The biosphere computes evolution by autoencoding interacting organisms into species and decoding species into ecosystems.

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Abstract Autoencoding is a machine-learning technique for extracting a compact representation of the essential features of input data; this representation then enables a variety of applications that rely on encoding and subsequent reconstruction based on decoding of the relevant data. Here, we document our discovery that the biosphere evolves by a natural process akin to autoencoding. We establish the following points:
1) A species is defined by its species interaction code. The species code consists of the fundamental, core interactions of the species with its external and internal environments; core interactions are encoded by multiscale networks including molecules-cells-organisms. Species interaction codes both map and construct the species’ environment.
2) The survival of fitted species is computed by natural autoencoding: the fittedness of species interactions is proven by successful decoding of evolving species into sustained ecosystems; survival of the fitted supplants Darwinian struggle and domination of the “fittest” only. DNA is only one element in natural autoencoding.
3) Natural autoencoding and artificial autoencoding techniques manifest defined similarities and differences. Biosphere autoencoding accounts for survival-of-the-fitted and sheds a new light on the mechanism of evolution. Evolutionary autoencoding renders evolution amenable to new approaches to computer modeling.

Keywords Evolution, Interaction, Survival of the Fitted, Species Interaction Code, Biosphere Autoencoding; Artificial Autoencoding; Encoding; Decoding.
1 Evolution emerges from cooperative interactions; basic definitions.

Evolution is the narrative of changes in species and their interactions over time (Koonin, 2011). Ever since Darwin (Darwin, 1860), the mechanism underlying evolution has been taught to be Natural Selection, which is based on a continuous struggle of variant individual organisms for survival and reproductive advantage in the face of limited resources; this struggle leads to survival of the fittest variants and their dominion over the less fit; proliferation of the winners determines the characters of species.

Darwin’s theory of Natural Selection has by now become an ideology applied to many aspects of human culture including ethics, economics, governance, social organization, and education (Wyllie, 1959; Auerswald and Branscomb, 2003; Browning et al., 2017; Bergman, 2014). However, new discoveries challenge the theory and ideology of survival of the fittest; for example, see (Laland et al., 2015).

In the interval since Darwin, science has learned that all living systems—cells, organisms, species (including Homo sapiens) and ecosystems—survive in extensive networks of interaction and group cooperation (Cohen and Marron, 2020; Sachs et al., 2004). A few examples include the dependence of every multicellular organism on a microbiome (Blaser, 2014); the symbiotic web of forest trees and fungi (Simard, 2018); and the collaboration and symbiosis that create a coral colony (Rosenberg et al., 2007). The biosphere is sustained by these interactions; the biosphere is a world wide web of interactions.

Survival-of-the-fittest is an alternative mechanism to account for evolution (Cohen and Marron, 2020; Cohen, 2000); surviving organisms and species are those that are integrated in networks of sustaining interactions. In the body of this paper, we shall demonstrate that survival-of-the-fitted is the outcome of a process we term natural autoencoding.

The substance of evolution, we have proposed, is the process of interaction (Cohen and Marron, 2020); interactions are what evolve. For example, individual brain cells of humans and apes, indeed, of cats and mice, may be quite similar. The differences between mammalian species and between individuals within a mammalian species can emerge from the different numbers and interaction networks of largely stereotypical cells (Striedter, 2005).

This paper uses the following terminology:

We have already used the term interaction: Interactions are mutual relationships between two or more entities (termed interactors) in which the interactors transmit or exchange energy, matter or information.

Sustainable types of interactions are characterized by repetition and sequence. Metabolic interactions, for example, are organized in repeating, sequential pathways—one interaction connected to the next in line (Judge and Dodd, 2020). Cycles of reproduction, growth, aging and death are mundane examples of the universality of repeated, sequential interactions.

Energy is the impetus behind motion and activity (Doige and Day, 2012), including the capacity to do work. Energy makes things happen.

Information we define according to Shannon as a particular non-random structure or arrangement of entities or processes (Shannon, 1948; Cohen, 2006). Arrangements bear information; but an arrangement by itself has no meaning unless it interacts with other arrangements to produce some effect (Cohen, 2006; Cohen, 2000). The consequences of the interactions of structured information constitute the meaning of the information. Written words, for example, have no meaning unless somebody or some thing can read them. A sequence of DNA, too, bears information that only gains meaning through expressed interactions including transcription and translation (Cohen et al., 2016). Interaction extracts meaning from information.

Matter itself is a product of interaction: the nuclei of atoms are created by interactions between fundamental particles; atoms are formed by interactions between nuclei and electrons; and molecules are formed by interactions between atoms.

So we must conclude that anything made of atoms or molecules, including living entities and the biosphere itself, is made of interactions. As stated by Feynman (Gleick, 1993) and others (Rovelli, 2017), interactions constitute reality.

2 Species are formed by core codes of interaction.

The concept of species is ancient, and species, since Darwin, are linked to evolution; this link is reflected in the title of Darwin’s foundational work on evolution: The Origin of Species (Darwin, 1860).

The definition of species, despite the term’s wide use, is controversial: A search in Google Scholar for species returns millions of publications; but there is not one universally accepted definition; scientists have proposed dozens of different definitions based on morphology, genetics, sexual reproduction, ecology, and other criteria (Mallet, 1995).

The concept of species has interested humans since antiquity. The Bible, for example, names species of animals that an observant person may or may not eat; the Bible then proceeds to amend the list with a functional code: a permitted species has cloven hoofs (a structural feature) and chews its cud (a dynamic process) (Leviticus 11:3-8 and Deuteronomy 14:4-8). Aristotle developed three codes, which he called "souls", to describe and distinguish between classes of living entities: plants (Vegetative Soul), animals (Sensitive Soul) and humans (Rational Soul) (See Britannica entry at www.britannica.com/biography/Aristotle/Philosophy-of-mind).
People may differ about the names of species; however abstract, a code is objective and testable; recall Juliet’s reference to smell in her code for defining a rose by any name (Shakespeare’s Romeo and Juliet, Act 2). In the spirit of codes, we here define a species as a collective of organisms that share a core code of potential, repetitive interactions with a jointly constructed external and internal environment, including both living and non-living components, both structural and dynamic. Thus, a species interaction code of sunflowers would include interactions that are common to all organisms, such as cell division, interactions that are common to all plants, such as photosynthesis, and interactions that characterize sunflowers among others, such as heliotropism. The core code of interactions emerges from the essential structures, processes and behaviors that characterize the members of a species. The core code enables the species to survive and thrive in its environment. All interacting organisms manifest their own species interaction codes. In principle, each species could be characterized by its core interactions.

A detailed list of a species interaction code for even the simplest species of bacteria would challenge experts. We suggest that a pairwise or set perspective might provide a manageable solution: given two related or interacting species or sets of species, we might focus only on the interactions that distinguish the pairs or the sets.

Beyond categories devised by human experts, the biosphere could have its own way of designating different species interaction codes; the autoencoding of species will be discussed below.

**Core codes map and construct the species environment.**

In addition to describing the program driving organisms in a species, the core code expresses an image of the environments with which the constituent organisms of the species interact (Cohen, 2000). This image of the environment is intrinsic to the species. For example, the shedding of their broad leaves by deciduous trees is an image of the recurrent winters the trees have evolved to endure (Hill and Broughton, 2009); nitrogen-fixing plants manifest structures and molecular processes that make possible their interactions with particular species of nitrogen-fixing bacteria—likewise, the bacteria engage in core interactions with their host plants (Vitousek et al., 2002); an animal’s teeth map the animal’s diet (Melstrom, 2017); the flowers of a plant are structural and visual images of the plant’s specific pollinators (Hu et al., 2008; Kritsky, 1991). Conceptually, these interactors and their environments map one another like locks and keys (Cohen, 2000).

Core codes not only map species environments, they can actually construct them (Scott-Phillips et al., 2014): beaver core interactions build dams to create beaver environments (Westbrook et al., 2006); birds’ nests and ant hills fashion the environments of these species; ants domesticate aphids (Depa et al., 2020). Modern humans, in contrast to now extinct versions of earlier humanoids, thrive in environments essentially constructed by modern humans (Jablonska, 2011); interactions between wolves and humans created the dog species (Nagasawa et al., 2015); in fact, all the species of plants, animals, bacteria and yeasts domesticated by humans evolved by virtue of innovative core interactions of these organisms with core interactions of humans.

The biosphere, in summary, is both mapped and constructed by the world wide web of core interactions of all its species.

An interactive system, like a species, that encodes an internal map of its environment can be termed a cognitive system (Cohen, 2000). In this sense, species are cognitive systems; each, thanks to its core code, bears an intrinsic representation of how it lives and where it lives. Matter alone, unlike living species, is not cognitive; other than its level of energy, matter bears no intrinsic representations of how or where it exists.

**Core species interactions may be shared and/or specialized.**

Some core interactions may be common to many different species: all organisms share cell division; all multi-cellular organisms interact with resident microorganisms (Blaser, 2014); all mammals interact with their fetuses by way of placentas (Wildman et al., 2006), but as far as we know, only H. sapiens, among mammals, features core codes that include social and conceptual interactions using verbal language (Christiansen and Kirby, 2003). The core code of interactions may include differences between individuals or classes within a species; for example, males and females perform different interactions; only queen bees produce fertile eggs; some collectives are controlled by dominant individuals; a variety of specializations exist within particular species.

Because of the specialization of organisms within a species, not every organism need perform all the interactions in the species’ list of core interactions.

**Circumstantial interactions can precede core interactions.**

Beyond a code of core interactions, many interactions are circumstantial; for example, most humans today interact with computers, but this interaction is only recent; the hooded crows in Rehovot interact with humans and cats to eat cat food and human garbage, but only recently. These circumstantial interactions are not core codes, but may be derived secondarily from core codes—for example, human interactions with computers evolved from the core code of human language; circumstantial core interactions with humans and cats evolved from crow core social intelligence (Kurosawa et al., 2003).

Some core interactions are likely to arise de novo from a critical change, such as a mutation; for example, genetic changes in the human larynx and voice box, which
Figure 1. Species are defined by codes of core interactions. Organisms (shown as circles), are grouped in species (distinguished by blue, red, green and black borders), where each species is defined by the set of its core sustaining essential interactions (shown as blue arrows); these interactions include those that are internal to each organism in the species, between members of the species, and with other species and with the inanimate environment. Species also engage in circumstantial interactions (shown as yellow dashed arrows), which are not part of the essential code. Organisms within a species vary (shown as different fill patterns).

are absent in the Neanderthals (Gokhman et al., 2020), may have had a critical influence on the core interactions mediated by human speech.

Other core species interactions may first have arisen as circumstantial interactions; the phenomenon of genetic assimilation described by Waddington is an example (Waddington, 1953): Waddington exposed Drosophila (fruit flies) to heat shock which led to a change in the structure of the animals’ wings; repeating the circumstantial heat shock over several generations eventually led to genetic fixation of the variant wing form, even in the absence of circumstantial heat shock. Many core genetic interactions are likely to have arisen from a history of circumstances. Figure 1 schematically summarizes the structure of the biosphere manifested through species codes of interactions.

Existing species disappear and new species arise.
A species becomes extinct in nature when, due to a lack of energy or offspring, an insufficient number of member organisms remain to fulfill the original species interaction code (Purvis et al., 2000). The evolution of a new species interaction code signifies the birth of a new species.

3 The biosphere has evolved interactions across scales of complexity.
Life’s interactions are scaled. We designate a higher scale when the interactions of entities in a given network, or complex system, express and process more information or manifest properties not previously present in constituent components (Crutchfield, 1994; Cohen and Harel, 2006).

Importantly, the scales of interactions in living systems are interwoven composites, one hidden within the other—molecules in cells, cells in organisms, organisms in species, and species in ecosystems. Repeated patterns of interactions, be they biochemical or social, form additional levels, albeit more dynamical than structural, within this multi-scale architecture. Molecular networks, emerging from the chemical evolution of matter, evolved into a primordial type of living cell that further evolved into families of prokaryote cells (Puigbò et al., 2010). Prokaryotes, then and now, survive in cooperative ecosystems (Keller and Segel, 1970; O’Toole et al., 2000).

Some billion years after their appearance, some prokaryote cells (bacteria and archaea) merged through endosymbiotic interactions to initiate a higher scale of evolution—the eukaryote cell (Margulis, 1981), which features complex organelles including nuclei, mitochondria, and more.

Yet higher-scale multi-cellular organisms arose from the interactions of single eukaryote cells. These more complex organisms continue to interact with earlier forms of life; for example, as we mentioned above, all multi-cellular organisms depend on an essential microbiome (Blaser, 2014).

Figure 2 depicts networks of interactions both within and between networks of molecules, prokaryote and eukaryote cells, and organisms, culminating in species, ecosystems and the biosphere itself. Cells and organisms evolved sequentially over eons of time, but all life is now integrated into one multi-scaled biosphere. But why has life evolved an architecture manifesting increasing scales of complexity? The answer still eludes...
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Figure 2. The multi-scale architecture of the biosphere. Scales include molecules; prokaryote cells; eukaryote cells; multicellular organisms; species; ecosystems; all comprising the biosphere. Not shown are dynamical arrangements and patterns like biochemical pathways or social behavior that are interwoven in the above, and other structures like biofilms. The blue arrows show that interactions can occur between entities at the same level and between entities across levels.

us, but this interaction-based architecture and the constraints it induces on its constituents suggests that the biosphere might perform a type of autoencoding. First, we shall briefly describe computer autoencoding, and then we shall apply the concept to the natural autoencoding of evolution.

4 Artificial autoencoding extracts the essential features of data sets.

Autoencoding is a term associated with artificial intelligence, machine learning, and artificial neural networks [Kramer, 1991; Ng et al., 2011]. An autoencoder is a computer program that learns key defining features of the individuals in a given population, and then represents each individual encoded as a value in a feature vector, or array. This code and its associated encoding constitutes a compact representation of the population and its individuals. For example, a 1000-by-1000 pixel picture of a straight line segment, may be encoded using just start and end coordinates, line width, and color.

An autoencoder is constructed by an iterative training process that discovers the exact computations that yield both a compact code and a faithful reconstruction of each encoded individual. The machinery of an artificial autoencoder includes three elements: (1) The encoder receives as input raw data about selected individuals, such as pixels of an image, an audio signal, or measurement data from some problem domain; the encoder outputs the learned feature vector with individual value assignments; this feature vector constitutes (2) The code. (3) The decoder accepts the code representing the encoding of a particular individual, and reconstructs the original data, such as the image or the speech segment.

In the training process that builds the encoder and decoder, the inputs and outputs are compared using a loss function to determine how close the reconstructed outputs are to the respective inputs. The internal parameters of encoder and decoder, which are commonly built using neural networks, are then adjusted and tuned, in a process termed backpropagation, usually carried out by gradient descent, to minimize the loss function.

Training an autoencoder is unsupervised: the data are not labeled, so the autoencoder does not know what it is encoding. The absence of supervision is reflected in the auto in autoencoding. It is only required that the outputs be very similar to the corresponding inputs. Once trained on a representative sample of a population, the autoencoder is able to encode and faithfully reconstruct many inputs from this population. Furthermore, certain autoencoders, termed variational, can use the code to generate new entities to be included in that population.

The array of features that comprises the numerical code may or may not include traits that a human observer would intuitively use to compactly describe the individual. Hence this code vector is often referred to as the latent, invisible vector, where only a properly trained decoder can "understand" its features.

Consequently, artificial autoencoding can function without its human operators assigning meaning to the details of the process, that is, how the multitude of connection weights and non-linear functions relate to the problem at hand. Autoencoding, as it were, takes place in a "black box"; humans choose the network architecture and the activation functions, select the input, and develop the loss function; however, autoencoder interpretability and explainability are still areas of research.

The opacity of autoencoding is important for our understanding of natural autoencoding of biosphere evolution, described below; biosphere autoencoding takes place without any access of the biosphere to external representations of the process.

Artificial autoencoders enable many uses, including face recognition, cleaning out image data by removing insignificant "noise", anomaly detection, classification and more.

Figure 3 depicts the training and deployment of a typical artificial autoencoding operation.

Encoding and decoding occur in nature: Music, for example.

Below, we shall apply autoencoding and encoding/decoding, to biological interactions and to evolution; here, we convey the concepts of encoding and decoding from the computer to the natural world by considering the example of human music [Fitch, 2006]:
A musical score is almost always the result of selective encoding by a composer of complex inputs into his or her brain of emotions, training, life experience, innate talent, previous compositions and other factors including constraints (see below) of time, budget and opportunity. The musical score is the resulting code, which is decoded by the performers into actual music, which is then encoded by listeners into their own brain state, which is then decoded into the listeners’ behavior, which might then be encoded into a state of family and social interactions.

In fact, words themselves are codes and everything with a name is a code. This chain of ongoing encoding-decoding-encoding interactions sets the stage for appreciating the autoencoding enterprises that mark biology and the evolution of the biosphere.

5 The evolution of the biosphere manifests autoencoding.

In this section, we describe biological evolution as a process of autoencoding: ongoing sustainable biological processes are manifestations of encoding and decoding according to species interaction codes (Section 2): these codes are established, changed, or eliminated in natural autoencoding following perturbations, innovations and new circumstances in organism interactions.

In everyday use, the word decoding refers to the extraction of the meaning of some coded information. In the realm of machine-learning with autoencoding, as in communications protocols and encryption, decoding focuses on re-creating the input. Encoding and decoding in the context of the biosphere, in contrast, refers to the indefinite repetition of biological interactions on planet earth. The realization that the biosphere is sustained by continuous encoding and decoding and transformation of the codes (Section 4) defines natural autoencoding: despite their differences, both the biosphere and particular machine-learning computational processes extract and decode hidden codes in diverse populations. This discovery is the basis of the present paper.

Each molecule, cell, and organism emerges from the set of its constituent interactions. In addition, the set of interactions that the entity may perform is a program, not unlike a computer program, which is described by its functions—a set of algorithms for reactive behavior. Conceptually, we have separated natural autoencoding into distinct encoding and decoding processes. The interactions of living systems, however, are integrated into functioning composites; thus it would be difficult to label a particular reproductive, developmental or metabolic process as purely encoding or purely decoding.

For example, the sequence of DNA is decoded into a linear amino acid sequence; which itself is a code that encodes a functionally folded protein. This protein then serves as a code that is subsequently decoded, in the case of an antibody, into an immune response, that can help encode a higher scale immune reaction that protects the organism from an infection. Indeed, a machine learning process has been invoked to account for the encoding of the state of the body by the mammalian immune system (Cohen and Efroni, 2019). More generally, every interaction, input, code, or output of a given autoencoder may also serve a function in another autoencoder (See Figure 5). Chained autoencoders may also be viewed in the aggregate, forming a higher scale autoencoding process.

Encoding and decoding processes can be used to describe essentially all biological interactions that emerge from genomic DNA including metabolic networks; growth, development and differentiation; the activities of the nervous, endocrine, cardiovascular, renal, respiratory and digestive systems; reproduction and aging, and more.

Note that the DNA codes of living entities actually emerge from the very biological structures and interactions encoded in DNA; the synthesis, sequence, recombination, and expressions of DNA emerge from biological interactions that encode and decode DNA. The organisms within a species are the instantiation of the species interaction code. The interactions that create biological structures, including molecules, organelles, cells, and entire multi-cellular organisms form the encoding and decoding processes. This includes all the interactions of life, including both local and universal adaptations (Cohen and Marron, 2020).

Constraints channel encoding and decoding.

Interactions in general are organized by limitations, or constraints, imposed on the interactors and on the environment; no structures can emerge when degrees of freedom are not limited (Grotzinger et al., 1995). Interactions result from constraints that channel the interactors to meet and interact. Moreover, interactions themselves generate new constraints on what may follow; interactions constrain degrees of freedom. Encoding and decoding, in this sense, are no different from other types of interactions; each instance of encoding and decoding is guided and organized by its own landscape of constraints.

Housekeeping encoding and decoding maintain existing species.

We distinguish housekeeping encoding and decoding from evolutionary autoencoding.

Housekeeping encoding and decoding refers to existing entities and ongoing interactions that have not been perturbed by unanticipated innovations. Biological *business as usual* is housekeeping—maintaining the house; innovations are the agents of evolution.
Figure 3. Artificial autoencoding. Typical autoencoders include three network-based elements: the encoder (blue circles), the code (red circles), and the decoder (orange circles). Individual inputs (handwritten digits, for example) are fed into the encoder, encoded as values in the code feature vector, and then reconstructed by the decoder.

During training (A), the differences between the output and the input are computed by a loss function, and the weights W of the connecting lines in the autoencoder’s neural net are adjusted to minimize the reconstruction loss. This is repeated using a finite set of examples. The process is termed backpropagation, and is often done using a gradient descent method.

Once training is completed, the autoencoder is deployed (B) to perform its application task. Encoding and decoding is now done using the fixed code and edge weights to process an unbounded number of inputs from the domain of interest.

Figure 4. Autoencoding evolution in response to innovations. In a sustained ecosystem (left), multiple species (as in Figure 1) interact. The three sets of interactions of each species (internal, intra-species and external) are respectively marked with A, B, C; D, E, F; G, H, J; and K, L, M. Following an innovation, biological or environmental (shown by a lightning bolt), an autoencoding process modifies the biosphere (right) by establishing one or more new species interaction codes. In this example, the sets of interactions C and F have changed into variants C’ and F’; the green species defined by the sets of interactions G, H, and J has gone extinct; and a new species has emerged, marked in purple, with interaction sets P, Q, and R.
Evolutionary autoencoding follows innovations.

Changes in species interaction codes emerge from innovations that lead to novel interactions of encoding and decoding. Innovations are changes that are not anticipated by existing core codes. Conceptually, there are two broad classes of innovations: either the environment has changed in a way that renders the core code ineffective in maintaining the species; or the core code has changed so that it is no longer relevant to the present environment. Of course, changes can take place both in the present code and in the environment—for example, genetically variant members of a hominoid species migrated out of Africa to evolve into the Neanderthal species in the European environment (Mellars, 2004).

An innovation can enter the biosphere at any scale, be it a molecular mutation, an infecting pathogen, an invading species, a cancer cell, a change in nutrients or in solar radiation, a natural cataclysm or a social or a technological invention; witness, for example, the industrial revolution and global warming (Rosenzweig et al., 2008). If the innovation is not integrated into a fitted configuration within a networked species interaction code, then an unfit interaction state can emerge, which may negatively affect molecules, cells, organisms, species, and ecosystems; the unfit innovation will ultimately fail to survive and become extinct. Figure 4 shows the effects of innovations on the evolution of the biosphere.

The transition from housekeeping encoding and decoding to new interaction codes are a regular feature of the evolution of species; the serial generation of new interaction codes from existing codes and the extinction of previous codes constitute the evolution of life. How does the biosphere decide which species interactions to keep and which to discard?

In nature there is no optimization step as in artificial autoencoding; instead, many interactors are formed and many interactions are triggered, and those that happen to repeat are retained by the fact that they work, not by a choice based on an external criterion such as the value of a loss function, or on a Darwinian "optimum" such as a reproductive advantage (Darwin, 1860). Species interaction codes, including species-specific life spans and reproductive rates, are decoded by the integration of a species into its particular ecosystem arrangement. Once formed, sustaining ecosystems can continue to grow, adding materials, organisms, species and energy flows.

Living systems manifest a great variety of interactions; however, living systems exist by virtue of two essential properties: their ability to reproduce their kind and their ability to metabolize the energy they require for maintenance and reproduction in their particular environment. Quite simply, species whose constituent organisms do not reproduce and metabolize cannot live (Dupré and O’Malley, 2013). We can link species autoencoding to these principles: the reproduction of kindred organisms is the process that encodes species, and the networks of metabolism that maintain species are ecosystems. The rest are details.

Autoencoding of interactions into species and decoding into ecosystems is not a strategic response to change; the encoding/decoding and autoencoding processes are the essence of the interactive existence of the biosphere; the decoding of species interaction codes into ecosystems is a product of survival of the fitted and the extinction of the unfitted. This paper establishes natural autoencoding of innovations as the underlying principle that accounts for evolution by survival-of-the-fitted (Cohen, 2016; Cohen and Marron, 2020). Figure 5 depicts an aspect of the simultaneous, parallel and overlapping flow of encoding and decoding interactions among multiple living entities.

6 Artificial and natural autoencoding manifest significant differences.

Here, we list differences between natural and artificial autoencoding. The comparison can help clarify both mechanisms.

1. Training input: Artificial autoencoding is generally unsupervised, but inputs are most often pre-selected from a designated class, such as images, numbers, or data records within some domain. The inputs into natural autoencoding are entire ecosystems, with all their diverse entities and dynamic interactions.

2. Input preparation for encoding: Artificial autoencoding features a preliminary representation, a "pre-encoding" step, to convert the subject of interest into a numerical computer input format. The inputs into natural autoencoding are biosphere interactions; there is no such pre-encoding; moreover, these input interactions actually perform the encoding and decoding.

3. Multi-scale connectivity: In typical artificial autoencoding, nodes at a particular network layer are connected only to nodes in the next higher layer; more general connectivity can be found in Boltzmann Machine architecture (Ackley et al., 1985), but this design does not include multiple built-in scales or hierarchies. Natural autoencoding features interactions both between and within scales—for example, in addition to the interactions between a cell and its host organism, a cell can interact with other cells in the same organism, and with other organisms as shown in Figure 2.

4. Goal orientation: Artificial autoencoding is devised by humans to perform an assigned function. Natural autoencoding processes are driven and determined inevitably by the laws of nature and the state of the biosphere.
Figure 5. Linked assemblies of biosphere autoencoders. Multiple autoencoders, including processes and entities, operate in parallel and are intertwined in a variety of ways forming chains and networks. Here for example, the immune system proteins decoded from DNA by Autoencoder A are then encoded into an immune response pattern by Autoencoder B to generate health. Autoencoder B may be connected to additional entities and processes (not shown). More generally, every interaction, input, code, or output of a given autoencoder may also serve a function in another autoencoder.

5. Features of interest: Artificial autoencoding is driven by optimization of the similarity of each output to its corresponding input. Biosphere autoencoding focuses on each entity’s interactions with other entities.

6. Evolving the autoencoder: Evolution of an artificial autoencoder is through iterative mathematical optimization of a loss function. The biosphere autoencoder evolves by the survival of newly fitted species in sustained ecosystems.

7. Recursion: In artificial autoencoding, the autoencoder itself is usually not part of the input; the reflection is in the backpropagation process, which exists in a different realm than the input and output data. In natural autoencoding, the biosphere incorporates the inputs, the outputs and the very machinery of autoencoding; the autoencoder recursively receives copies of earlier versions of itself as part of the input.

8. Handling of deviations and innovations: Artificial autoencoding is usually designed to avoid or trim changes, deviations and innovations; where allowed, they are constrained to a desired distribution. Biosphere autoencoding accommodates and retains diverse innovations that happen to be sustainable; this is evolution.

9. Number and separation of autoencoders: A typical artificial autoencoding application has one autoencoder; when applications are built from several autoencoders, they deal with disjoint subproblems and hence disjoint inputs. In natural autoencoding, there is a large number of intertwined autoencoders, sharing interactions, inputs, outputs, and codes.

7 Autoencoding clarifies the mechanism of evolution.

Darwin saw evolution as a gradual process; moreover, he believed that evolution in abrupt steps would leave an opening for creationist arguments (Darwin, 1860, Chapter 9). Many neo-Darwinians also supported gradualism. Fisher, for example, claimed that the probability of a mutation increasing the "Darwinian fitness coefficient" of an organism decreases proportionately with the magnitude of the mutation; survival of the fittest implies that any existing species must be close to its peak of fitness; when you are already near the peak, too great a step becomes a descent. Hence, any abrupt genetic change is likely to result in decreased fitness (Fisher, 1958). Evolution just had to proceed only in small, gradual steps (Pigliucci and Müller, 2010).

In contrast to gradual evolution, Eldredge and Gould in 1972 introduced the term punctuated equilibria to describe long periods of seeming stasis interrupted by bursts of new species in the fossil record (Gould and Eldredge, 1972). The authors interpreted the observation of stasis as a sign of silent equilibrium punctuated, as it were, by discrete periods of jumps in evolutionary activity—or "saltations", as described earlier by Goldschmidt (Goldschmidt, 1940; Dietrich, 2003).

In contrast to abrupt change, it is well documented that DNA mutations occur constantly and evolve at uniform rates, actually establishing a biological clock of uniformly gradual change (Lynch, 2010). Environments, too, constantly change (Lindsey et al., 2013). But the observation of stasis along with saltations raises a question: How can continuous genetic and environmental change be reconciled, on the one hand, with an apparently static equilibrium of species and, on the other hand, with sudden changes and saltations in the fossil record?

Autoencoding suggests a solution to the paradox: a stable DNA mutation rate indicates continuing molecular changes; environmental changes also tend to be small. However, the autoencoding process neutralizes most of these changes when they do not cause the species to leave its present ecosystem or to decode into a new ecosystem. Autoencoding enables evolutionary stasis on the macro-scale despite continuous changes at the micro-scale.
A given innovation may lead to a macroscopic evolutionary saltation only if the affected species were to decode into a new ecosystem. Successful ecosystem decoding might well depend on the circumstantial combination of a given innovation in one interactor together with other innovations in other interactors or environments.

The assumption that evolution of species must be driven by struggle and survival-of-the-fittest individual encumbers the perception of alternative mechanisms such as we have described here. Thomas Kuhn has pointed out the blinding power of entrenched paradigms: “What a man sees depends both upon what he looks at and also upon what his previous visual-conceptual experience has taught him to see...” [Kuhn, 1970].

The role of encoding and decoding in evolution has inspired us to consider new architectures and algorithms in natural, generative machine learning. Computer models of natural autoencoding can extend our understanding of the biosphere and might even provide new strategies for computer science.

Author contributions
IRC and AM contributed equally to the paper.

Competing interests
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