

Parallel Session

Evolutionary Dynamics IV

MAJOR EVOLUTIONARY TRANSITIONS AS STRUCTURE LEARNING OF BAYESIAN BELIEF NETWORKS

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Keywords: Multilevel selection, Evolutionary transitions, Bayesian modeling, Belief networks, Structure learning.

Complexity of life forms on Earth has increased tremendously, primarily driven by subsequent hierarchical evolutionary transitions, a mechanism in which units formerly being capable of independent replication combine to form a higher-level unit of replication. Although this process has been likened to the recursive combination of pre-adapted sub-solutions in the framework of learning theory, no general mathematical formalization of this analogy has been described yet. Here we show, building on former results connecting replicator dynamics and Bayesian update, that the Darwinian evolution of hierarchical population structure under multilevel selection is equivalent to Bayesian inference in a class of Bayesian belief networks. This allows for the transfer of concepts characterizing structured probabilistic models, such as conditional independence and d-separation; here we provide their evolutionary interpretation. Furthermore, hierarchical evolutionary transitions in this framework are equivalent to learning the structure of the corresponding Bayesian belief network. Indeed, comparing the average fitness of those replicators that are participating in the transition before and after the transition is equivalent to the comparison of model evidences of the corresponding Bayesian belief networks. This mathematical equivalence might make more elaborate methods of Bayesian learning theory accessible for modeling and understanding complex, hierarchical evolutionary processes.

Parallel Session**Evolutionary Dynamics IV****CAN WE DEFINE LIFE BY HOW IT EVOLVES?**

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Keywords: Cardiac loop, Mechano-physical cell model, Left-handed helix.

Definitions of life on earth have primarily focused on the metabolic and replicative/reproductive aspects of life as well as on the origin of cells and cell types. This converges with major experiments in astrobiology and more general theories of how, and by which mechanisms life evolves. Oparin and Miller, defenders of protein-first theories, were pioneers in demonstrating the spontaneous origin of coacervates and amino-acids; the discovery of ribozymes and the structure, transcription and translation of DNA enabled scholars such as Orgel, Eigen and Gilbert to formulate gene-first theories from within Neo-Darwinian frameworks; and research on the origin of cells and cell types associates with symbiogenesis theory (Mereschkowski, Wallin, Margulis). Natural selection, symbiogenesis, and instances of “spontaneous generation” that currently run under the name of autocatalytic networks, have also been used to mark major transitions in the evolution of life on earth, and the different theoretical frameworks have in addition put forth different units and levels of evolution (ranging from replicators to holobionts). Not so much attention has been given to the fact that the recognition that different evolutionary mechanisms, together, enable the origin and evolution of life forms, also calls out for a more universal definition of the phenomenon of evolution. I define evolution as the phenomenon that occurs when units evolve at levels of an ontological hierarchy by mechanisms, I examine how this definition of evolution can inform how we define and search for life, and I further analyze how life builds biological realities.

References

- [1] Gontier, N. & Bradié, M. 2018 “Acquiring knowledge on species-specific biorealities: The applied evolutionary epistemological approach.” In: Joyce, R. Routledge Handbook of Philosophy of Biology. Routledge
- [2] Gontier, N. 2018 A Universal Scheme for Evolution: The Applied Evolutionary Epistemological Approach. In: Kolb, Vera (ed). Handbook of Astrobiology. CRCPress

- [3] Gontier, N. 2016. "Guest-Editorial Introduction: Converging Evolutionary Patterns in Life and Culture." *Evolutionary Biology* 43 (4), 427-445
- [4] Gontier, N. 2016. "Symbiogenesis, History of." In: Kliman, R.L. (ed) *Encyclopedia of Evolutionary Biology* (261-271). Amsterdam: Elsevier <http://dx.doi.org/10.1016/b978-0-12-800049-6.00016-0>
- [5] Gontier, N. 2016. "Symbiosis, History of." In: Kliman, R.L. (ed) *Encyclopedia of Evolutionary Biology* (272-281). Amsterdam: Elsevier. <http://dx.doi.org/10.1016/b978-0-12-800049-6.00015-9>
- [6] Serrelli E, Gontier N, eds. 2015. *Macroevolution*. Dordrecht, Springer. Gontier, N, ed. 2016. *Reticulate Evolution*. Dordrecht, Springer.
- [7] Gontier, N. 2007. "Universal symbiogenesis: a genuine alternative to universal selectionist accounts." *Symbiosis* 44: 167-181
- [8] Gontier, N. 2004 *De oorsprong en evolutie van leven*. (The origin and evolution of life). Brussels (BE), VUBPress (In Dutch)

Parallel Session**Evolutionary Dynamics IV****MODELLING THE EVOLUTION OF GENERALIST VS. SPECIALIST PATHOGENS SPREADING ON A CLADE OF HOST SPECIES**

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Keywords: Coevolution, Host, Parasite, Competition, Phylogeny.

In recent decades, the rates of emerging infectious disease have increased significantly. Changing global conditions, rapid population growth and changing species distributions have all contributed to increasing the opportunity for host-shift events. While environmental factors have increased the rates at which host-shift events occur, the best predictor for a successful host-shift is often the phylogenetic distance between potential host species. The influence of host phylogenetic relationships on host-shift success is a result of parasites being limited to host species where their existing adaptations are applicable, with closely related host species being more likely to represent a compatible environment for shifting parasites. The ability of parasites to switch between species can vary depending on the species involved. Specialist parasites are highly restricted in their range of potential host species, while generalist parasites have a greater ability to shift between comparatively distantly related host species. Although attempts have been made to understand how parasites spread between host species, none investigate how specialism and generalism influence long-term, clade-wide evolutionary dynamics in a competitive context. This study explored competition between specialist and generalist parasites through the use of both deterministic mathematical models (ODEs) and stochastic computer simulations. An epidemiological analysis of the system ignoring the phylogenetic distance between species concluded that ultimately only one parasite lineage can remain stable on a host tree. As epidemiological analysis could not incorporate the phylogenetic distance between a dynamically changing host tree, simulations were used to provide a more realistic view of parasite switching between hosts over time. Generalist parasites were found to be more competitively successful in the initial stages of invading a host clade, as they were able to quickly spread across host phylogenetic trees. Specialist parasites were more susceptible to early lineage extinction when competing against generalists. However, in the long-term, surviving specialists slowly replaced generalist parasites on the host tree. Therefore, the success of a parasitic strategy can depend on the time scale being examined.

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Evolutionary Dynamics IV

WHEN DOES AN INVASION OF A NOVEL TRAIT IMPLY FIXATION?

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Keyword: Invasion implies substitution.

The focus of much of evolutionary biology is to identify the role of selection, in particular its strength and direction. Selection is said to be directional if an invasion of a novel phenotype implies that it fixes in the population in the sense that it substitutes its ancestral phenotype. Interestingly, when the invader and ancestor have a closely similar phenotype, meaning that the selection is effectively weak, such calculations can often be made exact under very general conditions - successful invasion generically implies fixation. Surprisingly, however, existing theory is divided according to the specific biological focus in mind with no up to date model that would unify the disparate results and biological interpretation. Here, by reviewing the existing literature and providing novel unpublished results, we outline the conditions on the genetic, spatial, demographic and ecological structure for which the outcome of invasion can be calculated. We discuss when the direction of selection can be expressed by a quantity that is proportional to a frequency-independent selection gradient, what role demographic stochasticity and reproductive values play, and then provide challenges for future research.

Parallel Session

Evolutionary Dynamics IV

PREDICTABILITY OF LONG-TERM, BUT NOT SHORT-TERM PHENOTYPIC EVOLUTION OF DROSOPHILA

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Keywords: Evolution, Predictability, Adaptation.

Combining real-time evolution experiments with a theoretical framework is a powerful approach to create and test expectations on the repeatability and predictability of evolution. Several studies have focused on this issue and have shown that repeatability of phenotypic evolution is generally pervasive. However, an important question that remains unanswered is how much short-term evolution can tell us about evolution in the long-term, and which one of these is easier to predict. We founded 5 new laboratory populations of *Drosophila subobscura* from two natural populations in Sintra and Arrábida, Portugal, in 3 different years (1998, 2001, 2005). We then followed the real-time evolution of life history and physiological traits in the 15 replicated populations throughout adaptation to the laboratory. Here, we compare the short and long-term (20 and 60 generations, respectively) evolutionary dynamics of these populations. We have previously shown⁴ that evolutionary contingencies during short-term adaptation were most prevalent for traits more loosely related with fitness, consistent with less selective pressure on these. Curiously, when performing the long-term analysis, we found differences in evolutionary rate for several traits, independently of their relationship to fitness. When analyzing the dependence of the overall evolutionary rate on the initial differentiation to the control populations, we found that differentiation is a good predictor for both short and long-term evolution. However, differences between populations seem to be more common in the initial period of adaptation. We also found that the short-term evolutionary rate (combining all traits) is a good predictor of long-term patterns in most cases. These results suggest that stochastic events play a role on both short and long-term evolution of each trait. The presence of these contingencies indicates that, despite a similar evolutionary trend between populations, the repeatability of evolution is not pervasive. Combining all analyzed traits, the strong dependency of short and long-term evolution on early differentiation and the later convergence supports the presence of a single phenotypic optimum, common to all populations. This suggests that adaptation to this environment is somewhat predictable. However, the specific evolutionary dynamics seem

to be different between populations, consistent with a role of stochastic events in the path taken towards this optimum. In light of these findings, we discuss a theoretical approach to combine information across traits in order to achieve a better characterization of the evolutionary dynamics and address the issue of how predictable phenotypic evolution is.