

sDiv working group meeting report

“sCaleWebs – third working group meeting”

Our working group seeks to understand general principles about how food webs are structured, including the drivers of structural change over broad spatial gradients in climate and biogeography. To realize this vision, in our previous two meetings we had to first transform our lists of invertebrate species in each of 1399 bromeliads into individual food webs. As we had more than 600 taxa in our database, such an endeavor exceeds any one methodology. We therefore built a software program that combines multiple sources of information (gut contents, feeding trials, experiments, field observations, literature obtained by project members or published databases), using a priority order for ranking the sources of information and Bernoulli trials for determining the probability of feeding trial results. We established a set of a priori constraints based on morphology and physiology which imposed forbidden links on the food webs. A key part of this was creating a new R package to impute body sizes for all individual invertebrates in food webs, in order to use size to constraint potential feeding links. This was done by participant Pierre Rogy, under contract by sDiv. Finally, we used our trait database to determine the degree to which information from related species could be used to infer the diet or predators of a focal taxa. For example, *Culex pipiens* mosquitoes had a “taxonomic scope” of genus: any diet information for other *Culex* species could be considered. The completed food webs have now undergone several iterations of improvement of these constraints and sources. Creating robust food webs occupied the first two in-person meetings, a substantial investment of time as our results are only as robust as our food webs are.

Simultaneously, along our first two-in person meetings we developed hypotheses as to the major environmental drivers of food web structure (meeting 1) and extracted the relevant predictor variables from online databases (meeting 2, plus contract to Melissa Guzman). One particular issue was that some species pools were defined at smaller spatial scales than the relevant climatic variables. We therefore needed to downscale the climate variables, and this feat of statistical imputation was achieved by Melisa Guzman. The process of combining different types of information into food webs has also led us to rethink how we interpret food webs in the context of different ecological questions. Benoit Gauzens has been leading a paper on this philosophical point.

Between the second and third (final) “in-person” meetings, we had several virtual meetings to divide up some of the writing of the first manuscript (“food web drivers”), led by Diane Srivastava, with deadlines for completion of tasks. In addition, we defined aims and questions for other two papers, namely “biomass pyramid” led by Paula Omena and Pablo Antiqueira, and “beta diversity” led by Gracielle Higino.

With these foundational data in hand and the first manuscript in progress, we were in good shape to capitalize on all this digital infrastructure that we have created. However, we have many more questions that we would like to use our database to answer. To realize this burst of productivity, however, we needed to have in-person discussions with fresh, creative in-

person brainstorming. Because of the COVID impediments, especially for members from countries where such disease was not well controlled, we decided to conduct our third meeting in three HUBs, following the idea and structure presented by D.S. Srivastava et al. (2021). Thus, we arranged a regional hub meeting, with hubs located at Leipzig (Germany), Montreal (Canada) and Campinas (Brazil). Montreal was chosen as the Canadian hub to facilitate the participation of researchers with small children and included all Canadian and US participants. Campinas was chosen as the Brazilian hub as three participants were already located there and others could easily travel to this location from within Brazil – for example, Ignacio Barberis, from Argentina, was able to join the Brazilian hub team. Leipzig would be convenient for the European researchers in our group (Germany, France, Austria, England). We used university facilities in Montreal and Campinas to reduce (to zero) expenses for meeting rooms.

*Srivastava, D.S., M. Winter, L.J. Gross, J.P. Metzger, J.S. Baron, N. Mouquet, T.R. Meagher, B.S. Halpern & V.D. Pillar. 2021. [Maintaining momentum for collaborative working groups in a post-pandemic world](#). *Nature Ecology & Evolution* 5:1188–1189.*

In our three-hub meeting, we worked on the three proposed papers ("food web drivers", "pyramid biomass"; "beta diversity"). For each paper, we established 3-5 people collaborating in-person in at least one hub, as well as remote collaborators. One to two persons led each paper. The choice to collaborate in each paper was previously assigned using Google Forms and previous virtual meetings. We coordinated each paper between hubs in daily Zoom meetings and on Slack, where we established what each team would work on and solve any problems that arise together. The main aim was to targetting proprietarily on the paper 1, and we achieved such goal. This paper is now about 50% completed. In addition, we were able to advance nicely on the analyses of pyramid biomass and beta diversity papers to the stage where we now have good momentum to start writing the papers. We encouraged the hubs and paper teams to experiment with different ways of collaborating after the meeting #3, to make progress and finish the three papers successfully.