

PROJECT: COMPUTATIONAL METHODS IN ECOLOGY AND EVOLUTION

Current project members: Alexandre Courtiol, Liam Bailey, Colin Vullioud, Christoph Alt

We develop computational methods to solve outstanding problems for ecologists and evolutionary biologists, which we distribute to the community by means of packages in the open source statistical software R. We identify challenging computational tasks in the research projects in which we are involved and implement general solutions that can be used by others. To complete these tasks, we combine our detailed biological knowledge on the topics with our practical knowledge of computer programming. Some of the tools we have created (or significantly contributed to) are used by many scientists all around the world (e.g. camtrapR, climwin). We also write scientific publications presenting these methods.

Established sub-projects:

- **camtrapR** (<https://cran.r-project.org/web/packages/camtrapR/index.html>): a toolkit for the management and data extraction of camera trap photographs in wildlife studies. Main collaborators: Jürgen Niedballa (former Phd student), Andreas Wilting (Dpt 6), Rahel Sollmann (UC Davis, California, US).
- **IsoriX** (<https://cran.r-project.org/web/packages/IsoriX/index.html>): a toolkit for building isoscapes using mixed models and inferring the geographic origin of organisms based on their isotopic ratios. Main collaborators: Stephanie Kramer-Schadt (Dpt 6), Christian Voigt (Dpt 1), François Rousset (Université de Montpellier, France).
- **spaMM** (<https://cran.r-project.org/web/packages/spaMM/index.html>): a toolkit to efficiently fit linear models of varying complexity, including mixed models with spatial autocorrelation. Main collaborator: François Rousset (Université de Montpellier, France).
- **climwin** (<https://cran.r-project.org/web/packages/climwin/index.html>): a toolkit to detect and visualise periods of climate sensitivity (climate windows) for a given biological response. Main collaborators: Viktoriia Radchuk (Dpt 6), Martijn van de Pol (Netherlands Institute of Ecology, Netherlands).

Sub-projects in preparation:

- **torpor**: a Bayesian method to assign metabolic rate measurements to either the torpor or the euthermia state, in heterothermic endotherm species. Main collaborators: Nicolas Fassel (University of Lausanne), Michel Genoud (University of Bern, University of Lausanne).
- **hyenaR**: a toolkit to manage the data of the long-term hyena project (IZW) and help to prepare data for downstream analyses. This package also serves as a model for other long-term projects. Main collaborator: Oliver Höner (Dpt 1).
- **Rato**: an adaptation of hyenaR tailored for the study of the Damaraland mole rats of the Kalahari Meerkat Project (University of Cambridge). Main collaborator: Philippe Vullioud (University of Cambridge).
- **estiMate**: a toolkit to estimate various aspects of mate choice from the observations of mating pairs in natural populations or genetic parentage analyses.

- **simulMate**: a toolkit to simulate pair formation according to specific mating rules and population constraints.
- **SPI-Birds** (<https://nioo.knaw.nl/en/spi-birds>): a project to convert individual level bird breeding data into a standard community data to facilitate collaboration and data transparency. Main collaborators: Antica Culina (Netherlands Institute of Ecology, Netherlands), Marcel Visser (Netherlands Institute of Ecology, Netherlands), Stefan Vriend (Norwegian University of Science and Technology, Norway).