

# Biological and Social Phases of Big History and Universal Evolution: Similarities, Differences, and the Growth of Complexity

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**Abstract:** In this paper, Grinin et al. survey general similarities and differences between biological and social macroevolution and phases of Big History. The comparison of biological and social evolution is an important but (regrettably) understudied subject. The authors have endeavored to make a systematic comparison between biological and social evolution at different levels of analysis and in various aspects. They have formulated a considerable number of general principles and rules of evolution, and worked to develop a common terminology to describe some key processes in biological and social evolution. In particular, Grinin et al. have introduced the notion of ‘social aromorphosis’ to describe the process of widely diffused social innovation that enhances the complexity, adaptability, integrity, and interconnectedness of a society or social system. This work has convinced the authors that it might be possible to find mathematical models that can describe important features of both biological and social macroevolution. In the Appendix the authors consider a concrete mathematical model that they deem capable of describing important features of both biological and social macroevolution.

**Keywords:** *social evolution, biological evolution, mathematical model, biodiversity, population growth, positive feedback, hyperbolic growth.*

## **Introductory Remarks**

In the recent decades the research of the Universe as a whole has made a significant progress. This is especially clearly manifested in the development of the Big History (Christian et al., 2013; Grinin et al., 2014; Spier, 2015; Rodrigue et al., 2015, 2016, 2017; Christian, 2017, 2019; Henriques et al., 2019; Voros, 2019; Panov et al., 2020; Henriques & Volk, 2023; LePoire et al., 2025a, 2025b, 2025c). Big History provides a unique opportunity to consider the development of the Universe as a single process. Big History approach regards the process of evolution as a continuous and unified process from the origins of the Universe to the present state of humankind and further to the future. Cosmic, geological/ biological, and social phases of Universal evolution have a genetic and structural continuity.

The importance of this approach is doubtless. Within Big History researchers distinguish some main evolutionary laws and principles (concerning energy and complexity, for example). However, it is very important to recognize that there are many more such integrating principles, laws, mechanisms and patterns of evolution at all its levels than it is usually supposed (Grinin et al., 2008, 2009, 2011, 2012; Grinin, 2014, 2017, 2018, 2019, 2020, 2023; Grinin & Grinin 2019, 2020, 2023; Korotayev, 2018, 2020a, 2020b, 2024; LePoire, 2020; Panov et al., 2020; Korotayev & LePoire, 2025; LePoire et al., 2025a, 2025b, 2025c).

In our paper we will demonstrate that one can find common traits in development, functioning, and interaction of apparently rather different processes and phenomena of Big History if we regard this in connection with the macroevolutionary paradigm (see Grinin, Carneiro, et al., 2011).

On the one hand, Big History is very similar in content to a coherent description of the universal macroevolutionary process, because it shows the formation of new levels of complexity in the process of historical development of the Universe (see LePoire et al. 2025a, 2025b, 2025c). At the same time, the general features of the development, operation and interaction are found in many seemingly dissimilar

processes and phenomena, showing a particular aspect of universal evolution as real similarities that occur in a variety of manifestations at all levels and in all lines. Therefore, the combining of the potential of the Big History with evolutionary approaches can open new horizons in this direction.

We plan to analyze the biological and social phases of the Big History and global evolution to give ideas about the driving forces and patterns of transition from one phase to another. We will discuss common, i.e. cross phasing, evolutionary and Big History rules, principles, patterns and laws; at the same time, we will highlight the peculiarities of realization of those rules at each phase.

We believe that it is possible to identify a considerable number of such similarities and to group them into large blocks. In particular, we will consider such features as:

- Ability for self-preservation and self-organization.
- Law of life cycle of various objects.
- Rule of evolutionary block assemblage.
- Unevenness and catastrophes.
- Typical and unique objects.
- Recombination or circulation of matter in nature.

Comparison between different phases of Big History is especially important, because such an analysis suggests new promising possibilities to deepen our understanding of the course, trends, mechanisms and peculiarities of different phases of Big History.

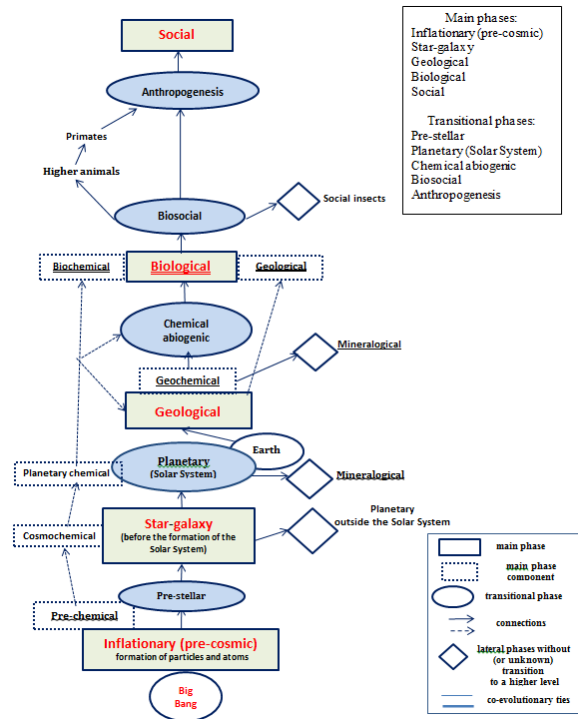
Each subsequent phase of Big History is accompanied by the emergence of new evolutionary mechanisms. For example, certain prerequisites and respective preadaptations can be normally detected within the previous phase; emergence of new evolutionary mechanisms does not imply the invalidation of those active during the previous phases.

One can observe the emergence of a complex system of interaction between various forces and mechanisms determining the evolution of new forms. For example, biological organisms operate in the framework of certain physical, chemical and

geological laws; behavior of social systems and people has certain biological limitations and so on. Some models (similar in principle) may emerge not only in the breakthrough points, changing the main line of evolution, but also in some directions that may be regarded as dead-ends (from the Big History leading line perspective). For example, the emergence of social life forms took place in many phyla and classes – from bacteria to insects, birds and mammals. Additionally, among insects, we can find rather high forms of social organization. See Fig. 1 for the place of this lateral phase as a sideline in the general scheme of Big History.

In this paper, we primarily analyze similarities and differences between social and biological evolution. This is moreover important because the comparison of biological and social evolution is a regrettably understudied subject,

We are still at the stage of a vigorous discussion about the applicability of Darwinian evolutionary theory to social/cultural evolution. Regrettably, we all are mostly dealing with a polarization of views. On the one hand, we confront a total rejection of Darwin's theory of social evolution. On the other, we deal with those who stress that cultural evolution demonstrates all the key Darwinian evolutionary characteristics.



**Fig. 1. Main and transitional phases of Big History**

We believe that, instead of following the outdated objectivist principle of ‘either – or’, we should concentrate on the search for methods that could allow us to apply achievements of biological evolutionary science to social evolution and *vice versa*. In other words, we should concentrate on the search for productive generalizations and analogies for analysis of evolutionary mechanisms. The Big History approach aims for inclusion of all mega-evolution within a single paradigm.<sup>1</sup> Hence, this approach provides an effective means to address the above-mentioned task.

### On evolutionary mechanisms

As is known, not only systems evolve, but mechanisms of evolution evolve too. This concept also appears rather fruitful as regards the development of Big History itself. Let us consider some of the parameters and examples that we might consider.

The emergence of each new phase of Big History is accompanied by the emergence of new evolutionary mechanisms; therefore, certain prerequisites and preadaptations can be detected within the previous

<sup>1</sup> This paradigm is discussed in Grinin, Carneiro et al., 2011.

phase. So, development of new mechanisms of evolution does not imply invalidation of evolutionary mechanisms that were active during previous phases (cf. LePoire et al., 2025b, 2025c). As a result, one can observe the emergence of a complex system of interaction of forces and mechanisms determining the evolution of new forms. Biological organisms operate in the framework of certain physical, chemical and geological laws (see Kutter, 2015 on this topic and also on the comparison between physical and biological evolution).

Likewise, the behaviors of social systems and people have certain biological limitations. New forms of evolution that determine Big History transition into a new phase may result from activities going in different directions. Some evolutionary forms that are similar in principle may emerge not only at a breakthrough point, but may also result in a dead-end – from the overall view of Big History. For example, the emergence of social forms of life took place in many phyla and classes – bacteria, insects, birds and mammals. Additionally, among insects, we can find rather high forms of socialization (See, e.g., Chittka & Rossi, 2022; Reznikova, 2011; Ryabko & Reznikova, 2009; Robson & Traniello, 2002). Despite the common trajectory and interrelation of social behaviors by these various life forms, there has been a large overall difference in the impact that each has had on the Earth.

What is more, as regards information transmission mechanisms, it appears possible to speak about certain ‘evolutionary freaks’. Some of those mechanisms (in particular, the horizontal exchange of genetic information) were spread rather widely in the biological evolution of simple organisms but were later discarded (or transformed into highly specialized mechanisms, e.g., sexual reproduction) among more complex organisms. Today, they are mostly confined to the simplest forms of life. We mean the horizontal exchange of genetic information (genes) among microorganisms, which makes many useful genetic

‘inventions’ literally a sort of ‘commons’ of microbe communities. Among the bacteria, the horizontal transmission of genes contributes to the fast development of antibiotic resistance (e.g., Markov & Naymark, 2009). It is important to keep in mind here that diversity, symbiosis, division of functions and information exchange are the original properties of earthly life (Markov, 2014: 32). It is important to keep in mind that viruses can be considered as basic information agents that transmit genetic information and are thus the basic molecular tool of evolution. Moreover, this tool is beginning to be used by humans for the genetic alteration of many organisms, including ourselves (Grinin A. 2025).

For the present paper, the following turns out to be important: The horizontal exchange of genetic information (in its general function) is distantly similar to those forms of information exchange that became extremely important for social evolution – the direct borrowing of innovations and their introduction into social life. Hence, principles and mechanisms that appear of marginal relevance at a certain phase of Big History may turn out to be extremely important in a later phase.<sup>2</sup>

These parallels suggest that analysis of similarities and differences between the mechanisms of evolution may help us to understand the general principles of megaevolution<sup>3</sup> and Big History in a much fuller way. They may also help us to better understand their driving forces and supra-phase mechanisms (mechanisms that operate in two or more phases of Big History) (Grinin & Korotayev, 2008, 2009a, 2009b; Grinin, Markov, & Korotayev, 2009, 2011, 2013, 2022; Grinin, Korotayev, & Markov, 2020; Korotayev, 2018, 2020b, 2024, 2025; LePoire et al., 2025a, 2025b, 2025c; Grinin & Grinin, 2025).

Let us return now to a comparison of biological and social evolution. It is important to describe similarities and differences between these two types of macroevolution – at various levels and in various aspects. This is necessary because such comparisons

<sup>2</sup> Note that in the biological macroevolution the ‘borrowing’ is found mostly at lower levels of the biological evolution, whereas it is found much less frequently at higher levels. The opposite situation is observed in social macroevolution – in general, the older the society, the lower its borrowing rate (incidentally, this accounts to a considerable extent for

a low rate of change in the majority of ancient societies).

<sup>3</sup> We denote as *megaevolution* all the process of evolution throughout the whole of Big History, whereas we denote as *macroevolution* the process of evolution during one of its particular phases.

tend to be deformed by conceptual extremes<sup>4</sup> and tend to be incomplete. These limitations are true even in respect of the above-mentioned paper by Mesoudi, Whiten and Laland (2006), as well as a rather thorough monograph by Christopher Hallpike, *Principles of Social Evolution* (1986). There, Hallpike offers a fairly complete analysis of similarities and differences between social and biological organisms, but does not provide a clear and systematic comparison between social and biological evolution.

### Section 1. Biological and Social Organisms: A Comparison at Various Levels of Evolution

There are a few important and understandable differences between biological and social macroevolution, nonetheless, it is possible to identify a number of fundamental similarities. One may single out at least three basic sets of shared factors.

- First of all, there are similarities that stem from very complex, non-equilibrium, but stable systems whose principles of function and evolution are described by General Systems Theory, as well as by a number of cybernetic principles and laws.

- Secondly, we are not dealing with isolated systems but with a complex interaction between organisms and their external environment. As a result, the reaction of systems to external challenges can be described in terms of general principles that express themselves within abiological reality and a social reality.

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<sup>4</sup> This is typical, for example, for a very interesting and controversial article by Mesoudi, Whiten and Laland *Towards a Unified Science of Cultural Evolution* (2006), where we clearly deal with an attempt to impose the Darwinian methodology on the study of social evolution (see also Mesoudi, 2021). The importance of the above-mentioned differences (including such fundamental differences as the absence in social evolution of a clear distinction between genotype and phenotype) is downplayed by a statement that those differences are either illusory or unimportant (*Ibid.*: 345). Such an approach also reduces the value of a rather interesting methodology that they propose.

<sup>5</sup> It appears appropriate to mention that the genomes of the humans and the chimpanzees differ by ten major genome reorganizations. Some time ago it turned out

- Thirdly, it is necessary to mention a direct ‘genetic’ link between the two types of macroevolution and their mutual influence.

It is important to emphasize that similarity between the two types of macroevolution does not imply commonality. Rather significant similarities are frequently accompanied by enormous differences. For example, the genomes of chimpanzees and the humans are 98 per cent similar. However, there are enormous intellectual and social differences between chimpanzees and humans that arise from the apparently ‘insignificant’ variations between the two genomes.<sup>5</sup>

It appears reasonable to continue the comparison between the two types of macroevolution on the basis of the analysis used by Hallpike (1986: 33), who singles out the following similarities between social and biological organisms:

1. ‘The institutions of societies are interrelated in a manner analogous to the organs of the body, and preserve their continuity despite changes of individual membership, just as individual cells are renewed in organs.’

2. ‘There is a specialization of organic functions analogous to the social division of labor.’

3. ‘In both cases self-maintenance and feedback processes occur.’

4. ‘There are adaptive responses to the physical environment.’

to be possible to sequence the genome of the rhesus macaque (a special issue of the *Science* was devoted to this subject; see in particular RMGSAC, 2007). This is the third primate genome that was sequenced (after the human and chimpanzee genomes). Up to that moment, when detecting differences between the genomes of the humans and the chimpanzees, specialist could not determine which of those differences emerged in the human evolutionary line, and which appeared in the evolutionary line of the chimpanzees. The reading of the rhesus macaque genome substantially facilitated this task. The comparison with the macaque genome allowed detecting that three of those differences happened in the human evolutionary line, whereas the other seven occurred in the evolutionary line of the chimpanzees (see Markov & Naymark, 2009 for more detail).

5. ‘In organisms we find the transmission of matter, energy, and information analogous to trade, communication, *etc.*, in societies.’

According to Hallpike (1986: 33–34), societies are unlike organisms in the following respects:

1. ‘They are not physical entities at all, since their individual members are linked by information bonds, not by those of a purely physical nature.’

2. ‘Societies are not clearly bounded, *e.g.*, two societies may be distinct politically, but not culturally or religiously.’

3. ‘Societies do not reproduce, so that cultural transmission from generation to generation is indistinguishable from general processes of self-maintenance.’<sup>6</sup>

4. ‘Societies are capable of metamorphosis to a degree only found in organic phylogeny.’

5. ‘The individual members of a society, unlike cells, are capable of acting with purpose and foresight, and of learning from experience.’

6. ‘Structure and function are far less closely related in societies than in organisms.’

Hallpike also comes to the sound conclusion that similarities between social and biological organisms are in general determined by similarities in organization and structure (we would say similarities between different types of systems). As a result, Hallpike believes that one can use certain analogies when institutions can be represented as similar to some organs. In this way, cells may be regarded as similar to individuals; central government similar to the brain, and so on. Herbert Spencer(1898) and Émile Durkheim(1893/1991) are important representatives of this tradition (see alsoHeylighen, 2011). Hallpike also has sufficient grounds to add Alfred Radcliffe-Brown and Talcott Parsons.

When comparing biological species and societies, Hallpike (1986: 34) singles out the following similarities:

1. ‘Species, like societies, do not reproduce.’
2. ‘Both have phylogenies and metamorphosis.’
3. ‘Both are composed of competing individuals.’

He also singles out the following difference: ‘*Unlike* species, however, societies are organized

systems, whereas species are simply collections of individual organisms’ (Hallpike, 1986: 34).

**Table 1.** Similarities and differences between social and biological organisms, as described by Hallpike (1986)

Similarities	Differences
Social institutions are interrelated in a manner analogous to the organs of the body.	Individual societies do not have clear boundaries. For example, two societies may be distinct politically, but not culturally or religiously.
Despite changes in membership, social institutions maintain continuity, as do biological organs when individual cells are replaced.	Unlike organic cells, the individuals within a society have agency and are capable of learning from experience.
The social division of labor is analogous to the specialization of organic functions.	Social structure and function are far less closely related than in organic structure and function.
Self-maintenance and feedback processes characterize both kinds of system.	Societies do not reproduce. Cultural transmission between generations cannot be distinguished from the processes of system maintenance.
Adaptive responses to the physical environment characterize both kinds of system.	Societies are more mutable than organisms, displaying a capacity for metamorphosis only seen in organic phylogeny.

<sup>6</sup> However, there are cases when societies create new societies rather similar (with basically the same ‘memotype’) to the ‘maternal’ ones, for example, with

the establishment of settler colonies. See the next section for more information on the differences in ways of information transmission.

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<p>The trade, communication, and other transmission processes that characterize social systems are analogous to the processes that transmit matter, energy, and information in biological organisms.</p>	<p>Societies are not physical entities, rather their individual members are linked by information bonds.</p>
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Further, Hallpike tries to demonstrate that, because of such differences between biological and social organisms,<sup>7</sup> the very idea of natural selection does not appear to be very productive with respect to social evolution. We believe that his proofs are not very convincing, although they make some sense in certain respects. In addition, his analysis is concentrated mostly at the level of an individual organism and an individual society. He hardly moves at the supra-organism level (though he, of course, discusses the evolution of species). We believe that with this, Hallpike (notwithstanding his desire to demonstrate the sterility of the application of Darwinian theory to social evolution) involuntarily amplifies the effect of similarity between biological and social evolution, because the analogy between the biological organism and society (as Hallpike admits himself) is rather salient indeed.

On the other hand, Hallpike does not take into account the point in social evolution where a few substantially new supra-socium levels of development emerge. We contend that it is very important to consider not only evolution at the level of a society but also at the level above individual societies, as well as the point at which both levels are interconnected. The

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<sup>7</sup> Because the systems of transmission of traits within biological and social systems are rather different; because of the higher degree of complexity of social systems, and so on.

<sup>8</sup> Though it cannot be excluded that this is still possible in primates who can borrow some patterns. At least we can talk about borrowing technologies during the period of anthropogenesis. And since some properties do not appear suddenly, but are the result of pre-adaptations, we can assume that to some extent the

supra-organism level is very important, as regards biological evolution (but, perhaps, less so with respect to social evolution). Thus, it might be more productive to compare societies with ecosystems rather than with organisms or species. However, this would demand the development of special methods, as in this case it would be necessary to consider the society not as a social organism, but as a part of a wider system, which includes the natural and social environment.

We identify the following differences between the social and biological evolution.

*A. At the Level of an Individual Society and an Individual Biological Organism*

1. As Hallpike (1986: 33) notes, societies are capable of such rapid evolutionary metamorphoses that they were not observed in the pre-human organic world. However, social systems are not only capable to change and transform, they are also capable to borrow innovations and new elements.

2. They may be also transformed consciously and with a certain purpose. Such characteristics are almost absent in natural biological evolution in any form.<sup>8</sup> In the process of social evolution the same social organism may experience radical transformation more than once.

3. Key information transmission differs significantly in biological and social evolution (we shall consider this point in more detail in the next section).

4. In biological evolution, the acquired characteristics are not inherited; thus, they do not influence the biological evolution that proceeds very slowly. This point will be also considered in more detail in the next section.

5. It appears very important to note that, though biological and social organisms are significantly

property of borrowing and transferring to new generations by learning could have existed before the hominids. It has also been suggested that “just as a biological species is characterized by its genetic information (genotype) and the biological traits of the corresponding organism (phenotype), a ‘species in a broader sense’ is characterized by a certain general information and the traits of the resulting form” (Glötzl, 2025: 268).

(actually ‘systemically’) similar, they are radically different in their capabilities to evolve. The biological organism does not evolve by itself; evolution may only take place at a higher level (population, species, etc.), whereas social evolution can often well be traced at the level of an individual social organism. What is more, it is frequently possible to trace the evolution of particular institutions and subsystems within a social organism.

### B. As Regards the Results of Social/Natural Selection

1. Biological evolution is more additive (cumulative) than substitutive; put in another way: ‘the new is added to the old’. In contrast, social evolution (especially during the two recent centuries) is more substitutive than additive: ‘the new replaces the old’ (Grinin, Markov, & Korotayev, 2011, 2022). However, it should be borne in mind that 97% of all species that existed on Earth no longer exist today, although they still had a certain influence on further evolution in the form of their contribution to the genome of currently existing species.

2. Since social evolution is different from biological evolution, in respect of mechanisms of emergence, fixation and diffusion of evolutionary breakthroughs (aromorphoses), this leads to long-term restructuring in size and complexity of social organisms. It is important to note that, in contrast to biological evolution, where some growth of complexity is also observed, such social reorganization becomes continuous. In recent decades, societies that do not experience a constant and significant evolution look inadequate and risk extinction. In addition, size of societies (and systems of societies) tends to grow constantly through more

and more tightly integrative links (this trend has become especially salient in recent millennia), whereas the trend towards increase in the size of biological organisms in nature is rather limited and far from general.

3. Within social evolution, we observe the formation of special suprasocietal systems that also tend to grow in size. This can be regarded as one of the results of social evolution and serves as a method of aromorphosis fixation and diffusion.

### C. At Supra-organic (Suprasocietal) Level

As a result of the above-mentioned differences, within the process of social evolution, we observe the formation of two types of special suprasocietal systems: A) amalgamations of societies with varieties of complexity that have analogies to biological evolution; B) emergence of elements and systems that do not belong to any society, in particular that lack many analogies to biological evolution.

Naturally, type B needs a special comment. The first type of supra-organic amalgamation is rather typical not only for social but also for biological evolution.<sup>9</sup> However, within biological evolution, amalgamations of organisms with more than one level of organization<sup>10</sup> are usually very unstable and are especially unstable among highly organized animals. Of course, analogues do exist within the communities of some social animals (e.g., social insects, primates). Neither should we forget that scale is important: while we might compare a society with an individual biological organism, we must also consider groups of organisms bound by cooperative relationships (see, e.g., Boyd & Richerson, 1996; Reeve & Hölldobler, 2007). Such groups are quite common among bacteria and even among viruses. These caveats aside, it remains the case that within social evolution, one observes<sup>11</sup> Within social evolution, we observe the emergence of more and more levels: from groups of

<sup>9</sup> There is, however, a major difference: any large enough society usually consists of a whole hierarchy of social systems (e.g., with respect to a typical agrarian empire these would be: nuclear family – extended family – clan community – village community – primary district – secondary district – province), so that it can hardly be compared with a single biological organism (though both systems can still be compared functionally, as is correctly noted by Hallpike [1986]).

<sup>10</sup> We could mention various flocks and packs of animals as examples of such amalgamations with one level of organization.

<sup>11</sup> More complex superorganic amalgamations may be found in the biological evolution among less complex organisms. This trend seems to be opposite to what is observed in the social evolution, though, say, village communities in more complex societies tend to be less complex than in more simple ones (see, e.g.,

small sociums to humankind as a whole. Of course, it makes sense to recollect analogies with social animals: social insects, primates and so on. Neither should we forget to compare society with the individual biological organism but also with groups of organisms bound by cooperative relationships. Such groups are widely present among bacteria and even among viruses (see Grinin A. 2025; see also Solé & Santiago, 2019; Wu, 2020).

It should be noted that modern biologists have developed well respected theories that account for the emergence of intragroup cooperation and altruism, including competition, kin selection, group selection and so on (see, *e.g.*, Reeve & Hölldobler, 2007). However, it is not clear if societies should be really compared with groups of organisms rather than individual organisms, whether we should not consider societies within the system of numerous intersocietal links?

In any case, it is clear that the level of analysis is very important for comparison of biological and social evolution. Which systems should be compared? Such analogies are more frequent when society (the social organism) is compared to a biological organism or species. However, in many cases, it may turn out to be more productive to compare societies with other levels of the biota's system organization: with populations, ecosystems and communities, with particular structural elements or blocks of communities (*e.g.*, with particular fragments of trophic networks or with particular symbiotic complexes), with colonies (with respect to colonial organisms), or finally – and this is the closest analogy – with groups of highly organized animals (cetaceans, primates, and other social mammals or termites, ants, bees and other social insects).

Thus, here we are confronting a rather complex and hardly studied methodological problem: which levels of biological and social processes are most congruent? What are the levels whose comparison could produce the most interesting results? In general, it seems clear that such an approach should not be a mechanical equation of 'social organism = biological organism' at all times and in every situation. The comparisons should be operational and instrumental. That means that we should choose the scale and level of social and

biological phenomena, forms and processes that are adequate for their respective tasks.

We would say again that sometimes it is more appropriate to compare an individual biological organism with a society, whereas in other cases it could well be more appropriate to compare a society with a community (of, say, ants or bees), a colony, a population or species. We believe that the issue of the 'presence' of the social ontogenesis (and its comparison with the biological ontogenesis) should be studied in this framework (see Grinin, Markov, & Korotayev, 2022: ch. 6 for more details). However, there are some cases when it seems more appropriate to compare social ontogenesis with biological phylogenesis. Hence, different scales and types of scientific problems need special approaches. This subject will be discussed further in the subsequent section of the present paper.

## Section 2. Similarities and Differences at the Level of Evolutionary Mechanisms

### 1. Biological and Social Aromorphoses

In certain respects, it appears reasonable to consider biological and social macro-evolution as a single macro-evolutionary process. This implies the necessity to comprehend the general laws and regularities that describe this process, though their manifestations may display significant variations, depending on properties of a specific evolving entity (biological or social). We believe that many similarities and differences in laws and driving forces in the biological and social phases of Big History can be comprehended more effectively if we apply the concepts of biological and social aromorphosis.

The application of the notion of biological and social aromorphosis has helped us to detect a number of regularities and rules that are common for biological and social evolution – 'payment for the arogenic progress', 'special conditions for the aromorphosis emergence', and so on. Such rules and regularities are similar for both biological and social phases of Big History. However, we shall not analyze them in the present paper.

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Korotayev, 1995, 2003: 75–90; 2022; Korotayev et al., 2000, 2011).

## 2. *On the Peculiarities of Key Information Transmission at Various Phases of Big History*

Replication on the basis of the matrix principle is a fundamental feature of all forms of life (see, *e.g.*, Timofeev-Ressovsky et al., 1969: 15–16). However, the process of such replication cannot be conducted with a 100 per cent accuracy; hence, the replication of a complete genome without any errors is virtually impossible. That is why the emergence of practically any new biological organism is accompanied by random change in genes (*i.e.*, mutations). However, a significant change of the genotype occurs extremely rarely. Yet, the role of mutations in biological evolution is extremely important and very well known, because the mutations are one of the main sources providing ‘raw materials’ for evolution (Timofeev-Ressovsky et al., 1969:72). However, there is also an opinion that the importance of mutations for evolution has been exaggerated, whereas the main source of new genetic material for major morphobiological reorganizations was provided by the gene duplication (see, *e.g.*, Shatalkin, 2005: 30). However, we still prefer to keep to the classical point of view on the role of mutation in the process of biological evolution.

However, it is important to emphasize that the number of distortions by which transmission of information is accompanied from generation to generation within social evolution (especially in complex societies) is orders of magnitude higher than that observed within biological evolution. There are grounds to maintain that the role of such ‘distortions’ in social macro-evolution tends to increase (in addition to conscious and purposeful alteration of cultural information). In the meantime, it appears that we observe just the opposite within biological macro-evolution. For example, among viruses and some bacteria, mutational variability is constantly necessary for their mere survival; on the other hand, in complex biological organisms, it is necessary only up to a very limited extent.

Within social evolution, some unconscious distortion of transmitted cultural information always takes place, which may be regarded to some extent as

analogous to biological mutations.<sup>12</sup> This, by itself, may lead to certain socio-evolutionary shifts (Korotayev, 2003; Grinin and Korotayev, 2007b, 2009b; Grinin & Grinin, 2020, 2023, 2025). However, the conscious directed alteration of the information by its carriers is significantly more important. Though many are still sure that ‘history never teaches anything to anybody’, already the elites of many complex agrarian societies quite often tried to take into account errors made by their predecessors and to modify the ‘socio-cultural genotype’ accordingly in order to avoid them in future.

One may recollect, for example, the conscious alteration of the social position of the military elite by the founders of the Sung dynasty in China (960–1279 CE), in order to prevent the military coups that jeopardized the political stability of their predecessors (Wright, 2001). Similarly, there was the conscious and purposeful replacement of traditional military systems with the modernized military systems of Western Europe by Peter the Great in Russia and Muhammad Ali in Egypt (see, *e.g.*, Grinin, 2006a; Grinin & Korotayev, 2009c, 2009d), and so on. Modernization is a very broad concept in relation to processes that have found their place in the history of many dozens of countries affecting very significantly their evolution, as well as the global social evolution in general (see, for example, Grinin, 2012a, 2012b, 2013, 2022; Grinin et al., 2024; Korotayev, Bilyuga et al., 2018; Korotayev, Slinko et al., 2020; Korotayev, Zinkina et al., 2019; Sawyer et al., 2022; Zinkina et al., 2018).

Thus, the major part of fixed socio-cultural alterations (supported by social selection) emerge not as a result of ‘random errors of copying’ (though, of course, such random errors do exist), but as a result of purposeful alteration of respective memes. Such ‘mutations’ are directional from the very beginning and do not seem to have any analogues in natural biological evolution.

However, in a broad mega-evolutionary sense, attempts to represent biological and social evolution in the general series of information development as the most characteristic through line of evolution are not without interest. Evolution is characterized by the fact that new types of information have developed in

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<sup>12</sup> Close results are arrived at by Dawkins (1993) in his theory of the ‘evolution of memes’.

leaps and bounds, each with new storage technologies, new duplication technologies and new processing technologies. This unified concept of evolution makes it possible, among other things, to achieve a unified view of biological and cultural evolution (Glötzl, 2025). In this respect, it makes sense to recollect that also viruses can be considered as basic information agents (Grinin A. 2025; see above). Also we can mention one more idea in megaevolution line. that the mindedness of animals is akin to the livingness of organisms and the cumulative cultural processes in human persons (Volk & Henriques, 2025).

### 3. *On the Inheritance of Acquired Characteristics*

The other (and perhaps even more important) difference is that, in the process of biological (but not social) evolution, the acquired characteristics are not inherited.<sup>13</sup> That is why socio-evolutionary changes are accumulated much faster than biologically useful changes of phenotype determined by mutation processes.

Thus, because the acquired characteristics do not influence biological evolution, biological evolutionary processes go extremely slowly (in comparison with social evolution). On the other hand, within social evolution, the acquired characteristics can be inherited, and, hence, social evolution goes ‘according to Lamarck’ rather than ‘according to Darwin’. This point has been noted many times by a number of evolutionists (see, *e.g.*, Mesoudi, Whiten, & Laland, 2006: 345–346). Consequently, social evolution proceeds much faster. In addition, as social evolution tended to go more and more ‘according to Lamarck’, it became more and more Lamarckian rather than Darwinian, which was one of the main factors for the acceleration of social evolution.

Still, it appears necessary to mention that in some rare cases one can observe the inheritance of acquired characteristics in complex biological organisms

(Zhivotovsky, 2002a). For example, somatic mutations may well be inherited in plants both with vegetative and sexual reproduction. In animals, viruses can insert themselves into the genome of gametes – subsequently the offspring inherit quite an ‘acquired characteristic’, the virus infection. The ability to inherit acquired characteristics is found in many plant-eating insects, in which specialized symbiotic bacteria live. Biochemical and ecological characteristics of such symbiotic complexes are determined up to a very large extent by bacteria (see, *e.g.*, Dunbar et al., 2007).

The possibility of inheritance of acquired characteristics through special particles (pangenes) was proposed by Darwin (1883) himself. Within the genomes of complex biological organisms one can find a very large number of retropseudogenes and even working copies of genes that emerged as a result of the ‘copying’ of genetic information from RNA molecules to the chromosome with special enzymes (such genes are characterized by the absence of introns). Thus, in biological evolution, one may observe the ‘copying’ into the genome of information on the structure of mature matrix RNA. Because the alternative splicing is quite a controlled process, regulated by the cell and subject of intermediate influence of external conditions (see, *e.g.*, Lareau et al., 2007), mature mRNA may actually carry some (albeit rather incomplete and fragmentary) information on ‘acquired phenotypic characteristics’, and this information may be transmitted to the genome of the germ line.

The impossibility of genetic inheritance ‘according to Lamarck’ postulated by the Synthetic Theory of Evolution exists because the mechanism of reverse translation does not appear to have emerged. That is why there is no way for changes that occur in an organism during its lifetime, at the level of proteins, to be recorded back into the genome.<sup>14</sup> On the other hand, at present, we know that the phenotype at the

<sup>13</sup> As one of the differences between social and biological evolution is connected with the absence in the former of clear equivalents of genotype and phenotype (see, *e.g.*, Mesoudi, Whiten and Laland, 2006: 344–345), it appears evident that the expressions ‘sociocultural genotype’ and ‘sociocultural phenotype’ should be regarded as metaphors rather than as exact scientific terms.

<sup>14</sup> On the other hand, there is a hypothesis that such a mechanism may have existed at the earliest phases of biological evolution. What is more, scientists have experimentally obtained RNA molecules that can perform certain stages of reverse translation (Nashimoto, 2001).

cellular level is determined not only by proteins, but also by a great variety of functional RNAs, whereas intravital changes of those molecules may well be written into the genome because here the mechanism of reverse transcription exists and is rather widely spread in biological organisms (including complex organisms). Hence, the point is not that within the biological evolution the 'Lamarckian' inheritance is totally impossible; rather the point is that such an inheritance is rather disadvantageous in most cases (see also Steele et al., 2002; Zhivotovsky, 2002b). Consequently, such an inheritance is not usually an important mechanism of evolution (and, especially, of arogenic evolution).

For example, it is evident that the hereditary fixation of adaptive modifications ('modification genocopying') is disadvantageous in many cases. Note that this includes those very consequences of the organ exercise whose inheritance played such an important role in Lamarck's theory. In order for an adaptive modification to appear, we should observe first a genetically determined capability for such a modification (e.g., the muscles' ability to grow as a result of exercise or the lymphocytes' ability to develop immunity against new pathogens). However, if such a genetically determined ability has appeared, the firm fixation in the genotype (the *genocopying*) of only one of many possible versions of the final state of the trait (e.g., a precise size of a muscle or an immunity toward a specific pathogene) will not be a progressive evolutionary change; it will be a degenerative evolutionary change, accompanied by a decrease of the organic complexity and a loss of one of the ontogenetic regulatory circuits. In biological evolution, such events take place rather frequently, but this is not the arogenic evolutionary pathway.

Within social evolution, there is no significant difference in the inheritance mechanisms between those traits that have been inherited from 'ancestral'

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<sup>15</sup> On the other hand, we observe another trend in connection with some sorts of regulation mechanisms. One should not think that the only evolutionary mechanism in social evolution is a conscious change of existing objects. There is also an opposite trend that may be denoted as institutionalization. In many cases certain relationships are fixed by customs or laws in order to avoid excessive variation/equivocality that may often be harmful for a social system. For

societies and the ones that have been acquired throughout the history of existence of a given society. There could be some insignificant difference as regards the firmness of the fixation of the respective alterations, the easiness of their acceptance, and so on, but it is impossible to say that acquired social characteristics are transmitted to new generations with significantly more difficulties (especially in complex societies).

A serious obstacle for the operation of the 'Lamarckian' mechanism can be seen in traditionalism, which holds negative attitudes toward innovation and glorifies everything inherited from ancestors. This was very typical for simple traditional societies. However, such attitudes have weakened in a significant way in modern complex social systems.<sup>15</sup> This might be connected with the development of the means, methods and technologies of forecasting, which is the conscious evaluation of innovation. Forecasting makes those characteristics that might be considered dangerous or disadvantageous by traditionalists (in particular, a very low precision of the 'memotype' replication and 'Lamarckian' inheritance) to become more acceptable in a society.

#### 4. On the Nature of Hereditary Variation

Hereditary variation is a key issue in the theory of evolution. This is the issue, around which the main discussions between representatives of various schools of evolutionary thought (classical Darwinism, Synthetic Theory of Evolution, Orthogenesis, Nomogenesis, Neolamarckism and so on) are concentrated. *Variation is the main material basis of evolution; its character, mechanisms, factor, and emergence rates determine to a very high extent the character of the evolutionary process.* These mechanisms of variation are one of the most

example, one could observe the development of rather rigid marriage institutions, various legal codes and constitutions that can be only altered with significant difficulties (that are usually consciously established by respective norms aimed at the provision of the stability of respective codes and constitutions). In this respect the trend toward the canalization of changes may be also traced in the social macroevolution.

fundamental areas of difference between biological and social evolution.<sup>16</sup>

Starting with Darwin, biologists have based their evolutionary theories on the idea that hereditary variation is basically ‘indeterminate’ or undirected, that is, random. However, as we have noted, within biological evolution, one can still detect a trend toward a decrease of randomness, both in mutational and recombinational variation. In some sense, this trend continues into social evolution, where variation is even less random and more directed.<sup>17</sup>

As mentioned above, there are significant differences between biological and social evolution in regard to the accuracy of copying (reproduction of replicators), because in general the precision of copying of genes (and, correspondingly, periods of their existence in a recognizable form) exceeds by orders of magnitude values of analogous indicators for memes. That is why ‘memetics’ (in contrast with genetics) has to deal with a much lower precision of replication and with a much higher speed of mutagenesis, though some replicators (memes) may have rather long periods of life.

For example, according to some recent estimates, roots of some most widely used words may be preserved in a recognizable form for about 10,000 (and even more) years of linguistic evolution (Pagelet et al., 2007). Another example can be provided by ‘long-lived’ folklore-mythological motifs that can survive for dozens thousand years (see, e.g., Korotayev & Khaltourina, 2011; Berezkin, 2007; Korotayev, 2006; Korotayev et al., 2006, 2017). The same can be said

about a very long life of some technical methods, for example, the production of stone tools. However, it makes sense to distinguish between various types of information transmission, depending on the number of copies in which the information is stored and reproduced (as well as the forms of that reproduction).

There could be situations in which there is just a single carrier of important information. An ancient engineer could take his secrets of construction to the grave so that nobody could continue his techniques any more. There are lots of historical facts known to us from just one source; and if, in the process of transmission, there was distortion of the initial text, this could affect our current knowledge of the past. Those unique ancient books that disappeared in fire did not let us know the important information contained in them, and so on. These are examples of distortion or loss of information by functioning social systems.

It seems appropriate here to recollect the information irreplaceability principle (Lyapunov principle). According to this principle, information that has entirely disappeared cannot be reconstructed in its entirety – what can be replaced are portions of information coming from a common source (see Rautian, 1988a, 1988b). We confront a different case when we deal with information that is used by numerous carriers (as in the case of the use of a mass language). In such cases, changes in a living language should not be always regarded as information distortion; we should rather speak about some drift in the use of linguistic matrices and patterns (similar to

<sup>16</sup> It appears that this is relevant not only for the biological and social phases of Big History, but also to all its preceding phases.

<sup>17</sup> When we make such comparisons, we compare genotype with that totality of sociocultural information (it may be denoted as ‘memotype’), which is transmitted from generation to generation and determines main characteristics of social systems. In social systems, in addition to biological generations, parents and children, we find other types of continuity (that could be sometimes even more important) like institutional and legal continuity whose role increases constantly. That is, we observe the growth of the importance of information transmission in the framework of institutions, corporations, organizations, and so on, that is

conducted not between biological generations (from parents to children), but, say, from an experienced worker to an inexperienced one, or from a teacher to a pupil. In addition, the emergence of external information carriers (in form of books, electronic records, and so on) allows conducting a distance transmission of information without any direct contact between respective people, which, incidentally, contributes to the growth of the sociocultural evolution rate. Actually, as a result, in complex social systems the number of information transmission channels grows by orders of magnitude (especially with the emergence of external information carriers). In some sense, this growth already starts with the development of social life among the animals.

gene drift in populations), because language carriers may well know older forms, but prefer new ones. One may even observe the coexistence of persons using differently linguistic forms and lexemes (similarly within one population there could be different phenotypes). However, with time, some forms win the competition and language changes.

When we speak about the accuracy of transmission of biological information, it is necessary to take into account that biological evolution has worked out rather effective molecular mechanisms that allow for sharply reduced precision of DNA replication when necessary (for example, *SOS-response* among bacteria). For some primitive biological objects, such as viruses, too high a precision of replication can even be lethal; in order to successfully go through their life cycles they need very low precision of replication or, in other words, a very high rate of mutation (mutagenesis). Especially when some viruses use RNA as a genome (Solé & Santiago, 2019). For such organisms, evolutionary changes turn out to be necessary components of their everyday life (Vignuzziet al., 2005; Grinin A., 2025)!

Generally, however, in biological evolution, replication accuracy increases rather than decreases with the growth of the organismal complexity. In this sense, the reduction of precision that is observed in the transition from biological to social phase of the Big History looks as if this were a 'step backward'. However, this observation is rather superficial, as it does not take into account the nature of those errors that emerge in the process of replication, notably the degree of their randomness/directionality.

Within biological systems, replication errors are basically random. Taking into consideration the decrease of randomness, this may be interpreted in the following way: nature has not developed any biological mechanisms that allow us to forecast results of concrete genetic changes and to plan them. Though a cell (for example, a lymphocyte) may 'know' in advance that, in order to achieve a needed result, it should alter some particular part of the genome, it, however, lacks mechanisms that would allow it to forecast results of a concrete genetic alteration. That is why, in the framework of biological evolution, the acceleration of adaptatio-genesis through a radical reduction of the precision of replication is a very expensive and risky strategy that can be afforded only

by very primitive forms of life. The situation changes radically if the replication 'errors' become not random, but actually purposeful, based on forecast of the possible results of concrete changes introduced into the 'memotype' of a social system.

The presence of 'directed mutations' (in addition to undirected ones) radically distinguishes the process of 'mutational variation' in the evolution of memes from what is observed within the evolution of genes, where all the mutations are basically undirected.

That is why we believe that the difference between biological and social evolution in respect to randomness/directionality of hereditary variation is more fundamental than the differences in precision of replicator copying or mutation rate. In the process of 'sociocultural mutagenesis', the element of randomness is significantly smaller, because people possess the ability (albeit limited) to foresee results of certain concrete 'mutations'. That is why human creativity (say, in development of new judicial laws or new technologies) may differ qualitatively from the 'creativity' of biological evolution – especially, as regards the effectiveness and the speed with which the respective results are achieved.

On the other hand, one should not exaggerate the role of conscious planning in relation to social innovation. Random search, trial and error remains very important in social evolution (Grinin, 1997, 2006b, 2007a, 2011, 2012a, 2013a, 2017, 2020; Korotayev 2003, 2004), although there has been a clear decreasing trend in randomness in recent centuries (see, e.g., Korotayev, 2003, 2004, 2007; Korotayev, Malkov, & Khaltourina, 2006a, 2006b; Grinin, 1997, 2007a, 2009a; Grininet al., 2024). Thus, it is not sufficient just to have respective challenges in order that serious transformations could take place. Most societies 'respond' to new problems in old, habitual, tested and familiar ways, as they choose – not from a set of hypothetical alternatives – but from a set of accessible alternatives (Van Parijs, 1981: 51). In other words, they use actually known measures instead of potential ones (Claessen, 1989). In these situations, their behavior is often quite similar to that of social animals. Naturally, not all such 'responses' are effective. As a result, many societies perish, disappear or lose their independence (Grinin, 2011).

For example, after the Roman regiments were withdrawn from Britain in 410 CE, the Britons

(Romanized British Celts) sought protection from the raids of their Irish and Scottish neighbors. They invited Saxons to defend them in return for plots of land in Britain. Actually, this was a variation of the very well-known Roman method ‘to use barbarians to fight barbarians’. However, the Saxons, after they had seen the Britons military weakness, stopped obeying local authorities and became masters of the country (together with Angles and Jutes). In this way, the Britons, notwithstanding their fierce and long resistance, were partly evicted, partly destroyed and partly enslaved. As a result, barbarian Anglo-Saxon states were found in place of the state of the Britons (Blair, 1966: 149–168; Chadwick, 1987: 71; Philippov, 1990: 77).

If we take into account general historical contexts, we see that an extremely small fraction of all responses to various challenges turned out to be capable of becoming sources for system aromorphoses. This implies that most societies turned out to be incapable to move to new qualitative levels: they did not have the necessary potential for change, their construction had certain ‘defects’, the system might have been too rigid to transform easily, or some necessary conditions were lacking, and so on (Grinin, 2011; Grinin and Korotayev, 2009e).

##### *5. The Ability to Borrow and the Horizontal Exchange of Genetic Information*

These facts illustrate a rather strange situation. There are similarities in biological and social evolution, such as the transmission of information, variability, community complexity, *etc.* However, these similarities occur at the lower stages of biological evolution (involving simple biological organisms), whereas they are absent in higher stages of biological evolution (involving complex biological organisms). It is important to take into consideration that far from every organism is independent in propagation, since sexual reproduction intrinsically needs another organism for genetic exchange. We will see below that there is a reason to believe that the cell nucleus itself is of viral origin. Since the nucleus plays a central role

in sexual reproduction in eukaryotes, this suggests that reproduction itself was most likely not invented by eukaryotes, but rather “borrowed” from viruses. (Grinin A., 2025: 52).<sup>18</sup>

One of the main differences between social and biological evolution is the ability of social systems to not just change and transform, but also to borrow new elements. However, in this respect, social evolution resembles the biological processes that prevailed during the epoch of the ‘prokaryotic biosphere’ (and those processes continue up to the present among prokaryotes and monocellular eukaryotes). Among the prokaryotes, we find the ability to ‘transform naturally’ – to absorb DNA from the environment and to insert it into their genome, which leads to an immediate transformation of the phenotype. There is also, of course, a significant difference between this biological and social analogue: in society the borrowings are usually made consciously.

Horizontal gene transfer produces many useful genetic ‘inventions’, a sort of commons for microbe communities. For example, communities of marine planktonic microbes use the genes of proteorhodopsins – proteins that allow them to partly utilize sunlight. In contrast to the proteins that participate in real photosynthesis, proteorhodopsins do not need the help of many other specialized proteins. Thus, in order to acquire a useful function, it is sufficient for a microorganism to borrow a single gene (Frigaard et al., 2006).

Complex borrowing of entire gene systems is observed much less frequently, but when they occur, they have more significant consequences. An original and wide-spread version of such ‘borrowing’ results in the emergence of symbiotic systems, which sometimes actually leads to the formation of a new organism out of several other organisms. The role of such systems is often underestimated, but all functioning of the modern biosphere is based on them.

There are many examples. *Terrestrial plants* would not have been able to achieve evolutionary success without symbiosis with mycorrhizal fungi and

*canalization, and then again to its free (but now conscious) borrowing’. ‘From contraposition of biological (genetic) and social mechanisms of evolution (within the process of anthropogenesis and sociogenesis) to genetic evolution controlled by the humans.’*

<sup>18</sup> We do not have a full explanation of this phenomenon, but one may think about the application to the macro- and even megaevolution of the law of the negation of the negation, which in this case may be interpreted in the following way: ‘From a free borrowing of information to its rigid isolation and

nitrogen-fixing bacteria. *Herbivorous animals*, both insects and vertebrates, are unable to digest plant food without symbiosis with specialized microorganisms. Indeed, the principle ecological, biospheric role of animals is precisely to process plant food!

In highly complex biological organisms, in contrast to social organisms and human societies, large-scale ‘borrowings’ in the form of symbiotic relations or alien genetic material rarely take place, but many of the most important aromorphoses are connected just with them.

##### *5. Analogues of ‘Suprasocietal Institutions’ in Biological Evolution*

Let us come back to the question: Are there analogues of such structures in the evolution of the biosphere? The answer will depend on the level of the biosphere's system organization. Society is frequently compared with biological organisms, but – in this case – we are comparing supra-societal amalgamations with supra-organic systems: populations, species, ecosystems, groups of social animals, and so on. However, this is probably not quite an appropriate scale of analysis, so we need to compare suprasocietal institutions of a global scale (like the United Nations) with biological objects of immeasurably smaller scale, *e.g.*, with particular ‘casts’ of the ant family.<sup>19</sup>

At any scale, it is difficult to find good analogies to the formation of suprasocietal institutions within biological evolution. This becomes even more evident if we compare societies, not with organisms, but with supra-organic biological systems (*e.g.*, populations or species). Although those biological systems (like societies) can amalgamate into systems of a higher order (ecosystems or the biosphere), these higher-order systems are not centralized but are weakly integrated – nothing like supra-societal institutions as the World Health Organization, UNESCO, or even a complex tribal confederation with its own supra-tribal regulation organs. For example, one can observe the formation of rather complex links between species in ecosystems; certain key species may produce a decisive influence on other species in the community, but this does not result in the formation of any ‘supra-species institutions’.

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<sup>19</sup> On the other hand, a large anthill or termitary may well be compared with a large village community.

On the one hand, it is possible to see in this comparison one of the fundamental differences between social and biological macro-evolution. On the other hand, some biological analogues of ‘suprasocietal institutions’ did emerge. In the Holocene (the last 10,000 years, starting with the Agrarian Revolution), human societies developed suprasocietal institutions. In the course of the socio-biological evolution of the resulting ‘anthroposphere’, we observe a parallel growth in the integration of humankind and integration and coordination of evolutionary changes of biological populations, species and ecosystems. In other words, the development of the global human community (the World System) may be regarded as a factor of integration of biological evolution at its upper level.

Thus, social and biological evolution are related processes that supplement and maintain each other. Indeed, there is a tendency toward their fusion into a single complex process, one leading to the development of an ‘anthropo-biosphere’. In this respect, it appears to be possible to speak about the co-evolution of biological and social development.

##### *6. On the Role of Selection in Biological and Social Evolution*

The role of selection in social evolution differs significantly from the one in biological evolution. In the biological world, the main source of stable, heritable innovations (mutational and recombinational variation) is characterized by a high degree of randomness and unpredictability (although, of course, it is also necessary to take into consideration all the above-mentioned qualifications about the means of optimization). In this situation, ‘post factum selection’, the selection among the deviations that have already emerged and have found their realization in the phenotype, becomes the only way to give the process a certain directionality (in this case – to secure the additive character of changes). About our views on the role of selection in evolution see Grinin, 2020; Grinin& Grinin, 2020; Markov&Naymark, 2019).

In the social world, the main sources of heritable innovations are not random errors of copying and reproduction but conscious and purposeful correction

and alteration of memes. However, such purposefulness is unable to foresee not only all the consequences of its actions but even the near consequences. That is why intentional actions may appear random. Throughout human history, failures of some societies have been a sort of payment for the success of others (what we denote as ‘a rule of payment for the arogenic progress’), from which the role of selection in the search for successful aromorphic variants acquires an especially important meaning (Grinin, Markov, & Korotayev, 2011, 2022; Grinin, Korotayev, & Markov, 2020; Grinin, 1997, 2007a; Grinin & Korotayev, 2009b; Korotayev, 2004). Societies frequently confront such situations when an old system does not work. Those who do not change or look for more effective means perish.

Selection at the gene/meme level plays a less important role in social evolution than it does in biological evolution. However, selection in social evolution takes place not so much at the level of memes but more at the level of organizations, institutions and social systems. At the level of inter-societal competition, until recently, social selection acted in an especially tough way: ‘the victor gets more or everything; the defeated may lose himself’ (Grinin, 2003, 2004, 2009a, 2009b, 2010a, 2011, 2020; Grinin & Grinin, 2023; Grinin & Korotayev, 2009e, 2015). So, this is a selection mechanism that is rather different from the one found in biological evolution.

One more important aspect of social selection that is absent in biological evolution is the struggle for the selection of a certain model (model of reforms, model of unification, ideological model) at the level of individual societies, as well as at the inter-societal level. Everywhere, we can observe the selection of leaders, models, courses, central positions and so on. The decisive advantage could be rather different in different cases. In some cases, this could be a very capable and talented leader (Grinin, 2010b); in others this could be an advantageous geographic position; in still other situations this could be just a lucky contingency.

Thus, although we are dealing with rather different mechanisms of selection in biological and social evolution, their roles are very important in both cases. Still, within biological evolution, selection process is more important, because there is no alternative,

whereas such an alternative exists within social evolution.

### **Section 3. Some Preconditions of the Transition from Biological to Social Phase of the Big History**

#### *1. Social Evolution as a Logical Result of the Development of Adaptogenesis Mechanisms*

In addition to what has been already said about the organic links between biological and social evolution, one should consider another aspect of adaptogenesis. The process of adaptation that constitutes the principal contents of biological evolution may proceed at different levels: 1) the organism structure; 2) its behavior; 3) structure and behavior of a socium as a superorganic amalgamation.

At all those levels, one may observe the transition from primary, primitive and slow methods of adaptogenesis based on random mutations, recombination and selection to more progressive, effective and rapid ways of evolutionary change. Not only organisms, species and societies evolve; mechanisms of evolution evolve too. The general direction of this evolutionary movement may be characterized as a trend to the reduction of the role of random processes and the growth of systematic controlled processes. The initial and primary evolutionary algorithm is the random search, the trial-and-error method. However, at all levels of adaptogenesis, one may observe a gradual development of such mechanisms that decrease the role of randomness and, thus, optimize this algorithm; though it appears impossible to exclude entirely an element of randomness either from biological or from social evolution.

**1) The organism structure level.** Even at the basic level of biochemistry, physiology and morphology, many forms of life have developed ways of adaptogenesis that are faster and more effective than the random search conducted according to the scheme of ‘random mutations + selection’. One of these mechanisms is regulation of the mutagenesis rate, depending on available conditions: under favorable conditions, the mutagenesis rate is low; in unfavorable conditions it increases (Grinin, Markov, & Korotayev, 2022: ch. 6, §6.8).

It is also appropriate to mention epigenetic changes of hereditary material that are transmitted to a number of generations, in particular parental genomic imprinting that became especially developed in the most complex organisms, such as mammals and flowering plants (Jablonka & Lamb, 1999). Imprinting is actually a sort of purposeful manipulation of hereditary properties of offspring. With the maturation of male and female gametes, certain parts of the genome are marked in a special way, for example through methylation. The methylation of DNA is not a chaotic process but is regulated by complex molecular systems. What is especially important is that methylation of particular nucleotides increases the probability of their mutating. Thus, through the methylation (or non-methylation) of particular nucleotides, cells can in principle regulate the probability of their mutation (Vanyushin, 2004).

Another example of the purposeful change of hereditary information is provided by the development of adaptive (acquired) immunity through combining genetic blocks, subsequent somatic hypermutation, and clonal selection. Both the combining of DNA fragments (V-(D)-J recombination) and hyper-mutation are processes that are only partly random. In other words, the limits of randomness in this case are rather accurately demarcated (Grinin, Markov, & Korotayev, 2022: ch. 4, §4.2.4). The combination of DNA fragments is conducted from a precisely defined set and the hyper-mutation takes place at a rather accurately demarcated part of a gene, while the selection of lymphocyte clones makes the whole process unequivocally directional. As a result, the final outcome of such a 'sequence of random events' turns out to be quite deterministic.

Such a mechanism may be designated as 'optimized random search'.<sup>20</sup> Note that in the case of the acquired immunity, from a 'technical' point of

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<sup>20</sup> In this way, a more flexible reaction to unknown situations develops; this may be compared with multifunctional institutions in human societies that while remaining apparently the same institutions may allow social systems to behave differently in different situations, whereas respective institutions would experience certain changes with the change of situations. Thus, army may be relatively small during the time of peace, and then it would grow sharply in

view, the achieved result may well be transmitted to the offspring, for example, via the mechanism of reverse transcription and transmission of the genetic material from lymphocytes to gametes through endogenous retroviruses (Steele et al., 2002). However, this does not happen, because it is more advantageous to transmit not a concrete immunity to a particular pathogen to the offspring but a universal capability to develop immunity against any pathogen.

In general, such mechanisms of purposeful genome alteration do not have a universal presence in biological organisms, and the overwhelming majority of mutations take place in a quite random way.

Biologists rarely consider that assortative (selective) mating, mediated sometimes through extremely complex mechanisms of mate-choice; this is nothing but an extremely effective mechanism for management of recombinational variation. However, in the real biological world, absolutely unselective, random mating is hardly ever observed. Indeed, random mating is a scientific abstraction, like an 'ideal gas', or an 'absolutely dark body'. With growth in the level of organization of biological organisms, the complexity and effectiveness of mate-choice also grew, whereas the recombinational variation became less random as a result.

**2) Level of individual behavior.** One can trace the transition from predominantly hereditary and genetically determined behavioral patterns to more flexible learning-based ones. As we saw above, in the case of immunity, it was more advantageous to transmit to the offspring a universal capability to 'learn' instead of a rigidly determined means of resistance to a particular pathogen. In an analogous way, in the general course of evolution, it has turned out to be more advantageous to transmit the ability to learn rather than to transmit rigidly fixed behavioral stereotypes.<sup>21</sup> No doubt, the emergence of the capability to learn is a major aromorphosis, though it

size as a result of mobilization, whereas its functions also substantially change. The same can be said about the flexibility of the family, the village community and many other social groups and institutions.

<sup>21</sup> It appears necessary to note that in both cases the ability to learn does not replace entirely the genetically determined concrete adaptations; the former is added to the latter. In the immunity system

is very stretched over time. Even unicellular organisms have some inchoate abilities to learn (sensitization, habituation), let alone such highly organized animals as ants or bees.

**3) Biological socium level** (social adaptogenesis). A wide variety of living organisms – from bacteria to mammals – lead a social way of life. The socium as a whole has certain system characteristics that can be more or less adaptive (Popov, 2006). Here, we also observe the transition from rigidly genetically determined forms of social relationships to more flexible versions, within which a social system may adequately (adaptively) react to changes in its environment. For example, the size of subsidiary colonies of an anthill may change in a reasonable, that is, adaptive way, depending on resource availability (Zakharov, 1978: 49). However, in general, for all the pre-human forms of life, such possibilities are limited. The human development of the ability to evolve socially, which implies the possibility of an almost limitless change in the structure of social systems, appears to be a natural (though qualitatively higher) continuation of this evolutionary trend.

## 2. One of the 'Preadaptations' that Facilitated the Transition from Biological to Social Evolution

The issue of how biological evolution transformed into social evolution is among the most important questions of Big History and Evolutionary Studies. What 'preadaptations' were needed for the transition from biological to social phase of the Big History? This is a very complex subject. And here we shall restrict ourselves to consideration of just one of those preconditions.

Social macro-evolution (and, hence, the start of the Big History social phase) became possible due to the emergence of an uniquely human ability denoted as 'ultra-sociality' (Boyd & Richerson, 1996). This is only found among humans and designates the ability to change their social organization radically and almost limitlessly in response to internal and external challenges. Only humans are capable of forming collectivities that could be entirely different as regards

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of higher organisms, the system of innate immunity is preserved in addition to a new system of adaptive (acquired throughout the life) immunity; similarly, in the behavior of higher animals, behavioral patterns

their structure, their traditions, their norms of behavior, their modes of subsistence, their systems of intragroup relationships, their family types, etc.

Whatever the complexity of the collectivities of non-human primates, they do not have such flexibility (Butovskaya et al., 2020). Each species usually has only one type of social organization; some cultural differences are observed, but they are incomparable with the ones observed in *Homo sapiens*. Yet, some animals possess a limited ability to adaptively change the structure of their socium. For example, in disadvantageous circumstances, one may observe growth in the rigidity of social hierarchy (the 'power vertical'), whereas the relationships become more egalitarian under more favorable conditions. Sometimes the transition to a social way of life occurs during unfavorable conditions, whereas the same animals may return to solitary life with improvement of conditions (Popov, 2006).<sup>75</sup> Those adaptive modifications of social structure in animal communities are still significantly inferior in their scale to what is observed in human societies; in addition, among other animals, they are characterized by a much higher degree of predictability.

The emergence of ultra-sociality was a natural result of the preceding *co-development of intellect and social relations* among our ancestors. The progressive development of the brain and intellectual capacities in primates is inseparably linked with a social way of life – with the necessity to predict actions of other members of their group, to manipulate them, to learn from them, to achieve an optimum combination of altruism and egoism in their behavior. At present, this is the point of view of the majority of primatologists (e.g., Byrne, 2022; Byrne & Whiten, 1988; Byrne & Bates, 2007).

The idea that the primates intellect developed first of all for, say, effective search for fruit (the 'ecological intellect hypothesis') does not now have many supporters. It cannot explain why primates need such a large brain, if many other animals, such as squirrels, perfectly manage similar tasks, though their brain remains small. In contrast, the 'social intellect hypothesis' is supported by facts. Scientists have

developed throughout the life through the learning are combined with innate genetically determined behavioral traits.

detected a significant positive correlation between brain size in primates and the size of their social groups (Dunbar, 2003, 2024). It is necessary to note that primates (in contrast to the majority of other social animals) know all the members of their group 'by sight' and have particular relationships with each of them. There are grounds to maintain that individualized pair relationships are the most intellectually 'resource-intensive' (Dunbar & Shultz, 2007).

A positive feedback appears to have existed between the development of social intelligence and the growth of complexity in social relationships of hominids.<sup>22</sup> Those individuals that managed to achieve a higher status within a social hierarchy, due to a higher intellect or a better ability to foresee actions of others, left more numerous offspring, which in turn led to the general intellectual growth of the socium. As a result, in subsequent generations, in order to move up the social ladder, it was necessary for individuals to possess an even more developed social intellect, and so on (Speechley et al., 2024).

Interesting experimental facts have been obtained. They indicate that intellectual abilities of a 'social' character, which allow for resolution of social tasks, developed in our ancestors earlier in comparison with the intellectual capabilities of the other types (e.g., the ones that allow to solve 'physical' and instrumental tasks) (Herrmann et al., 2007).

In order to function effectively in a complex, constantly changing socio-cultural environment, our pre-human ancestors had to develop intellectual abilities of a rather concrete type: abilities of effective communication, learning and – most importantly – of understanding not only actions, but also thoughts and desires of members of their groups (Vygotsky, 1978; Markov & Markov, 2020). It is quite evident that abilities of this kind should become apparent in early childhood, in the period of active learning and social adaptation. There are two alternative hypotheses about possible mechanisms in the evolutionary development of these social abilities.

The first hypothesis suggests that they emerged as a result of the uniform development of the intellect as a whole (*general intelligence hypothesis*). The second suggests that this was the directed development of

specific socially-oriented abilities, whereas all the other abilities (such as abilities to think logically, to detect cause-and-effect links in the physical world, and so on) developed later, as something additional and secondary. This is called the *cultural intelligence hypothesis* (Barkow, et al., 1992; Shettleworth, 1998; Herrmann et al., 2007; Henrich, 2015).

At first glance, the *general intelligence hypothesis* looks more plausible, but, it is also possible to provide evidence in support of the *cultural intelligence hypothesis*. For example, it is known that specific intellectual abilities develop locally in many animals, but their overall intellectual level does not grow (or grows insignificantly). One can mention, for example, the birds' unique orientation abilities (Shettleworth, 1998). Special experiments have been conducted in order to test these hypotheses.

The experiments were based on the following reasoning: If the *cultural intelligence hypothesis* is true, then there should be an age in the individual development of humans when we are not different in our 'physical' intellect from the apes, even though we are already far above them in our 'cultural-social' intellect. Experiments have confirmed the *cultural intellect hypothesis*: it turns out that 2.5 year old children have the same level of development as adult chimpanzees and orangutans in respect to solving physical tasks (spatial, quantitative, detection of cause-and-effect relationships, and so on), but they are significantly superior as regards the effectiveness with which they solve tasks of a social nature, such as those connected with the prediction of others' actions, communication, learning, and so on (Herrmann et al., 2007; Henrich, 2015; Markov & Markov, 2020, 2021).

In general, present-day anthropological data suggests the following:

1) The development of social relationships and intellectual abilities in the higher primates (in general) and the hominids (in particular) proceeded within a single evolutionary process that was accelerated by the above-mentioned positive feedback.

2) This process tended to lead to the growth of complexity and flexibility of social relationships. Thus, the development of ultra-sociality and the ability to evolve socially within one of the groups of

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<sup>22</sup> This social intellect is also called the 'Machiavellian intellect' (e.g., Byrne & Whiten, 1988).

primates was a natural and logical result of the development of a trend that started among the primates long before the emergence of *Homo sapiens*.

### **TRANSITIONAL PHASES TO BIOLOGICAL AND SOCIAL PHASES**

The transition to both the biological and social phases did not occur immediately.

In both cases, we are dealing with transitional phases, in which there were many aromorphoses, although not all of them are known to us. See Fig. 1 above for the place of these intermediate phases in the general scheme of Big History. Let us briefly consider these transitional phases. *истории*.

The **abiogenic chemical phase**. The abiogenic chemical phase began after the emergence of our planet and lasted for several hundred million years, as a result of geological and geochemical processes on Earth. It is very important to emphasize this, because the abiogenic chemical phase was pivotal for the emergence of life. There are various hypotheses about abiogenic chemical evolution and the origin of life including the so-called RNA world. Although some progress has been made in many respects, especially in the last fifteen years, none of them seems to be completely satisfactory yet. We believe that the first pre-living systems (the so-called protobionts) should not be considered as direct ancestors of the first living organisms, but as their analogues. These analogues were already comparable to the most primitive living systems in a number of functions. But in general, they were organized differently (it is now extremely difficult to say exactly how). In addition, one should also take into account that the conditions on the young Earth were peculiar. Consequently, such structures could have formed, but modern scientists are unlikely to believe in their existence until concrete facts are available. The evolution of abiogenic organic matter occurred in the following different directions:

- a) increasing complexity of chemical compounds and structures;
- b) increasing energy output and reaction rate;
- c) selection of elements and compounds according to certain parameters;
- d) concentration of substances;
- e) the ability of complex compounds and proto-organisms to expand and grow fast;

f) the selectivity and recognition of some substances by others, according to the important evolutionary pattern for self and non-self discrimination.

For details, see Grinin 2020, 2024. For processes developing in the abiotic phase and points of view on these processes, see Anisimov, 2013; Markov, 2013, 2014, 2015, 2016; Markov et al., 2010; Mitrofanov, 2017.

The **Biosocial phase**. After the emergence and development of life, evolution begins to develop in the direction of social processes among living organisms. This is the biosocial phase.

The biosocial phase is of great interest from the point of view of the growing complexity of Big History. In the previous volume of our series, a great attention is paid to many of the most important processes of this phase: the development of the capacity for brain activity, the continued growth of the brain, the increase in psychological and cognitive complexity, and so on (Volk & Henriques, 2025; Hoggard, 2025; LePoire, 2025; see also Aunger, 2007; Gilbert 2014; LePoire, 2016).

The biosocial phase shows a powerful breakthrough in **cephalization** that evolution has made. In essence, at this phase we see evolution gradually searching for new directions of development. The first of these is the activity of the brain, psyche and consciousness. We see this in higher animals, especially in primates, whose behavioral lability is exceptionally high. Secondly, this is growth in terms of collectivism, a superstructure over ordinary biology in terms of creating a "super-organism" in the form of a large and organized group of animals. In fact, this is another step in terms of enlarging organisms, no less important than the transition from unicellular to multicellular organisms. This should be called **socialization**. In the biological world, we can distinguish several attempts at socialization. These are social insects. In Fig. 1, this line is a dead end. However, another line develops through higher animals and becomes more complex. First, there are the herd animals, then there is a complication in the primates and then the hominids. Thus, in this line there was a connection between two directions: cephalization and socialization, which led to a new transitional phase – anthropogenesis.

**Anthropogenesis** came as a transition to the social phase of Big History. It was the second transitional

phase from biological to social phase.

The transition from the biological to social phase of Big History was a very complex process that we do not quite understand even now. *Within this transition it appears possible to speak about a phase change of a few subtypes of macro-evolution: the biological type of macro-evolution was first transformed into the biological-social type, then the biological-social type was transformed into the social-biological type; and, finally, the latter was transformed into the social type of macro-evolution already in the framework of the unequivocally human society* (see Grinin & Korotayev, 2009b: ch. 1; Grinin & Korotayev 2025; Korotayev, 2025).

In the course of anthropogenesis, biological macro-evolution was transformed into bio-social evolution. The discoveries of recent decades have moved the dating of the emergence of our species deep in the past to about 200,000–300,000 BP (see, e.g., Callaway, 2017; Culotta, 1999; Gibbons, 1997; Guran et al., 2024; Hublin et al., 2017; Kaufman, 1999; Korotayev, 2025; Pääbo, 1995; Richter et al., 2017; Stringer, 2016; Stringer & Galway-Witham, 2017; Stringer & Crété, 2022; White et al., 2016).

However, the borderline around 60,000 – 40,000 BP (the so-called “Upper Paleolithic Revolution”) still retains an immense importance (Barton & Clark, 2021; Bar-Yosef, 2002, 2007; Bar-Yosef & Kuhn, 2016; Goder-Goldberger et al., 2023; Sánchez-Yustos

et al., 2024; Shea, 2013; Zwyns, 2021). This is the point from which we can speak with a complete confidence about the global presence of not only anatomically, but also behaviorally modern humans, ‘really human’ culture (e.g., Conard et al., 2009; Cuenca-Solana et al., 2013; Giacobini, 2007; Korotayev, 2025; Lbova, 2021; Lewis-Williams, 2002; Marshack, 1991; Oktaviana et al., 2024; Pettitt, 2011; Stiner, 2014; Zilhão, 2005). There is, of course, some hypothesis that human language appeared long before 50,000 – 40,000 BP. Although this is contested by other scientists, everybody agrees that by 40,000 BP fully developed languages existed wherever humans lived (e.g., Holden, 1998: 1455; Rozov, 2023).<sup>23</sup>

We believe that the evolutionary driving forces were still mostly biological when modern humans first emerged, but that the social forces gradually increased in their importance and prevailed over the biological ones at a certain point. Naturally, this was a rather prolonged process, within which the breakthrough point could hardly be identified. We contend that the social component became dominant after 50,000 – 40,000 BP. However, it did not become absolutely dominant, as biological adaptation and physical anthropological transformation continued in many important ways. The point is that they did not disappear, but their role significantly decreased.<sup>24</sup>

<sup>23</sup> Richard Klein, an anthropologist from Stanford University proposed the following hypothesis to explain the gap between the emergence of anatomically modern *Homo sapiens sapiens* and the emergence of language and cultural artifacts that took place much later. According to Klein, the modern brain is a result of rapid genetic changes. He hypothesized that such changes took place around 50,000 BP, pointing out that the affluence of cultural artifacts starts just after that date, as well as the migration of anatomically modern humans out of Africa (see Zimmer, 2003: 41ff). Thus, according to him, the emergence of *Homo sapiens* did not automatically result in social macro-evolution proper.

<sup>24</sup> On the one hand, in no way the biological evolution of the humans stopped 50 thousand years ago; in fact, it definitely continues, and in recent millennia (especially, after the Neolithic Revolution) it has even very significantly accelerated (Cochran

& Harpending, 2009; Hawks, 2014; Hawks et al., 2007; Kerner et al., 2023; Wilde et al., 2014). However, there is no evidence that this resulted in any increase in biological complexity of humans. After 50,000 BP human evolution mostly led to idioadaptations (sometimes very significant, like emergence of lactase persistence [or the ability to digest milk after weaning, e.g., Check, 2006; Curry, 2013]), sometimes degenerations, but never to aromorphoses that would have increased the biological complexity of humans. There is no evidence that at present human babies are born with more complex brain than Upper Paleolithic babies. In fact, the average brain size of the Upper Paleolithic Cro-Magnons in Europe was a bit larger than the one of present-day Europeans (e.g., Balzeau et al., 2013). This, of course, does not mean that Upper Paleolithic people were more complex biologically than present-

Thus, starting with the Upper Paleolithic Revolution, we may speak about *the transition from socio-biological evolution to social evolution*, a process that was finalized by the Agrarian Revolution.

### **Afterword. The Formation of Social Evolution's Own Mechanisms**

There were not so many major aromorphoses in the hunter-gatherer production principle (Grinin, 2006b, 2009a; Grinin, Grinin 2015, 2016; Grinin, Grinin, Korotayev 2024), which is why the overall rates of socio-evolutionary processes were slow and their directionality rather vague. HOWEVER, THEY WERE both in technical sphere and in social one. *Such a type of social macro-evolution may be denoted as socio-natural.* As a result of a system of inter-related aromorphoses connected with the agrarian revolution, one could observe the transition to the socio-historical type of macro-evolution. As a result of this, social macro-evolution changed its algorithm in a rather significant way, resulting in modification of certain evolutionary laws. We shall consider below how the significance of laws of evolution and the process of social macro-evolution changed as a result of the Agrarian Revolution.

Main factors of social change in foraging societies were the result of adaptation to new and various environments – from the deserts of Australia to the pack ice of the Arctic. This was only possible through the modification of socio-cultural systems. This made it possible for humans to people most of the world's landmass,<sup>25</sup> to create an enormous variety of tools and

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day humans, but, naturally, this is not congruent with any substantial increase of biological complexity of humans after 50,000 BP. Finally, 50,000 years do not look like a sufficient time for the development of a serious biological aromorphosis leading to a serious increase in biological complexity. On the other hand, it is quite clear that the complexity of human planetary system has increased enormously since 50,000 BP; and it has increased exclusively (or almost exclusively) through the increase in its sociocultural, not biological complexity.

<sup>25</sup> It involved crossing the Bab-el-Mandeb straits and movement along the Arabian Peninsula coast to Iran, then to India, South-East Asia, New Guinea and Melanesia, reaching Australia by around 50,000 BP

crafts, as well as social and other institutions. Effective adaptations let people not only survive, but sometimes also live relatively 'comfortable' lives (Sahlins, 1972) see below. The character of human relations with their environment varied significantly, but generally these were ones of human adaptation to the natural world (see, e.g., Grinin, 2006b: 82–83; Grinin & Grinin 2015, 2019, 2020a).

In the agrarian epoch, the character of those inter-relations changed significantly through the transition to much more conscious and effective change of the environments at a rather wide scale (irrigation, clearing of forests, plowing of steppes, soil fertilization, construction of cities, roads and so on). Natural forces (animal, wind and water energy) started to be used on a much wider scale (earlier humans actively used only fire). Natural raw materials started to be transformed into entirely new products (metals, fabrics, ceramics, glass) (Grinin & Grinin, 2015, 2019, 2020a).

Thus, within social evolution process a more and more significant role started to be played by peculiarly social factors that (in contrast with natural factors) are connected to conscious goal-setting and goal-achieving. Gradually, with economic-technological progress, the growth of surplus accumulation capacities, as well as general cultural complexity of social systems, their evolution became almost purely social. As a result, the 'vector' of evolutionary selection turned out to be directed toward societal capabilities to adapt to social (rather than natural) environments, which implies the capacity to compete

(see, e.g., Kealey et al., 2018; O'Connell et al., 2018; Korotayev, 2025). Around 55,000 BP Homo sapiens reached southern parts of China (Hublin, 2021: 3), around 45,000 BP modern humans appeared in Europe (Hublin et al., 2020; Prüfer et al., 2021; Teyssandier, 2023) and Siberia (Fu et al., 2014; Li et al., 2020; Rybin et al., 2023), about 40,000 BP they reached Northern China (Bae et al., 2017; Li et al., 2020), around 38,000 BP they arrived in Japan (e.g., Cooke et al., 2021), and so on. In the later Upper Paleolithic Homo sapiens peopled the New World, most likely in a few waves (e.g., Becerra-Valdivia & Higham, 2020; Gruhn, 2023; Korotayev, 2006; Korotayev et al., 2006, 2017; Meltzer, 2009; Stanford & Bradley, 2012).

with neighboring social systems in economic, military, commercial, cultural, ideological and other spheres.

Finally, we would like to mention the following important changes in the ‘algorithm’ of social evolution:

- *The start of the mechanism for resource accumulation.*

In the tens of thousands of years of the human foraging epoch, long-term material resource accumulation was relatively insignificant when compared to subsequent epochs. There was, of course, a certain amount of accumulation, of knowledge, traditions and technologies, albeit at a limited scale. This accumulation took place not in every society, but was observed at the global scale and was due to the overall demographic growth, increase in numbers of social systems, emergence of new tools, products, etc. There was practically no special accumulation sector prior to the Agrarian Revolution.<sup>26</sup>

In many cases, people could produce more than they actually needed, and sometimes even so-called ‘original affluent societies’ could emerge (Sahlins, 1972).

For example, with respect to the gatherers of sago in New Guinea, people would spend a minor part of their time securing food for themselves, whereas they would spend the rest of the time at other activities and leisure (Shnirelman, 1983, 1989). The impossibility to accumulate and/or the absence of the desire to accumulate slowed down development, which contributed to the slow speed of social evolution (Grinin, 2006b, 2009a). *In simple social systems of agriculturalists and pastoralists, the emergence of the possibility (and, later, the desire) to accumulate led to numerous transformations in the spheres of functional differentiation, distribution, social stratification, exchange, trade, development of property relationships, increasing political complexity and so on.*

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<sup>26</sup> With a possible exception of some highly specialized hunters (usually of large aquatic animals), gatherers, and fishers – for example, some social systems described ethnographically for the North-Western Coast of America (see, e.g., Averkieva, 1978; Shnirelman, 1986; Townsend,

- *Strengthening of the ability of social systems to change.*

Agrarian societies turned out to be more capable of serious social transformations than hunter-gatherers, while complex agrarian societies turned out to be much more capable of such transformations than simple agriculturalist and pastoralist systems. The growth of social systems' ability to change provides a vivid demonstration of the main difference between social and biological evolution – that humans were capable of consciously transforming their social systems, with preconceived goals.

- *Intersocietal contacts become the leading factor of social evolution.*

The importance of various contacts increased sharply, and this contributed to a more active adaptation of social systems to their environments. The growth of the role of contacts dramatically raised the importance of external social driving forces (Grinin, 1997: 23; 2007a: 177). Note that this had an enormous importance for the development of the World System and for the humankind as a whole. Military and other interactions stimulated improvements in administration, defense, culture, technology and so on. All this contributed to development of a single global process involving numerous societies and peoples.

It is also appropriate to note that the growth of societal size is not only due to natural demographic growth, but is more importantly due to the integration and unification of social systems. Thus, external contact factors become most important with respect to societal evolution.

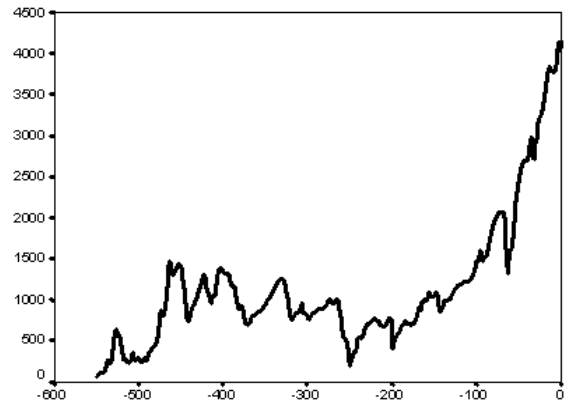
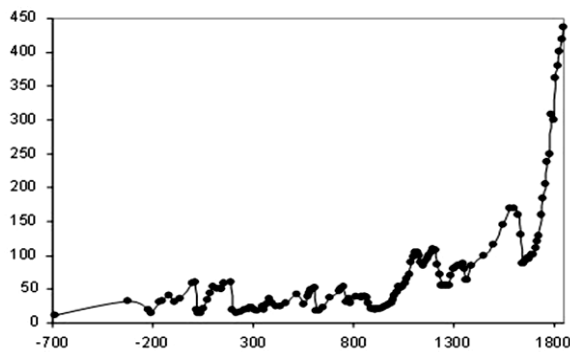
## **Appendix. Mathematical Modeling of Biological and Social Macroevolution**

In this appendix we consider a specific mathematical model capable of describing important features of

1985). See also about other most complex societies of the Hunter-Gatherer Production Principle: Ammerman & Cavalli-Sforza, 2014; Conte et al., 2018; Lozovskaya et al., 2018; March, 2013; Shnirelman, 1983; Tanno et al., 2013).

both biological and social macroevolution. In mathematical models of historical macrodynamics, a hyperbolic pattern of world population growth arises from non-linear, second-order positive feedback between demographic growth and technological development. Based on diverse paleontological data and an analogy with macrosociological models, we suggest that the hyperbolic character of biodiversity growth can be similarly accounted for by non-linear, second-order positive feedback between diversity growth and the complexity of community structure. We further discuss how such positive feedback mechanisms can be modelled mathematically.

The authors of this paper met for the first time in 2005, in the town of Dubna (near Moscow), at what seems to have been the first ever international conference dedicated specifically to Big History studies (see Korotayev & Markov, 2014, 2015). Without advance knowledge of one another, we found ourselves in a single session. During the course of the session, we presented two different diagrams. One illustrated population dynamics in China between 700 BCE and 1851 CE, the other illustrated the dynamics of marine Phanerozoic biodiversity over the past 542 million years (Fig. 1).



**Fig. 1.** Similarity between the long-term population dynamics of China (top: millions of people, following Korotayev, Malkov, *et al.* 2006b: 47–88) and the dynamics of Phanerozoic marine biodiversity (bottom: number of genera,  $N$ . Data source: Markov & Korotayev, 2007)

The similarity between the two diagrams was striking. This, despite the fact that they depicted the development of very different systems (human population *vs.* biota) at different time scales (hundreds of years *vs.* millions of years), and had been generated using the methods of different sciences (historical demography *vs.* paleontology) with different sources (demographic estimates *vs.* paleontological data). What could have caused similarity of developmental dynamics in very different systems?

\* \* \*

In 1960, von Foerster *et al.* published a striking discovery in the journal *Science* (von Foerster *et al.*, 1960). They showed that between 1 and 1958 CE, the world's population ( $N$ ) dynamics could be described in an extremely accurate way with an astonishingly simple equation:<sup>27</sup>

$$N_t = \frac{C}{(t_0 - t)}, \quad (\text{Eq. 1})$$

<sup>27</sup> To be exact, the equation proposed by von Foerster and his colleagues looked as follows:  $N_t = \frac{C}{(t_0 - t)^{0.99}}$ .

However, as von Hoerner (1975) and Kapitza (1996) showed, it can be simplified as  $N_t = \frac{C}{t_0 - t}$ .

where  $N_t$  is the world population at time  $t$ , and  $C$  and  $t_0$  are constants, with  $t_0$  corresponding to an absolute limit ('singularity' point) at which  $N$  would become infinite. Parameter  $t_0$  was estimated by von Foerster and his colleagues as 2026.87, which corresponds to November 13, 2026; this made it possible for them to supply their article with a title that was a public-relations masterpiece: 'Doomsday: Friday, 13 November, A.D. 2026'.

Of course, von Foerster and his colleagues did not imply that the world population on that day could actually become infinite. The real implication was that the world population growth pattern that operated for many centuries prior to 1960 was about to end and be transformed into a radically different pattern. This prediction began to be fulfilled only a few years after the 'Doomsday' paper was published as World System

$$\frac{dN}{dt} = aN^2 \quad (\text{Eq. 3})$$

growth (and world population growth in particular) began to diverge more and more from the previous blow-up regime. Now no longer hyperbolic, the world population growth pattern is closer to a logistic one (see, e.g., Korotayev, Malkov *et al.* 2006a; Korotayev, 2009).

Fig. 2 presents the overall correlation between the curve generated by von Foerster *et al.*'s equation and the most detailed series of empirical estimates of world population (McEvedy & Jones, 1978, for the period 1000–1950; U.S. Bureau of the Census, 2025 and UN Population Division, 2025, for 1950–1970). The formal characteristics are:  $R = 0.998$ ;  $R^2 = 0.996$ ;  $p = 9.4 \times 10^{-17} \approx 1 \times 10^{-16}$ . For readers unfamiliar with mathematical statistics:  $R^2$  can be regarded as a measure of the fit between the dynamics generated by a mathematical model and the empirically observed situation, and can be interpreted as the proportion of

the variation accounted for by the respective equation. Note that 0.996 also can be expressed as 99.6 per cent.<sup>28</sup> Thus, von Foerster *et al.*'s equation accounts for an astonishing 99.6 per cent of all the macrovariation in world population, from 1000 CE through 1970, as estimated by McEvedy and Jones (1978) and UN Population Division (2025). Note also that the empirical estimates of world population find themselves aligned in an extremely neat way along the hyperbolic curve, which convincingly justifies the designation of the pre-1970s world population growth pattern as 'hyperbolic'.

The von Foerster *et al.*'s equation, , is the solution for the following differential equation (see, e.g., Korotayev, Malkov *et al.* 2006a: 119–120):

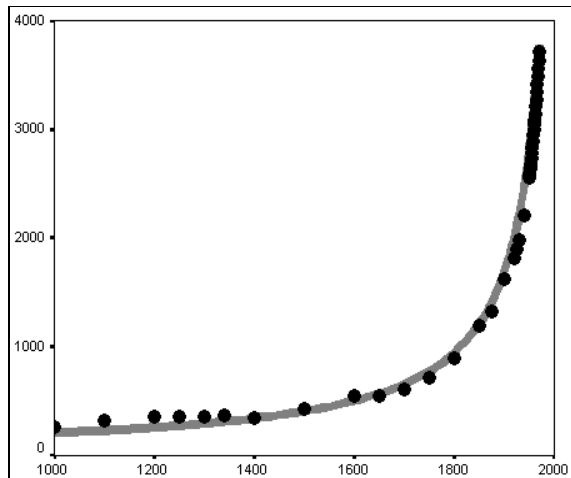
$$\frac{dN}{dt} = \frac{N^2}{C} \quad (\text{Eq. 2})$$

This equation can be also written as:

$$\text{where } a = \frac{1}{C}.$$

<sup>28</sup> The second characteristic ( $p$ , standing for 'probability') is a measure of the correlation's statistical significance. A bit counter-intuitively, the lower the value of  $p$ , the higher the statistical significance of the respective correlation. This is because  $p$  indicates the probability that the observed correlation could be accounted solely by chance. Thus,  $p = 0.99$  indicates an extremely low statistical significance, as it means that there are 99 chances out of 100 that the observed correlation is the result of a

coincidence, and, thus, we can be quite confident that there is no systematic relationship (at least, of the kind that we study) between the two respective variables. On the other hand,  $p = 1 \times 10^{-16}$  indicates an extremely high statistical significance for the correlation, as it means that there is only one chance out of 10,000,000,000,000,000 that the observed correlation is the result of pure coincidence (a correlation is usually considered statistically significant once  $p < 0.05$ ).



**Fig. 2.** Correlation between empirical estimates of world population (black, in millions of people, 1000–1970) and the curve generated by von Foerster *et al.*'s equation (grey)

What is the meaning of this mathematical expression? In our context,  $dN/dt$  denotes the absolute population growth rate at a certain moment in time. Hence, this equation states that the absolute population growth rate at any moment in time should be proportional to the square of world population at this moment. This significantly demystifies the problem of hyperbolic growth. To explain this hyperbolic growth, one need only explain why for many millennia the world population's absolute growth rate tended to be proportional to the square of the population.

The main mathematical models of hyperbolic growth in the world population (Cohen, 1995; Golosovsky, 2010; Grinin, Markov *et al.*, 2013; Korotayev, 2005, 2007, 2008, 2009, 2013, 2018, 2020b, 2024, 2025a; Korotayev, Malkov *et al.*, 2006a: 21–36; Korotayev & Malkov, 2012; Kremer, 1993; Podlazov, 2017; Taagapera, 1976, 1979; Tsirel, 2004) are based on the following two assumptions:

- (1) 'the Malthusian (Malthus, 1778 [1798]) assumption that population is limited by the available technology, so that the growth rate of population is proportional to the growth

<sup>29</sup> In addition to this, the absolute growth rate is proportional to the population itself. With a given relative growth rate, a larger population will increase more in absolute number than a smaller one.

rate of technology' (Kremer, 1993, 681–682),<sup>29</sup> and

(2) the idea that '[h]igh population spurs technological change because it increases the number of potential inventors... In a larger population there will be proportionally more people lucky or smart enough to come up with new ideas', thus, 'the growth rate of technology is proportional to total population' (Kremer, 1993, 685).<sup>30</sup>

Here Kremer uses the main assumption of Endogenous Technological Growth theory (see, *e.g.*, Kuznets, 1960; Grossman & Helpman, 1991; Aghion & Howitt, 1998; Simon, 1977, 2000; Komlos & Nefedov, 2002; Jones, 1995, 2005).

The first assumption looks quite convincing. Indeed, throughout most of human history the world population was limited by the technologically determined ceiling of the carrying capacity of land. For example, with foraging subsistence technologies the Earth could not support more than a few million people because the amount of naturally available useful biomass on this planet is limited. The world population could only grow over this limit when people started to apply various means to artificially increase the amount of available biomass that is with the transition from foraging to food production. Extensive agriculture is also limited in terms of the number of people that it can support. Thus, further growth of the world population only became possible with the intensification of agriculture and other technological improvements (see, *e.g.*, Turchin, 2003; Korotayev, Malkov *et al.* 2006a, 2006b; Korotayev & Khaltourina, 2006).

However, as is well known, the technological level is not constant, but variable (see, *e.g.*, Grinin 2006b; Grinin & Korotayev, 2015; Grinin, Grinin, & Korotayev, 2024), and in order to describe its dynamics the second basic assumption is employed. In general, we find this assumption rather plausible – in fact, it is quite probable that, other things being equal, within a given period of time, five million people will

<sup>30</sup> Note that 'the growth rate of technology' here means the relative growth rate (*i.e.*, the level to which technology will grow in a given unit of time in proportion to the level observed at the beginning of this period).

make approximately five times more inventions than one million people.

This assumption was expressed mathematically by Kremer in the following way:

$$\frac{dT}{dt} = kNT. \quad (\text{Eq. 4})$$

This equation simply says that the absolute technological growth rate at a given moment in time ( $dT/dt$ ) is proportional to the technological level ( $T$ ) observed at this moment (the wider the technological base, the higher the number of inventions that can be made on its basis). On the other hand, this growth rate is also proportional to the population ( $N$ ): the larger the population, the larger the number of potential inventors.<sup>31</sup>

When united in one system, Malthusian and Kuznetsian equations account quite well for the hyperbolic growth of the world population observed before the early 1990s (see, e.g., Korotayev 2005, 2007, 2008, 2013, 2018, 2020b, 2024, 2025a; Korotayev, Malkov *et al.* 2006a). The resultant models provide a rather convincing explanation of *why*, throughout most of human history, the world population followed the hyperbolic pattern with the absolute population growth rate tending to be proportional to  $N^2$ . For example, why would the growth of population from, say, 10 million to 100 million, result in the growth of  $dN/dt$  100 times? The above mentioned models explain this rather convincingly. The point is that the growth of world population from 10 to 100 million implies that human subsistence technologies also grew approximately 10 times (given that it will have proven, after all, to be able to support a population ten times larger). On the other hand, the tenfold population growth also implies a tenfold growth in the number of potential inventors, and, hence, a tenfold increase in the relative technological growth rate. Thus, the absolute technological growth rate would expand  $10 \times 10 = 100$  times as, in accordance with Eq. 4, an order of magnitude higher number of people having at their disposal an order of magnitude wider technological base would tend to make two orders of magnitude more inventions. As throughout the Malthusian epoch, the world population ( $N$ ) tended toward the

technologically determined carrying capacity of the Earth, we have good reason to expect that  $dN/dt$  should also grow just by about 100 times.

In fact, it can be shown (see, e.g., Korotayev, Malkov *et al.* 2006a, 2006b; Korotayev & Khaltourina, 2006) that the hyperbolic pattern of the world's population growth could be accounted for by a nonlinear second-order positive feedback mechanism that was long ago shown to generate just the hyperbolic growth, also known as the 'blow-up regime' (see, e.g., Kurdyumov, 1999). In our case, this nonlinear second-order positive feedback looks as follows: more people – more potential inventors – faster technological growth – faster growth of the Earth's carrying capacity – faster population growth – more people allow for more potential inventors – faster technological growth, and so on (see Fig. 3).

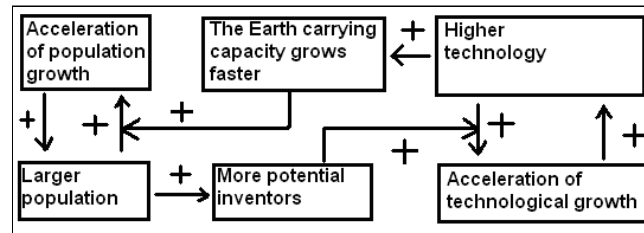


Fig. 3. Cognitive scheme of the nonlinear second order positive feedback between technological development and demographic growth

Note that the relationship between technological development and demographic growth cannot be analyzed through any simple cause-and-effect model, as we observe a true dynamic relationship between these two processes – each of them is both the cause and the effect of the other.

The feedback system described here should be identified with the process of 'collective learning' described, principally, by Christian (2005: 146–148; see also Baker, 2016). The mathematical models of World System development discussed in this paper can be interpreted as models of the influence that collective learning has on global social evolution (*i.e.*, the evolution of the World System). Thus, the rather peculiar hyperbolic shape of accelerated global development prior to the early 1970s may be regarded as a product of global collective learning. We have

<sup>31</sup> Kremer did not test this hypothesis empirically in a direct way. Note, however, that our own empirical

test of this hypothesis has supported it (see Korotayev, Malkov *et al.* 2006b: 141–146).

also shown (Korotayev, Malkov *et al.* 2006a: 34–66) that, for the period prior to the 1970s, World System economic and demographic macrodynamics, driven by the above-mentioned positive feedback loops, can simply and accurately be described with the following model:

$$\frac{dN}{dt} = aSN, \quad (\text{Eq. 5})$$

$$\frac{dS}{dt} = bNS. \quad (\text{Eq. 6})$$

The world GDP ( $G$ ) can be calculated using the following equation:

$$G = mN + SN, \quad (\text{Eq. 7})$$

where  $G$  is the world GDP,  $N$  is population, and  $S$  is the produced surplus per capita, over the subsistence amount ( $m$ ) that is minimally necessary to reproduce the population with a zero growth rate in a Malthusian system (thus,  $S = g - m$ , where  $g$  denotes per capita GDP);  $a$  and  $b$  are parameters.

The mathematical analysis of the basic model (not described here) suggests that up to the 1970s, the amount of  $S$  should be proportional, in the long run, to the World System's population:  $S = kN$ . Our statistical analysis of available empirical data has confirmed this theoretical proportionality (Korotayev, Malkov *et al.* 2006a: 49–50). Thus, in the right-hand side of Eq. 6,  $S$  can be replaced with  $kN$ , resulting in the following equation:

$$\frac{dN}{dt} = kaN^2.$$

Recall that the solution of this type of differential equations is:

$$N_t = \frac{C}{(t_0 - t)},$$

which produces a simple hyperbolic curve.

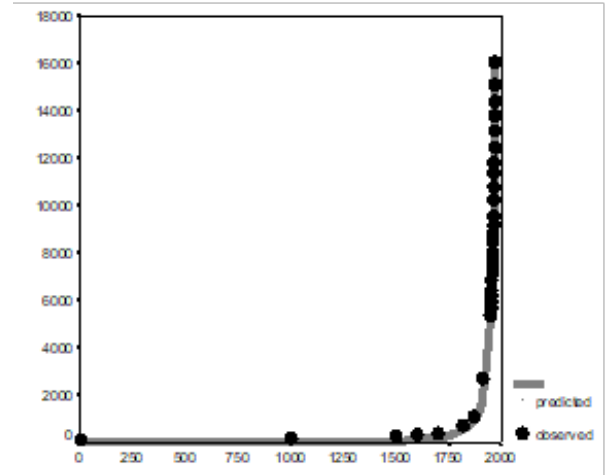
As, according to our model,  $S$  can be approximated as  $kN$ , its long-term dynamics can be approximated with the following equation:

$$S = \frac{kC}{t_0 - t}. \quad (\text{Eq. 8})$$

Thus, the long-term dynamics of the most dynamic component of the world GDP,  $SN$ , the ‘world surplus product’, can be approximated as follows:

$$SN = \frac{kC^2}{(t_0 - t)^2}. \quad (\text{Eq. 9})$$

This suggests that the long-term world GDP dynamics up to the early 1970s must be approximated better by a quadratic hyperbola, rather than by a simple one. As shown in Fig. 4, this approximation works very effectively indeed.

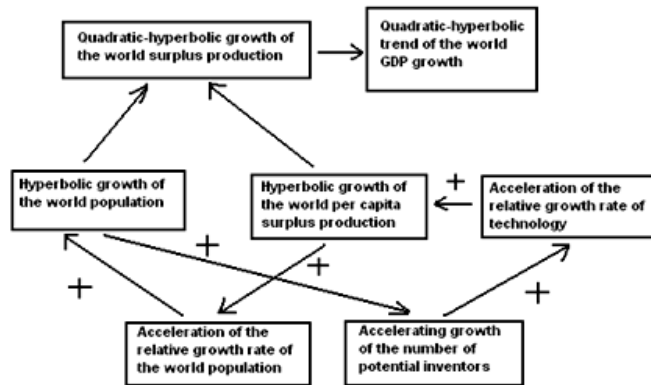


**Fig. 4.** The fit between predictions of a quadratic-hyperbolic model and observed world GDP dynamics, 1–1973 CE (in billions of 1990 international dollars, PPP)

*Note:*  $R = .9993$ ,  $R^2 = .9986$ ,  $p \ll .0001$ . The black markers correspond to Maddison's (2001) estimates (Maddison's estimates of the world per capita GDP for 1000 CE has been corrected on the basis of [Meliantsev, 2004]). The grey solid line has been generated by the following equation:

$$G = \frac{17749573.1}{(2006 - t)^2}.$$

Thus, up to the 1970s the hyperbolic growth of the world population was accompanied by the quadratic-hyperbolic growth of the world GDP, as suggested by our model. Note that the hyperbolic growth of the world population and the quadratic-hyperbolic growth of the world GDP are very tightly connected processes, actually two sides of the same coin, two dimensions of one process propelled by nonlinear second-order positive feedback loops between the technological development and demographic growth (see Fig. 5).



**Fig. 5.** Cognitive scheme of the world economic growth generated by nonlinear second-order positive feedback between technological development and demographic growth

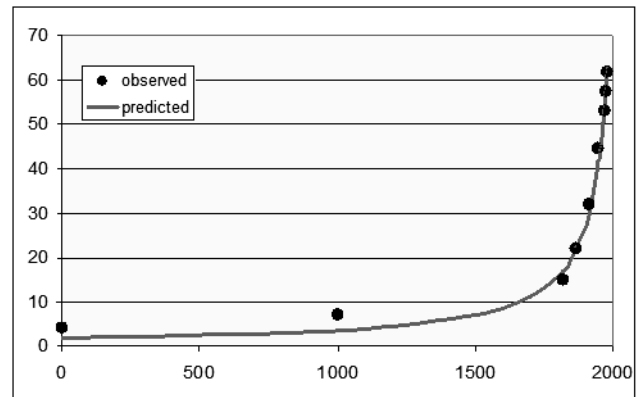
We have also demonstrated (Korotayev, Malkov *et al.* 2006a: 67–80) that the World System population's literacy ( $l$ ) dynamics are rather accurately described by the following differential equation:

$$\frac{dl}{dt} = aSl(1-l), \quad (\text{eq.10})$$

where  $l$  is the proportion of the population that is literate,  $S$  is per capita surplus, and  $a$  is a constant. In fact, this is a version of the autocatalytic model. Literacy growth is proportional to the fraction of the population that is literate,  $l$  (potential teachers), to the fraction of the population that is illiterate,  $(1 - l)$  (potential pupils), and to the amount of per capita surplus  $S$ , since it can be used to support educational programs. (Additionally,  $S$  reflects the technological level  $T$  that implies, among other things, the level of development of educational technologies.) From a mathematical point of view, Eq. 9 can be regarded as logistic where saturation is reached at literacy level  $l = 1$ .  $S$  is responsible for the speed with which this level is being approached.

It is important to stress that with low values of  $l$  (which correspond to most of human history, with recent decades being the exception), the rate of increase in world literacy generated by this model (against the background of hyperbolic growth of  $S$ ) can be approximated rather accurately as hyperbolic (see Fig. 6).

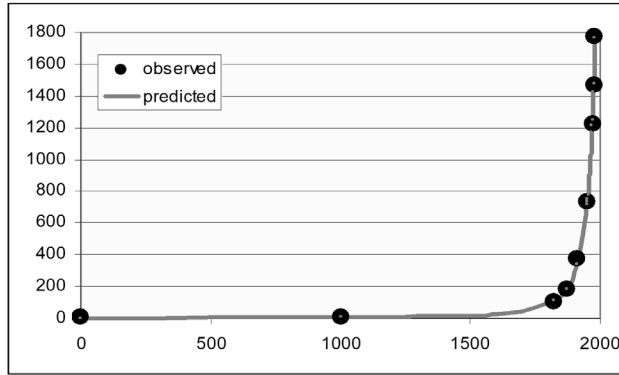
<sup>32</sup> Since literacy appeared, almost all of the Earth's literate population has lived within the World System; hence, the literate population of the Earth



**Fig. 6.** The fit between predictions of the hyperbolic model and observed world literacy dynamics, 1–1980 CE (%). Note:  $R = 0.997$ ,  $R^2 = 0.994$ ,  $p < 0.0001$ . Black dots correspond to World Bank (2013) estimates for the period since 1970, and to Meliantsev's (2004) estimates for the earlier period. The grey solid line has been generated by the following equation:  $l_t = \frac{3769.264}{(2040-t)^2}$ . The best-fit values of parameters  $C$  (3769.264) and  $t_0$  (2040) have been calculated with the least squares method.

The overall number of literate people is proportional both to the literacy level and to the overall population. As both of these variables experienced hyperbolic growth until the 1960s/1970s, one has sufficient grounds to expect that until recently the overall number of literate people in the world ( $L$ )<sup>32</sup> was growing not just hyperbolicly, but rather in a quadratic-hyperbolic way (as was world GDP). Our empirical test has confirmed this – the quadratic-hyperbolic model describes the growth of the literate population of this planet with an extremely good fit indeed (see Fig. 7).

and the literate population of the World System have been almost perfectly synonymous.

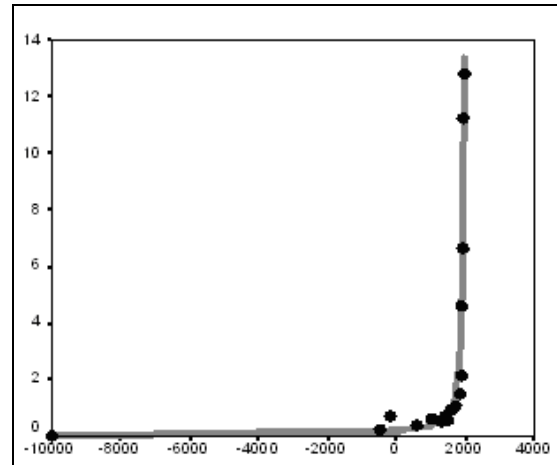


**Fig. 7.** The fit between predictions of the quadratic-hyperbolic model and observed world literate population dynamics, 1–1980 CE ( $L$ , millions). Note:  $R = 0.9997$ ,  $R^2 = 0.9994$ ,  $p < 0.0001$ . The black dots correspond to UNESCO/World Bank (2025) estimates for the period since 1970, and to Meliantsev's (2004) estimates for the earlier period; we have also taken into account the changes of age structure on the basis of UN Population Division (2025) data. The grey solid line has been generated by the following equation:  $L_t = \frac{4958551}{(2033 - t)^2}$ . The best-fit values of parameters  $C$  (4958551) and  $t_0$  (2033) have been calculated with the least squares method.

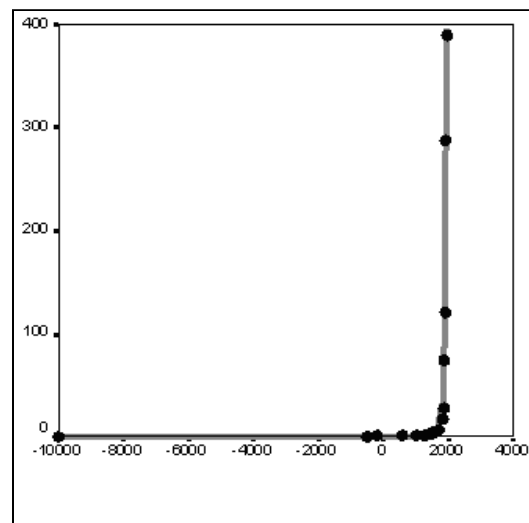
Similar processes are observed with respect to world urbanization, the macrodynamics of which appear to be described by the differential equation:

$$\frac{du}{dt} = bSu(u_{lim} - u), \quad (\text{Eq. 11})$$

where  $u$  is the proportion of the population that is urban,  $S$  is per capita surplus produced with the given level of the World System's technological development,  $b$  is a constant, and  $u_{lim}$  is the maximum possible proportion of the population that can be urban. Note that this model implies that during the Malthusian-Kuznetsian era of the blow-up regime, the hyperbolic growth of world urbanization must have been accompanied by a quadratic-hyperbolic growth of the urban population of the world, as supported by our empirical tests (see Figs 8–9).



**Fig. 8.** The fit between predictions of the hyperbolic model and empirical estimates of world megaurbanization dynamics (% of the world population living in cities with > 250,000 inhabitants), 10,000 BCE – 1960 CE. Note:  $R = 0.987$ ,  $R^2 = 0.974$ ,  $p < 0.0001$ . The black dots correspond to estimates of Chandler (1987), UN Population Division (2025), Modelski (2003), and Gruebler (2006). The grey solid line has been generated by the following equation:  $u_t = \frac{403.012}{(1990 - t)}$ . The best-fit values of parameters  $C$  (403.012) and  $t_0$  (1990) have been calculated with the least squares method. For comparison, the best fit ( $R^2$ ) obtained here for the exponential model is 0.492.

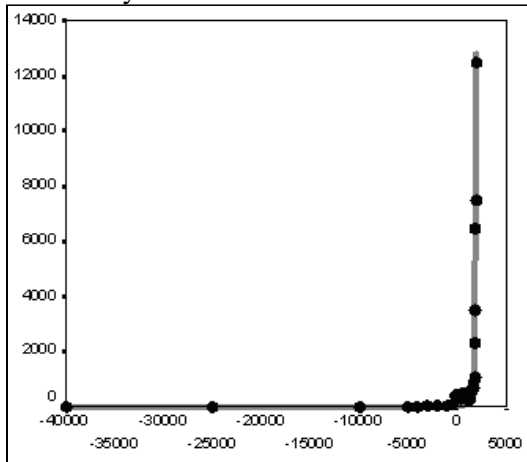


**Fig. 9.** The fit between predictions of the quadratic-hyperbolic model and the observed dynamics of world urban population living in cities with > 250,000 inhabitants (millions), 10,000 BCE – 1960 CE. Note:  $R = 0.998$ ,  $R^2 = 0.996$ ,  $p < 0.0001$ . The black markers

correspond to estimates of Chandler (1987) and UN Population Division (2025). The grey solid line has been generated by the following equation:  $U_t = \frac{912057.9}{(2008 - t)^2}$ . The best-fit values of parameters  $C$  (912057.9) and  $t_0$  (2008) have been calculated with the least squares method. For comparison, the best fit ( $R^2$ ) obtained here for the exponential model is 0.637.

Within this context it is hardly surprising to find that the general macrodynamics of largest settlements within the World System are also quadratic-hyperbolic (see Fig. 10).

As was long ago demonstrated by cross-cultural anthropologists (see, e.g., Naroll & Divale, 1976; Levinson & Malone, 1980: 34), for pre-agrarian, agrarian, and early industrial cultures the size of the largest settlement is a rather effective indicator of the general sociocultural complexity of a social system. This, of course, suggests that the World System's general sociocultural complexity also grew, in the Malthusian-Kuznetsian era, in a generally quadratic-hyperbolic way.

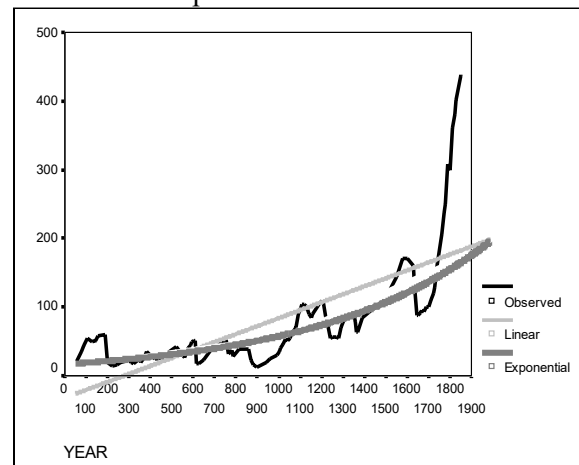


**Fig. 10.** The fit between predictions of the quadratic-hyperbolic model and the observed dynamics of size of the largest settlement of the world (thousands of inhabitants), 10,000 BCE – 1950 CE. Note:  $R = 0.992$ ,  $R^2 = 0.984$ ,  $p < 0.0001$ . The black markers correspond to estimates of Modelski (2003) and Chandler (1987). The grey solid line has been generated by the following equation:  $U_{\max t} = \frac{104020618.573}{(2040 - t)^2}$ . The best-fit values of parameters  $C$  (104020618.5) and  $t_0$  (2040) have been calculated with the least squares method. For

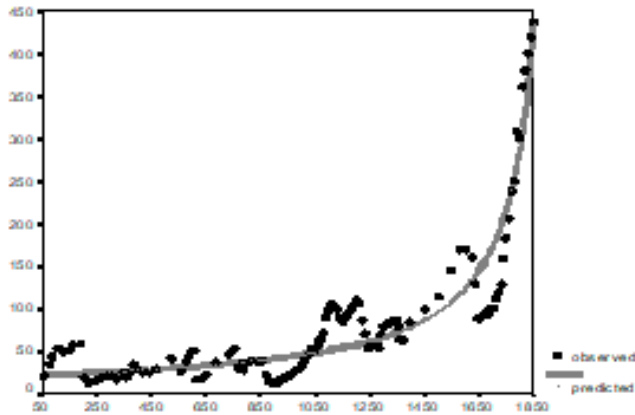
comparison, the best fit ( $R^2$ ) obtained here for the exponential model is 0.747.

Turning to a more concrete case study, as suggested at the beginning of this section, the hyperbolic model is particularly effective for describing the long-term population dynamics of China, the country with the best-known long-term demographic history. The Chinese population curve reflects not only a hyperbolic trend, but also cyclical and stochastic dynamics. These components of long-term population dynamics in China, as well as in other complex agrarian societies, have been discussed extensively (see, e.g., Alexander, 2016; Chu & Lee, 1994; Goldstone, 1991; Hoyer et al., 2024; Komlos & Nefedov, 2002; Kondor & Turchin, 2024; Korotayev & Khaltourina, 2006; Korotayev, Malkov et al., 2006b; Korotayev & Zinkina, 2015; Korotayev, Zinkina et al., 2016; Korotayev, 2017; Nefedov, 2004, 2012, 2013, 2025; Turchin, 2003, 2005; Turchin & Korotayev, 2006; Turchin & Nefedov, 2009; Usher, 1989; Wittmann & Kuehn, 2024).

As we have observed with respect to world population dynamics, even before the start of its intensive modernization, the population dynamics of China were characterized by a pronounced hyperbolic trend (Figs 11 and 12). The hyperbolic model describes traditional Chinese population dynamics *much* more accurately than either linear or exponential models.



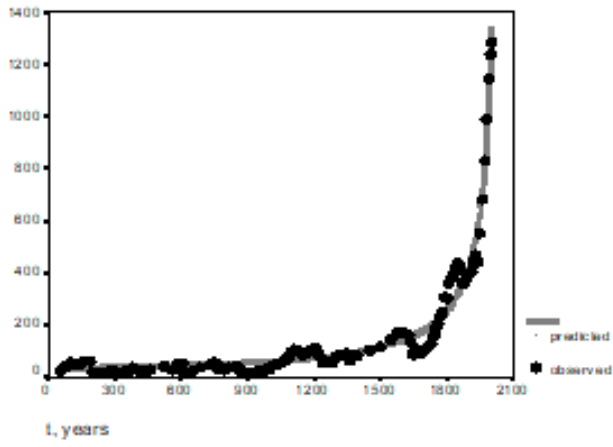
**Fig. 11.** Population dynamics of China (million people, following Korotayev, Malkov, et al. 2006b: 47–88), 57–1851 CE. Fit with Linear and Exponential Models. Note: Linear model:  $R^2 = 0.469$ . Exponential model:  $R^2 = 0.600$ .



**Fig. 12.** Fit between a hyperbolic model and observed population dynamics of China (million people), 57–1851 CE Note:  $R^2 = 0.884$ . The grey solid line has been generated by the following equation:

$$N_t = \frac{33431}{1915 - t}$$

The hyperbolic model describes the population dynamics of China in an especially accurate way if we take the modern period into account (Fig. 13).



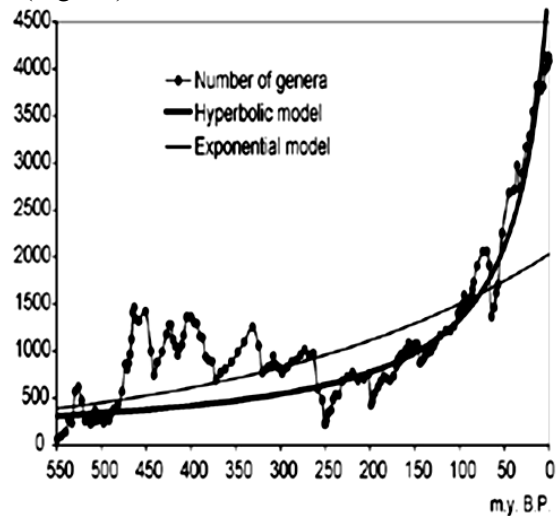
**Fig. 13.** Fit between a hyperbolic model and observed population dynamics of China (million people, following Korotayev, Malkov, *et al.* 2006b: 47–88), 57–2003 CE Note:  $R^2 = 0.968$ . The grey solid line has been generated by the following equation:

$$N_t = \frac{63150}{2050 - t}$$

It is curious that, as we noted above, the dynamics of marine biodiversity are strikingly similar to the population dynamics of China. The similarity

probably derives from the fact that both curves are produced by the interference of the same three components (the general hyperbolic trend, as well as cyclical and stochastic dynamics). In fact, there is a lot of evidence that some aspects of biodiversity dynamics are stochastic (Raup *et al.*, 1973; Sepkoski, 1994; Markov, 2001; Cornette & Lieberman, 2004), while others are periodic (Raup & Sepkoski, 1984; Rohde & Muller, 2005; Roberts, Mannion, 2019). In any event, the hyperbolic model describes marine biodiversity (measured by number of genera) through the Phanerozoic much more accurately than an exponential model (Fig. 14).

When measured by number of species, the fit between the empirically observed marine biodiversity dynamics and the hyperbolic model becomes even better (Fig. 15).



**Fig. 14.** Global change in marine biodiversity (number of genera,  $N$ ) through the Phanerozoic (following Korotayev & Markov, 2014). Note: Exponential model:  $R^2 = 0.463$ . Hyperbolic model:  $R^2 = 0.854$ . The hyperbolic line has been generated by the following equation:

$$N_t = \frac{183320}{37 - t}$$

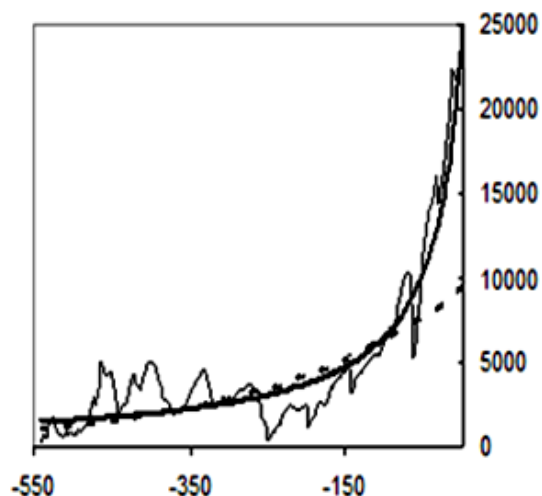


Fig.

15. Global change in marine biodiversity (number of species,  $N$ ) through the Phanerozoic (following Korotayev & Markov, 2014). Note: Exponential model:  $R^2 = 0.51$ . Hyperbolic model:  $R^2 = 0.91$ . The hyperbolic line has been

generated by the following equation: 
$$N_t = \frac{892874}{35 - t}$$

Likewise, the hyperbolic model describes continental biodiversity in an especially accurate way (Fig. 16).

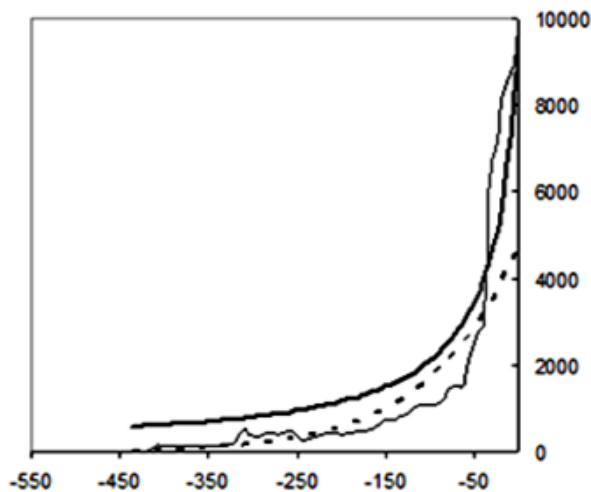


Fig. 16. Global change in continental biodiversity (number of genera,  $N$ ) through the Phanerozoic (following Korotayev & Markov, 2014), Note: Exponential model:  $R^2 = 0.86$ . Hyperbolic model:  $R^2 = 0.94$ . The hyperbolic line has been generated by the following equation: 
$$N_t = \frac{272095}{29 - t}$$

However, the best fit between the hyperbolic model and the empirical data is observed when the hyperbolic model is used to describe the dynamics of total (marine and continental) global biodiversity (Fig. 17).

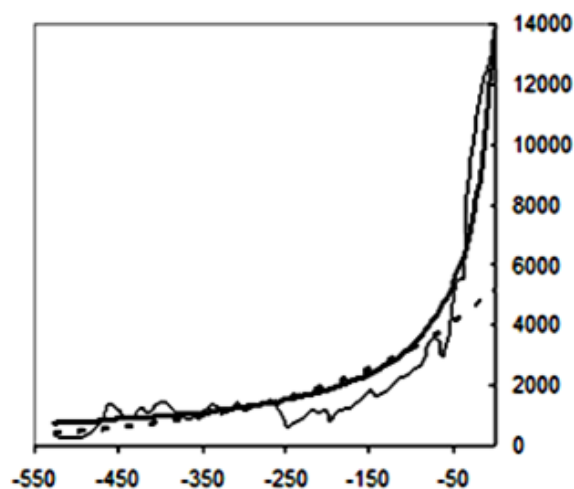


Fig. 17. Global change in total biodiversity (number of genera,  $N$ ) through the Phanerozoic (following Korotayev & Markov, 2014) Note: Exponential model:  $R^2 = 0.67$ . Hyperbolic model:  $R^2 = 0.95$ . The hyperbolic line has been generated by the following equation:

$$N_t = \frac{434635}{30 - t}$$

The hyperbolic dynamics are most prominent when both marine and continental biotas are considered together. This fact can be interpreted as a proof of the integrated nature of the biosphere. But why, throughout the Phanerozoic, did global biodiversity tend to follow a hyperbolic trend similar to that which we observed for the World System in general and China in particular?

As we have noted above, in sociological models of macrohistorical dynamics, the hyperbolic pattern of world population growth arises from non-linear second-order positive feedback (more or less identical with the mechanism of collective learning) between demographic growth and technological development. Based on analogy with these sociological models and diverse paleontological data, we suggest that the hyperbolic character of biodiversity growth can be similarly accounted for by non-linear second-order positive feedback between diversity growth and the

complexity of community structure: more genera – higher alpha diversity – enhanced stability and ‘buffering’ of communities – lengthening of average life span of genera, accompanied by a decrease in the extinction rate – faster diversity growth – more genera – higher alpha diversity, and so on. Indeed, this begins to appear as a (rather imperfect) analogue of the collective learning mechanism active in social macroevolution.

The growth of genus richness throughout the Phanerozoic was mainly due to an increase in the average longevity of genera and a gradual accumulation of long-lived (stable) genera in the biota. This pattern reveals itself in a decrease in the extinction rate. Interestingly, in both biota and humanity, growth was facilitated by a decrease in mortality rather than by an increase in the birth rate. The longevity of newly arising genera was growing in a stepwise manner. The most short-lived genera appeared during the Cambrian; more long-lived genera appeared in Ordovician to Permian; the next two stages correspond to the Mesozoic and Cenozoic (Markov, 2001, 2002). We suggest that diversity growth can facilitate the increase in genus longevity via progressive stepwise changes in the structure of communities.

Most authors agree that three major biotic changes resulted in the fundamental reorganization of community structure during the Phanerozoic: Ordovician radiation, end-Permian extinction, and end-Cretaceous extinction (Bambach, 1977; Sepkoski et al., 1981; Sepkoski, 1988; Markov, 2001; Bambach et al., 2002; Benton, Wu, 2022; Wu et al., 2024). Generally, after each major crisis, the communities became more complex, diverse, and stable. The stepwise increase of alpha diversity (*i.e.*, the average number of species or genera in a community) through the Phanerozoic was demonstrated by Bambach (1977) and Sepkoski (1988). Although Powell and Kowalewski (2002) have argued that the observed increase in alpha diversity might be an artifact caused by several specific biases that influenced the taxonomic richness of different parts of the fossil record, there is evidence that these biases largely compensated for one another so that the observed increase in alpha diversity was probably underestimated rather than overestimated (Bush & Bambach, 2004; Markov, 2009).

Another important symptom of progressive development of communities is an increase in the evenness of species (or genus) abundance distribution. In primitive, pioneer, or suppressed communities, this distribution is strongly uneven: the community is overwhelmingly dominated by a few very abundant species. In more advanced, climax, or flourishing communities, this distribution is more even (Magurran, 1988). The former type of community is generally more vulnerable. The evenness of species richness distribution in communities increased substantially during the Phanerozoic (Powell & Kowalewski, 2002; Bush & Bambach, 2004). It is most likely there was also an increase in habitat utilization, total biomass, and the rate of trophic flow in biota through the Phanerozoic (Powell & Kowalewski, 2002).

The more complex the community, the more stable it is due to the development of effective interspecies interactions and homeostatic mechanisms based on the negative feedback principle. In a complex community, when the abundance of a species decreases, many factors arise that facilitate its recovery (*e.g.*, food resources rebound while predator populations decline) (Foote, 2023). Even if the species becomes extinct, its vacant niche may ‘recruit’ another species, most probably a related one that may acquire morphological similarity with its predecessor and thus will be assigned to the same genus by taxonomists. So a complex community can facilitate the stability (and longevity) of its components, such as niches, taxa and morphotypes. This effect reveals itself in the phenomenon of ‘coordinated stasis’. The fossil record contains many examples in which particular communities persist for million years while the rates of extinction and taxonomic turnover are minimized (Brett et al., 1996, 2007; Roopnarine, 2025).

Selective extinction leads to the accumulation of ‘extinction-tolerant’ taxa in the biota (Sepkoski, 1991b). Although there is evidence that mass extinctions can be nonselective in some aspects (Jablonski, 2005), they are obviously highly selective with respect to the ability of taxa to endure unpredictable environmental changes (Payne et al., 2023). This can be seen, for instance, in the selectivity of the end-Cretaceous mass extinction with respect to the time of the first occurrence of genera. In younger

cohorts, the extinction level was higher than that of the older cohorts (see Markov & Korotayev, 2007: fig. 2). The same pattern can be observed during the periods of ‘background’ extinction as well. This means that genera differ in their ability to survive extinction events, and that extinction-tolerant genera accumulate in each cohort over the course of time. Thus, taxa generally become more stable and long-lived through the course of evolution, apart from the effects of communities. The communities composed of more stable taxa would be, in turn, more stable themselves, thus creating positive feedback.

The stepwise change of dominant taxa plays a major role in biotic evolution. This pattern is maintained not only by the selectivity of extinction (discussed above), but also by the selectivity of the recovery after crises (Bambach et al., 2002). The taxonomic structure of the Phanerozoic biota was changing in a stepwise way, as demonstrated by the concept of three sequential ‘evolutionary faunas’ (Sepkoski, 1992). There were also stepwise changes in the proportion of major groups of animals with different ecological and physiological parameters. There was stepwise growth in the proportion of motile genera to non-motile, ‘physiologically buffered’ genera to ‘unbuffered’, and predators to prey (Bambach et al., 2002). All these trends should have facilitated the stability of communities. For example, the diversification of predators implies that they became more specialized. A specialized predator regulates its prey’s abundance more effectively than a non-specialized predator.

There is also another possible mechanism of second-order positive feedback between diversity and its growth rate. Some research has demonstrated a shift in typical relative-abundance distributions in paleocommunities after the Paleozoic (Wagner et al., 2006). One possible interpretation of this shift is that community structure and the interactions between species in the communities became more complex. In post-Paleozoic communities, new species probably increased ecospace more efficiently, either by facilitating opportunities for additional species or by niche construction (Wagner et al., 2006; Solé et al., 2002; Laland et al., 1999; Antell, Saupe, 2021). This possibility makes the mechanisms underlying the hyperbolic growth of biodiversity and human population even more similar, because the total

ecospace of the biota is analogous to the ‘carrying capacity of the Earth’ in demography. As far as new species can increase ecospace and facilitate opportunities for additional species entering the community, they are analogous to the ‘inventors’ of the demographic-economic models whose inventions increase the carrying capacity of the Earth.

Exponential and logistic models of biodiversity imply several possible ways in which the rates of origination and extinction may change through time (Sepkoski, 1991a; Foote, 2023). For instance, exponential growth can be derived from constant per-taxon extinction and origination rates, the latter being higher than the former. However, actual paleontological data suggest that origination and extinction rates did not follow any distinct trend through the Phanerozoic, and their changes through time look very much like chaotic fluctuations (Cornette & Lieberman, 2004). Therefore, it is more difficult to find a simple mathematical approximation for the origination and extinction rates than for the total diversity. In fact, the only critical requirement of the exponential model is that the difference between the origination and extinction through time should be proportional to the current diversity level:

$$(N_o - N_e) / \Delta t \approx kN, \quad (\text{Eq. 12})$$

where  $N_o$  and  $N_e$  are the numbers of genera with, respectively, first and last occurrences within the time interval  $\Delta t$ , and  $N$  is the mean diversity level during the interval. The same is true for the hyperbolic model. It does not predict the exact way in which origination and extinction should change, but it does predict that their difference should be roughly proportional to the square of the current diversity level:

$$(N_o - N_e) / \Delta t \approx kN^2. \quad (\text{Eq. 13})$$

In the demographic models discussed above, the hyperbolic growth of the world population was not decomposed into separate trends of birth and death rates. The main driving force of this growth was presumably an increase in the carrying capacity of the Earth. The way in which this capacity was realized – either by decreasing death rate or by increasing birth rate, or both – depended upon many factors and may varied from time to time.

The same is probably true for biodiversity. The overall shape of the diversity curve depends mostly on the differences in the mean rates of diversity growth in the Paleozoic (low), Mesozoic (moderate), and

Cenozoic (high). The Mesozoic increase was mainly due to a lower extinction rate (compared to the Paleozoic), while the Cenozoic increase was largely due to a higher origination rate (compared to the Mesozoic) (see Markov & Korotayev, 2007: 316, Figs. 3a and b). This probably means that the acceleration of diversity growth during the last two eras was driven by different mechanisms of positive feedback between diversity and its growth rate. Generally, the increment rate  $((N_o - N_e)/\Delta t)$  was changing in a more regular way than the origination rate  $N_o/\Delta t$  and extinction rate  $N_e/\Delta t$ . The large-scale changes in the increment rate correlate better with  $N^2$  than with  $N$  (see Markov & Korotayev, 2007: 316, Figs. 3c and d), thus supporting the hyperbolic rather than the exponential model.

## Conclusion

In mathematical models of historical macrodynamics, a hyperbolic pattern of world population growth arises from non-linear second-order positive feedback between the demographic growth and technological development. Based on the analogy with macrosociological models and diverse paleontological data, we suggest that the hyperbolic character of biodiversity growth can be similarly accounted for by non-linear second-order positive feedback between the diversity growth and the complexity of community structure. This hints at the presence, within the biosphere, of a certain analogue to the collective learning mechanism. The feedback can work via two parallel mechanisms: (1) a decreasing extinction rate (more surviving taxa – higher alpha diversity – communities become more complex and stable – extinction rate decreases – more taxa, and so on), and (2) an increasing origination rate (new taxa – niche construction – newly formed niches occupied by the next ‘generation’ of taxa – new taxa, and so on). The latter possibility makes the mechanisms underlying the hyperbolic growth of biodiversity and human population even more similar, because the total ecospace of the biota is analogous to the ‘carrying capacity of the Earth’ in economic demography. As far as new species can increase ecospace and facilitate opportunities for additional species entering the community, they are analogous to the ‘inventors’ of the economic-demographic models

whose inventions increase the carrying capacity of the Earth.

The hyperbolic growth of Phanerozoic biodiversity suggests that ‘cooperative’ interactions between taxa can play an important role in evolution, along with generally accepted competitive interactions. Due to this ‘cooperation’ (which may be roughly analogous to ‘collective learning’), the evolution of biodiversity acquires some features of a self-accelerating process. The same is naturally true of cooperation/collective learning in global social evolution. This analysis suggests that we can trace rather similar macropatterns within both the biological and social phases of Big History. These macropatterns can be represented by relatively similar curves and described accurately with very simple mathematical models (see Korotayev, 2018, 2020b, 2024, 2025a for more detail).

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