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sDiv working group meeting summary "sEnigmas: Seeing the forest instead of the trees: identifying the common mechanisms behind enigmas of biodiversity"

General working atmosphere and feedback on sDiv support

The general working atmosphere of our group was very lively, collegial and collaborative. Support of the sDiv administrative team was again of the highest standard. The support in helping maintain our agenda, providing access to multiple small and large meeting spaces, and coordination of lunch and evening meals was exceptionally helpful and allowed us to focus our energy on discussions, brainstorming and accomplishing the goals of our group.

General structure of the week

The composition of our group was approximately 50% in-person and 50% remote for this meeting. Our 1st meeting had been focused on theoretical synthesis, with much progress made in this direction, so our plan for the 2nd meeting was to focus on model development. Through a number of different, unrelated, and unforeseen circumstances, the large majority of our group members with modeling expertise were either absent or present remotely with limited availability. Because of this, we pivoted the focus of the meeting toward refinement of the conceptual synthesis, with some work on the modeling, primarily in better understanding the requirements of modeled processes and patterns. The general structure of the meeting followed that of our first meeting, with a balance between plenary sessions for brainstorming, and focused small group sessions on specific topics.

Focal areas of discussion + main results/conclusions + open questions

The broad areas of discussion followed our three enigmatic patterns: Lewontin's paradox, the species-genetic diversity correlation (SGDC), and the diversification rate-genetic diversity correlation (DGDC). We dedicated focal work sessions to each of the enigmas, with the intention of addressing each enigma from an orthogonal direction, in other words taking into consideration processes previously unconsidered or outside the scope of previous attempts to understand each pattern. For example, with Lewontin's paradox we discussed potential macroevolutionary and community ecological processes which might generate this pattern.

One of the most interesting lines of discussion, and something that remains an open question is: What is constraining genetic diversity within species/populations? In a way, this is the central question for each of the focal enigmas, though for slightly different reasons, and a great deal of our discussion revolved around articulating our ideas around this. It will also be important to consider the extent to which genetic diversity is either the 'predictor' or the 'response' variable within each of the enigmas, in other words, how important is the feedback between the accumulation or depletion of genetic diversity and the processes of



speciation and/or community assembly. It's most clear to see how this feedback may be important within the framework of the DGDC: How does macroevolution result from and also constrain intraspecific genetic variation?

General research ideas, questions & directions discussed

Many of the concrete outcomes of this meeting related to refining the outline of and developing content for the synthesis paper, which included developments on several fronts:

Conceptual Synthesis Figures: With intraspecific genetic diversity as our fundamental unit of biodiversity currency, we mapped out two ideas for synthesis figures. In one, we discussed having a figure illustrating spatial, temporal, and hierarchical scales (individuals to species), with processes and interactions across scales that can affect genetic diversity. Another figure we code named "Climbing Mount Synthesis", within which we intend to plot MESS, Gen3sis, and other integrative models on the mountain of biodiversity synthesis models, with Island Biogeography and Neutral Biodiversity Theory as foundational models. The idea being that there has been a historical precedent for conceptually integrated models, that these models build upon one another, and that we can envision the pinnacle of this effort as a truly unified biodiversity model.

Conceptual Synthesis Table: We also envision a complementary table connected to the "mountain of biodiversity synthesis" figure, and briefly describing strengths, weaknesses, and innovations of current and past models attempting to unify macro/micro-evolution and ecology. We want to show what current and past models can do, what they might do better, and what efforts can be extended beyond them, focusing on where the models are incomplete in the needs of integration.

sEnigmas Modeling Approach: Our discussions on modeling focused on identifying the conceptual ingredients for predicting genetic diversity across scales. We agreed that all the ingredients are needed for all the enigmas: Ne, Nc, speciation rate, genetic diversity, species diversity. We also agreed that our target is an integrative framework that can make predictions across the three enigmas simultaneously.

Content of presentations

On Wednesday afternoon the sEnigmas team gave two brief presentations at the regular iDiv seminar. Co-PIs Overcast and Silva first presented a high-level overview of the sEnigmas project, highlighting the work of our group to develop a theoretical framework to synthesize processes across levels of biological organization. Then, sEnigmas team member Rolland spoke about using fossils and present-day data to study how climatic preferences of vertebrates evolved over long time scales.

Next steps & upcoming deliverables

Our next steps will be to continue writing up our conceptual synthesis paper, and to compose figures and boxes to support our lines of reasoning. On the modeling end, members of our group (Overcast & Hagen) have already shown a proof of concept model unification linking macro- and micro-scale processes, so the next step with model development is to scale the

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model up from an individual patch to a 'sub-continent' to investigate model parameters which do or do not recapitulate our focal enigmatic patterns.