

sDiv working group meeting summary

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

The first meeting of the sECURE working group took place in Leipzig in mid May of 2017 and successfully brought together a collaborative network of early career scientists, postdocs, senior researchers and professors with a broad and highly interdisciplinary background in ecology and evolution. In addition to the diversity of career stages and scientific backgrounds, participants came from a variety of different countries, including: Germany, England, Brazil, Ireland, Greece, Spain, Denmark, Sweden, Turkey, Poland, Croatia, and Finland. With this wonderful group of major data holders and world-leading experts from multiple disciplines, we worked in this first workshop towards identifying analytical pathways allowing the best use of species traits, ecological characteristics and phylogenetic information to predict the impacts of drivers of global change on species co-occurrence, community assembly and biodiversity, with a focus on European butterflies. Overall, we divided our time in a number of presentations on key concepts and ideas (20%), brainstorming in small groups (50%), and large group information exchange and task division (30%).

The scientific novelty and power of our synthesis relies on the integration of multiple data sets on species distribution and abundance with high temporal and spatial resolution and extent in combination with comprehensive information on species traits, their niche characteristics and phylogenetic relationships. Hence, on day one we started with a stirring talk by Oliver Schweiger, who laid down some of the original ideas and specific aims of the sECURE project. His talk was then followed by a series of presentations on the available datasets, which included: LepiDiv – European Distributions data (Oliver Schweiger); eBMS – European Butterfly Monitoring Scheme (Reto Schmucki); European butterfly trait data (Martin Musche); and European butterfly phylogenetic data (Martin Wiemers). In the afternoon, the new postdoc associated with this working group, Andros Gianuca, gave a presentation about his previous research on trait- and phylogenetic-based metacommunity ecology as well as on his future perspectives within the sECURE project.

Still on day one, after the first series of stimulating presentations and discussions, which set out the general framework and identified available datasets, we organized three subgroups for further brainstorming on the following topics: (i) Spatial and temporal scaling of biodiversity patterns and processes; (ii) butterfly niche and trait evolution and its relation to global change; and (iii) hierarchical modeling of species and community responses to environmental change (including abiotic filtering and biotic interactions).

To boost scientific exchange and creativity throughout the meeting, we allowed some dispersal of attendees among subgroups, forming something more like a “metacomunity” rather than islands of ideas, which proved to be successful.

The second day started with an inspiring talk by Jonathan Chase, entitled: “Embracing scale-dependent biodiversity change in space and time to achieve synthesis”. A number of ideas presented by Chase were especially useful for the subgroup dealing with spatial and temporal scaling, and he also assumed a leading role in this subgroup in the remaining days of the meeting.

The third day was packed with insightful presentations and group discussions. The day started with a great talk by Toke Høye on the long-term trends in European butterfly species richness and functional traits. A bit later, Robert Wilson contributed an inspiring public talk to the iDiv seminar series, in which he talked about the influence of microclimate and phenology on species and community responses to climate change, with emphasis on butterfly species at range margins. Please, find below a short summary of each subgroup discussions.

Subgroup (i) Spatial and temporal scaling of biodiversity patterns and processes

There is a fierce debate going on about whether or not biodiversity is similarly decreasing at local, regional and continental spatial scales and what are the main drivers of biodiversity change across scales. Whereas results based on meta-analysis remain inconclusive at best, solving this issue requires high quality abundance data gathered in a standardized way across a range of spatial and temporal scales. Here we are going to use abundance data from the European Butterfly Monitoring Scheme (eBMS) to investigate (i) what are the main drivers of biodiversity change across scales; and (ii) how patterns of species richness, functional and phylogenetic diversity across spatial and temporal scales reflect changes in total abundance, rarity and/or aggregation of individuals. During the first workshop we defined a number of hypotheses about drivers of biodiversity change across spatial scales, identified available datasets, and divided tasks. Three manuscripts will be written on this topic, one of which is already in progress and will be discussed in detail on the next meeting, planned by the beginning of 2018.

Subgroup (ii) Butterfly niche and trait evolution and its relation to global change

The first main goal of this subgroup was to identify gaps in the trait and phylogenetic dataset covering (almost) all European butterfly species and to propose potential approaches to reliably fill such gaps, if any. Secondly, we

aim at understanding how evolution of single traits, or combinations of correlated traits, influence species vulnerability to global change. A potential approach that was proposed is the use of “phylogenetic confirmatory path analysis” to identify causal links among traits and their influences on species responses to global change. We outlined a plan for building a more complete and robust trait database for European butterflies that will be made public available after the completion of this project. Also, two manuscripts were sketched and are expected to be in advanced stage before the next meeting.

Subgroup (iii) Hierarchical modeling of species and community responses to environmental change (including abiotic filtering and biotic interactions)

The main goals of this subgroup were to identify available datasets and outline a framework to test (i) the role of abiotic and biotic factors in driving continental patterns of community composition based on species traits and phylogenetic relationships and (ii) to generate practical applications of the results for conservation. Based on group discussions, we outlined three manuscripts, two of which will be ready for submission by the next meeting, at the beginning of 2018.

General summary and feedback

In all, we are confident that this was a very successful week of work for all participants, made possible by an excellent organization provided by the iDiv team. The facilities were really great, the atmosphere was amazing and the group stick together and enthusiastically discussed science even during breakfast and dinner, which was a lot of fun. This friendly and positive attitude of all attendees combined with the wonderful support provided by iDiv was key to the flourishing of ideas and creativity as well as to outline our future working plans and scientific output.