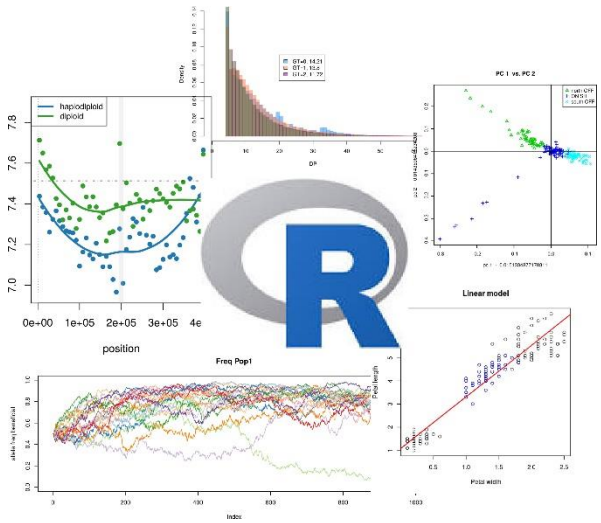

Advanced R for Ecology and Evolutionary Biology

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Calendar: June 30th – July 4th 2025
Duration: 36 hours (contact hours)
Schedule: 9h-12h30 and 14h-17h30, Monday-Thursday; 9h-13h and 14h-18h Friday

Objectives:

Provide students with statistical knowledge and tools to manipulate, analyze and visualize biological data with R. Introduction to modeling, simulations and Bayesian statistics.

Topics:

- Refresher into R
- Exploratory analysis for ecology and evolution (Principal Component Analysis)
- Linear regression and ANOVA
- Hypothesis testing using bootstrap and permutations
- Introduction to analysis of population genetics in R
- Modeling and simulation of dynamics systems
- Bayesian statistics and advanced inference algorithms (Markov chain Monte Carlo)

- Students case studies

Detailed Plan:

- **Refresher into R.** A very quick refresher on R language to be sure that all students know basic R programming
- **Exploratory analysis for ecology and evolution (Principal Component Analysis).** The students will learn how to perform and interpret the results of Principal Component Analyses (PCA) and Multivariate Evolutionary Analyses.
- **Linear regression and ANOVA** (factorial and nested ANOVA). Students will learn how to perform and interpret results from general linear models.
- **Hypotheses testing using resampling approaches** (e.g. bootstrap and jackknife). Many datasets in ecology and evolution violate assumptions of classical statistical tests, and hence resampling approaches became common practice. Students will learn how to perform hypothesis testing using permutation tests, bootstrap and jackknife.
- **Introduction to analysis of population genetics in R:** the students will learn how to compute the basic genetic statistics (genetic diversity, FST), test Hardy Weinberg equilibrium, compare genetic diversity between populations and perform PCA with genomic data.
- **Modeling and simulation of dynamics systems** We will use examples from population genetics (genetic drift) and population dynamics (Lotka-Volterra predator-prey model) to illustrate how R can be used to perform simulations. The students will learn how to model and perform simulations of populations evolving through time.
- **Introduction to Bayesian statistics.** The students will learn how to use a Markov chain Monte Carlo (MCMC) algorithm to estimate parameters of different models of population dynamics.
- **Student's case studies.**

Throughout the course, students will be encouraged to apply the knowledge obtained to data from their own work. Depending on the interests of the participants some of the content can be adjusted to focus more on examples from evolutionary biology or from ecology. On the last day, each student will do a small presentation with data available from their own work, or with possible applications to their research question.

Participants have to be present at 85% of the contact hours (this means that they can miss one half-day), and actively participate in all activities.

This course can give credits to PhD programmes at FCUL or of programmes with partnership from FCUL and other institutions with 6h-7h of contact hours per ECT, as a function of specific requirements. **For these students additionally to the exercises done during the week the delivery of a written report done after the course is mandatory.** For programmes with less hours of contact per ECT (6h/ECT, getting 6 ECTs from the course) students need to do an additional assignment

(summary report). If needed 1 or 2 additional hours of contact may be added. Such report(s) are also advised for other students requesting accreditation of the course in their institutions.

Location: Faculdade de Ciências da Universidade de Lisboa

Nº (min, max) students: 10 – 20

Minimum formation: - Knowledge of R programming syntax and Rstudio. Preference will be given to participants that attend the introductory course in R or that have previous knowledge in R.

Directed to: PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics

Fee: free for 1st year PhD students in Doctoral programmes at FCUL (e.g. Biologia), Biodiversity, Genetics and Evolution (BIODIV UL; UP), Biology and Ecology of Global Changes (BEAG UL, UA) or Sustainability Science (UL, several institutions), when the course counts credits for their formation, in which case the delivery of a final report done after the course is mandatory; the course is also free for more advanced PhD students of the BIODIV programme (ULisboa or UPorto); 50 € for more advanced PhD students of cE3c; 80 € for PhD students of the PEERS network (CFE); 125 € for FCUL Master students and unemployed; 180 € for BTI, BI and other PhD students*; 250 € for Professional and postdocs.

(* For PhD students also doing the Introduction to R course the fee is reduced to 120 €)

When the maximum number of students is reached, 10 vacancies will be available for non-paying 1st year PhD students mentioned above, being, by order of preference students from: 1) cE3c; 2) BIODIV (not from cE3c); 3) FCUL (not from cE3c); 4) Sustainability Science (not from cE3c or FCUL); 5) BEAG (not from cE3c or FCUL).

Deadline for applications: May 23rd 2025

How to apply

Candidates should fill a FORMULARY that will be available after the call is open.

This formulary is strictly confidential, as explained in the introduction, and the data are required because the cE3c Advanced Courses are also offered as part of the PRR programme of FCUL.

When filling the formulary mind to:

1) FILL ALL THE MANDATORY FIELDS
2) UPLOAD CV AND MOTIVATION LETTER, both mandatory; use the names as instructed there
3) If you want to resume later SAVE the formulary, otherwise you will need to fill everything again
4) At the end SUBMIT the formulary before exiting

For any doubts please contact the cE3c coordinator of the cE3c courses Margarida Matos (mmmatos@fc.ul.pt) and the teacher Inês Fragata (irfragata@fc.ul.pt)