* because the codon sequences in the code must correspond to the sequences of nucleotide bases in DNA. At the same time, it is a paraphrase because, in the process of protein biosynthesis, the order of assembly of amino acids into protein structures reflects the order of the bases coding them. The next element of this level is Motoo Kimura's neutralistic theory of molecular evolution (NTEM)²⁶, which is methodologically related to the idea of DNA (4) *intra-level correspondence relation*. This is a correspondence in the sense that while the rules of the genetic code determine the correct assembly sequence of the structure of proteins, which are therefore not subject to selection, (NTEM) defines a set of molecular structures which – due to the neutral nature of these molecules—also it is not subject to the action of selection but only to the random action of genetic drift; in other words, natural selection “does not see” these molecular structures.²⁷ The last element of this level is the so-called Tomoko Ohta's extension. It consists in the fact that, in addition to neutral nucleotide mutations, there are also non-neutral mutations in molecular sequences, i.e. those that are either beneficial changes (very rare) or harmful, negative changes (common). Both of them—by conditioning the course of numerous stages of gene expression—are then recognized by the mechanism of natural selection and as such, they will be preserved (beneficial mutations) or eliminated (harmful mutations). Ohta's extension is related to Kimura's theory by the (3) *concretization relation* because we obtain it when we remove the assumption about the occurrence of neutral mutations.

²⁶ Kimura's theory is the so-called non-Darwinian theory of evolution because the primary mechanism of changes that occur at this level is genetic drift. Its effect can only be discovered when the intensity of natural selection on the molecular endowment of the population is minimal, i.e. almost zero.

²⁷ A detailed analysis of this issue is presented by W. Makalowski (1991) in his work *Mechanizmy ewolucji molekularnej w świetle syntetycznej i neutralistycznej teorii ewolucji. Ewolucja genów tRNA jako kryterium powiązań teoretycznych i stosowalności empirycznej obu teorii*, [Mechanisms of Molecular Evolution in the Light of the Synthetic and Neutral Theory of Evolution. Evolution of tRNA Genes as a Criterion of Theoretical Connections and Empirical Applicability of Both Theories], (doctoral dissertation), AMU, Poznań 1991.

The vertical dimension of the map

I will now move on to the description of inter-level connections. This procedure requires the assumption of disaggregation of relevant biological research structures. Therefore, I will consider connections in the vertical dimension (Maps II).

Let us start from the upper left corner (Map II), where the (5) *disaggregating paraphrase relation* is shown, which connects Linnaeus' ideas with Mendel's gene hypothesis, Watson and Crick's discovery, and Lamarck's concept. This way, we obtain the following findings: (5a) The Linnean morphological description of the species is then replaced—in Mendel's language—by the description of a set of genes determining traits; (5b) the discovery of the structure of DNA, in turn, allows us to state that the specific structure of species DNA is responsible for the appropriate determination of features (Mendel's hypothesis); (5c) it can also be said that this relation determines Lamarck's position towards Linnaeus; this means that the variability of the organism must violate the ideal pattern of phenotypic characteristics that is—according to Linnaeus—assigned to a given species; (5d) the same relation connects Darwin's theory with Schmalhauzen's concept in such a way that when Darwin claims that natural selection selects an adaptively optimal fraction, Schmalhauzen says that this fraction is a consequence of the action of stabilizing selection, because in this mechanism of evolution it is crucial to optimize the intensity of adaptive features during the body's epigenesis. This relation (in variant 5e) also occurs between Darwin's theory and the genetic-population theory of evolution and, as a result, reduces the evolution of a species to the description of the effects of selection in the gene pool without taking into account the test of natural selection (from a methodological point of view, this is a conceptual peculiarity of population genetics)²⁸. This paraphrases the concept of natural selection because, in the language of the genetic-population theory of evolution, it corresponds—by definition—to the concept of adaptive value, the intensity of which is reduced by the selection coefficient theoretically assumed in the research.

The (6) *inter-level disaggregation relation* (in variant 6a) links Mendel's hypothesis with the idea of the genetic code because the rules of the genetic code reflect the order of gene determination in the process of epigenesis; variant (6b) of this relationship also works between STE and the genetic-population theory of evolution, and in variant (6c) between the genetic-population theory of evolution and Ohta's extension, as well as between the H-W law and Kimura's theory—this is variant (6d). However, variant (6b)

²⁸ S. Ginnobili discusses the issue of the conceptual and linguistic discrepancy indicated here in the article *Missing Concepts in Natural Selection Theory Reconstruction*, *History and Philosophy of the Life Sciences*, 2016, 38 (8), pp. 4–6.

transforms the qualitative description of the effects of selection on the basis of STE into a quantitative description of the effects of selection in the language of the genetic-population theory of evolution; the following variant (6c) indicates what frequencies of molecules described in Kimura's theory and indicated in Ohta's extension correspond to the frequencies of genotypes subject to selection in the description of the population-genetic theory of evolution. Variant (6d) of this relationship indicates the appropriateness of the frequency balance of genotypes in the population's genetic structure determined by the H-W law in relation to the frequency of neutral molecules that guarantee the survival of the population according to Kimura's theory.

A particularly interesting variant of connections is the relation of (7) *paraphrased inter-level correspondence* (concretization-disaggregation), which has two variants: [#] when it occurs between Darwin's theory and STE and [##] when it connects the H-W law with the genetic-population theory of evolution. The [#] variant transforms the description of evolution from natural terms (traits) into the language of Mendelian genetics (genes) because it introduces the concept of mutation and recombination into the STE structure. However, the [##] variant transforms the description of the state of equilibrium in the genetic structure of the population (H-W law) into a description of the state of unstable equilibrium because the selection is limited to indicating the number of genetically impaired individuals. It is also a specification of the H-W law because it considers the selection factor.

Map II also indicates the relation of the (8) *aggregation paraphrase*. This relationship links three theoretical structures: the H-W law (gene level) with Schmalhauzen's concept (individual level), the H-W law with STE (species level) and Kimura's theory (molecular level) with the theory of genetic polymorphism (gene level). The first one is that the content of the H-W law (the state of equilibrium in the genetic structure of a population), expressed in genetic terms, is transformed into a description in natural terms (traits), which allows STE to aggregate evolutionary changes described in terms of frequency and intensity of features. The second aggregation connection is a paraphrase of H-W in the language of Schmalhauzen's concept, which means that the idea of balance in the H-W law (at the gene level) corresponds to Schmalhauzen's idea of stabilization of the evolutionary process (at the individual level). The third connection is the aggregation relationship between Kimura's theory (molecular level) and the genetic polymorphism theory (gene level). In this case, the aggregation means that the concept of genetic polymorphism (as a specification of the H-W law) can also include the idea of neutral mutations in parallel with other factors of this theory, such as non-neutral mutations and migration.

2.2. Selected examples and interpretations from the map of biological ideas

1. In the given scheme, more complex inter-level transitions can be interpreted. Let us take, for example, the connection between Linnaeus' idea and the H-W law. Linnaeus assumes that the species is not subject to change; Mendel shows what gene composition determines the stability of inheritance of traits, and the H-W law quantitatively describes the state of equilibrium (and thus relative stability) of the genetic structure of a population at given gene proportions. Consequently, the connection of these three ideas (i.e. Linnaeus, Mendel and the H-W law) allows us to justify genetically in which situation Linnaeus is right and in which Mendel is right. In this way, we obtain a genetic interpretation of the initial concept (non-genetic—Linnaeus), a thesis that is doubly paraphrased and disaggregated (through two levels of complexity). In this way, the thesis about species constancy receives a genetic equivalent (state of equilibrium) in the language of population genetics (i.e. the H-W law).

2. [Map II] shows that the concept of evolution generally exhibits a multi-level nature (Łastowski, 1987, 2015). The form presented is a theory spanning several (i.e. four) levels of biological knowledge. STE [MS], population genetic theory of evolution and the latest version of the extended evolutionary synthesis [EES] have just such an inter—and multi-level character.

3. The inter-level order is determined by the relationship of disaggregation, to which ideas of a higher level are subject to those of a lower one. The aggregation relation determines the intra-level order. Which relationship a researcher uses depends on his or her research views (including theoretical assumptions).

4. The historical development of biological ideas occurred in both horizontal and vertical dimensions. Discoveries and theories proposed since Linnaeus can be mapped according to the types of simplifying assumptions researchers made. Some dealt with species or gene pools, and others chose to reflect on individuals. And in the last 50.70. years, a clearly disaggregated approach was developed, as it focused on the gene and molecular levels.

5. The classic approach to research on the development of science emphasizes intra-level analysis of theory. We can, therefore, identify four levels at which methodological analysis conducted in a traditional style would be carried out. These are the species, individual, gene and molecular levels. Each of them contains achievements that are interesting from the methodological point of view, e.g. the “Linnaeus → Darwin” line, the “Schmalhauzen → Stearns” line, the “Darwin → STE” line, the “H-W → population genetics” line. Each path of connections distinguished here is individually interesting

cognitively for both a methodologist and a biologist with a historical orientation.

6. The vertical structure of the map indicates groundbreaking achievements in biology. Such a turn means that researchers “opted for” a different level of their research (e.g. Lamarck) or discovered an animate structure different from the traditionally accepted one. They also tried to show the cognitive consequences of these decisions. An example is the “descent” from the individual level to the gene level (as a result of which Mendelian genetics is created). An example of “descent” from the gene to the molecular level is not only the discovery of the DNA helix structure but also Kimura’s formulation of the non-Darwinian neutralistic theory of molecular evolution.

7. Also interesting are changes in the opposite direction, i.e. aggregation of the research object. Important examples are: the transition from the H-W law to STE or to population genetics, or from the theory of life histories (Stearns) to the Verhulst-Pearl law. These are not all possible and interesting consequences of the development of biological ideas in the second half of the 20th and early 21st centuries. Only selected ones are indicated; unfortunately, there is no space for other, more detailed ones.

CONCLUSION

In summary, it is worth noting other important methodological issues:

1. The reconstructed relationships prove that the theory of evolution is a multi-level theory—it describes phenomena from different levels of the organization of life. The vertical dimension shows the levels of complexity of the studied phenomena, and the horizontal dimension shows the development of biological ideas (theories) within a given level.
2. They enable building arguments in a methodologically controlled way, i.e. moving between levels according to needs and cognitive abilities.
3. These relations not only bind the relevant theories of biological (evolutionary) knowledge. Their theoretical applications include, among other things, the fact that they can be combined into sequences and used to explain evolutionary phenomena at various levels of complexity. This trend in scientific knowledge creation involves constructing complex narratives that explain the processes of biological phenomena, including evolutionary ones. Evidence of this cognitive activity is found not only in the book edited by Pigliucci and Müller (2010) but

also in the article by Laland et al. (2015) that further develops its ideas.

Map II shows the main biological (and evolutionary) ideas. As mentioned in the Introduction, the dynamic development of biological knowledge also affects “neighbouring” fields, e.g. the humanities and social sciences. Thanks to some researchers, such as the achievements of Edward O. Wilson, we are dealing with an overlap of inspirations flowing from the biological sciences to the social sciences. The main result of this interaction is the overlap of selected biological and social ideas (e.g. in research on the determinants of behaviour). One result of this influence is sociobiology. Another direction in which biological-evolutionary ideas overlap with the area of humanities research is psychology and cognitive sciences. Due to Leda Cosmides, John Tooby, Steven Pinker, and David Buss, evolutionary ideas permeated psychology, contributing to the emergence of evolutionary psychology. And although this impact has not turned out to be groundbreaking so far, it does not mean that selected biological ideas will not inspire researchers in the humanities and social sciences in the near future. However, it is undoubtedly true that reflection on the methodological structure of the currently dominant field of knowledge, i.e. biological sciences, will make the inspiration for new areas of research particularly creative. The first signs of this phenomenon can already be seen, for example, in attempts at molecular research (using molecular structures, so-called markers) in the course of selected developmental pathways constituting the processes of epigenetic development. In this way, regularities and connections between the development of the organism and its molecular endowment are sought.

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