

Eco-Evolutionary Neutral Dynamics of Mutualistic Webs

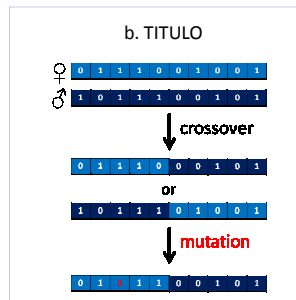
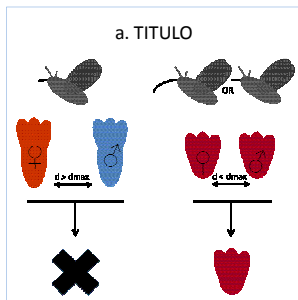
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1. Introduction

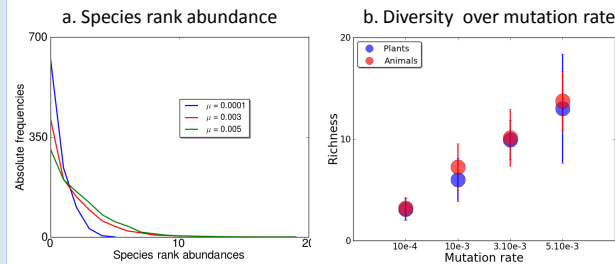
Plant animal mutualistic interactions show a rich variety of patterns, from highly specialized to generalized interactive species that generate different patterns of nestedness across broad geographic regions. The observed patterns are thought to be driven by niche mechanisms. However, there is a lack mechanistic models connecting evolutionary and ecological dynamics in spatial networks to detect the emergence of diversity and network structure. We developed an individual based spatially explicit model of mutualistic interactions between plants and animals. Our model is explained below. We show in this poster the preliminary results of the model. These results suggest **evolutionary convergence** of mutualistic traits and the **de novo emergence of network structure** patterns (nestedness)

2. The Model

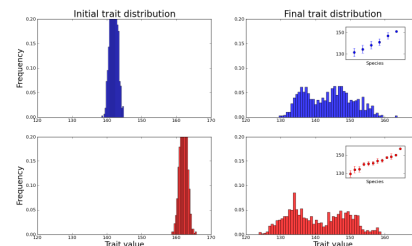
We consider the eco-evolutionary dynamics of plants (P) and pollinators (A). The two guilds interact mutually, they need each other to reproduce. Stochastic individual-based model with overlapping generations and birth-death zero-sum dynamics. Each gild population consists of haploid individuals which reproduce sexually in a spatially explicit landscape. Geographical distance ($d_{ij} < d_{max}$) and genetic distance ($q_{ij} > q_{min}$) between sexual partners determine whether two individuals can reproduce¹. For the pollinators or the plants to mate they need their mutualistic partner to be within their geographical range ($d_{ij}^{PA} < d_{max}^{PA}$). Additionally, for the plants to mate the pollinators need to have a proboscis (p) equal or longer than their corolla (c). Each individual has one quantitative trait (p or c) determined by their genome (L = 150) and an environmental effect (m=0; var = 1). Initially, all individuals have identical genomes. Genetic variation increases over generations through mutation and recombination. We performed 2000 generations with a 1000 individuals for each gild. We ran 500 replicates for each parameter combination with fixed $d_{max} = 0.7$ and $q_{min} = 0.97$.



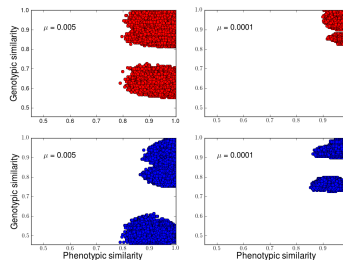
3. Results



c. Trait distribution

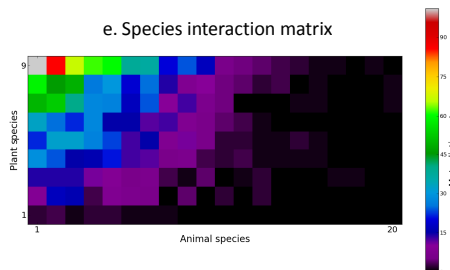


d. Genotype-phenotype relationship



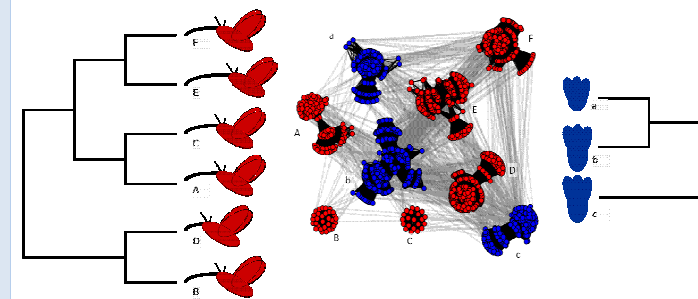
e. Species interaction matrix

Average interaction matrix shows high nestedness and low connectance



3. Results continued

f. Evolutionary convergence and complementarity



4. Discussion

Niche and neutral ecological processes are known to be responsible of several properties of plant-animal mutualistic networks. Co-evolutionary processes are mainly thought to promote evolutionary convergence and complementarity of mutualistic traits between mutualistic partners. However, the signal and strength of these selective forces is still almost completely unknown. Our preliminary results show that neutral eco-evolutionary processes can explain some important network properties and the emergence of evolutionary convergence and complementarity. We find de novo evolution [or emergence?] of network structure (e.g. nestedness) and genotypic-phenotypic trait distribution. Evolutionary convergence and complementarity occurs about 20% of the cases in average, meaning that physical restrictions of plant-animal interactions and neutral eco-evolutionary processes can be sufficient to observe the emergence of 'syndromes' (e.g. pollination syndromes) and trait-matching. However, we have only examined a limited range of the parameter space. Therefore, future work aims to get a deeper understanding of the model by numerical exploration and analytical approximations. The results of the model are promising and it can be used to test model predictions using high-resolution data about diversity and mutualistic traits. We conclude that observed network structure and convergence and complementarity of mutualistic traits seem plausible only by considering neutral processes.

¹MRefs