Back to the future: Reintegrating biology to understand how past eco-evolutionary change can predict future outcomes

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Summary:

The last two decades have been characterized by an exponential growth in computational and experimental methodologies to produce detailed analyses of the biosphere. However, most of these analyses are still domain-specific, with little integration among sub-fields. This traditional approach to science hinders our ability to identify common eco-evolutionary patterns that are shared by many species and that can be interpreted to model biological systems' responses to current and future environmental challenges. To overcome this narrow vision of life, we envision future, highly collaborative projects that will be rooted in the synergy of approaches, datasets, and discoveries from all fields of biology and beyond. Starting from currently available knowledge, we propose an integration of current information that is scattered among databases and other resources and promote the development of a common language that will allow the use of these data across fields. Using these new, integrated resources, we discuss some examples of future projects that will explore the predictive aspect of eco-evolutionary studies. We expect that the potential impact of this integrative approach to understand Earth's biosphere will be large for humans specifically (e.g., counteract human-driven climate change) and for the environment in general (e.g., preservation of biodiversity) and will also lead into a new institutional awareness of the importance of interdisciplinary training for researchers of all levels (from students to faculty).

Glossary of Terms:

Biodiversity - The variability among living organisms including variation in genetic, phenotypic, phylogenetic, and functional attributes, as well as changes in abundance and distribution over time and space within and among species, biological communities and ecosystems.

Eco-evolutionary dynamics - The web of interactions between ecological and evolutionary processes.

Novel ecosystems - System of abiotic, biotic and social components (and their interactions) that, by virtue of human influence, differs from those that prevailed historically.

Interactome- the myriad interconnections between biological processes at all scales of life

Tree of life - Phylogenetic representation of all known organisms that shows species relationships based on genetic similarities.

INTRODUCTION

Harnessing the predictive power of evolution

During the last few decades, biologists have made remarkable progress in understanding the rules of life. The unprecedented availability of new biological data has led to an improved understanding of the complex interplay of evolutionary mechanisms at various scales of life, from molecules to ecosystems, and at different timescales, from rapid adaptive responses over months or years to evolutionary divergence at the scale of tens of million years. Increasing evidence shows the potential for rapid evolutionary changes to affect ecosystems while the slow buildup of genetic variability provides the raw material for organismal and ecosystem responses (Lankau, 2011). Despite this improved knowledge, large gaps still remain in our understanding of the connection between genetic innovation and phenotypic evolution and how evolution responds to environmental pressures. This has led to a suboptimal utilization of this knowledge to benefit society, preserve ecosystems, and manage our world.

A key step to transform evolutionary concepts into applicable guidelines is to integrate all biological and time scales of evolution into a unified view of the connection between biological changes and innovations. To achieve this, we propose harnessing our current understanding of evolutionary processes to develop models that can successfully predict future evolutionary outcomes. This will require an expansion of our framework to study evolution, including processes such as genetic drift, epigenetic effects, and plasticity in phenotypes. It also requires understanding the role of humans as agents of evolutionary change. By understanding how genomes, individuals, populations, and ecosystems have responded to challenges in the past, we can predict responses to the likely environmental and evolutionary changes of the future. Accurate models and the ability to anticipate how evolution will play out across the scales of life has the potential for numerous, tangible benefits to human health and wellbeing, ecosystem health, biodiversity, and scientific advancements.

From an anthropogenic perspective, the ability to accurately understand and predict evolutionary changes would be transformational to humanity's interaction with the world. The interactome—the myriad interconnections between biological processes at all scales of life—could be modified to benefit humanity without the deleterious effects that current environmental manipulations (even those that have been well intended) have produced (Andrés et al., 2012). Predicting eco-evolutionary outcomes may enable us to preserve biodiversity (at genetic, organismal, and ecosystem scales), allowing us to create effective interventions for species facing extinction or to preserve specific genes for future genetic engineering. Such predictive power could, for example, be used to mitigate the predicted impacts of climate change on human food supplies by preventing crop failures and reduced crop productivity, or the crashing of marine food sources (Hoegh-Guldberg et al., 2018). This understanding could allow us to engineer functional, self-sustaining ecosystems, allowing remediation of debilitated environments, colonization of new worlds, or alteration of biological dynamics to reduce disease transmission.

Recent transformations in biology facilitate eco-evolutionary modeling

Creating a predictive framework of biology is timely as our world is currently in a state of rapid change. Humans have been modifying the environment for millennia but it is only over the last two centuries that anthropogenically induced alterations have become prevalent across the world, with documented impacts on natural systems (Boivin et al., 2016). Climate change is likely the most well known example and is expected to lead to massive loss of biodiversity in the coming decades (Hoegh-Guldberg et al., 2018). Humans have also drastically changed both terrestrial and marine landscapes directly, through deforestation, conversion of natural lands into agricultural areas, pollution (e.g., hazardous waste sites), and accumulated refuse (e.g., ocean garbage patches). Global urbanization represents a major transition that might accelerate evolutionary change and potential ecosystem feedback. On smaller biological scales, humans have altered systems by introducing chemicals into the environment, such as the release of pesticides or neuroendocrine disruptors that can influence cellular level processes (Kabir et al., 2015). We can expect that the scale and rate of changes we are currently experiencing will result in widespread and innovative evolutionary changes in the near future. An integrated approach to modeling and predicting future outcomes will allow humans to harness the knowledge of past evolutionary events to predict potential future outcomes and, possibly, influence them in directions that will benefit human societies and the planet's biosphere.

Our current and expanding tools in biology have made the development of sophisticated models from large-scale datasets more feasible. Advances in massive '-omics' datasets (e.g., genomics, transcriptomics, proteomics, metabolomics, etc.) have enabled modeling from subcellular to organismal and macroevolutionary scale, while the increasing centralization and accessibility of museum specimens, geolocation data, and ethnobotanical knowledge have facilitated similar capacity from the organismal to the ecosystem scales. Mass data collection mechanisms such as citizen science, high-throughput phenotyping techniques (e.g., remote sensing, 3D scanning, microCT) and automated biologging have also rapidly increased our knowledge of biological systems. These innovations have been paired with an exponentially increasing computational capacity to store and statistically analyze these 'big' data. These recent scientific transformations facilitate the use of a large-scale, model-based approach to predict future eco-evolutionary outcomes from past events.

Emerging models of eco-evolutionary dynamics can provide a powerful framework to identify key mechanisms linking ecology and evolution, and predict eco-evolutionary outcomes under alternative future scenarios. However, current models are still limited and lack important mechanisms that influence the responses of communities to environmental change such as demographic, dispersal, evolution, and species interactions (Urban et al., 2012; De Meester et al., 2018). They are also limited in representing interactions across space and the complex local-regional dynamics of metacommunities (Govaert et al., 2019). Furthermore, current models make simple assumptions about human agency and the interactions with other drivers of change.

Creating functional models to predict evolutionary outcomes will require expertise spanning the sub-fields of biology. This includes uniting ecology and evolution to ask questions across evolutionary time scales, from population dynamics to lineage diversification (McGill et al., 2019), while supporting the analysis of these datasets with the expertise of theoretical, statistical, and computational biologists. The scales of life are intricately interconnected, where changes at a molecular level can have consequential impacts on scales up to individual organisms and ecosystems. Likewise, changes at the ecosystem scale can have top-down impacts on smaller scales, such as cellular or genetic processes of an organism. In our increasingly human-dominated world, such models will need to fully integrate coupled human-natural system dynamics. Creating holistic models to comprehensively predict evolution, and even engineer biological systems, will necessitate integrating knowledge across all sub-disciplines, and enhance our ability to translate eco-evolutionary effects across the scales of life.

Key barriers and challenges that will need to be overcome

The traditional insular approach to scientific investigation is now posing a significant limitation on our ability to connect information across disciplines. Barriers in communication (e.g., terminology usage) and in practices to share data (e.g., databases) are compounded by a predominantly field-specific educational training that does not often allow for the development of an integrated vision of biological evolution at multiple scales. Despite the recent development in large, integrated databases, often times datasets remain scattered in large and small databases, on personal websites with no guarantee of long term access, are only “available upon reasonable request”, and are often without proper documentation of metadata. Incentives to encourage individual researchers to properly archive data with common standards need to be further developed. Such practice should be the norm of all subdisciplines to enable a common dialog. For example, the Timetree database (timetree.org) combines high-level information from the geosciences world (e.g., luminosity, carbon dioxide levels) with phylogenetics and evolutionary concepts to provide a user-friendly picture of Earth at a given point in time. There is great potential to create reintegrated databases such as Timetree, for example merging geological data, paleontological data, with information in museum collections, or connecting phenotype and genetic innovations through time.

Recent fields, such as astrobiology, that are inherently interdisciplinary, have started addressing the issues of bringing together subdisciplines with new training models driven by a shift in vision from detailed-oriented to big-picture focused. For example, a strong emphasis is placed on developing communication skills for audiences outside of one's field of study by reducing the complexities of each field to general trends. These efforts create a general basis of understanding across fields that can then be expanded into the unique strengths and challenges of each research area. There are many steps to achieve before reaching an integrated vision of biology but an initial one could be to integrate datasets with information across fields and provide easy-to-access explanations of the meaning of each dataset.

As science becomes more global, language and cultural barriers in communicating science emerge not only across subdisciplines, but also across scientists trained in different languages and cultural settings. In turn, accessing scientific literature and resources in less-funded regions and institutions pose additional barriers to effective scientific communication. Modern technology has the huge potential to democratize scientific information through automated translation, open source databases/computer code/publications, and online training in both language skills and domain-specific scientific knowledges.

Intent of this vision document

We intend for this vision, and any of its realized products, to be disseminated as broadly as possible, both within and outside the scientific community. Modeling future evolutionary outcomes will require expertise across a variety of disciplines. Participation by biologists of all stripes--ecologists, evolutionary biologists, paleontologists, sociobiologists, and 'omics' researchers, as well as the funding agencies supporting these scientists-- will be crucial to generating the needed data, and data repositories, to supply sophisticated and accurate models. Bioinformaticians, mathematical modelers, and computational scientists will be needed to generate the models and predict future outcomes. Due to potential societal impacts, ethicists, cultural leaders, and politicians should be involved in harnessing models to engineer new biological systems. Discussions would ideally play out over a wide audience, amongst scientists, resource management experts, and community stakeholders that will be impacted by the 'real-world' applications of this new biological potential.

We have structured our vision for the biological sciences' path forward in using past and present data to inform predictions of future eco-evolutionary changes by covering short, medium, and long term objectives. Short-term targets utilize existing data sets and observational or experimental set-ups to better understand biological responses to environmental changes. Medium-term activities are predictive and will require the development of integrative models. Long-term goals require collaborative, repeated projects across the globe toward influencing ecosystems to remain resilient to further change. Each of these objectives will both impact and be impacted by human nature and activities so that we must consider the needed resources for each step and their implications on society.

SHORT-TERM OBJECTIVES: Using current resources to understand how biological systems respond to environmental changes.

Earth's ecosystems are experiencing a profound transition. Human-driven alterations to biological systems, through processes such as urbanization and climate change, are only the latest example of strong selective pressures that organisms have been facing for 4 billion years of evolution. Whether it be disruptions in physiological processes, loss of genetic diversity within populations, loss of individuals within populations, species extirpation resulting in decreased species diversity within ecosystems or other challenges, ecosystems have periodically faced, throughout time, loss in productivity and resilience that have resulted in often dramatic changes in the structure of the ecosystems themselves. Understanding how biological systems are responding or have responded in the past to changing environmental conditions will allow us to understand the key factors maintaining ecosystem function and evolutionary potential. This knowledge is key to understand past and present ecosystem changes, predict possible future modifications, and, possibly, intervene to protect the viability of our planet. There are a number of questions that will aid in our understanding of the mechanisms that maintain biological resilience that can be explored with resources currently available to the research community.

Key questions that can currently be addressed

How does environmental change alter behavioral responses?

Novel tracking and monitoring systems are making it possible to simultaneously track the movement of hundreds of animals and whole ecological communities of relatively large taxa. These systems also allow data collection on a number of physiological parameters and behavioral states (Kays et al., 2015; Warne et al., 2019). Future miniaturization and refinement of these technologies can be used to comprehensively study ever smaller taxa such as insects and other invertebrates in both terrestrial and aquatic/marine systems. Increasing accuracy and data storage capacity of data loggers and multimedia recording devices is also making it possible for a tremendous amount of data being remotely and constantly collected by an array of loggers, the spatial extent of which is generally only limited by the number of loggers that can be acquired and safely deployed. Machine learning approaches such as artificial neural networks are advancing our ability to rapidly and efficiently extract and analyze behavioral data from these big data projects. A combination of advanced animal tracking technology and machine learning is already enabling scientists to understand and predict complex behaviors such as schooling in fish and other group-living animals (Berdahl et al., 2018; Zador, 2019). Broadening the scope of these studies to multi-species, multi-community and eventually a whole ecosystem level approach will uncover the importance of behavioral ecology in driving ecosystems. Similar efforts are also starting to appear in the microbial world where genetic networks are being integrated into mathematical frameworks to predict behavioral responses to environmental stimuli (Tagkopoulos et al., 2008; Baskerville et al., 2018).

Which mechanisms drive species interactions?

At present, most studies of species interactions are restricted to modeling a handful of species at a time. With the advent of algorithms developed for social network analyses and advanced tracking technologies, more and more species can be looped into their interconnected networks, for instance by interpreting interactions from radiotracking data even when animals are not directly observed (Shizuka and Johnson, 2019). An important current challenge is to layer behavioral interactions across taxa into these networks to understand the motives behind the interactions and the nodes that form among individuals or taxa in the social networks (Papageorgiou et al., 2019). For example, simultaneous tracking and monitoring of multiple taxa can reveal mechanisms such as predation, parasitism, frugivory, pollination, and competition that may be driving strong associations among taxa. Comprehensive networks that incorporate all "macro" organisms in a relatively species poor ecosystem may be an important first step towards assembling interactomes for increasingly complex communities. Taking these "bird's-eye" views of potential species interactions may highlight species interactions that need to be more closely observed or ones that may reveal important interactions for human welfare, such as unknown links among taxa that drive disease transmission.

Are evolutionary processes shared within and among species?

Within the subfields of biology, evolutionary processes at the macro- and micro-evolutionary level are often analyzed independently. While part of this separation is rooted in the origins of comparative analyses that initially were based on phenotypically visible characters available only for multicellular species, a unified vision of macro- and micro- evolution has been hard to reach despite the widespread and shared use in both fields of molecular data in the past three decades. This is partly due to the different assumptions and analytical methods commonly employed by macro- vs. micro-evolutionary analyses. Macroevolutionary research often assume species being a homogeneous entity, and speciation is an equal split of the parental species. However, microevolutionary patterns and processes, such as metapopulation structure, may leave lasting legacy shaping long-term patterns of diversification. A second example is that genetic exchange beyond speciation, such as introgression/reticulate evolution/horizontal gene transfer, are often considered at the microevolutionary scale but rarely so at the macroevolutionary scale. The analytical frameworks designed to track phylogenetic networks are still in their infancy. Thus, supporting and encouraging the current effort to unify macro- and micro- evolutionary processes should be a fundamental step towards a reintegrated view of biology and a necessary paradigm shift that will allow us to create more comprehensive models for evolutionary predictions at any scale of life.

How are trait changes across time and space related across branches of the tree of life?

Traditionally evolutionary mechanisms and hypotheses have been developed independently for the multicellular and the unicellular world. When transposed onto the Tree of Life, this means that some branches of the tree are expected to evolve with mechanisms different from other branches, primarily pinning multicellular eukaryotes *vs.* the microbial world (eukaryotes and prokaryotes). The perceived difference in mechanisms is also driven by the different timescales of evolution of macro *vs*. micro organisms that are allowing in-depth experimental evolution studies for one (micro-) but rarely for the other (macro-organisms) (Bell, 2016). Moreover, existing macroevolutionary modeling studies often rely on singular events that lack statistical power (Uyeda et al., 2018) and that often capture superficial associations, and lack mechanistic interpretation. Work to view these macroevolutionary associations as starting points to generate hypotheses and seek mechanistic explanations (perhaps working with geneticist and ecologists for manipulated experiments), will eventually generate more nuanced models that have more reliable predictive powers. This approach is being used for microorganisms that are easier to manipulate in an experimental setting but comparisons of the identified mechanisms in macro- and micro- organisms is still lacking.

Despite this separation, there is little evidence that the most basic evolutionary mechanisms, those at the molecular level, are different between the two worlds. Indeed, even the common definition of species using the biological species concept (Mayr, 1942), that has been traditionally applied to sexually reproducing multicellular organisms, is now starting to be considered, with some variations in terminology, for the unicellular world. For example, the concept of gene flow, that the biological species concept is based on, could be applied to any branch of the tree of life if it is expanded to consider both vertical and horizontal gene acquisitions (Bobay and Ochman, 2018; Moldovan and Gelfand, 2018). However, it remains to be seen how universal are the rules that govern the accumulation of changes. Considerations based on past drastic changes, such as those during the Cenozoic, have revealed common trends across multiple species within mammals but it is not known yet if similar trends would be applicable to other species as well (Blois and Hadly, 2009). It is likely that, at a very broad scale, some responses shared across the tree of life will eventually be identified, such as variations in energy input/output, characters tradeoff for survival, dispersal, and reproduction, or common phenotypic responses to similar global changes.

Existing resources to examine past and current responses to environmental change

Museum and herbarium collections

Museums and herbariums provide a wealth of information regarding our planet's ecological past (Lendemer et al., 2019). The digitization of many of the collections has also increase their access to researchers across the globe. These hundreds of millions of plant, fungi and animal specimens can provide snap-shots of community structure within a given ecosystem, population characteristics across environmental gradients, and provide clues into how populations within each environment have changed over time. Herbarium collections can be used to examine changes in morphology, phenology, physiology, and genetics within populations (e.g., Willis et al., 2017; MacLean et al., 2018), as well as explore how communities may have shifted overtime within specific ecosystems (Meineke et al., 2018). They can also provide information on how human driven land use alters populations. A recent study by DeLeo et al. (2019) used museum specimens collected over an approximately 200 year period to examine changes in *Arabidopsis thaliana* (a flowering plant) populations within their native ranges. The temporal changes within these populations that were consistent with changes in environmental factors, including land use changes and temperature shifts. Specimens can also be used to follow environmental changes over time. Avian populations have been used to track the rise and fall in black soot pollution within the U.S. industrial complex as manufacturing within this region began to grow in the late 1800's - 1920's and then became more regulated in the mid-1950's as the air pollution control act was implemented (Dubay and Fuldner, 2017). Museums collections can also provide information about shifts in community biodiversity and species interactions (Meineke et al., 2018). Plant-pollinator interactions have been examined using insect and plant collections to examine how relationships have been altered with increasing temperatures and urbanization (Meineke and Davies, 2018). Collections can also provide information regarding levels of biodiversity that we did not even realize existed (Drew et al., 2013). By examining museum artifacts (shark-toothed weapons) at the Natural History Museum in Washington, D.C., Drew et al. (2013) identified two species of sharks in the Gilbertese Islands that were present during the late 19th century, yet were never reported in any taxonomic history for that area.

In order to form robust predictive models for assessing future eco-evolutionary dynamics, a key question that needs to be addressed is whether there are variables that elicit common biological responses to abrupt and significant environmental perturbations. In other words, do taxa respond in similar ways to environmental changes, and how can we quantify those responses? We can begin to explore this question by examining the fossil record. With biologists working jointly with geologists, paleontologists, anthropologists and climatologist, we can couple the fossil record with global climate data to ask whether we see similar patterns of change across taxa globally and how these changes might be tied to specific climate conditions. If there are general patterns of change, be it genetic (e.g., changes in genetic diversity), morphological (e.g., body size: Weeks et al., in press) or behavioral (e.g., migration pattern), do these changes break down at a certain taxonomic-level or given life history? How much of an influence does evolutionary history or geography have on this similarity? Similar questions have been addressed in specific taxa (i.e., mammals: Blois and Hadly 2009) but applying this across different branches of the tree of life, will provide a more robust analysis for future predictive work.

Not only can we look at macroevolutionary changes using these collection but recent advances in ancient and fossil DNA and protein extraction and sequencing techniques allow researchers to use museum collections to examine microevolutionary processes. Sufficient DNA for genome sequencing may persist in biominerals for hundreds of thousands of years (Orlando, 2013) and allow reconstruction of population dynamics (e.g., Orlando, 2002). Additionally, protein preservation, particularly in vertebrate bone can resolve phylogenetic status of long-deceased taxa including dinosaurs species (Schroeter, 2017). Headway is beginning to be made in comparable analyses of invertebrates (e.g., Marin, 2018). However, as invertebrate biominerals contain much amounts of organic matter, extracting sufficient undegraded material from fossil invertebrates has proven difficult. Because these collections can also represent a type of time-series data, researchers can address important questions using these molecular tools that are needed to predict eco-evolutionary dynamic models. Examples include the relative contribution of genetic versus plastic adaptive responses to environmental change (Lang et al., 2019), and what genetic changes are important to developing resistance (Less et al., 2011).

Indigenous knowledge

Knowledge of indigenous groups around the globe represents an important resource of historic population data that is under-utilized by researchers. These communities often have information on ecological communities and methods for sustainable use practices that are missed with current research practices. With this information, we can further piece together historic species distribution, range expansions, potential human-mediated dispersal patterns, community biodiversity, and how these patterns have been altered with our changing ecological landscape. While some current databases containing this information exist, such as the Native American Ethnobotany Database, including local indigenous groups directly into these research practices will gain new and improved insight into ways of designing and maintaining sustainable populations. By increasing the diversity of voices in STEM, for example, through programs such as UCLA's Center for Diverse Leadership in Science with a sub-focus on indigenous people and First Nations: https://www.ioes.ucla.edu/project/environmental-justice-and-first-nations), we will gain a better understanding of how to address these important questions.

Long term ecological research stations

NSF-funded long term ecological research (LTER) sites serve a unique purpose in providing a window into seasonal and annual variability and stability of ecosystem processes and interactions over decadal time scales for a well-defined geographic location (https://lternet.edu; Gosz, 2010). The first LTERs were established in 1980, and the 28 extant sites fulfill NSF's goals of advancing scientific knowledge and positively benefiting society. They also provide a trove of nearly 40 years' worth of data in addition to the infrastructure to collect new, highly targeted data to address eco-evolutionary dynamics and to test predictive models. Beyond monitoring, LTERs incorporate smaller-scale *in situ* environmental manipulations to test outcomes of predicted future conditions, such as the effects of ocean acidification on calcification rates in corals (e.g., Carpenter, 2018; Edmunds, 2019).

Individual LTERs focus on ecosystems spanning the tropics (Moorea LTER) to the poles (Arctic Tundra, Palmer Station, and McMurdo Station LTERs). Additionally, Urban Long-Term Research Area Exploratory (ULTRA-EX) grants, partnerships between NSF, the United States Department of Agriculture's Forest Service, researchers, and local stakeholders have been awarded for 29 studies since 2009; these projects complement the Central Arizona-Phoenix and Baltimore Ecosystem Study urban LTERs. Recognizing the utility of these permanent urban research sites, NSF's Division of Environmental Biology will be accepting proposals for new urban LTER sites in 2020. The multitude of ecosystems studied as LTERs, both minimally distrubed historical systems and novel ones emerging as cities expand in number and size, and the time over which they are studied may allow for better prediction of system process resilience in the face of climate change (Kratz, 2003).

MEDIUM-TERM OBJECTIVES: Projects that require the integration of multiple resources from research groups with different expertise (i.e., synthesis centers).

Potential questions to be addressed

What is the parameter space of evolution?

A long-term view of how the biosphere of Earth changed over time has the power of informing us on the “viable” paths life has taken and might take in the future. Whether driven by random chance or by adaptive responses, the amount of genetic and phenotypic combinations potentially accessible to life (from all possible combinations of the four nucleotides in the DNA of a species to the possible ecological interactions of multiple species) is astronomically larger than what we have observed over our planet’s history and what we can observe today. This suggests that, through deterministic processes such as selection and stochastic processes, some evolutionary paths may be now unavailable (or highly unlikely) to future species (Greenbury et al., 2016). Knowing the parameter space that evolution used in the past can provide valuable information to predict future evolutionary paths of species, such as predicting new emerging pathogens or new species interactions within a changing ecosystem.

How does urbanization affect eco-evolutionary dynamics?

Increasing evidence shows that cities across the globe are accelerating phenotypic changes in wildlife, including animals, plants, fungi, and other organisms. Some of these changes are evolutionary (Alberti et al., 2017; Johnson and Munshi-South, 2017). In urban environments multiple selection pressures are caused by changes in habitat structure and biogeochemical processes and changes in biotic interactions. Cities also exhibit novel disturbance regimes and habitat heterogeneity. Because of the co-occurrence of multiple pressures, urban environments provide an opportunity to explore whether organisms are adapting to specific pressures or their combined effect (Alberti, 2015).

Interacting effects of urbanization and climate change may also have important consequences on eco-evolutionary dynamics. Climate change and global urbanization are two major drivers that will determine future biodiversity. Their interplay controls the dynamics between adaptation, dispersal, and species interactions. Complex feedback between multiple drivers of eco-evolutionary change are difficult to tackle with current eco-evolutionary models. For example, different patterns of urbanization may affect the priority and monopolization effects resulting from climate change by modifying the spatial and temporal patterns of environmental changes. Ignoring such interactions may bias predictions. Alternative scenarios may emerge depending on the characterization of the urban and climate interplay and key assumptions on the future patterns of urbanization.

The emerging field of urban eco-evolutionary dynamics is still at its infancy. We do not know how urbanization is driving evolutionary change and its potential ecosystem feedback. Despite the remarkable progress in studying eco-evolutionary feedbacks over the last decade, empirical studies are still limited (Johnson and Munshi-South, 2017). In particular, we do not know what role human activity plays in the reciprocal interactions between ecological and evolutionary processes (Alberti et al., 2017). To achieve an understanding of how rapid global urbanization affect eco-evolutionary changes and their effects on ecosystem function we will need to consider the complex interactions eco-evolutionary dynamics of coupled human natural systems across time and space. We will also need to establish the genetic basis of these changes through the design and implementation of long-term common garden experiments across cities and regions.

Cities are microcosms of the changes that are occurring on a planetary scale, and thus provide a natural laboratory to study global human-induced eco-evolutionary dynamics. Cities also share ecological features and thus enable us to test hypotheses about the repeatability of evolution and convergence of trait changes across species. They also provide an opportunity to determine how multiple selective pressures operating across space and time and their interactions generate divergent outcomes. Designing global eco-evolutionary experiments across cities will require a new formidable collaboration across disciplines and a new partnership among research teams across different world regions. Yet its outcome could transform biological science and catalyze a new collaboration across scientific fields. As one example, the NSF RCN Network is currently building a large geo-referenced database of urban driven genetic and phenotypic observations across multiple taxa in diverse regions of the world (https://www.urbanecoevo.net/).

How can we harness rapidly evolving organisms for understanding eco-evolutionary dynamics?

Fast-evolving systems blur the boundary between ecology and evolution and are ideal systems for exploring the predictive power of eco-evolutionary dynamics. Given the fast evolutionary rates of viral pathogens, disease dynamics blur the boundary between ecology and evolution. In fact, disease dynamics are at the forefront of applying the predictive power of evolutionary models. For example, we are getting better at predicting which flu strings will be prevalent in the next flu season, and what are the most likely mutations. Although not 100% effective, flu vaccines are improving from year to year. A second example is combination therapy in HIV treatment that is successful in blocking some of the key evolutionary paths in HIV. Similarly, eco-evolutionary models can be applied to niche and evolution of cancer for developing better treatments.

When are novel ecosystems created and how do biological systems adapt to these new environments?

Just as climate regimes may be lost due to anthropogenic climate change over the coming decades, novel climate regimes will also likely appear (Williams, 2007). These new climate states, not presently found at their current locations, represent new sources of interactions between species and their environments with predicted species loss or gain in specific locations and establishment of novel ecosystems. Scenarios of higher CO_2 emissions are predicted to result in greater area covered by these novel climates by the end of the century relative to scenarios in which CO_2 emissions are minimized, such as countries meeting their intended nationally determined contributions from the 2015 Paris Agreement (e.g., Williams, 2007; Mahoney, 2017).

Novel ecosystems are different from past or present systems in biological and abiotic composition as well as in function (Perring, 2013). The relatively rapid rate of change from a historical ecosystem to a novel one is linked to human action, but maintenance of new ecosystems is not dependent on further human intervention (Hobbs, 2006). Novel ecosystems can vary widely in construction and scale. They can be the result of large-scale urbanization leading to new species interactions (as detailed in other areas of this paper). The creation of new habitats can also be microscopic, such as through the colonization of bacteria and algae on microplastic pollution. The 'plastisphere', or plastics marine debris with associated microbial communities (Zettler, 2013), may represent a novel marine ecosystem with no historical analog under any climate conditions. Due to slow rates of plastic degradation and persistence of microplastics across the full water column of the ocean (Andrady, 2017), once formed, individual plastispheres may exist for centuries or longer. As microbes within these ecosystems are consumed by higher organisms such as filter feeders, the microplastics themselves may be transferred to higher trophic levels with potential negative effects up the trophic scale (Galloway, 2017). These plastics also have the potential to sequester additional toxins, thus increasing the stress on organisms that consume them (Cole et al., 2011). Many questions remain surrounding plastispheres including the mechanisms of their establishment, their duration, and their ultimate function in the larger ocean system. Thus, not only is it important for us to understand how organisms are responding in their current environment, but as humans continue to alter the environmental landscape, we need to be able to predict the novel ecosystems that may be created.

Potential new resources to be created

Shared databases

Reintegration of biology requires that scientists move from investigator-specific databases of limited utility to those allowing a large number of researchers (and non-scientists) to access a wider and more complex set of data (Porter, 2018). One prominent example of the utility of large, international databases is the consortia that have been sharing cancer genetics information (e.g., International Cancer Genome Consortium, 2010), with the downstream results of more efficient and effective targeted cancer drug development (Santos, 2017). Further, 'open data' and 'open science' are proposed to improve scientific output and speed (Reichmann, 2011).

A variety of extensive databases presently exist to catalog information on genetic and proteomic data (e.g., NCBI), biological collections (e.g., iDigBio), biological, chemical, and physical oceanographic data (e.g., BCO-DMO), and botanical data (e.g., BIEN) among other datasets. However, the utility of these databases, or even knowledge of their existence, may be limited to sub-fields within biology and they are often not included in online database networks. We therefore propose the creation of a centralized directory of such databases, which would be beneficial to efforts to reintegrate biology and which is easily achievable. Efforts to compile large-scale, searchable resources are already underway within the private sector (e.g., Google

Dataset Search) and could be leveraged to include datasets and databases of multiple scientific fields. Additionally, initiatives to facilitate the storage and transfer of big datasets have started to appear (e.g., OSIRIS). While these are only first steps, they are the core of what could become larger initiatives that will provide platforms to share scientific knowledge across fields and across the world.

Novel modeling approaches to integrate ‘eco’ and ‘evo’ across the scales of life

Reintegrating biology will provide the opportunity to develop novel modeling approaches to predict eco-evolutionary dynamics. Current eco-evolutionary models provide a useful framework to begin to investigate interactions between ecological and evolutionary mechanisms. Yet they lack important mechanisms that mediate organisms’ responses such as demographics, dispersal, evolution and species interactions. These models also disregard cross-scale spatial and temporal interactions. To incorporate the complex eco-evolutionary dynamics, we need to develop spatial-explicit dynamic individual based models, representing populations, species, and higher taxonomic groups, as well as how they interact with biotic and abiotic environments in an evolving meta-community framework.

Current modeling endeavors are at variable stages of development across biological systems. To build predictive models will require raising all systems to a sufficient level of complexity. For instance, while we can model ecosystem biomass based on temperature and rainfall, and often can predict thermal limits for individual organisms, we have a less complete understanding of community-level inter-species interactions at varying temperatures. Likewise, we can map out entire genomes, as well as measure individual organisms’ phenotypes, but a complete understanding of how genotype, together with complex epigenetics and environmental factors together affect phenotypes has proven more difficult to develop. Filling these gaps for biological systems that lack sufficient data or theoretical understanding is an important first step for generating models with predictive power.

Once these gaps have been filled, integration across the scales of life will be needed. An improved understanding of how the scales of life, from molecules to ecosystems, interact with one another will require greater collaboration between biological sub-disciplines. Drawing on the above example, these inter-scale dynamics may include how animals’ physiological thermal limits impact their community level interactions, or vice versa, understanding how community level dynamics such as competition impact animals’ response to temperature changes. Similarly, models must include a thorough representation of the interactions between biotic and abiotic factors. These will become particularly important as we move towards implementing models’ predictive capacity. Engineering new ecosystems will require fine-tuning of the impact of abiotic factors on life, for example soil chemistry’s impact on plant growth, or the effects of ocean acidification on marine life. Increasing our ability to comprehensively model the dynamic nature of biological systems across the scales of life will be essential to creating a meta-community framework for predictions.

Lastly, eco-evolutionary models must incorporate the spatial and temporal complexity of life. Many biological systems show a high degree of spatial heterogeneity—from clumped plant distributions or microclimates utilized by animals to localized differences in genes and gene expression within an organism (Porter et al., 2010; Wang et al., 2010; Yizhak et al., 2019). Predictive models will need mechanisms to factor in this spatial heterogeneity, as well as the interactions between space and time. Abiotic temporal effects, from daily cycles (e.g. light/dark or temperature cycles), yearly seasons (e.g. summer/winter, wet/dry season), to multi-year phenomena (e.g., El Niño/La Niña weather patterns) have dynamic effects on biological systems. Biological processes are mutable across temporal scales as well, as seen in predator-prey population cycles, ecological succession, or the progression of disease outbreaks. Designing models that include explicit spatial and temporal dynamics is integral to replicating the complexity of life in a predictive framework.

Trait shifts across diverse taxa are likely a result of both shifts in allele frequencies (evolution) and phenotypic plasticity. One of the key challenges in eco-evolutionary dynamics involves the assessment of the relative contribution of evolution, ecology and their interaction. Eco-evolutionary partition metrics can help quantify the contributions of ecology and evolution to observed trait change (Govaert et al., 2016) to separate the contribution of phenotypic plasticity and evolutionary change. Such metrics have been recently extended to partition community trait change in a temporal setting into effects of plasticity, evolution, species sorting and eco-evolutionary interactions.

Developing novel integrated models that account for the complexity of coupled eco-evolutionary dynamics is necessary to improve predictions of biodiversity under rapid environmental change. Improving such predictions will involve designing additional long-term experiments to test our predictions with empirical observations.

Replicated experiments at different sites across the global scale

A number of large-scale ecological experiments are carried out by researchers in many sites across the world using a mutually agreed set of protocols, with coordinated data collecting schemes. These experiments have the power to discover generalizable rules in these systems. Some examples of such experiments include the Forest Global Earth Observatory (ForestGEO https://forestgeo.si.edu), the Long Term Ecological Research Network (LTER), and The Nutrient Network (NutNet https://nutnet.org/). Looking into the future such long-term research infrastructure and networks have the potential to continue to further our understanding of eco-evolutionary dynamics, in ways that are sometimes unexpected.

LONG-TERM OBJECTIVES: Aspiring future projects to manage and protect Earth's biosphere

A desired outcome of achieving a deep understanding of evolutionary processes over time is to use and manipulate these processes to protect and manage our planet's biosphere. With the quick advancement of biotechnologies, this once fictional goal can now be considered within our reach in the next few decades, provided that solid scientific foundations are laid. Very small steps are already being taken, for example with modifications of species fertility (e.g., mosquito vector) to reduce the incidence of some infectious diseases (e.g., malaria), but these are often unsuccessful because we are still lacking a full understanding of how biological systems react to what are perceived as challenges to their survival (Hammond et al., 2016; Flores and O'Neill, 2018; Noble et al., 2018).

Managing ecosystems for improved resilience to climate change

One of the grand ideas of implementing our vision would be to manage existing ecosystems (both natural and anthropogenic) to make them more resilient and adaptable to rapid global change. The focus should be for these ecosystems to be globally interconnected and collectively house a rich biodiversity of extant communities, species, tissues, cells, and genes, and the interactions each those have with other biological entities and their environment. Building on principles of restoration ecology, these ecosystems will include new habitats and ecological niches created by humans such as vast urbanized landscapes and regions of human waste accumulation in a network that maximizes the movement of genes, organisms and information across the globe. The benefits from such ecosystems would be manifold for humanity through provision of a vast range of stable/dependable ecosystem services while helping arrest current rates of global change to more near natural rates of change (as have been documented over ecological/evolutionary time) that allow for organic and cultural adaptation by both ecological communities and human societies. This execution of scientific tools at such planetary proportions will not only require significant advances in computing and data acquisition, analysis and interpretation but also a broader scientific outlook that integrates multiple fields from biochemistry to social sciences.

Understanding and applying knowledge from genomes, pathways, and adaptive strategies

Genomes of organisms on Earth not only hold a vast genetic diversity but many lineages have also convergently evolved to overcome similar eco-environmental challenges. Understanding and safe-gaurding the diversity of evolutionary pathways that lead to convergent phenotypes may be an important reason for taking a pan-genome approach for biological conservation at the whole ecosystem level. In addition to satisfying the internationally recommended goal of protecting evolutionary potential (IPBES, 2019), such a pan-genomic approach also gives us the ability to undertake bio-exploration of genes and their function which could be used to benefit humans or help make species/populations resilient to environmental change and disease. For example, genes for combatting low temperatures in high elevation grasses may be used to engineer crop species that can be planted in the highlands. Taking a broad comparative approach towards understanding the diversity of evolutionary pathways leading to the convergent phenotype of cold tolerance may offer genomic alternatives and highlight life-history trade-offs while engineering such a change in crops selecting the ideal candidate genes from the right candidate taxon.

Biological interactions at all scales of biocomplexity

Biological interactions occur within and across all scales of biocomplexity. Cross-scale interactions are poorly understood and difficult to predict. However, these interactions are crucial in maintaining the stability of biological systems. An important goal for the future is to use integrative biology to simultaneously study interactions within and across multiple scales. For example, all chemical interactions between microbes in the soil, or all behavioral interactions between macro-organisms. Going beyond an organismal approach, such studies may reveal new “keystone” interactions that maintain community stability.

New human-driven ecosystems

Human-induced environmental and land-use changes are giving rise to novel ecosystems such as highly “built-up” cityscapes, landfill sites, and large marine garbage patches. Although these novel habitats are here to stay, we could change them to increase the biodiversity they support with the hope of making them more stable and resilient. Findings from urban planning and restoration ecology will be critical in this process. These new ecosystems are crucibles of evolution. The role of an integrated biology will be to direct how these systems can be made beneficial to people who live in or near them while being rich biological communities.

Maintaining evolutionary potential

To maintain ecosystem function in a rapidly changing will require reframing conservation within an eco-evolutionary dynamic framework. Rather than maintaining habitats as they are, novel conservation strategies should aim to promote evolutionary potential through policies and principles that maintain evolutionary potential and protect genetic diversity. As highlighted in the recent IPBES Report (IPBES, 2019) “understanding and monitoring these biological evolutionary changes is as important for informed policy decisions as it is in cases of ecological change.” IPBES calls for “sustainable management strategies” designed to influence evolutionary trajectories so as to protect vulnerable species and reduce the impact of unwanted species (such as weeds, pests or pathogens).

OVERARCHING CONSIDERATIONS

Ethical considerations

An expansive, forward-looking scientific program such as this is fraught with serious ethical considerations. As we study, influence, change, and engineer ecosystems in an integrative approach, it is important to consider “who” we are doing this for. Such a broad approach will traverse multiple political, cultural and ethnic boundaries of societies that differ in cultural value systems. Quantifying proximate and ultimate costs of such a program for the world’s human population and keeping them as equitable as possible across the globe will be extremely challenging. Building consensus on what is the “right” thing to do will require communication between science, policy and social decision makers. So the execution of this research program will require significant inputs from social scientists and ethics experts.

Current funding opportunities

Below, we provide a non-exhaustive list of grants and fellowships that specifically address the integration of various biological sub-fields. This list encompasses both U.S. and internationally-focused programs at multiple career stages and those that are specifically intended to be collaborative and/or cross-disciplinary.

Grant or Fellowship	**Purpose**	**Career Stage**
NSF - Integrative Graduate Education and Research Traineeship	Promote interdisciplinary and collaborative research and education	Graduate
NSF - Postdoctoral Research Fellowships in Biology	(1) Broadening Participation of Groups Underrepresented in Biology, (2) Interdisciplinary Research Using Biological Collections, (3) National Plant Genome Initiative (NPGI) Postdoctoral Research Fellowships and (4) Integrative Research Investigating the Rules of Life Governing Interactions Between Genomes, Environment and Phenotypes.	Postdoctoral
NASA Astrobiology Early Career Collaboration Award	Encourages circulation between two or more laboratories supported by the NASA Astrobiology Program	Undergraduate through junior faculty
NSF - Advances in Biological Informatics	Development of bioinformatic tools	Tenure and non-tenure track researchers
NSF - Accelerating Research through International Network-to-Network Collaborations (AccelNet)	Enable multi-team international collaborations (NSF-wide)	Tenure and non-tenure track researchers
NSF - Long-Term Ecological Research: New Urban Site	Interaction of human activities in urban settings with natural processes to determine ecological outcomes	Tenure and non-tenure track researchers

NSF - Biological Integration Institutes	Integration of biological disciplines	Tenure and non-tenure track researchers
NSF - Rules of Life	Understanding fundamental biological processes across scales	Tenure and non-tenure track researchers
Human Frontier Science Program - Research Grants	Funds basic research into fundamental biological processes across nationality and discipline	Tenure and non-tenure track researchers
Department of Energy - Computational Tool Development for Integrative Systems Biology Data Analysis	Develop computational approaches to integrate large, disparate data types from multiple and heterogeneous sources	Tenure and non-tenure track researchers
NASA - Research Opportunities in Space and Earth Science (Exobiology)	Supports research at the interface of biology and other natural sciences	Tenure and non-tenure track researchers

Institutional changes towards integrating subfields of biology

Student training

In order to train the next-generation of integrative biologists, student training should focus less on memorization and instead on big picture, inquiry-driven approaches, and the ability to research information into sub-disciplines. Specific measurements include flexibility for undergraduate students to create their own core curriculum, cross disciplinary graduate programs, and courses that effectively create interdisciplinary dialog. To further facilitate cross-disciplinary dialog, it is beneficial to actively engage with other STEM departments and create team-taught undergraduate and introductory graduate classes that specifically integrate scientific topics across multiple scales (biochemical, cellular, genetics, ecology, evolution) to give students a broader perspective of how these disciplines connect with one another. One such training model at the graduate level that focused on interdisciplinary learning is the Integrative Graduate Education and Research Traineeship (IGERT, http://www.igert.org/). This is a cross-disciplinary, fully supported Ph.D. program that gears toward training students to think and engage across across STEM fields. The program includes team-taught classes, and a dissertation chapter can be co-authored. However, the program is very expensive both time- and money-wise.

Funding streams & reviewer education

While the type of ‘jumpstart’ programs recently hosted by NSF are a step forward in advancing a more interdisciplinary approach to studying biological systems, there can still be resistance to including these interdisciplinary approaches in the biological community as a whole. This resistance is most acutely felt during the grant review process, when proposals are penalized for taking these types of integrative approaches. Providing funding streams to target projects that prioritize interdisciplinary questions is one approach to solving this challenge. In addition, forming integrated review panels and educating individuals serving on these panels on the review process for these streams (similar to what is required before serving as an NSF Graduate Research Fellowship Program reviewer) would improve the overall quality of the review process.

Broader impacts

With the power of predictive models for eco-evolutionary dynamics, we would be able to benefit human health in a number of ways. This would include better forecasting the spread route and prevalence of disease epidemics, and taking precautions to control the spread of infectious disease. These include developing better vaccines that target the most virulent strings of the coming season, advise people on behavioral changes that reduce the chance for getting infected, carrying out screening in major traffic hubs to prevent global pandemic, and policy decisions on travel advisory and travel ban. Similarly, more effectively predicting hotspots for drug resistance would lead to better decision making for the patient, medical workers, and public health workers. By better understanding cancer evolution and the “niche” for cancer proliferation would lead to better treatment strategies.

Predictive models of eco-evolutionary dynamics will improve our ability to secure human food resources under future rapid global changes. These models’ forecast could lead to proactive measures against invasive species and weeds that reduce crop production, develop herbicide resistance, and displace native species. These will result in policy decisions and conservation strategies for healthier, more sustainable natural as well as human-associated ecosystems including cities and agricultural fields.

Finally, the looming global change poses the need to manage ecosystems and facilitate climate resilience in both natural and artificial ecosystems, such as remediate polluted sites, sustainable crop ecosystems, and attract citizen scientists for continued monitoring of biodiversity and environmental factors such as community managed sensor networks. Perhaps eventually humans will even create novel ecosystems in space. For these reasons, understanding the natural mechanics of eco-evolutionary dynamics is critical for not only making these endeavors feasible, but also help communicating to the public (not just scientists) the value of the ability to design ecosystems.

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