Wednesday, 27th January 2021, 13:00 – 16:00h

**Simulation-based ecological modelling**

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This tutorial contains three parts corresponding to different types of spatially explicit simulation models: (A) basic metapopulation model, (B) individual-based metacommunity model, and (C) population-based metacommunity model. The objective of the tutorial is to provide the basic computational tools for performing simulation modelling with R, and to practice with metacommunity models that have been used for approaching ecological questions. The basic background knowledge has been introduced in the lecture "Ecology across scales" and more specific content will be introduced in brief presentations in the beginning of each part. Each part will consist of three steps: (1) introduction by the instructor, (2) R tutorial by the instructor (where students run the R code simultaneously), and (3) individual exercises. The basic task for the exercises will be to vary a model parameter of interest (i.e. a parameter controlling a given ecological process) and investigate its effect on model outputs (i.e. biodiversity patterns). All the R code is in the script "Metacommunity\_simulations.R".

**A. Basic metapopulation model**

Q1: How does connectivity among patches vary as a function of the dispersal exponent ("exp.rate")? Manually vary the exponent (e.g. values from 0.01 to 1) and visually inspect the connectivity pattern.

Q2: Given a dispersal exponent ("exp.rate") of 1, what is the spatial structure of the metapopulation after 100 generations (random, regular or clustered)? Why?

Q3: How does the spatial structure of the metapopulation after 100 generations change depending on the dispersal ability ("exp.rate" varying from 1 to 0.01)?

**B. Individual-based metacommunity model**

Reference parameter values:

* dispersal ability ("sd.disp"): 0.7
* niche breadth ("sd.niche"): 5

*B1. Variation in metacommunity archetypes.*

Q4. What is the relative importance of the environment to explain species composition under the different types of metacommunity dynamics? Set the different metacommunity archetypes ("meta.type") and perform variation partitioning.

*B2. Variation in dispersal ability.* Set dispersal ability to vary between 0.1 and 4.

Q5. Under a neutral model (NM), what is the effect of variation in dispersal ability on alpha-, beta-, and gamma-diversity?

*B2. Variation in niche breadth.* Set the niche breadth to vary between 1 and 50.

Q6. Under a species sorting (SS) model, what is the effect of varying niche breadth on alpha-, beta-, and gamma-diversity?

Q7. Under a species sorting (SS) model, what is the effect of varying niche breadth on the relative importance of the environment to explain species composition?

*Tip: perform variation partitioning.*

**C. Population-based metacommunity model**

Q8. Under a model without interspecific competition (set "min\_inter" and "max\_inter" to 0), what is the effect of varying niche breadth on alpha-, beta-, and gamma-diversity? Is the effect comparable to the individual-based model (Q6 in Part B)?

Q9. How does density-dependent competition affect the relationships found in Q8? Run the same simulations under the four different types of competition. For setting the different competition scenarios, check the R package repository (https://github.com/plthompson/mcomsimr). Include also a model without interspecific competition.

Q10. Under a model in which species are neutral in relation to abiotic environment (set the niche breadth really high; e.g. 10), how do you expect species abundances to covary under the four types of competition (write down the predictions)? Now calculate the pairwise correlations in space and time. How does the median pairwise correlation varies among the different types of competition? Compare to your predictions.