sDiv working group meeting summary

"sEcoEvo 2 - Biodiversity Dynamics: The Nexus Between Space & Time"

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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 second sDiv meeting was held 13-17 August 2018.

The meeting started off with project updates – new developments on the theoretical model led by Isaac Overcast (MESS; Massive Eco-evolutionary Synthesis Simulations),,; Alpha/Beta led byLuke Mahler and Ben Peter; and then Island Ontogeny led byBrent Emerson. We then heard short presentations from people that had not attended the previous meeting (Brent Emerson, Pedro Neves). We then had Prof. Henrik Krehenwinkel (Trier University) visit the group, and he presented on data that will be extremely useful for us as we move forward. He described the data format and how it can be used. We then heard a summary of a Research Coordination Effort (NSF RCN, PIs Ana Carnaval, Bette Loiselle, and Jeanine Cavender-Bares) that links to the sEcoEvo (Hickerson, Gillespie, Rominger).

Over the subsequent days at sDiv, we had multiple breakout sessions, except for a talk by Henrique Miguel Pereira from the Earth Observations Biodiversity Observation Network (GEO BON) and the Wednesday talk which was given by Luke Harmon and Michael Hickerson on "*The perils of inferring history: time dependence of speciation rates and the pipe dream of comparative phylogeography*".

Progress was made on several fronts and we summarize where we are at with the different 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).** As we reported earlier, the theoretical framework for this is being lead by Isaac Overcast, working with Michael Hickerson, Luke Harmon, and Andy Rominger, with graduate students Megan Ruffley and Bob Weeks. MESS is a mechanistic model of community assembly, rooted in classic island biogeography theory, to make temporally explicit joint predictions of biodiversity metrics across three major diversity axes: i) species richness and abundance; ii) genetic diversity and divergence; and iii) trait evolution within the context of phylogenetic diversification. It uses supervised machine

learning to estimate model parameters and test competing models of community assembly and evolution. It can be used to estimate the strength of deterministic non-neutral community assembly proccesses using only community-scale abundance and genetic diversity data; moreover, adding community-scale trait information allows it to distinguish models of competition and environmental filtering. Major recent accomplishments are as follows:

- The MESS team leads met at the Santa Fe Institute in Feb 2019 to discuss developments of MESS and next steps.
- The paper describing the model is close to being submitted to *Ecology Letters*, Overcast et al. "A mechanistic model linking the distribution of abundance, genetic diversity, and trait diversity with the processes controlling the assembly of ecological communities".
- Isaac Overcast has given six presentations on the model, including at the *International Biogeography Society*, Malaga, Spain, Jan 2019; the *Island Biology Conference*, Reunion Island, July 2019; Instituto Gulbenkian de Ciência, Oeiras, Portugal, 2018; Smithsonian Institution National Museum of Natural History, Washington DC, 2018; Santa Fe Institute, Science Symposium, Santa Fe, NM, 2019; and Rutgers University, 2019.
- Starting in November 2019, Isaac will be building on this work through a postdoctoral fellowship with Prof. Hélène Morlon, and connecting with a related effort funded through the European Twinning Project, "*Island Biodiversity Genomics*" (iBioGen) that aims to unify data collection across Island Genomic Observatories and to develop models adapted to the interpretation of this data in order to improve our understanding of the processes that shape the diversity and dynamics of island communities (PIs Anna Papadopoulou (University of Cyprus), Brent Emerson (CSIC, Tenerife) and Alfried Vogler (NHM, London), in addition to Hélène Morlon).

2) **A Rules Of Life Engine (RoLE) Model to Uncover Fundamental Processes Governing Biodiversity** – A proposal was submitted last February, led by Andy Rominger, that builds on the sEcoEvo effort. The proposal has now been awarded (PI Andy Rominger; co-PIs Mike Hickerson, Rob Guralnick, Renato Figueiredo, Ana Carnaval, Rosemary Gillespie, Mike Dawson). The argument is that there is now an unprecedented opportunity to advance understanding and synthesis of the rules of life as cross-scale, multidimensional biodiversity data become increasingly available, yet the modeling frameworks needed to derive more mechanistic understanding of system states are still missing. This effort will make use of the MESS model described above.

3) **Framework - Macroecology + Macroevolution.** As we discussed in the last report, the fields of microevolution, macroevolution, micro-ecology (traditional population and community ecology), and macroecology are currently practiced in four separate fields. Over the 20th century major trends drove ecology and evolution apart and pushed an emphasis towards the micro perspective in both disciplines. Macroecology and macroevolution reemerged as self-consciously distinct fields in the 1970s and 1980s, but they remain largely separated from each other. A framework to link macroecology

and macroevolution has now been developed, lead by Brian McGill. The paper is in press:

- McGill, Brian J.; Chase, Jonathan; Hortal, Joaquín; Overcast, Isaac; Rosindell, James; Borges, Paulo A. V.; Emerson, Brent C.; Etienne, Rampal; Hickerson, Michael J.; Mahler, Luke; Massol, Francois; McGaughran, Angela; Neves, Pedro; Parent, Christine; Ruffley, Megan; Wagner, Catherine E.; Gillespie, Rosemary G. 2019. Unifying macroecology and macroevolution to answer fundamental questions about biodiversity. *Global Ecology and Biogeography*. In press

4) **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 and Pedro Neves, working with Jairo Patino and Rosemary Gillespie. The ideas here will form the core of the PhD dissertation of Pedro Neves. Building on these ideas:

- Gillespie, Patino, and Jun Ying Lim worked with Rampal Etienne and Pedro Neves at the Groningen Institute for Evolutionary Life Sciences, University of Groningen, January 2019. The idea here was to determine whether we can compare across lineages in the Hawaiian Islands to assess signatures of the dynamic nature of the islands, and hence how communities assemble over time.
- Gillespie, Patino, Jun Ying Lim and Pedro Neves met again in Prague in July 2019 to further develop the effort.

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. The group has now assembled four data sets and developed a pipeline for testing the influence of macroevolution patterns of alpha and beta diversity. Next steps for this group are to finish cleaning and analyzing data, and to write a manuscript, with this work slated for late 2019 and early 2020.