**Current laws of biological evolution**

Science uses evidence-based inductive reasoning to build theories, principles, and laws. A common type of inductive reasoning is generalization, that is, projecting conclusions drawn from one or a few case studies onto a broader context. The reliability of generalizations depends upon the representativeness and the formal validation of the selected case studies, which is usually performed by hypothesis testing. Another usual type of inductive reasoning is prediction, which uses observations to develop general principles and laws that can predict or anticipate future outcomes. The reliability of these predictions is confirmed by the accomplishment of the anticipated situation. It is interesting to note that generalizations are based on the analysis of empirical evidence, whereas predictions are formulated before the desired empirical evidence, which is actually the target of the prediction, is available.

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The American philosopher of science Peter Lipton ([2005](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0009)) commented that we are commonly more impressed by predictions than by accommodations, as he called hypothesis testing. To illustrate this, Lipton used the discovery of Halley's Comet. In 1705, the British astronomer Edmond Halley proposed that the comets observed in 1531, 1607, and 1682 were actually the same comet with a periodic elliptical orbit. Back then, his hypothesis did not have much impact within the scientific community. However, when Halley's prediction was confirmed in 1758 by the return of the comet, the intellectual world in Europe widely accepted the existence of a single comet, which was subsequently named Halley's Comet. Halley's prediction may seem straightforward, even trivial, considering the characteristic periodicity of 75 years in previous observations. Yet, it was the predictive success, rather than prior observations, that convinced the scientific community of his conclusion.

Physics is considered one of the strongest branches of science—along with chemistry and mathematics—in regard to the generality and accuracy of its predictions. Biology seems still to be in its infancy, and the search for regularities that could lend to potential generalizations is the most common approach (Dodds, [2009](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0004)). This is due in part to the high level of complexity of the living world, its evolutionary change over time, and its relationships with the environment. As emphasized by the German evolutionary biologist Ernst Mayr ([2004](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0010)), these intrinsic and unique features of living beings, which are intimately associated with the genetic code, clearly differentiate biology from other natural sciences and make the fundamental laws of physics and chemistry insufficient to understand the living world.

The main aim of this essay is to discuss whether biological research is able to develop inductive predictions similar to physics or chemistry. First, I present some classical examples of physical and chemical discoveries based on inductive predictions, such as the Higgs boson, interstellar dark matter, and the periodic table of elements. As all these advances are based on the previous existence of fundamental laws, the question arises whether similar laws exist in biology to support physics-like inductive predictions. I suggest that, if these laws exist, they should emerge from the evolutionary process, which is the main biological singularity. Thus, it should be possible to make inductive predictions based on the fossil record, which is the fundamental evolutionary evidence. Indeed, it seems that the lack of evolutionary laws is the main drawback for inductive prediction in studying evolution, which cannot escape to Lipton’s accommodation procedures, that is, hypothesis testing and generalization.

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**Physical and chemical laws and predictions**

The existence of the Higgs boson was predicted in the 1960s to fulfil the standard model of particle physics (SMPP) that describes the subatomic particles and three of the four fundamental forces—electromagnetic force, weak atomic force, and strong nuclear force. The equations of the SMPP accurately describe the electroweak force—that is, the combination of electromagnetic and weak forces—which is responsible for electricity, magnetism, light, and some types of radioactivity—assuming that the particles involved do not have mass, which is true for photons but not for particles such as W and Z bosons. This inconsistency was solved by proposing the existence of the Higgs field, named after the British physicist Peter Higgs, which would grant mass to any particle interacting with it. The particle associated with this field was tentatively called the Higgs boson, and its mass, charge, and spin were estimated with the SMPP. In 2012, after five decades of experiments, the Higgs particle was eventually discovered at the CERN Large Hadron Collider (LHC), and Peter Higgs, together with his Belgian colleague François Englert, was awarded the Nobel Prize in 2013 for this fundamental finding (<https://home.cern/science/physics/higgs-boson>).

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Other physical predictions still await empirical confirmation, such as the existence of interstellar dark matter. Astrophysical observations of gravitational fields of galaxies are difficult to explain under gravitational laws, the fourth fundamental physical force, unless more matter is present than can be seen. This has led to the prediction that an unknown form of matter is abundant in the universe, which has been called dark because it does not interact with the electromagnetic field, that is, it does not absorb, reflect, or emit electromagnetic radiation and is therefore difficult to detect. However, dark matter particles are assumed to carry energy and momentum, and hence, they might theoretically be detectable in the LHC (<https://home.cern/science/physics/dark-matter>).

In chemistry, the periodic table is another example of successful predictive inference. The background behind this table is the periodic law, formulated in 1869 by the Russian chemist Dimitri Mendeleev, according to which the properties and atomic structures of the chemical elements are a periodic function of their atomic numbers (the number of protons in the nucleus), which is unique for each element. Mendeleev organized the chemical elements known at the time in a table according to their atomic numbers and observed gaps, which he considered to correspond to still unknown elements, and predicted the atomic composition of the unknown elements according to the periodic law. With time, these elements have progressively been identified to conform to the current periodic table.

A common feature of these predictions is the axiomatic nature of the fundamental background laws, in this case the SMPP, gravitational laws, and the periodic law of elements. Predictions of new subatomic particles, new chemical elements, or still undetected interstellar matter are necessary to prove these fundamental laws, and each time that a prediction is accomplished, it reinforces said laws. In other words, physicochemical laws are viewed as immutable rules, and knowledge advances by finding the evidence needed to fulfill these laws. A corollary is that the predictive approach seems better developed in scientific disciplines with well-established fundamental laws.

**Biological laws**

Among biologists is a lack of consensus whether general laws exist or not. Various scientists, including Mayr ([2004](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0010)), have contended that there are no laws in biology, owing to the contingent and unpredictable nature of living beings and their evolution. Others try to find regularities in biological contingency that could potentially inform general laws or they tentatively formulate biological laws, usually with a strong physical component and a recurrent emphasis on the laws of thermodynamics (Trevors & Saier, [2010](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0014); Brandon, [2013](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0001)). However, fitting biology with the laws of thermodynamics cannot be considered a biological law; it is a physical law. In contrast, the propensity of evolution to minimize entropy (Rull, [2012](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0013)), which presents a challenge to the universality of the second law of thermodynamics, may be the seed for developing a potential biological law. Notwithstanding, generally accepted laws specific to the biological world are still lacking. However, most theorists agree on a unique biological singularity: the diversity of living organisms and the complex spatial, temporal, functional, and ecological diversity patterns they generate emerge by evolution.

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It follows that if general laws specific to biology do exist, they will likely derive from the theory of evolution. Thus, it is worth exploring its potential, along with recent developments in genomics and molecular phylogenetics, to support inductive predictions. Given the contingent nature of biological evolution (Mayr, [2004](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0010)), predicting its future is still unworkable; but the possibility of making predictions similar to the Higgs boson, dark matter, or the lacking elements of the periodic table is worth a consideration. This endeavor should not be confused with a reductionist approach that aims to apply physical laws to biology; it is merely a conceptual and methodological comparison.

**Possible evolutionary predictions**

Whether biological evolution progresses gradually or in leaps is an old debate. An example is the controversy between phyletic gradualism (PG) and punctuated equilibrium (PE). The PG concept proposes that evolution progresses slowly and gradually to transform one species into another (anagenesis) acting by natural selection on species' populations. In contrast, PE contends that most evolution takes place as rapid speciation events that split one species into two distinct species (cladogenesis), followed by long phases without significant evolutionary changes (stasis). The PE concept was proposed by the American paleontologists Gould and Eldredge ([1977](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0006)), who argued that gradual change is not observable in the fossil record, which is instead dominated by long-ranging static fossil morphologies. The defenders of PG attributed these observations to the incompleteness and fragmentary nature of the fossil record.

The fossil record—similar to the first periodic table of Mendeleev, which was still incomplete—could be used as evidence to confirm either the PG or PE view. Under the PG rule, the fossil record should contain the whole range of intermediate morphologies that represent gradual anagenetic process. Furthermore, PG should eventually be able to predict these forms, as Mendeleev did with the hidden elements. There are three main limitations, however, that prevent such prediction: general or particular evolutionary laws of morphological change, similar to the periodic law of the elements, are lacking; fossil morphology represents usually the harder parts of a species and morphological changes in other, lost parts are unnoticed; and fossil morphology is just one of the possible phenotypic expressions of the genotype, which is the real evolutionary material. Even in the case that PG would be able to predict specific fossils, finding the necessary empirical evidence would be difficult owing to the intrinsic incompleteness of the morphological fossil record.

In contrast to PG, which is grounded in Darwin's theory of natural selection, PE is essentially based on the available morphological fossil record. Therefore, by definition, PE is comfortable with the fossil record as is and does not seem to have any predictions to do in this respect.

At present, the PG and PE proposals are considered two extreme views within the general context of evolutionary rates, which are not constant but variable across species (Futuyma, [2005](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0005)). It is worth noting that our ability to accurately predict the fossils needed to fit with any evolutionary model, regardless of the involved rates, might provide the basis for formulating evolutionary laws and, therefore, for predicting future evolution. However, the limitations mentioned above seem insurmountable. The situation is therefore similar to the proposal of dark matter, as a huge amount of still hidden “dark evolutionary matter” is needed to properly understand biological evolution. The main difference is that physicists know what the target evidence is (the predicted dark matter particles) and the suitable methodology for finding it (particle acceleration), whereas biologists seem to ignore what we are looking for.

**The dark matter of evolution**

Fortunately, our knowledge of the fossil record has greatly improved since the 1970s and 1980s, when the PG-PE debate was rampant. Recent technologies to sequence ancient genome, or parts of it, preserved in fossil remains have added a large amount of dark evolutionary matter to the morphological fossil record. Importantly, the DNA of fossil organisms (also called ancient DNA or aDNA) is the evolutionary subject and, hence, the fundamental evolutionary matter. This technology inaugurated the so-called field of paleogenomics, which may be able to reconstruct evolutionary trends, that is, the genetic changes in specific species over time. In spite of preservation constraints, paleogenomics has already provided direct insights into evolution that few would have predicted less than a decade ago (Cappellini *et al*, [2018](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-bib-0002)). However, this particular field of knowledge progresses by accumulation of empirical evidence, rather than by its prediction, as in the case of the missing elements of the periodic table or interstellar black matter.

Moreover, we can consider the genome of contemporary species as a compendium of their evolutionary history, similar to a miniature fossil record. Recent advances in DNA analysis have again allowed the detailed reconstruction of the phylogenetic history of many living beings, as DNA is the evolutionary material itself. This procedure is somewhat similar to the prediction of the Higgs boson in that we would be able to anticipate the genotypic and, eventually, the phenotypic features of still undiscovered predecessors or “evolutionary bosons” (Fig [2](https://www.embopress.org/doi/full/10.15252/embr.202154392#embr202154392-fig-0002)). It would help us to know what we are looking for in the fossil record, which could be useful for planning research, just as physicists adjust the parameters of the particle accelerators based on the physical properties of their predicted targets.

[](https://www.embopress.org/cms/asset/df676ba3-16d5-48c8-a920-d7774e7f454c/embr202154392-fig-0002-m.jpg%22%20%5Ct%20%22_blank)