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# sDiv working group meeting report

# "sCom - Advancing inference for eDNA and other novel, high-throughput community data "

## Feedback of the sCom group (PIs)

## Focal areas of discussion

The first sCom workshop focused on extensions to joint species distribution models (jSDMs) and the interface between eDNA data and jSDMs. We began our workshop with brainstorming sessions that identified two main areas of interest:

*Prediction and scaling* - For instance, under what conditions can jSDMs improve predictions? How can we incorporate observation error? Do jSDMs really perform better predicting rare species, given that jSDMS estimate species covariances? How can we optimise (eDNA) sampling design?

*Inference and synthesis* - For instance, given that community data (the 'Y matrix') only reveals realised niches (i.e. already include the effect of biotic interactions on species abundances and incidences), how is it possible to use jSDMs to infer the effects of species interactions? Is it possible parse the relative contributions of abiotic response, species associations, and spatiotemporal structure on variation in community structure (variation partitioning)?

We followed up in Days 2-5 with detailed planning of two review articles and (at least) two modelling studies, which we describe below.

## Content of presentations

On Day 3, Florian Hartig and Douglas Yu gave a joint presentation to iDiv on sCom and its objectives.

## Outputs discussed

**General-audience review paper:** We are planning to write a general review paper on the interface between joint species distribution models and novel community data (e.g. eDNA, bioacoustics, remote sensing).

**Technical review:** in a second paper, we want to review the techniques for producers and consumers of eDNA data for species distribution modelling. We anticipate two audiences: modellers who have heard about eDNA and want to take advantage of this new source of data and molecular ecologist who can create such datasets but have many sampling, laboratory, and bioinformatic design choices to make. Our technical review will step through the topics and decisions that the statistical ecologist and molecular ecologist should discuss with each other before embarking on the study: sample type, study design, laboratory protocol, bioinformatic pipeline, and modelling.

**Inference of species interactions from time-series data:** Because snapshot community data (the 'Y matrix') only reveal realised niches (i.e. already include the effect of biotic interactions on species abundances and incidences), the species covariances estimated by jSDMs are unlikely to reveal true biotic interactions (e.g. competitive exclusion). However, with time series data, it is possible to infer causality from the simple fact that causal events must happen before the events that they cause. We have set up a sub-group in sCom to work on this idea

**From metacommunity structure to ecosystem functional diversity:** A fourth subgroup is looking at the question if there a relationship between metacommunity complexity and functional diversity?

## Balance between work on outputs, general brainstorming/ information exchange and participants presentations in %

- work on outputs: 20%
- general brainstorming/information exchange: 70%

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- participant presentation:  10%

## Inspiration for own work and/or further cooperation

There is no single one idea / cooperation that we would like to highlight, but collaboration between participants has intensified in various aspects through the meeting, and we have received the feedback that participants found the meeting helpful also for their individual research.

## General working atmosphere and feedback on sDiv support

We ran a hybrid meeting format, with 10 in-person and 6 virtual participants. Despite smaller technical problems and the limitations of a hybrid format, meeting participants were overall happy with the organization and the opportunities to participate. We would like to thank iDiv for their great support!

## Next steps

After consultation, we have scheduled the second in-person meeting of sCom for the week of 9 May 2022. For the next meeting, which will probably also take a hybrid format. Our work plan is to make progress on all four projects before the next meeting.

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