

# Resource variation within and between patches: Where exploitation competition, local adaptation and kin selection meet

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## The topic

This theoretical study aims to understand how variation in resources drives biological diversity in resource consumers. While it is well known that resource variation between patches could lead to spatial diversity in consumers, and competition for local resource selects for diversity within patches, we study how both types of resource variation interact with each other. Using an mathematical invasion analysis and running individual-based simulations, we show that both types of variation add up and promote consumer diversity for a greater range of conditions. Importantly, we show how such evolution proceeds in structured populations, when limited dispersal and finite patch sizes impose competition among kin.

## Overview

The supplementary data allow to repeat the following steps of the analysis:

1. Running the individual-based simulations
2. Analyzing the simulation output
3. Recreating the figures of the manuscript

## File specifications

The following types of data are available:

- The source and header files to compile NEMO-AGE with resource competition (beta version). These files can be found in the directory ***NemoAge\_ResourceCompetition***.

This software version differs from the official release of NEMO-AGE (Cotto, Schmid, and Guillaume 2020) as the extension for resource competition was not released yet

when these simulations were run. The source and header files allow to compile Nemo-Age following instructions on <https://bitbucket.org/ecoevo/nemo-age-release/src/master/>

- The Nemo configuration files (ini-files) specify the parameter values for the simulations. The Nemo-Age ini-files can be found in the directory *ini\_files*.

The the name of each ini-file is indicative of the simulation scenario. The part “sc1” within the file name refers to resource competition with long exploitation time, and the last part indicates the resource distribution. For instance, “sigb1” indicates between-patch resource variation of  $\sigma_{r,b}^2 = 1$  while within-patch variation is absent  $\sigma_{r,w}^2 = 0$ . With an “\_s\_” being present in the file name, reproduction happens sexually and not clonally.

Further note that you can specify the path for the simulation output files in each ini file by adapting the input parameter *root\_dir*.

- The *external\_files* on *Dryad* are needed beside the ini-files to run the simulations. They contain text-files to specify the property and frequency of each resource type. Note that the path to these files on your computer needs to be adapted in each ini-file (i.e. adapting the path for the input parameters *cloning\_resource\_property* and *cloning\_resource\_proportion*).
- The R-scripts in the folder “*R\_scripts*” allow to reproduce the the analysis of the simulation data and the plotting of the Figures. We ran the R scripts with R (R Core Team 2019, version 4.3.0) and made use of the package *hierfstat* (Goudet 2005, version 0.5-11). In fact, you only need to open and run the script *Plots.R*. The script *Functions.R* only contain the functions used in the *Plots.R* script.

## References

- Cotto, Olivier, Max Schmid, and Frédéric Guillaume. 2020. “Nemo-Age: Spatially Explicit Simulations of Eco-Evolutionary Dynamics in Stage-Structured Populations under Changing Environments.” *Methods in Ecology and Evolution* 11 (10): 1227–36.
- Goudet, Jérôme. 2005. “HIERFSTAT, a Package for R to Compute and Test Hierarchical F-Statistics.” *Molecular Ecology Notes* 5 (1): 184–86. <https://doi.org/10.1111/j.1471-8278.2005.00111.x>.
- R Core Team. 2019. “R: A Language and Environment for Statistical Computing.” Vienna, Austria: R Foundation for Statistical Computing,. <http://www.r-project.org>.