

sDiv working group meeting summary

“ Separating Environmental Changes and their effects on commUnity tRaits in European butterflies (sECURE)”

Following the success of our first meeting, when the main ideas and concepts were discussed and developed, the main goals of our second meeting were to develop efficient code to standardize massive abundance datasets and to extract explanatory variables at multiple resolutions for the entire Europe, organize and fill the gaps of a large life-history traits database, run analyses and prepare manuscripts. The first day started with a number of presentations, including a welcome talk by Oliver Schweiger, who also highlighted important progress and challenges faced during the first year of the sECURE project. Andros Gianuca talked about the progress of a manuscript on drivers of climatic risk in European butterflies and Reto Schmucki offered his insights on the challenging task of standardizing abundance data from the e-BMS gathered in many different countries across Europe. In addition, Shane Blowes from iDiv gave a very interesting talk on methods to disentangle potential mechanisms behind spatial scaling of biodiversity patterns. Prof. Niklaus Zimmermann gave an inspiring talk in the mid of the week about the assumptions, challenges and recent progresses in species distribution models. On the other days, three break-out groups were formed to work on several key subprojects, as follows:

- 1) Spatial scaling of biodiversity: This subgroup worked mainly on writing code to standardize e-BMS abundance data, using a nested design with multiple resolutions, ranging from 5 km² to 200 km². In addition, this group started analyses aiming at separating potential mechanisms that might cause scale-dependent patterns of biodiversity.
- 2) European butterfly trait-data: This subgroup was engaged in compiling trait datasets from multiple sources. Also discussed was the potential to use imputation methods to estimate some trait values to fill gaps in this comprehensive database. In addition, some new ideas were developed on how to best use trait data to inform butterflies' responses to environmental change through time.
- 3) Hierarchical modelling of species communities: This subgroup worked on many complementary aspects, including writing an efficient code to extract environmental data across multiple nested scales, organizing datasets and writing scripts to run analyses (i.e., HMSC) as well as outlining a manuscript for submission.

iDiv again proved an excellent, enjoyable working environment, based on the support and organization provided by the iDiv team. Building on relationships formed at the first meeting and also with new participants, the atmosphere was friendly and highly productive, both in the formal meeting times as well as with informal exchanges of ideas afterwards.

As future plans, in addition to the publication of at least four papers that are currently in progress, we hope to organize a writing retreat to further develop some articles for publication, including one on drivers of metapopulation and metacommunity stability and another on evolution-mediated responses to environmental change.