

In-Lab Units: Applied Ecological & Evolutionary Sciences

Concepts, questions and methods in experimental evolution

Stéphanie Bedhomme (stephanie.bedhomme@cefe.cnrs.fr), CEFE.

Experimental evolution is a powerful method to answer a diversity of questions in evolutionary biology. In this Inlab, the students will be provided with an overview of the different ways of performing experimental evolution and the diversity of questions that can be addressed with this approach. Then students will choose their own question that they would like to address with bacteria experimental evolution, design the experimental protocol that would allow them to answer this question and will try to perform the first steps in the CEFE microbiology lab. In a last session, students will discover and learn how to analyse the whole-genome sequencing data of experimentally evolved population to identify loci likely to contribute to adaptation.

The students will learn the principles of experimental evolution design, some basic evolutionary microbiology skills and WGS analysis.

Developing individual-based eco-evolutionary models

Jhelam Deshpande (jhelam-nitin.deshpande@umontpellier.fr) &
Emanuel A. Fronhofer (emanuel.fronhofer@umontpellier.fr), ISEM.

Concepts: Ecology and evolution often happen at similar time-scales and in spatially complex settings. Studying spatial eco-evolutionary dynamics, that is, ecology and evolution in metapopulations, is often complex and requires simulation based approaches. We will use one such simulation-based framework, individual-based models, in order to investigate dispersal evolution in metapopulations.

Methods: Students will develop their own individual-based metapopulation model in C++ that will allow them to study both ecological and evolutionary dynamics of spatially structured populations. Simple coding in C++ will be combined with version control using git/github and results analyses in R.

Competences:

- Basic coding in C++
- Building simple individual-based models in C++.
- Version control using git/github.

An introduction to laboratory experimentation in community ecology

Emanuel A. Fronhofer (emanuel.fronhofer@umontpellier.fr), ISEM.

Concepts: Causal inference requires experimentation, but experiments in ecology may involve large spatial or temporal scales and be therefore de facto impossible. We will here get to know how to perform experimental community ecology in the lab using model organisms, such as freshwater protists. We will test classical predictions from community ecology, such as Gause's competitive exclusion principle and confront ecological experiments with corresponding, simple mathematical models.

Methods: Students will be introduced to experimental community ecology using standard microbiology laboratory techniques. Time series of abundances will be analysed using mathematical models (ordinary differential equations, ODEs; Lotka-Volterra competition models). We will use Bayesian approaches to fit these dynamical models to experimental time series data.

Competences:

- Microbial ecology lab techniques
- Building simple mathematical models using ODEs
- Fitting of ODEs to experimental data using Stan.

How to infer the structure of complex food webs?

Claire Jacquet (claire.jacquet@umontpellier.fr), ISEM.

Concepts: Feeding interactions between species, the process by which energy and resources pass through living organisms, play a fundamental role in the functioning of ecosystems. Food webs describe the topology of these interactions and are therefore a central tool for studying ecosystem structure and dynamics. In this In Lab teaching session, you will study the structure of complex food webs composed of a large number of interacting species. You will tackle the following questions:

1. How to describe food web structure?
2. What are the general rules that yield food web structure?
3. How to infer food web structure from presence/absence data and species body-size?

Methods: The course consists of short discussions on key concepts and their application using R programming:

1. Use of metrics from network sciences to describe food web structure, use of the package `igraph` to visualize complex food webs
2. Presentation and application of the niche model (Williams and Martinez 2000) to draw complex food webs from simple assembly rules
3. Parameterization of the niche model with data on predator-prey body-size relationships of a marine ecosystem, comparison between observed and predicted food web structure

Ref: Williams, R. J., & Martinez, N. D. (2000). Simple rules yield complex food webs. *Nature*, 404 (6774), 180–183.

Competences:

- Understanding of food web structure and its importance for ecosystem dynamics
- Experience of using R to study a specific ecological topic
- Experience in combining a theoretical approach and observational data

Swimming performance in fish larva challenged to an environmental stress

Catherine Lorin-Nebel (catherine.lorin@umontpellier.fr), Marbec.

Our InLab aims at investigating individual differences and behavioral traits following an exposure to an environmental stressor (here: low pH) in teleost fish larvae. Acidification of aquatic environments is recognized as a global environmental problem. The zebrafish *D. rerio* will be used as a model fish to determine if a low pH affects swimming performance and other behavioral traits. We will test different challenges (such as, a dark/light challenge that elicits an anxiety-like response, or a threatening stimuli that induces an escape behavior) and analyze different behavioral phenotypes (such as, swimming velocity, distance moved, acceleration) in control animals as well as fish that were challenged to lower pH levels.

To investigate these different behavioral traits, we will use the DanioVision system that was designed to track zebrafish larvae and then compare data between different pH conditions. The students will learn to use the DanioVision software and will develop their experimental design according to the available literature. Following the acquisition of the data, students will quantify behavioral traits and interpret data. Students will gain concepts in physiology (acid-base regulation), learn to handle fish larvae and provide a critical analysis of biological data.

Environmental DNA time series in Ecology and Evolution

Christelle Tougard (christelle.tougard@umontpellier.fr), ISEM.

Ecological communities change in time and space, but long-term dynamics at the century-to-millennia scale are poorly documented due to lack of relevant data sets. Nevertheless, understanding long-term dynamics is important for explaining present-day biodiversity patterns and placing conservation goals in a historical context (Bálint et al., 2018: doi10.1016/j.tree.2018.09.03).

To explore past biodiversity, we will use a metabarcoding approach in a paleogenetics context. DNA extraction will be performed from sediments in a dedicated lab (<https://plateformeadndegrade.wordpress.com/>) under strict experimental conditions (lab under UV, bleach cleaning, protection suit) to avoid exogenous contaminations. As it will not be possible to analyse results just after extraction, some examples of research applications will be presented through selected literature.

No particular experimental skills are requested to attend this InLab. However, to avoid contamination by exogenous DNA, rigor and precision will be requested during lab work.