



## Review article

# Evolutionary epistemology: Reviewing and reviving with new data the research programme for distributed biological intelligence



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## ABSTRACT

Numerous studies in microbiology, eukaryotic cell biology, plant biology, biomimetics, synthetic biology, and philosophy of science appear to support the principles of the epistemological theory inspired by evolution, also known as “Evolutionary Epistemology”, or EE. However, that none of the studies acknowledged EE suggests that its principles have not been formulated with sufficient clarity and depth to resonate with the interests of the empirical research community. In this paper I review evidence in favor of EE, and also reformulate EE principles to better inform future research. The revamped programme may be tentatively called Research Programme for Distributed Biological Intelligence. Intelligence I define as the capacity of organisms to gain information about their environment, process that information internally, and translate it into phenotypic forms. This multistage progression may be expressed through the acronym IGPT (information-gain-process-translate). The key principles of the programme may be summarized as follows. (i) Intelligence, a universal biological phenomenon promoting individual fitness, is required for effective organism–environment interactions. Given that animals represent less than 0.01% of the planetary biomass, neural intelligence is not the evolutionary norm. (ii) The basic unit of intelligence is a single cell prokaryote. All other forms of intelligence are derived. (iii) Intelligence is hierarchical. It ranges from bacteria to the biosphere or Gaia. (iv) The concept of “information” acquires a new meaning because information processing is at the heart of biological intelligence. All biological systems, from bacteria to Gaia, are intelligent, open thermodynamic systems that exchange information, matter and energy with the environment. (v) The organism–environment interaction is cybernetic. As much as the organism changes due to the influence of the environment, the organism’s responses to induced changes affect the environment and subsequent organism–environment interactions. Based on the above principles a new research agenda can be formulated to explore different forms of biological intelligence.

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**Abbreviations:** BCT, bacterial cognitive toolkit; EE, evolutionary epistemology; EET, evolutionary epistemology theories; EEM, evolutionary epistemology mechanisms; EKT, evolutionary knowledge transfer; IGPT, information gain process translate; IOI, individual organism intelligence; MLS, multiple level selection; SBOL, synthetic biology open language; SI, social intelligence; TRIZ, teorija reshenija izobretatelskih zadach in Russian; VOC, volatile organic chemicals.

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## 1. Introduction

Evolutionary epistemology (EE) is a programme of research in biology and philosophy of science centered around the following principles: (i) living systems are knowledge systems, (ii) evolution is the process of gaining knowledge, and (iii) there are features shared by all forms of knowledge gain (Plotkin, 1982). The origins of EE can be traced to the writings of Simmel (1858–1918) and Piaget (1896–1980) (Simmel, 1895; Piaget, 1982). However, Campbell (1916–1996) is credited with initiating the actual research programme and coining the term EE (Campbell, 1960, 1974). Quine (1908–2000) independently promoted the view of naturalized epistemologies but was not involved in the EE programme (Quine, 1969).

One of the most prominent supporters of EE was Popper (1902–1994). He strongly promoted the analogy that the growth of scientific knowledge is reminiscent of biological evolution: hypotheses are blind trials and selection is the filter distinguishing successful from non-successful trials (Popper, 1972). Popper's analogy attracted a degree of criticism and it is considered controversial by some authors (Kronfeldner, 2010, 2011). Critics focused on the notion that the acquisition of human knowledge is a directed process whereas biological evolution resembles a blind trial-and-error process lacking direction. Although Popper's misconceptions about biology are well documented (Vecchi and Baravalle, 2015), a new analysis argues in favor of the original analogy, provided that some features of EE are revised (Baravalle and Vecchi, 2016). The branch of EE based on Popper's analogy is formally known as EET (T for theories).

Given the perceived controversy I will avoid EET in this paper, and instead focus on the other branch of EE known as EEM concerned with investigating nature of cognitive mechanisms (M). EEM is purely biology-centered and it is based on empirical research, whereas EET is a speculative philosophical programme, which has supporters and opponents. According to Bradie (1986), EEM attempts “. . . to account for the characteristics of cognitive mechanisms in animals and humans by a straightforward extension of the biological theory of evolution to those aspects or traits of animals which are biological substrates of cognitive activity, e.g., their brains, sensory systems, motor systems etc.” Furthermore, Bradie (1986) stated that “EEM programs are genuine, EET programs are not”. He also argued that the above three principles (see the first paragraph) are primarily biological and not philosophical. Plotkin (1982) presented the most authoritative summary of EEM in an edited volume consisting of twenty essays. This volume will serve as the benchmark for the current study.

In recent years numerous publications emerged promoting the original principles of EEM (see below), without realizing that these principles have been defined in the past. The only explanation for the discrepancy is that the authors in question have not been aware of EEM. I will argue later in this text that in the past EEM principles have not been formulated with sufficient clarity and depth to

resonate appropriately with the interests of the empirical research community. This creates a problem similar to the following analogy. If a scientist invents a concept A, and her colleague discovers the same concept many years later without being aware of its primary form and names it B, duplication occurs: the same concept has two forms A and B. This violates the principle, *Non sunt multiplicanda entia sine necessitate* (Entities must not multiply beyond necessity), known as Ockham's razor or the parsimony principle – one of the principles behind the scientific method.

The aim of the present paper is to show that: (i) several investigative areas within at least six different research disciplines including microbiology, eukaryotic cell biology, plant biology, biomimetics, synthetic biology, and philosophy of science share the basic principles of EEM, (ii) if research areas which have shared interest are unified under one umbrella, advances are more likely than if they remain separated, and (iii) given that none of the above mentioned investigative areas refer to EEM, the existence of a unified umbrella will prevent violation of the parsimony principle. I start with a brief overview of EEM in light of new developments that mark a departure from the classical neo-Darwinian paradigm. I then reformulate EEM principles with the aim of making them more attractive to empirical research. Finally, I discuss relevant developments in each of the above-mentioned six disciplines to prepare the ground for presenting a new synthetic view aimed at informing future research.

## 2. A brief overview of EEM

In this Section I briefly summarize key aspects of EEM and define the basis for the reformulation of EEM principles. For more detailed accounts of the EEM basics the reader may refer to both older (Plotkin 1982; Bradie 1986) and more recent texts (Anderson, 2008; Gontier, 2010; Baravalle and Vecchi, 2016). Three key EEM principles include: (i) living systems are knowledge systems, (ii) evolution is the process of gaining knowledge and, (iii) there are features shared by all forms of knowledge acquisition. I will analyze each principle separately and provide an appropriate update in light of recent literature.

### 2.1. Living systems as knowledge systems

According to the standard EEM account, the term living system refers to individual organisms, and the term knowledge refers to the process of adaptation of organisms to their environments (Plotkin, 1982). The underlying assumptions are: (i) adaptations are attributes of phenotypes; (ii) each adaptation must reduce the energy cost of the phenotype, or increase its chances for survival, or both; and (iii) each adaptation reflects some aspect of the environment (Plotkin, 1982).

The last point means that the relationship between adaptation and the environment has a goal- or end-directedness, a view

that departs from the classical neo-Darwinian stance, which interprets this relationship as a blind process. For example, in the neo-Darwinian account of evolution, adaptations are determined exclusively by genetic factors: either changes in genes (mutations) or their frequencies (Futuyma, 1998). The genetic changes occur randomly without any direction from the environment. Organisms containing random genetic changes compatible with their survival in certain environmental conditions are then selectively propagated. Thus, the process of adaptation is one-sided. Organisms evolve to fit into pre-existing environments. (This view is blind to the fact that the environment itself consists largely of organisms; see below).

By contrast, EEM interprets the interaction between organisms and the environment as a complex process starting with “a series of challenges to the integrity of the organism”. These challenges trigger the process of the active organism–environment interaction (Plotkin, 1982). Organisms react to challenges by a collective set of adaptations, the function of which is to solve problems posed by the organism–environment interaction. Adaptations are not determined by genetic factors only, but also by subsequent interactions with the environment and other phenotypic features that emerge in the process of translating the organism–environment interactions into phenotypic forms (epigenetics). Thus, the capacity of organisms to adapt is not random. Instead, adaptations are goal-directed: they are aimed at coping with problems arising from the organism–environment interactions. Adaptations must incorporate into themselves aspects of the environment representing a particular problem.

Understood in this way adaptations become, at least in part, products of the epistemic process because organisms behave as cognitive systems. Organisms have the capacity to (G)ain information about the environment, (P)rocess that information internally, and (T)ranslate the information into a phenotypic trait. The entire (I)nteraction–(G)ain–(P)rocess–(T)ranslation (IGPT) cycle is adaptation. Each adaptation is tested by the selective filter: natural selection at the ecological level. If the newly emerging phenotypic form arising from the cognitive process of adaptation is retained and further sharpened after repeated testing by natural selection, the adaptation becomes a contributing factor to phenotypic fitness of the organism (Fig. 1).

A recent challenge to the classical neo-Darwinian account of evolution known as the Extended Evolutionary Synthesis (Pigliucci and Müller, 2010; Laland et al., 2014, 2015; Noble et al., 2014) contains elements which appear to conform to EEM’s interpretation of organism–environment interactions. For example, proponents of the Extended Evolutionary Synthesis state (Laland et al., 2014): “Living things do not evolve to fit into pre-existing environments, but co-construct and coevolve with their environments, in the

process changing the structure of ecosystems” thus emphasizing the active complexity of the organism–environment interactions expressed through the term “coevolution”. From the perspective of EEM the term “coevolution” may be synonymous with the phrase “organism–environment interactions” in the sense that both represent the active cybernetic processes leading to the emergence of biological novelty.

Furthermore, the Extended Evolutionary Synthesis acknowledges that the exclusivity of random genetic changes as the only explanation for the emergence of biological novelty has become outdated (Jablonka and Raz, 2009). Inheritance is not only genetic but may also include inheritance of acquired characters e.g., transgenerational epigenetic inheritance, ecological inheritance, psychological inheritance etc. (Laland et al., 2015), and the inheritance of genomes through predation (Margulis and Sagan, 2002, 2008).

Other researchers have expressed similar views. For example, various forms of transgenerational epigenetic inheritance were experimentally observed in mice (Skinner, 2011, 2014). Skinner (2015) suggested that these neo-Lamarckian forms of inheritance should be integrated with the mainstream thinking. This line of reasoning is also visible within EEM through acknowledging the importance of non-genetic forms of inheritance, in particular those described by Conrad Waddington, an early challenger of classical neo-Darwinian views, who coined the term epigenetics (Waddington, 1982).

Another aspect of EEM, which is unwittingly taken up by new research, involves the concept of information in a biological or evolutionary sense. In the context of EEM, the terms “knowledge” and “information” are used interchangeably and they can never be disembodied (Plotkin, 1982). Thus, EEM implies that information represents an essential component of the organism–environment interaction. Here is an excerpt from a paper, illustrating emergence of a potential paradigm shift in biology (Shapiro, 2007), that is in line with EEM thinking: “Matter, the focus of classical molecular biology, is giving way to information as the essential feature used to understand how living systems work. Informatics rather than mechanics is now the key to explaining cell biology and cell activities. The traditional mechanistic view held that the structure of biological molecules determines the actions of cells in some kind of linear fashion. But today we know that biological molecules change their structures as they interact with other molecules and that these structural changes contain information about the external environment and conditions within the cell.” This line of reasoning reveals the organism–environment cybernetics in which information becomes a form of a flexible biological “unit” convertible on both sides of the line separating the organism and the environment (Fig. 1).

## 2.2. Evolution as the process of gaining knowledge

The ambition of EEM was to explain all biological phenomena, not only those related to the level of individual organisms (Plotkin, 1982). This inevitably included the old question of types of selection: selection targeting individual organisms via genes i.e. “differential propagation of alternative alleles in the gene pool of a breeding population”, or multiple level selection targeting social groups, ecological units or even cultural units (Plotkin and Odling-Smee, 1981). EEM acknowledged the importance of both types of selection in line with the contemporary thinking that interprets kin selection or inclusive fitness theory (Hamilton, 1964) and multi-level selection theory (MLS) (Wilson, 1975; Wilson et al., 2008) as equivalent (Okasha, 2005). For EEM both forms of selection were consonant with the principle that adaptations that exist at multiple levels including (i) genetic and molecular substrates (ii) cellular and morphological phenotypic features and (iii) social and ecologi-

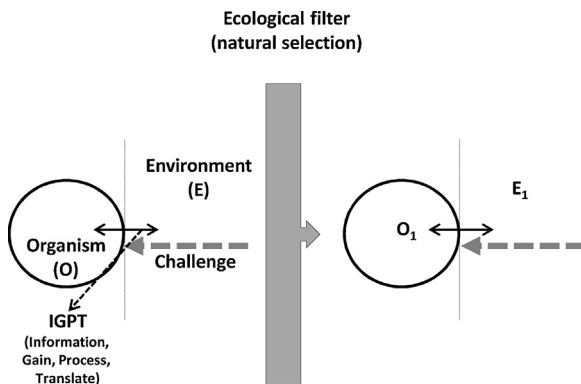


Fig. 1. Schematic representation of IOI.  $O_1$  – organism after adaptation (after IGPT).  $E_1$  – environment after organism adaptation.

cal interactions are, in part, the product of IGPT or the evolutionary “knowledge process” (Plotkin, 1982).

The question for EEM was whether all levels of IGPT are explainable by a “single algorithm”, or whether there are significant differences in terms of knowledge gain at different levels. EEM was not able to give a definitive answer. It was argued that at the more fundamental levels of IGPT (genetic, epigenetic, individual learning) a single algorithm might be sufficient.

However, placing a solitary organism into the social context changes the nature of the organism–environment interaction. In a social context any organism, irrespective of whether it is a bacterium or an ant, interprets other members of its social group as part of the environment (Okasha, 2005). For example, bacteria, traditionally viewed as single-celled organisms, actually live as colonies (Shapiro, 1988). Individual bacterial cells use sophisticated forms of communication including quorum-sensing, chemotactic signaling, and plasmid exchange (Shapiro, 1988; Bassler, 2002), which in turn allow formation of highly organized colonies, that possess environmental adaptability (Ben-Jacob, 1998). The emergence of colonial identity may lead to intentional collective behavior and collective decision-making, which represent forms of adaptation at the level of the social group. A similar situation is observable in the case of social insects. The sacrifice of individuality on the part of members of ant or termite colonies is required for the emergence of the highly integrated collectives termed superorganisms (Wilson and Hölldobler, 2005).

Thus, a different form of IGPT or “knowledge process” operating at the organism–environment interface may exist in the case of social groups requiring a sophisticated form of communication among individual members (Fig. 2) relative to the equivalent applicable to solitary organisms (Fig. 1). This potentially means that different algorithms are applicable at different levels of selection: selection targeting individual organisms (kin selection theory or inclusive fitness) and selection targeting social groups (MLS).

### 2.3. Features shared by all forms of knowledge

Irrespective of whether it involves individual organisms (Fig. 1) or social groups (Fig. 2) IGPT always occurs *a posteriori*. That is, it must be validated by the ecological selection filter, which retains successful variant forms and project them into the future (Plotkin, 1982). This means that biological systems are never prescient, even though the adaptation process at individual or collective levels is directed to some degree, to satisfy the active nature of the organism–environment interactions (see above). However, prescience may be simulated by biological systems in certain circumstances. This occurs when IGPT, which originally occurred *a posteriori* at one level, emerges again at another level of hierarchy where it appears to be a form of *a priori* IGPT. In other words, knowledge forms are “copied” from one level to another because seemingly different problems of the organism–environment inter-

action require the same solutions. To EEM proponents this looked as if many forms of knowledge share certain features.

Some authors call this phenomenon biological periodicity. Biological functions, such as flight or vision, emerge periodically in different organisms and at different evolutionary times as ready-made solutions to particular problems of the organism–environment interaction (Lima de Faria, 1997). For example, Campbell (1974) argued that: (i) the evolutionary “knowledge process” is hierarchical, (ii) knowledge can be exchanged between hierarchies and hence so too can its shared basis/periodicity and, (iii) that the top of the hierarchy of “knowledge process” is occupied by the emergence of science as the attempt of human neural intelligence to understand its environment.

Campbell (1974) used communication among social organisms as an example of the “knowledge process” periodicity being the consequence of the shared basis of knowledge forms. He thought, for example, that the “language of the bees” fulfills a social communication function analogous to human language. Thus, the roots of “language” as a means of communication among members of a social group may be found within groups of organisms that practiced social behavior in evolution for the first time. This also means that all social groups may share the same communication “algorithm” as a consequence of the shared basis of knowledge forms.

It is important to stress that the term “algorithm” is not used in the precise mathematical sense but rather in a weak sense to mean a set of rules describing a sequence of events within a specific biological operation. If the term algorithm is interpreted in this weaker sense then there are certain biological operations, that could be considered algorithm-like, including human language as a means of communication among individual members of human social groups. According to the universal grammar theory, universal syntactic rules are at the core of all natural languages (Chomsky, 1957). Syntactic grammar (organization of phrases and sentences according to grammar rules) and lexical rules (formation of words) allow the emergence of semantic and pragmatic meaning (Hauser, 1996; Warnow, 1997; Searls, 2002). This is the algorithm-like situation: the input represents meaning-independent lexicon and syntax; the output is the emergence of semantic and pragmatic meaning. In a wider biological sense the function of communication algorithms, such as language (Ben-Jacob et al., 2004) or semiotics (communication through symbols) (Uexküll, 2010), is exchange of information and exchange of meaning among members of social groups.

It has been argued, independently of EEM, that the bacterial communication system contains all elements of exchange of information/meaning analogous to human linguistics (Ben-Jacob et al., 2004). Bacteria use their genomic plasticity to conduct collective linguistic communication relying on shared interpretation of chemical cues and exchange of chemical messages (semantic) and dialogues (pragmatic). The exchange of meanings through bacterial linguistics may lead to the emergence of colonial identity, intentional behavior and collective decision-making (Ben-Jacob,

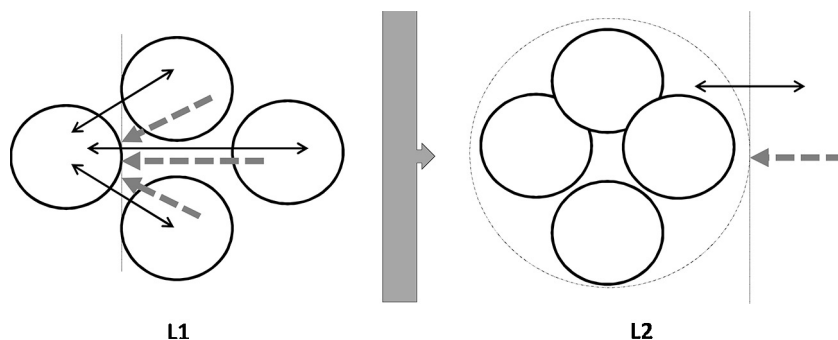


Fig. 2. Schematic representation of IGPT at the level of social group. L-level. Other symbols as in Fig. 1.



1998), all of which represent forms of adaptation at the level of social group.

A similar style of thinking is emerging among plant biologists. For example, some scientists argue that communication between plants has a form of natural language (this point will be discussed in Section 3).

Thus, social communication systems (language; semiotics) may represent a universal algorithm equally applicable to all social organisms including bacteria, protists, plants, social insects, other social animals and humans. This also means that the exchange of knowledge across biological hierarchies is possible because many forms of knowledge share certain features.

### 3. Reformulated EEM principles

Having presented key principles of EEM, which are now several decades old, and exposed them to a limited set of recent studies, I will next reformulate them with the aim of facilitating correspondence of the original principles with contemporary research in a more productive manner.

There are three reasons for reformulation of EEM principles. First, even though EEM claimed to be a universal or near-universal evolutionary theory (Plotkin, 1982), in reality it was limited to explaining behavior of “humans and animals”. This constitutes a discrepancy because any principle of biological universality should be aimed at covering the majority of biological forms. EEM proponents overlooked the fact that animals constitute only a small section of the biological biomass, which is dominated by plants and microbes. For example, the plant terrestrial biomass exceeds the animal biomass by 1000 times (Mancuso and Viola, 2015). Similarly, microbial biomass exceeds animal biomass and it constitutes, according to estimates, between 10% and 90% of plant biomass (Whitman et al., 1998; Kallmeyer et al., 2012). Therefore, if EEM is to retain the initially projected principle of universality it must include all organisms, not only animals.

Second, a careful reading of selected recent papers in microbiology, cell biology, plant biology and some other fields dealing with the cognitive side of the organism-environment interactions (see Section 4) reveals a general agreement with EEM principles. However, there was no single example in which EEM was acknowledged as the source of information or the guiding motivation behind the conducted research. This suggests that principles of EEM had not been formulated sufficiently clearly, and with sufficient depth, to constitute an attractive and wide-ranging proposition, that will resonate well with the empirical research community. By contrast, philosophers found EE and EEM more attractive judging by the fact that the philosophical nature of EEM principles is still debated today (Kronfeldner, 2010, 2011; Baravalle and Vecchi, 2016). Therefore, there is a need to make EEM principles more attractive to empirical research. Operating on the assumption that the integration of disparate areas of common interest may exceed the sum of their individual parts and lead to advances in knowledge, the benefits to empirical research from a reformulated EEM may be considerable.

Third, the knowledge base upon which EEM principles had been formulated has expanded significantly in recent years. Thus, there is a need to incorporate new streams of knowledge into the theory.

I will reformulate EEM principles in line with the above considerations in the following way.

#### • Principle No. 1:

“Living systems as knowledge systems” → **Individual organism intelligence (IOI).**

The term “individual organism” refers to any organism – any biological entity capable of actively interacting with the environ-

ment in an autonomous way: bacteria and archaea, protists, fungi (unicellular and multicellular), plants and animals.

In the new formulation terms such as “cognition”, “knowledge process”, “epistemology” etc. are replaced by the term “intelligence”. This term may resonate better with the empirical research community because it encompasses all the above terms as exemplified by its use in the well-known field of AI (artificial intelligence). If intelligence can be ascribed to man-made machines (McCorduck, 2004), there is no reason why the same property should not be ascribed to “natural machines” – the anthropocentric term some scientists and philosophers use to describe living organisms (e.g. Dawkins, 1976).

The term “intelligence” refers to the capacity of organisms to (i) gain information about the environment, (ii) process the information internally, and (iii) translate the information into a phenotypic form. This capacity was named IGPT earlier. It is important to stress that IGPT encompasses perception, memory, learning, anticipation, decision-making, and communication (Lyon, 2015; see also Section 4). The purpose of IOI is to increase organismal fitness. Increases in organismal fitness brought about by IOI are subject to the ecological filter of natural selection.

Through IOI, organisms have the capacity to change the environment, which in turn may react or respond to this change. The organism-environment cybernetics is synonymous with the term co-evolution (Laland et al., 2015).

The biological mechanisms behind IOI include genetic mechanisms, epigenetic mechanisms, symbiotic mechanisms, natural computation, inheritance of acquired characters, ecological inheritance, psychological inheritance etc. (Jablonka and Raz, 2009; Laland et al., 2015; Skinner, 2015; Wilson et al., 2008).

#### • Principle No. 2:

“Evolution as the process of gaining knowledge” → **Collective intelligence.**

Intelligence is hierarchical and it ranges from the intelligence of bacteria and archaea to the intelligence of the planetary ecological system (the biosphere or Gaia), which integrates all types of intelligence (Lovelock and Margulis, 1974). The term collective intelligence covers two types of supra-organismal intelligence called Social Intelligence (SI) 1 and 2. SI1 is defined as the type of intelligence resulting from the emergence of the communication system among individual organisms of the same species. It has been argued that the bacterial communication system contains basic elements analogous to human linguistic communication: interpretation of chemical cues, and exchange of chemical messages (semantic) and dialogues (pragmatic) (Ben-Jacob et al., 2004).

Similarly to bacteria, other groups of organisms, including protists (Flowers et al., 2010), plants (Trewavas, 2016, 2017), and insects (Schulz and Höftling, 2015) are capable of exchanging chemical and other messages (Cocroft and Rodriguez, 2005). Furthermore, cells in multicellular organisms communicate through sophisticated signal transduction pathways (King, 2004). A consequence of the effective communication system among individual organisms or cells may be the emergence of the supra-organismal entities capable of adaptation on their own – a bacterial colony, a multicellular plant or animal, or an insect superorganism. These supra-organismal entities acquire the capacity to coordinate IOI in a novel way in which individual organisms adjust and integrate their own IOI capacities in line with the needs of the supraorganismal entities. Also, supra-organismal entities have a greater capacity to change the environment. Exemplary is the change of the planetary atmosphere composition by cyanobacteria, which could only occur through the emergence of bacterial colonies capable of “conquering” a large proportion of habitats at Earth’s surface (Schirrmeister et al., 2011).

A second type of collective intelligence may be called SI2. In contrast to SI1, in which interactions occur among organisms of the same species, in SI2 interactions occur among organisms of different species. The most fundamental example of SI2 are eukaryotic cells as mergers of at least two (amoebae, animals, fungi etc.) or three (algae, plants etc.) endosymbiotic partners into functioning composite organisms or chimeras (Sagan, 1967). Modern phylogenomic studies indicate that the merger at the heart of the eukaryotic cell occurred between an archaeal host and a eubacterial partner (Williams et al., 2013).

Another example of SI2 is insect agriculture. Leafcutter ants (genera *Atta* and *Acromyrmex*) use fungi from two genera *Leucogaricus* and *Leucocoprinus* as the biological “convertor” of green leaves into food for the entire ant colony (Hölldobler and Wilson, 2011). This mutualistic symbiosis may involve some form of chemical communication between ants and the fungi (Vasse et al., 2017).

A further example of SI2 is the manipulation of insects by plants, through chemical signals, as a means for protection against herbivory (McCormick, 2016). Still another example of SI2 is the close communication between all plants and animals on one side and their associated microbial collectives known as microbiomes, resulting in the communities known as holobionts (Margulis 1993; Zilber-Rosenberg and Rosenberg, 2008), on the other. New studies use the term “cross-kingdom communication” to describe communication between microbiomes and their hosts, some of which exploit prions as signal-sending molecules (Jarosz et al., 2014). Furthermore, integration of SI1 and SI2 may be a key to the emergence of ecological dominance as in the case of plants (Mancuso and Viola, 2015), social insects (Wilson, 2012), and humans (Lewis and Maslin, 2015).

At the highest ecological level (the biosphere) self-regulation and stability exist (Lovelock and Margulis, 1974), suggesting that all forms of SI1 and SI2 are integrated into their ecological systems. For example, new research suggests the capacity of plants to “engineer” biomes (Sheffer et al., 2015). However, judging by the mass extinctions, or ecological catastrophes, which occur periodically (Rohde and Muller, 2005), ecological stability is not the evolutionary norm. Mass extinctions may constitute an ecological filter, which shapes the biosphere in a blind way. (Mass extinctions may depend on time scale. Biomimesis for human survival suggests we mirror the bio-intelligence of stably recycling ecosystems [climax ecosystems in Amazon, mature Douglas fir forests etc.] not the aftermath of vulcanism, celestial bombardment, or cyanobacterial global atmospheric regime change.)

- Principle No. 3:

“Features shared by all forms of knowledge” → **Evolutionary knowledge transfer (EKT).**

As argued by Campbell (1974) the peak of SI1 intelligence is science – the human analytical capacity aimed at understanding its own environment. This also includes analysis of all types of IOI/SI1/SI2 intelligence present in the biosphere, including the generation of new forms of intelligence such as AI and employment of intelligent technologies for exploration of the environment. The current state of human technological development may be characterized as the fourth industrial revolution – the emergence of cyber-physical-biological systems (Schwab, 2016).

Given that IGPT forms are shared across species, social group and ecosystem boundaries, many types of knowledge may be evolutionarily shared (Plotkin, 1982). Thus, an important applied aspect of science is to identify those types of knowledge that may be useful to human technologies. For example, it is possible that a solution to a particular problem of the organism-environment interaction “invented” by species X may be used as the solution to a particular problem faced by human technology Y.

**Table 1**

Reformulated EEM principles in different areas of empirical research. For detail see Section 4. IOI – Individual Organism Intelligence; SI Social Intelligence; EKT – Evolutionary Knowledge Transfer.

	IOI	SI1/SI2	EKT
Microbiology	+	+	
Eukaryotic Cell Biology	+	+	+
Plant Biology	+	+	
Biomimetics			+
Synthetic Biology			+
Philosophy of Science			+

An excellent example is the “honeybee algorithm” (Nakrani and Tovey, 2007) a biomimetic mathematical model developed to address the problem of Internet server allocations. After analyzing the honeybee self-organizing model for optimal nectar collection and assessing its homology to the problem of the server allocation, an algorithm was developed which is highly adaptive and competitive against the benchmark and conventional algorithms. The success of the “honeybee algorithm” is measured in both financial terms (\$ 10 billion saving to the Internet server industry; Professor Thomas Seeley, personal communication) and its value to the scientific community (it received a Golden Goose award from AAAS in 2016). However, many similar attempts to use bio-intelligent solutions for problems of human technologies failed (summarized in Nakrani and Tovey, 2007).

Thus, one function of science is to identify the most effective way for assessing the suitability of various forms of IOI/SI1/SI2 as solutions to problems of human technologies. This may also help search for solutions to ecological problems facing humanity provided that due attention is paid to the ecological scale of bio-intelligence.

#### 4. New research-based evidence for EEM principles

In this Section I will present evidence from modern research in line with EEM principles. I will focus only on non-neural forms of intelligence<sup>1</sup> as observed in microbes (prokaryotic and eukaryotic) and plants. Animal intelligence is beyond the scope of this study because of insufficient space. As stressed earlier, all relevant studies consulted in this section lacked the awareness of EEM.

The investigative fields covered in this section belong to the following major research areas: microbiology, eukaryotic cell biology, plant biology, synthetic biology, biomimetics, and philosophy of science. Table 1 is a summary of the correspondence of investigative areas with individual EEM principles. For example, the plus sign (+) identifies one of the principles (see above) corresponding to a particular investigative area. Each investigative area will be briefly discussed and major points highlighted.

##### 4.1. Microbiology

###### 4.1.1. IOI

Traditionally, bacteria have been viewed as single cell microbes – autonomous free-living organisms. However, this view does not reflect reality, as bacteria are highly “social” organisms living in colonies. Some researchers consider bacterial colonies multi-cell-organism-like entities (Shapiro, 1988, 1889; Ben-Jacob, 1998; Ben-Jacob et al., 2004). Nevertheless, in certain circumstances of their social lives bacteria are required to carry out solitary living. For example, they may search for the new food sources on behalf of the colony at locations far away from the main body of the colony. Using the process called chemotaxis individual bacteria determine their

<sup>1</sup> Neural intelligence, which typifies animals, relies on neurons as the means of communication between (i) the central processing unit (brain) and the body and (ii) exchange of information between brain areas.

movement, in response to chemical stimuli present in the environment. The process of bacterial chemotaxis is a typical example of IOI that conforms to the IGPT formula (Fig. 1).

For example, some *E. coli* strains are motile because they possess flagella. Individual cylindrical-shaped bacteria swim in the liquid medium in the direction of their long axis at the speed of 35 diameters per second (Berg, 2000). They often change the course of movement but rarely stop. The flagellum has three parts: the basal body or motor embedded into the cell wall, a short proximal hook which constitutes a universal joint, and a helical filament which plays the role of a propeller (Berg, 2000). The motor runs clockwise and counter-clockwise in alternating fashion. When the motor turns clockwise the movement is erratic – the cell tumbles. When motor turns counter-clockwise the movement is steady – the cell runs. These two alternating motor modes are responsible for the capacity of *E. coli* cells to move around.

The molecular machinery behind the control of the flagellum is integrated with the cellular sensing system. Sensors are proteins of different classes embedded into the cell wall opposite the flagellum. The protein sensors act as receptors for environmental chemical cues. Each receptor has multiple binding sites, which recognize a wide range of chemical stimuli. Information received by receptors is processed internally by the complex signal transduction system involving a range of molecules. In brief, information in the form of chemical stimuli flows from outside the cell through holes in the cell wall called porins. Upon entering the periplasmic space these chemical stimuli, such as amino acids for example, bind to appropriate receptors. This in turn causes changes on the cytoplasmic side of the receptor in the form of a chemical reaction such as methylation. By constantly analyzing the occupancy of the binding site and comparing it with the level of methylation at the cytoplasmic side of the receptor, the bacterial cell determines the action of the flagellum and thus its own movement (Berg, 2000). The cell also has a temporal perspective. The occupancy of the binding site reflects the current conditions. Level of methylation reflects the past conditions.

The above brief summary of chemotaxis in *E. coli* represents only a fragment of a much wider bacterial IOI repertoire (Shapiro, 1991; Vertosick, 2002; Marijuán et al., 2010; Trewavas, 2014; Lahoz-Beltra et al., 2014; Baluška and Levin, 2016). Lyon (2015) named this repertoire the “Bacterial Cognitive Toolkit” (BCT). She used a range of references to justify bacterial behavior as intelligent but curiously did not mention EEM. Nevertheless, papers describing BCT (Lyon, 2015, 2017) constitute the most comprehensive evidence in favor of bacterial IOI.

Here is the summary of BCT, or in my formulation IOI, directly taken from Lyon (2015):

- **sensing/perception** – the capacity to sense and recognize (recognize) existentially salient features of the surrounding milieu;
- **valence** – the capacity of an organism to assign a value to the summary of information about its surroundings at a given moment, relative to its own current state;
- **behavior** – the capacity of an organism to adapt via changing its spatial, structural or functional relation to its external or internal milieu;
- **memory** – the capacity to retain information about the immediate (and possibly distant) past, and to calibrate the sensorium to take account of this information, for example, via signal amplification;
- **learning** – the capacity to adapt behavior according to past experience, enabling a faster response time;
- **anticipation** – the capacity to predict what is likely to happen next based on an early stimulus;
- **signal integration or decision making** – the capacity to combine information from multiple sources, because all organisms

appear to sense more than one thing, and some bacterial species are equipped to sense dozens of different states of affairs;

- **communication** – the capacity to interact with conspecifics, including initiating collective action, which may or may not include an explicit method of differentiating “us” from “them”.

#### 4.1.2. Collective intelligence

The classical neo-Darwinian stance favors rigid lines between individual organisms and social groups, and permits only individual organisms as units of selection via genes (Hamilton, 1964; Laland et al., 2014). By contrast, for some researchers the perception of biological individuals and collectives is more in line with the concept of holon – an ambiguous part-whole entity (Koestler, 1967). For example, Margulis and Sagan (2000) and others (Martin, 1999) advocate that hierarchy (holarchy in Koestler’s terminology) of life is not in line with the classical Darwinian tree, but rather it represents a complex web with multiple levels of hierarchy. Each level of hierarchy can be a unit of selection: individuals, mergers of individuals (symbionts including holobionts), social groups, groups of different species making an integrated ecological unit etc.

In line with this view, James Shapiro argued that bacterial populations behave as multicellular organisms (Shapiro 1988). The “conquest” of the planet by bacteria and the birth of geochemical processes dependent on them would not be possible if bacteria behaved as purely single-cell microbes. Other researchers accepted this view and suggested that communication systems relying on chemical messaging were crucial for bacterial ecological expansion. Different terms are used to describe bacterial communication including “bacterial linguistics” (Ben-Jacob et al., 2004), bacterial “small talk” (Bassler, 2002) and “bacterial communication” (Lyon 2015). In the terminology of revised EEM principles this would fall under the category of SI1 because communication occurs between conspecifics.

The molecular mechanism behind bacterial communication is autoinduction or indirect sensing via proxies. This is a process in which individual bacteria secrete a class of molecules called autoinducers (Bassler, 2002). In brief, bacterial cells produce their own chemical messages (autoinducers), release them into the environment, and detect them and respond to a threshold concentration of the released autoinducer molecule. This type of communication is also called quorum sensing. It occurs only when bacteria are at high population densities. Quorum sensing regulates bioluminescence, virulence factor expression, biofilm formation, sporulation, and mating. In quorum sensing communication emerges spontaneously once the sufficient bacterial density or quorum is achieved. Autoinducers in quorum sensing include a range of molecules such as AHL, HAI-1, AI-2, butyrolactone, macrolide, and mixtures of amino acids etc. (Shapiro, 1988; Bassler, 2002). It is also interesting to mention the concept of “alarmones” (alarm + hormones) – social hormones based on cAMP widely used by bacteria (Lazcano et al., 2011).

However, bacterial populations in natural habitats are complex conglomerates consisting of multiple species or strains. They represent highly ordered communities suggesting that the order may be regulated through communication between different kinds of bacteria. Autoinducers for inter-species communication include AI-2 and some other chemicals (Bassler, 2002). They are used by multiple gram-positive and gram-negative bacteria. Therefore, in bacterial linguistics AI-2-mediated communication represents a universal interspecies chemical language. In the terminology of the revised EEM principles this would represent an example of SI2.

However, social communication on its own would be a chaotic process without a unifying mechanism capable of keeping it under control and providing some meaning to it. This unifying mechanism encompasses memory, learning, anticipation, and decision making. Ben-Jacob (1998) made a compelling case for bacterial



collective intelligence (SI1 and 2). He criticized the conventional neo-Darwinian approach and its reductionist-mechanistic stance, which precludes collective creativity resulting from the emergence of collective “mind” which has the capacity to retain information about the immediate and distant past, and adapt to new conditions. This excerpt sums up his stance (Ben-Jacob, 1998):

“Progress happens when organisms are exposed to paradoxical environmental conditions – conflicting external constraints that force the organism to respond in contradicting manners. Clearly, an organism cannot do it within its current framework. The new picture of creative cooperative evolution is based on the cybernetic capacity of the genome. . . and the emergence of creativity as the solution cooperative complex systems apply to an existential paradox.”

The genome is not only a storage device but also “a sophisticated cybernetic entity well beyond a universal Turing machine” because it changes adaptively during computations to satisfy the needs dictated by computations. The notion of the genome as an agent of memory that is creative has also been entertained by Shapiro (2016). He uses the term “read-write genome” to describe the capacity of the genome to evolve as part of an active and creative biological process. Shapiro suggests that the processes of horizontal gene transfer, integration of viruses into bacterial genomes and other processes that neo-Darwinism sees as non-classical, play a prominent role in the emergence of biological novelty.

One of the problems for the above line of thinking is how to express it in mathematical terms. Ben-Jacob suggested that current approaches of logic and mathematics may be limited in interpreting biology. For example, our mathematical thinking is based on the notion of a set composed of elements in which sets and elements are static and fixed. Mathematical sets are closed and lack any internal structures, thus leading to the Gödel incompleteness theorem as the symbol of a misfit between mathematics and biology. Instead, Ben-Jacob suggested that the notion of elements should be replaced by the notion of agents with internal structure. The agents, neither static nor passive, include biomolecules such as nucleic acids (DNA and RNA) and proteins, which collectively form the genome. However, the genome cannot exist on its own. It must be functionally integrated into the cell through the universal genetic code. Ben-Jacob (1998) argued further:

“The notion of a set is replaced by a cell, which refers to a collection of agents with a common goal and mutual dependence. It also implies that the system of agents is open, i.e. it exchanges energy and information with the environment. I argue that, in order for a cell of agents to be self-aware, it must have an advanced language, i.e. a language which permits self-reference to sentences and to its grammar. The language also enables the individual agents to have information about the entire system. In addition the cell has strong coupling with the environment. The ‘self’ emerges through this coupling. There is no meaning of ‘self’ in a closed system.”

The cited paragraph summarizes effectively SI1 (Fig. 2) and it also provides some mathematical perspective which may be combined further with systems biology approaches. Taken together, the arguments presented in the last two sections are in line with the EEM principles and yet all cited papers ignore EEM.

## 4.2. Eukaryotic cell biology

### 4.2.1. IOI, SI1 and SI2

Any organism above the level of bacteria and archaea is a chimera (Margulis et al., 2011). Thus, single-cell eukaryotes, such as protists, already incorporate into their structure the SI2 type

intelligence by virtue of the endosymbiotic origin of the eukaryotic cell, which constitutes an autonomous cognitive system consisting of two independent prokaryotic organisms (Sagan, 1967), most likely an archaeal host and a eubacterial partner (Williams et al., 2013), which fused together and established permanent chemical communication. In the case of algae and plants a third type of endosymbiotic partner is the plastid, the photosynthetic organelles. The transition from bacteria to eukaryotes (single- and multi-cell) is also known as SET (serial endosymbiotic theory) (Margulis, 2004).

There is strong evidence for IOI in protists. The most commonly investigated organism is the slime mold, *Physarum polycephalum*. This is an ameboid multi-nuclear single cell, visible without the microscope and consisting of multiple tubular structures called plasmodia (Dussutour et al., 2010). Plasmodia are “distributed information processors” that allow *P. polycephalum* to carry out various cognitive tasks including finding the shortest route through a maze in search of food (Reid et al., 2012), anticipating timing of periodic events (Saigusa et al., 2008) and solving complex foraging problems (Nakagaki et al., 2016).

In addition, *P. polycephalum* shows chemotactic abilities and capacity for learning through the process known as habitation (Boisseau et al., 2016). Habitation, or the simplest form of learning, is usually defined as reduction in response to a frequently repeated stimulus. *P. polycephalum* learnt to ignore chemical stimuli (quinine and caffeine) when repetitive, but responded after the stimuli were withheld for a period of time. Therefore, according to the above studies, *P. polycephalum* shows all components of the cognitive toolkit typical of bacteria (see BCT components above), or IOI, except communication.

However, other slime moulds such as *Dictyostelium discoideum* show forms of communicative social behavior in line with SI1. In the absence of food *D. discoideum* cells, which start life as haploid amoebas, start to communicate and form aggregates (Buttery et al., 2009; Flowers et al., 2010; O’Day and Keszei, 2012) which are known as plasmodia. After aggregation the new entities (cytoplasms of individual cells fuse transforming into a giant single cytoplasm with multiple nuclei) may undergo one of two possible collective reproductive options. The first option is the formation of a “fruiting body.” Aggregated cells form a slug, which migrates collectively until a suitable location is found to form a fruiting body. Cells at the front of the slug form a stalk and the rest form spores that will be dispersed by the wind. The second option is to form a structure known as a macrocyst. Here, after aggregation, cells do not form a slug but instead two cells merge to form a zygote, which then eats all the other aggregating cells. The resulting giant cell forms a hard cellulose wall and germinates after a few weeks. It has been shown that various chemicals regulate communication between aggregating cells (O’Day and Keszei, 2012) in line with SI1.

The eukaryotic SI1 is most apparent in true multicellular organisms such as plants and animals. Transition to multicellularity requires a hierarchical shift in which cells sacrifice their individuality in deference to of the corporate body. In other words, individual cells must adjust and integrate their own IOI capacities in line with the needs of the corporate body (King, 2004; Marijuán et al., 2013). This leads to the shift from cell-level individuality to that of the corporate body-level individuality and thence to the emergence of a supraorganismal type of IOI. Also, there is a selection shift in which the corporate body is subject to MLS-type selection (Gardner, 2014).

Phylogenomic studies indicate that fundamentals of multicellularity include (i) cell adhesion, (ii) signal transduction as the means for cell communication and (iii) differentiation including the soma-germline split, division of labour, and apoptosis as the filter for descendents (King, 2004). It is also worth remembering Ben-Jacob’s notion of the genome as the cybernetic unit and the agent of memory, and also the concept of cell as the biological set of agents (see



above). The genomic perspective in the case of eukaryotic multicellularity shifts somewhat relative to its bacterial counterpart. First, there is a greater emphasis on epigenetics and its roles in cell memory and heredity. Control mechanisms involved in epigenetic inheritance include chromatin markers, structural inheritance and RNA based inheritance, all of which are in line with the greater complexities of eukaryotic genomes relative to bacterial genomes as the cybernetic units behind corporate bodies (Jablonka and Lamb, 2006; Jablonka and Raz, 2009; Slijepcevic, 2016). The emergence of the corporate body as an independent multicellular entity shifts the emphasis from individual components of the body – cells as independent sets of agents – to the body as the set of sets in which sets and its agents are now subject to the much more stringent rules imposed by epigenetic mechanisms and the need to maintain genome stability over many generations in the germline and in each generation in the soma (Slijepcevic, 2016).

With regard to SI2 in protists a good example may be the primitive practice of agriculture by the social amoeba *D. discoideum*. This amoeba forms a primitive farming symbiosis with bacteria the purpose of which is the husbandry of those bacteria, which are eventually incorporated into fruiting bodies (Brock et al., 2011). Furthermore, in the choanoflagellate *Salpingoeca rosetta*, the putative closest living protist relative of animals, lipids produced by the bacterium *Algoriphagus machipongonensis* regulate multi-cell rosette formation (Woznica et al., 2016); and also in *S. rosetta* chondroitinase, produced by the bacterium *Vibrio fischeri*, induces their sexual reproduction (Woznica et al., 2017).

#### 4.2.2. EKT

Prominent cell biologists use metaphors and analogies in line with the principle of EKT. The direction of EKT in science is almost always from nature to human technologies as shown in the case of the “honeybee algorithm”. However, the opposite direction is also possible, e.g., some forms of individual-level, social-level and technological-level human organization may be used as the means for understanding intricacies of the molecular organization of the eukaryotic cell.

For example, plant biologist Barbara McClintock stated in her Nobel acceptance speech that: “A goal for the future would be to determine the extent of knowledge the cell (organism) has of itself and how it utilizes this knowledge in a thoughtful manner when challenged” (McClintock, 1984). This is a useful analogy because it suggests that the neural intelligence that typifies animals is not essential for intelligence.

In a further example, cells are seen as elaborate factories consisting from numerous interlocking production lines comprised by assemblies of protein machines (Alberts, 1998). The term “protein machine” stems from the fact that all major processes in the cell are carried out by assemblies of ten or more protein molecules. As in a human-made machine-based factory line, assemblies of protein molecules contain highly coordinated moving parts whose effects can be traced from an output C, to an output B, to an output A. The number of proteins in a cell is difficult to estimate. Assuming that there are 100,000 proteins/eukaryotic cell (Trewavas, 2017), the factory thus represents an interactome, which integrates all possible protein machines into a functioning whole.

Similarly, a molecular biologist used the metaphor of a “metropolitan city” to describe the eukaryotic cell in which the bustling community of macromolecules must be precisely organized including, for example, those for intracellular transport (Vale 2003). Intracellular cargos of various protein assemblies and organelles are transported efficiently by protein motors along cytoskeletal tracks reminiscent of the roads and railways in the transport system of a metropolis.

### 4.3. Plant biology

The notion of plant intelligence has been a hotly debated topic. The emerging picture suggests that plant intelligence has been underestimated relative to animal intelligence, mostly as a result of the prejudice summed up by the phrase “brain chauvinism” (Trewavas, 2005). Brain and nervous system are evolutionary routes required for rapid movement and rapid assessment of the changing organism–environment interactions that typify life for animals. By contrast, plants are sedentary organisms and their relative lack of movement obscures a fight for local space. As a result, their intelligence is distributed or modular, and it lacks a central processing unit. Nevertheless, plants show IOI, SI1 and SI2, as do other non-neural organisms such as microbes.

#### 4.3.1. IOI

Individual plants are capable of sensing a range of stimuli from the environment and responding to them in an intelligent way consistent with the IGPT formula (see above). These include (i) abiotic stimuli: light, temperature, mechanical signals such as touch, bending and wind, soil obstacles to roots, vibrations and sound, patchy mineral distribution and soil impedance variation, loss of turgor due to low water availability, gravity, and variation in the atmospheric gas concentrations, anaerobic conditions, and volatile and non volatile chemicals; and (ii) biotic stimuli: competition and cooperation, trampling, herbivory, disease, symbiosis and mutualism (reviewed in Trewavas, 2017).

To respond to all the above stimuli in an intelligent way plants rely on internal signals, which travel through the plant vascular system in the absence of animal style neural network. But signals are there nonetheless: they include mRNA and various types of small inhibitory RNAs (Pierik and deWit, 2013), numerous proteins and peptides (Aphalo et al., 1999), hormones, hydraulic and mineral signals (Trewavas, 2017) and action potentials (Choi et al., 2016). The speed of signal travel varies, the fastest signal typically moving at the speed of  $1 \text{ m s}^{-1}$  (Trewavas, 2017).

A good example of IOI in plants is the mechanism for regulation of stomata opening. Stomata are apertures located on leaves and distributed at densities of hundreds per  $\text{mm}^2$  (Peak et al., 2004). The function of stomata opening is the  $\text{CO}_2$  intake required for photosynthesis. At the same time stomata opening causes water evaporation and water loss. Therefore, the process must be regulated to preserve individual fitness. The importance of the process of regulating the opening of stomata is highlighted by the fact that 99% of terrestrial carbon fixation and 99% of terrestrial water loss is dependent on it. Research has shown that the process of stomata opening is equivalent to sophisticated biological computation, and reminiscent of computer-based simulations of locally connected networks known as cellular automata (Peak et al., 2004). This suggests that plants engage in a form of emergent, distributed computation, a process in line with IOI. Some other examples of IOI in plants include kin recognition (Dudley and File, 2007), decision-making by root tips about when to stop dormancy and initiate germination (Topham et al., 2017), and adaptive variability to light in response to crowding (Pierik and deWit, 2013). The most up-to-date summary of various forms of plant IOI can be found in Trewavas (2017).

#### 4.3.2. SI1 and SI2

Plants communicate through emitting volatile organic chemicals or VOCs. Any part of the plant body can emit VOCs: leaves, roots, shoots, bark, fruits, and flowers (Trewavas, 2017). It is estimated that 1% of carbon fixed by plants is used for production of VOCs (Trewavas, 2017). VOCs emitted by one plant are detected by conspecifics (SI1) (Dudareva et al., 2006), or even by plants from different species (SI2) (Runyon et al., 2006). The purpose of emission

and detection of VOCs by conspecifics is usually defense against herbivore attacks or mechanical wounding. VOC detection by plants from non-emitting species is frequently associated with parasitism. There is also evidence of interaction among plant roots, rhizosphere bacteria, and mycorrhizae through VOCs (Castulo-Rubio et al., 2015), which provides another example of SI2.

Some scientists interpret plant communication as a form of language. This is similar to Ben-Jacob's interpretation of communication in bacteria. Individual VOCs are likened to "words", whereas several VOCs in combination are seen as a "sentence" – the emergence of the "words" which make it up (Holopainen and Blande, 2012). "Sentences" must convey meaning, as in the bacterial communication explained earlier. If meanings emitted by "sentences" are not coherent (e.g. missing VOCs or "words") the consequence is that the intended biological process will fail (Kikuta et al., 2011; Trewavas, 2017).

Given that plants constitute the majority of the planetary biomass (Mancuso and Viola, 2015), plant intelligence may have wider ecological reach. A recent study favors this possibility through demonstration that plants have the capacity to strategically influence entire biomes and in this way dictate productivity and resilience of their environment (Sheffer et al., 2015). By controlling nitrogen-fixing bacteria and strategically distributing this control, nitrogen fixing plants behave in a smart and strategic way. This possibility is in line with the ecological-level SI2 which could have important implications for resolving current ecological problems related to forest carbon sinks and removal of CO<sub>2</sub> from the atmosphere (Sheffer et al., 2015).

Taken together, all the examples presented above strongly suggest intelligence in plants in line with EEM principles. Again, none of the screened references acknowledged the existence of EEM principles.

#### 4.4. Biomimetics

The field of biomimetics accords with the EKT principle of EEM (Table 1). Next, I will briefly summarize principles of biomimetics in light of EEM.

Nature has been an inspiration for human technologies for millennia. An organized extraction of engineering ideas from nature started in 1950s. A major pioneer who saw great potential in extraction of engineering solutions for humans from biological scenarios was Otto Schmitt (1913–1998), one of the most prominent biophysicists of the 20th century (Vincent et al., 2006). He coined the term biomimetics to describe exploration of biological processes as potential solutions for the human engineering or design problems. His ideas resonated well within the scientific community leading to the establishment of biomimetics, an interdisciplinary field also known as bionics, biomimicry, biomimesis and biologically inspired design (Vincent et al., 2006). The key principle of biomimetics is formalization of procedures for effective translation of biological scenarios into the field of human technology and engineering. Typical examples include invention of Velcro (Velcro 1955), invention of Lotusan using the self-cleaning property of lotus leaves (Barthlott and Neinhuis, 1997), and invention of anti-reflective surfaces on solar panels based on their equivalents on insect eyes or plant leaves (Bernhard et al., 1965; Parker et al., 1998). Three large efforts to use biomimetic principles in manufacturing have emerged in recent years: (i) biomimetic fabrication; (ii) micro and nano fabrication and surface manipulation; and (iii) production systems and organization based on biological solutions (Shu et al., 2011).

In line with EEM, but without being aware of it, biomimetics implies that biological systems are cognitive systems – any human engineering attempt, which involves biological systems, relies on organisms' prior evolutionary "expertise". The clear benefit for

human engineers is that solutions to the evolutionary problems encountered in the past by various cognitive systems, from cells to ecosystems, can be attempted as potential solutions to problems encountered in human technologies. The "honeybee algorithm" described earlier is a perfect example of a bio-intelligent solution to a human technological problem.

However, numerous attempts to apply biological scenarios to human technological problems had varying degrees of success. For example, algorithms based on ACO (ant colony optimization) were not competitive against alternative methods (Applegate et al., 1998). This suggests that a highly formalized and stringent procedure for translation from biology to technology is required. One such procedure is known as TRIZ. Originally developed in Russia, TRIZ (Teorija Reshenija Izobretatelskih Zadach in Russian) roughly translates as "Theory of Inventive Problem Solving" (Vincent et al., 2006). In brief, TRIZ relies on the dialectic thesis-antithesis approach to identify the most promising solution for a particular technological problem. A contradiction matrix is formed in which desired inventive principles from existing patents are matched against antithetic features. The contradiction matrix consisting of 39 features then serves as a lookup table for identifying optimal solutions. TRIZ has recently been modified into PRIZM (roughly translated as The Rules of Inventive Problem Solving, Modernized) to make it more effective (Vincent et al., 2006). Interestingly, application of TRIZ and PRIZM suggest that biological processes are less "concerned" with manipulating usage of energy and more concerned with the problems of information and structure, thus indirectly acknowledging the importance of IGPT at all levels.

#### 4.5. Synthetic biology

The culmination of biologically inspired technologies is synthetic biology – a growing interdisciplinary field that combines genetic engineering, biotechnology, molecular biology and engineering, systems biology, electrical and computer engineering, evolutionary biology, and other disciplines with the aim of exploring living organisms as the new technological medium.

The first synthetic genome has been generated and transferred into a recipient bacterial cell, which was successfully propagated (Gibson et al., 2010). This paved the way for creating the minimal artificial genome required for a bacterial cell to survive (Hutchison et al., 2016). To enable a smooth interchange of ideas and designs between versatile fields, a set of common standards known as SBOL (Synthetic Biology Open Language) has also been created (Galdzicki et al., 2014).

Synthetic biology relies on EKT almost in the entire provision (Table 1). For example, without the use of restriction enzymes manipulation of DNA for the purposes of genetic engineering in the last forty years would not be possible. Scientists who discovered restriction enzymes relied on the evolutionary solution bacteria invented to fight viral infections (Smith and Wilcox, 1970). Similarly, more recent molecular technologies such as RNAi (Stram and Kuznatova, 2006) and CRISPR-Cas (Barrangou, 2015) are copies of earlier evolutionary inventions. Even the construction of the first artificial genome would not work without using genome-free bacterial cells as the evolutionary knowledge platform.

Interestingly, scientists working on bacterial synthetic biology still do not appreciate SI1 and SI2. This perhaps reflects our rudimentary knowledge of the social lives of bacteria and their potential effects on ecosystems. Given bacterial capacity to adapt quickly to many new environmental conditions through "the read-write genome" (Shapiro, 2016) it is essential that synthetic biology fully appreciates bacterial SI1 and SI2. At present, neither bacterial intelligence nor EEM principles feature in synthetic biology.

#### 4.6. Philosophy of science

In recent years changes in our understanding of bacterial intelligence have attracted philosophers of biology in recent years (O'Malley and Dupré, 2007; Dupre and O'Malley, 2009). However, EEM principles have not been mentioned at all. In addition, other philosophers attempted to present an integrated picture of cognitive biological systems, again without acknowledging EEM (Cazalis et al., 2017). This is somewhat unexpected because philosophers still actively pursue EE, as exemplified by recent papers (Anderson, 2008; Gontier, 2010; Baravalle and Vecchi, 2016). The closest philosophers of biology came to recognizing EE was through quoting Popper's thought that there is only one step between amoeba and Einstein but without acknowledging the wider context (Lyon, 2015). However, in a different study Lyon (2017) searched for explanations of cognitive mechanisms in bacteria, a pursuit similar to the goals of EEM. Thus, it would seem that, as in empirical research, philosophy of science is not acknowledging EEM (Table 1).

### 5. Synthetic overview and concluding remarks

Given that (i) all organisms adapt to their environments, (ii) the process of adaptation determines organismal fitness, (iii) the process of adaptation is, at least in part epistemic, and (iv) the process of adaptation is hierarchical, biological intelligence should be investigated holistically, from a new angle on that is not disconnected in fragments. In this way we may be able to facilitate a broader, deeper understanding of the multibillion year old eco-evolutionary intelligence of which we are, after all, only a recent part.

A holistic approach to the study of evolutionary cognitive mechanisms was the original intention of EEM. Unfortunately, EEM principles did not resonate well with the empirical research community for the reasons explained in Section 3. The reformulated EEM framework (Section 3) provides a new platform for investigating intelligence as a universal biological phenomenon. The new platform may be tentatively called Research Programme for Distributed Biological Intelligence.

The new Biological Intelligence framework should incorporate AI. Given that AI represents only one form of intelligence, derived from the complex hierarchy of Biological Intelligence, it may not be justifiable to keep AI as an independent research programme unrelated to the framework from which it has been derived. Here is the list of key principles that stem from the framework (Section 3) and recent research (Section 4).

- Intelligence is a universal biological phenomenon promoting individual fitness and required for effective organism-environment interactions. Given that animals represent less than 0.01% of the planetary biomass, neural intelligence is not the evolutionary norm.
- The basic unit of intelligence is a single cell prokaryote. All other forms of intelligence are derived.
- Intelligence is hierarchical. It ranges from bacteria to Gaia.
- The concept of “information” acquires a new meaning because the IGPT process is at the heart of biological intelligence. All biological systems, from bacteria to Gaia, are intelligent and open thermodynamic systems, which exchange information, matter, and energy with the environment.
- The organism-environment interaction is cybernetic. As much as the organism changes due to influence of the environment, the organism's reaction to induced changes affects the environment and subsequent organism-environment interactions.

Based on these principles a new research agenda can be formulated along the following lines:

- The links should be built between disparate investigative areas focusing on microbial (prokaryotic and eukaryotic), fungal, plant, animal, and ecosemiotic intelligence. This should create an empirical research programme the aim of which should be to understand principles of biological intelligence. The resulting new research programme should gradually integrate with AI research. The expected benefit for the AI research community should be better understanding of fundamental principles of biological intelligence as the eco-evolutionary context from which AI should be critically assessed.
- Understanding the concept of “information” in a biological sense is still rudimentary. The new biological intelligence framework offers an opportunity to investigate this concept hierarchically starting from bacteria and gradually building a wider picture applicable to other levels of the hierarchy. This will allow assessment of common features shared by different hierarchical levels. For example, it may be feasible to test whether various communication forms (e.g., bacterial language and plant language; see Section 4) share common features. In addition, the new framework may help understanding viruses, which pose a problem in terms of biological classification. Given their perceived dormancy outside bodies of organisms, viruses may be considered pieces of dormant biological information, which come to life upon integration into the bodies of metabolizing organisms. Thus, viruses may act in some cases as an ecological filter by prompting organisms to develop strong internal counter-measures (anti-viral defenses), which may have the effect of protecting accumulated biological information in a storage state. Viruses as “unwanted information proxies” (computer viruses) crop up in AI, suggesting a potential example of EKT.
- The fields of biomimetics and synthetic biology may benefit from some form of integration. For example, synthetic biology lacks proper appreciation of SI1 and SI2. At what point does SI1 lead to organismhood at higher levels of integration? Is this an example of SI2?
- Investigation of organism-environment cybernetics can help identify potential solutions to ecological problems highlighted by climate change and mass species extinction.

Taken together, this paper represents an attempt to revamp EEM principles and adapt them to facilitate better integration with empirical research.

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