

sDiv working group meeting summary

“sEcoEvo - Biodiversity Dynamics: The Nexus Between Space & Time”

Biodiversity is critical for providing ecosystem services and sustaining functioning ecosystems, yet we lack a robust understanding of the relative roles of ecological and evolutionary processes in its origins and maintenance. Participants with expertise at the intersection of macroecology, population genomics, and phylogenetics, are developing an integrative and predictive theoretical framework, synthesizing data from plants, insects, and vertebrates, and using natural experiments provided by insular systems replicated across snapshots of ecological to evolutionary time. Our first sDiv meeting was held 19-23rd March 2018.

The meeting started off with short discussions of the work of the different participants and how it fit within the framework of the meeting: Participants coming from a more theoretical perspective were [Mike Hickerson](#) (comparative phylogeography, hierarchical Bayesian models, co-expansion across different taxa); [Luke Harmon](#) (speciation and how to connect across scales); [Isaac Overcast](#) (importance of linking population genetics with macroecology and the role of scale); [Megan Ruffley](#) and [Bob Weeks](#) (students working with Luke Harmon and Isaac Overcast, initially using random forest approaches); [Jon Chase](#) (when do we have to worry about evolutionary processes and the role of beta diversity); [Andy Rominger](#) (non equilibrium dynamics, and the role information entropy in telling us something about the status); [James Rosindell](#) (using neutral theory to look at patterns of biodiversity); [Rampal Etienne](#) (asking whether island biotas are in equilibrium and looking at effects of island ontogeny); [Ben Peter](#) (population geneticists to look at general patterns of diversity); [Angela McGaughan](#) (population genetics); [Francois Massol](#) (evolution of life history traits, and spatial networks and metapopulations), [Pietr Kiel](#) (scale and using statistics and machine learning to look at taxonomic and phylogenetic diversity area relationships); [Brian McGill](#) (macroecology meets macroevolution and how niche breadth changes over time); and [Joaquin Hortal](#) (creating models at different scales). Participants coming from a more empirical perspective came with data from insular systems: [Jairo Patino](#) (Canary Islands), [Luke Mahler](#) (Caribbean); [Paulo Borges](#) (Azores); [Christine Parent](#) (Galapagos); and [Rosemary Gillespie](#) (Hawaii).

Our next step was to outline progress that the core members of the team had made at a preliminary meeting held at the Santa Fe Institute, 27-30 November 2017. Here, the goal was to describe a hierarchical framework of biological processes which models all essential causal mechanisms; so, integration of processes (demographic, eco-evolutionary, biotic interactions), across ecological scales (individual, population, species, community, metacommunity, biome) and temporal scales (community assembly, population genetic, & phylogenetic). Then we would plan to construct a more complex model and call for adequate (next-gen) data to test this model. Major modeling questions emerging from the meeting were: Can we fit the SAD (species abundance distribution), the phylogeny, the

population genetic content, and traits all within the same model? Can we build an ecological model of evolution - or an evolutionary model of ecology? "Scale" is system dependent, so how can we reconcile ecological and evolutionary time? What is the relationship between space and time? Empirical questions included: Are there general rules of macroevolutionary structure? How can we test whether specific species radiations are exceptional or not? How are distributions of abundances partitioned among clades? Are clade age and species richness correlated? Does co-existence predict persistence? Is there a correlation between trait diversity and genetic diversity? Are ecological patterns across taxonomic scales similar or different? What are the limits to species richness?

Over the subsequent days at sDiv, we built on the core model (the MESS model) and developed several satellite efforts:

- 1) **MESS (Massive Eco-evolutionary Synthesis Simulations). A major focus has been on the development of a model that can integrate across three realms that are traditionally treated separately (population genetic, phylogenetic and ecological).** The idea here is to use MESS under the Mainland-island/plot forward time model (Rosindell and Harmon 2013) to generate phylogenies and underlying population genetic data under a range of ecological parameter values (ie dispersal rate, environmental filtering, population size/abundance, allopatric speciation rate, and in situ speciation rate). By re-scaling of underlying ecological parameters into population genetic parameters, the model can generate population genetic distributions (Theta's, diversities, Fsts etc) building off of Overcast et al. (*in review*). Multi-dimensional data (ie abundances, population genetic, phylogenies and traits) for this could include cichlids, Galapagos gastropods, Galapagos reptiles, Hawaiian Arthropods, Galapagos land birds, Azores Spiders and Beetles (Terceira island). The theoretical framework for this is being lead by Mike Hickerson, Luke Harmon, Andy Rominger, and Isaac Overcast, with Megan Ruffley and Bob Weeks.
- 2) **Alpha/Beta - The role of diversification in shaping local community structure on islands.** Recent work suggests that island species richness (gamma) increases more rapidly with area if species can be gained via in situ diversification, rather than solely via immigration. The impact of in situ diversification on the structure of *local ecological communities* within islands is much less clear. If diversification produces species that are segregated spatially among local communities, and these communities are no richer than expected under an "immigration-only" model, it would suggest that diversification augments island richness at the beta scale, with little impact on alpha community structure. Conversely, if such local communities are richer than expected by immigration alone, it would suggest an important role for macroevolution in determining the structure of local communities. This effort is being led by Luke Mahler, with contributions from Jon Chase, François Massol, Brian McGill, Paulo Borges, Megan Ruffley, and Christine Parent.
- 3) **Framework - Macroecology + Macroevolution.** The fields of microevolution, macroevolution, micro-ecology (traditional population and community ecology), and macroecology are currently practiced in four separate fields. Efforts to link microevolution and macroevolution

and micro-ecology and macroecology are ongoing but difficult. Efforts to link microevolution and micro-ecology have been a major focus for the last decade. Efforts to link macroecology and macroevolution have been by comparison much more limited but are urgently needed. A framework to link macroecology and macroevolution is being developed, lead by Brian McGill.

- 4) **Alpha/Beta** - Alpha/beta area curves under a neutral island model. Possible approaches here are (1) to use James Rosindell's spatially explicit neutral model, with extensions covering the questions we want to address (alpha, beta measures; genetic diversity and species diversity). (2) to develop a spatially implicit coalescent approach, with a hierarchical structure (plot within island within metacommunity, speciation happening at the island/gamma level). The lead in this effort is Ben Peter.
- 5) **Island Ontogeny** - Effect of island ontogeny/habitat dynamics on diversity patterns. The idea here is to see whether island ontogeny – or the change in area of islands through time – leaves its imprint on a phylogeny. The plan is to use the DAISIE (Dynamical Assembly of Islands by Speciation, Immigration and Extinction) model and apply it to multiple phylogenies across diverse islands. The leads here are Rampal Etienne, working with Jairo Patino.

Additional, and somewhat more focused, side projects included (1) Why radiate? (led by Andy Rominger and James Rosindell); (2) Do abundant island clades radiate more than rares? An empirical aspect of this is being led by Katie Wagner; a more theoretical component by Andy Rominger.