

## **sDiv working group meeting summary**

### **“sEnigmas: Seeing the forest instead of the trees: identifying the common mechanisms behind enigmas of biodiversity”**

The sEnigmas working group arose out of conversations among some of the participants with specializations in community ecology, population genetics, and macroevolution. We each had encountered as yet unexplained patterns within our specific fields (the 'enigmas'): the species genetic diversity correlation (SGDC) within community ecology, Lewontin's paradox within population genetics, and the relationship between speciation rate and genetic diversity in macroevolution. We began to interrogate the nature of these patterns, and we realized that the enigmas may be an outcome of the fact that models that consider individual hierarchical levels of biodiversity tend to ignore processes either above or below their scale of interest. This was the germination of the sEnigmas group. With the support of sDiv, we resolved to bring together theoreticians, modelers, and empirical biologists with experience in the relevant disciplines, and with demonstrated interest in bridging processes or investigating patterns across scales, in order to expand upon these lines of thinking and potentially gain better understanding of how biodiversity is generated and maintained.

We began the first day with an introduction to the project and a brief statement from the co-PIs about what we hoped to accomplish, both in the first meeting, and more broadly across the duration of the working group. These broader goals being: a synthesis paper proposing a unified approach to understanding the processes across scales that give rise to the enigmas and; a mechanistic modeling framework based on this synthesis with which to investigate these. This was followed by brief self-introductions by each of the participants, during which they were asked to discuss their work, in very general terms, and also what they saw as their role in our group, and what benefit they hoped to obtain from participation. During the remainder of the first day we spent a considerable amount of time reviewing and discussing in deeper detail each of the focal enigmas.

Throughout the 4 days we spent an equal amount of time in free-form brainstorming sessions around specific topics, in presentations by various group members, and in small group focused work sessions. Presentations were given by participants Overcast (on the MESS and PIED models), Hagen (on the Gen3sis model), Afonso Silva (on empirical data with focus on what is available and where are the gaps), and Aristide (on the relationship between speciation rates and molecular rates). Overall, the working atmosphere was very collegial, energizing, and productive, and all

working group members actively participated and made meaningful contributions to the discussions. We did receive feedback that the lively and productive atmosphere was facilitated by the ECR status of the working group members. Additionally, in every aspect of the working group, the support we received from sDiv was impeccable and critical to our success, including all the help with lodging and travel arrangements, and all the onsite technical and administrative support.

Through the course of the meeting, with respect to the focal enigmas and developing progress toward our proposed synthesis we came to three main conclusions, each of which also generated questions which will need to be addressed to successfully develop both the synthesis and the model. First, we came to the conclusion that genetic diversity is the common currency among all the enigmas, which raises the following questions: How can we measure genetic diversity using more than one statistic, and how do measures of genetic diversity change across scales? How do the four forces at the core of Ecology and Evolution (drift, migration, selection, and speciation/mutation) interact with life history traits such as fecundity, longevity, dispersal ability, etc., to generate patterns of genetic diversity? Second, while spatial context is important, it is often overlooked (e.g. in Lewontin's paradox and in models of diversification). Hence, we need to understand better how these enigmas emerge across different spatial and taxonomic scales. If the enigmas emerge as multi-scale patterns, then we need our models to operate across scales as well. Third, the timescales of different processes must be reconciled. This is a classic problem faced when trying to link micro- to macro-scale processes, so developing a more rigorous framework for thinking about unifying processes across timescales will be critical for both the model and the synthesis.

As the working group drew to a close, we revisited our broader stated goals of writing a synthesis paper and developing a computational model to investigate the enigmas. We held a breakout group session to discuss the structure of the synthesis paper and to sketch an outline of our model. The outline produced by the synthesis paper breakout group provided a good first step for moving forward. We created a google doc where we organized our questions into broad topics and participants self-assigned to work on areas of the paper based on interest and expertise. We then agreed on roles in driving the synthesis paper forward during the intervening months and committed to meeting every 3 weeks on zoom to keep up the momentum. The modeling breakout group perhaps had a harder task, and so the progress on the sketch of the model was more limited. Because of this we agreed that the next steps for the core group of modelers are to develop concrete models that can be evaluated at the next meeting, and that the immediate next steps of the larger group should be on developing the synthesis paper prior to the next meeting.