German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
Deutscher Platz 5e, 04103 Leipzig, Germany

sDiv working group meeting summary
"sCaleWebs – Unifying environmental and spatial determinants of food web structure across spatial scales"

PI report on sCaleWebs meeting 2, December 2019

The empirical goal of this meeting was to build models predicting food web structure at two spatial scales: at the community level (the aquatic invertebrates within a single bromeliad) and at the meta-community level (for the many bromeliads within a site).

We had an unconventional meeting structure that ending up working extremely well. At Leipzig we had a team of 12 researchers who worked during the day on tasks. Towards the end of day, we had a Skype meeting with three participants based across the Atlantic to bring then up to date about what had been achieved during the day and then to hand the coding baton to them. These participants then worked through their day (the Leipzig night) to complete the coding and modelling tasks they had been handed. When the Leipzig team woke up the next morning, they were then able to pick up where the midnight coders had left off. We were able to double the productivity of our working group through this workflow. Essential elements included the use of Github to help pass the digital baton between teams, and the 1.5 hour hand-off meeting via Skype. We also rotated facilitators each plenary session, and this helped keep the organization fresh and the group cohesive. We developed in tandem an ideas paper relating the method by which researchers construct ecological networks to the questions such networks can answer. This more philosophical discussion, conducted in part by walk-and-talks in sub groups of three, unexpectedly ended up influencing some of the thornier methodological decisions that we had to make. Finally, Regis Céréghino and Diane Srivastava presented a sDiv seminar entitled: "Are the aquatic invertebrates in bromeliads functionally convergent across the Neotropics?". Melissa

Guzman helped with slide preparation. This well-attended seminar summarized recent analyses originating from a CESAB working group on trait-based analyses of bromeliad invertebrates.

Our second meeting met all our goals. Between the first and the second meeting we had finished integrating many different types of information about trophic relationships among taxa. When direct observations were missing, we inferred feeding from that known from taxonomically similar species in our database or from the literature. An important part of this process was developing algorithms that ranked the information in terms of confidence, and developing rigorous thresholds for excluding information. We then used a probabilistic model to impute missing values based on the information in the matrix. In the second meeting, we evaluated these final food web matrices, and iteratively improved our algorithms. We then characterized the structure of each food web using conventional food web metrics. Simultaneously, we downloaded bioclimatic data for each of the fieldsites, with a particular emphasis on variables related to productivity and drought disturbance. By the end of the meeting, we had a final data matrix of food web metrics and environmental/climatic variables at two spatial scales: within each of >1000 bromeliads, and aggregated at the level of species pool. We will have video-conferences every two months over the next year to keep the momentum with the next tasks in the workflow, specifically building and refining the models that identify the environmental and climatic drivers underlying spatial variance in food web structure at multiple scales.

Diane Srivastava, (University of Britsh Columbia, Canada)

Gustavo Romero, (State University of Campinas, Brazil)