# 465990-HS2025-0:
# Theoretical ecology and evolution, research practical
# Introduction

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# About me

Diplom in Mathematics from University of Bielefeld (Germany) - **Modeling recombination**

PhD in Population Genetics from Vetmeduni Vienna (Austria) with some months at UT Austin (Texas) - **Modeling speciation**

Postdoc at EPFL (Switzerland) with some months at UC Berkeley (California) - **Evaluating fitness landscape models with experimental data**

Group Leader at the Gulbenkian Science Institute in Oeiras (Portugal) - **Evolutionary Dynamics**

Since 1 Oct 2020: Professor at IEE, Head of Division **Theoretical Ecology and Evolution**

**(**Since 1 Aug 2024: Institute Director, IEE)

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# Co-Teacher intro

Dr. Franziska Brenninger (Evolving Interactions)

Russ Jasper (THEE)

Julio Ayala (THEE)

Dr. Ana-Hermina Ghenu (IBU)

# About you (<1 min/person)

Name

Study program, year and field of study

Something that fascinates you about biology OR Your favorite course so far

*“All models are wrong, but some are useful.”*

–George Box

# Learning Outcomes of the next 3 weeks

Upon completion of this course the students are able to…

- Write small pieces of code in R to analyze data/a model and to visualize results
- Follow the most important steps for reproducible (computational) research
- Interpret data/results related to the course projects
- Define and use common terms related to the course projects
- Criticize model assumptions
- Phrase theory questions and hypotheses
- Present and discuss modeling, data analysis, and coding challenges and solutions

# Why is this important?

Ecology and evolution are built on models & theory

Models help build intuition and testable hypotheses

Models are everywhere and come in different complexities (often underlying “big data” studies too)

Model choice/approach/assumptions crucially affect results

Almost no way to get around coding in biology today

Presenting and discussing a problem is often its solution

Reproducibility is key to good scientific work (and helps you too)

# Our expectations

**Talk to us! Ask if anything is unclear and give feedback, especially if you feel bored or overwhelmed.**

Be on time for check-ins and pay attention during tutorials

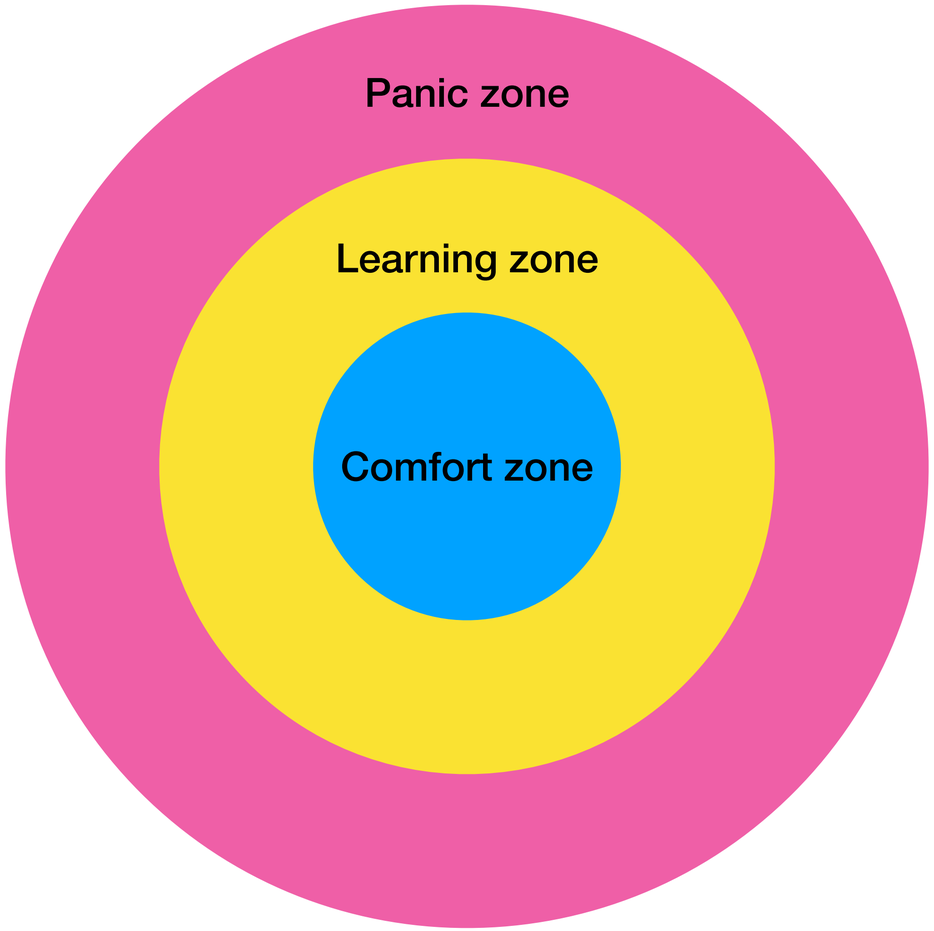
First try out things on your own, then ask for help - both equally important!

Embrace the experience - I am expecting fun 3 weeks

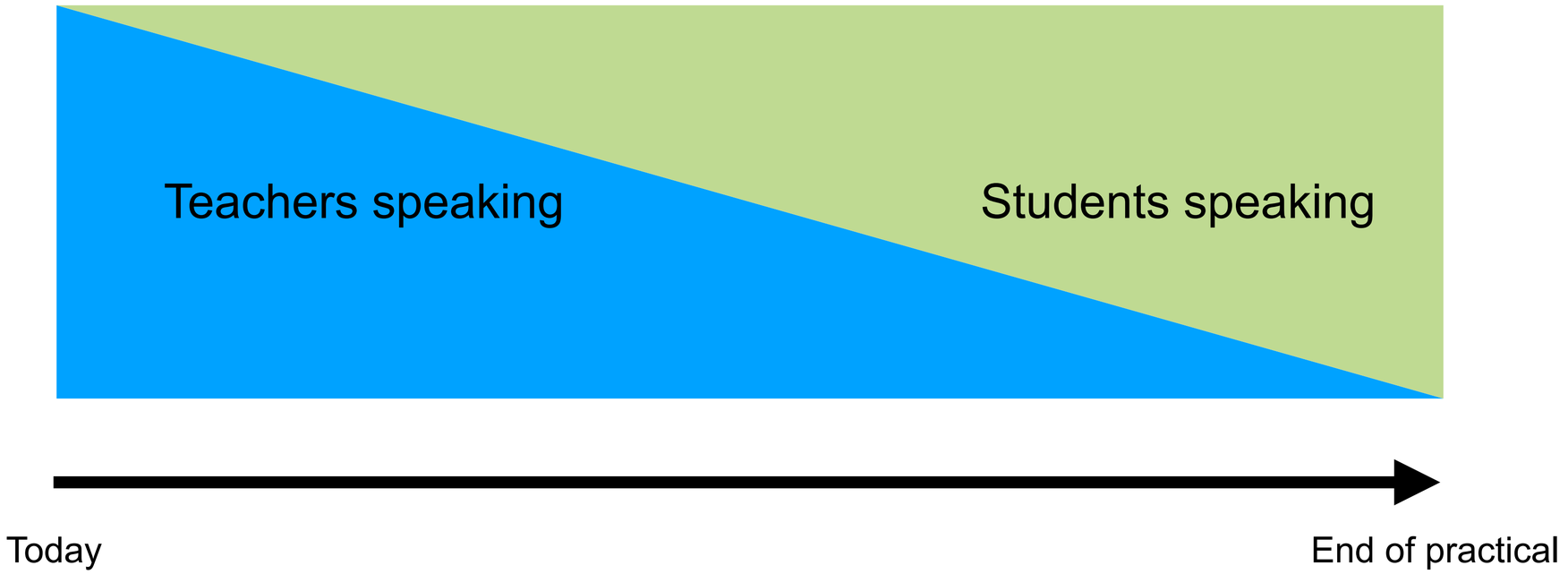
Friendly teamwork and collaboration

Use Teams for virtual communication - preferably share questions with group rather than via PM

# The learning zone model



# Our hope


Teachers speaking
Students speaking
Today
End of practical

# Grading criteria

Presence during check-ins and tutorials

Active participation during discussions

Completed project (see Data Management Plan)

Quality of code, report, & presentation

5 ECTS credits ≈ 125-150 hours of work, of which ≈ 63 during the official practical hours

# Your expectations

Why did you choose this practical?

What do you expect to learn?

# Schedule

Week 1 - coding camp & getting to know your project

Week 2 - getting & visualizing results

Week 3 - writing & preparing presentation

Key dates:

30 October 9:15: your presentations to the THEE lab

7 Nov 23:59: share project folder with draft of report

14 Nov 23:59: return feedback to your colleagues

5 Dec 23:59: share final version of project folder & report

# Rough schedule for this week

Tuesday: warming up to coding; reproducibility

Wednesday: brainstorming of topics; meet & greet your project

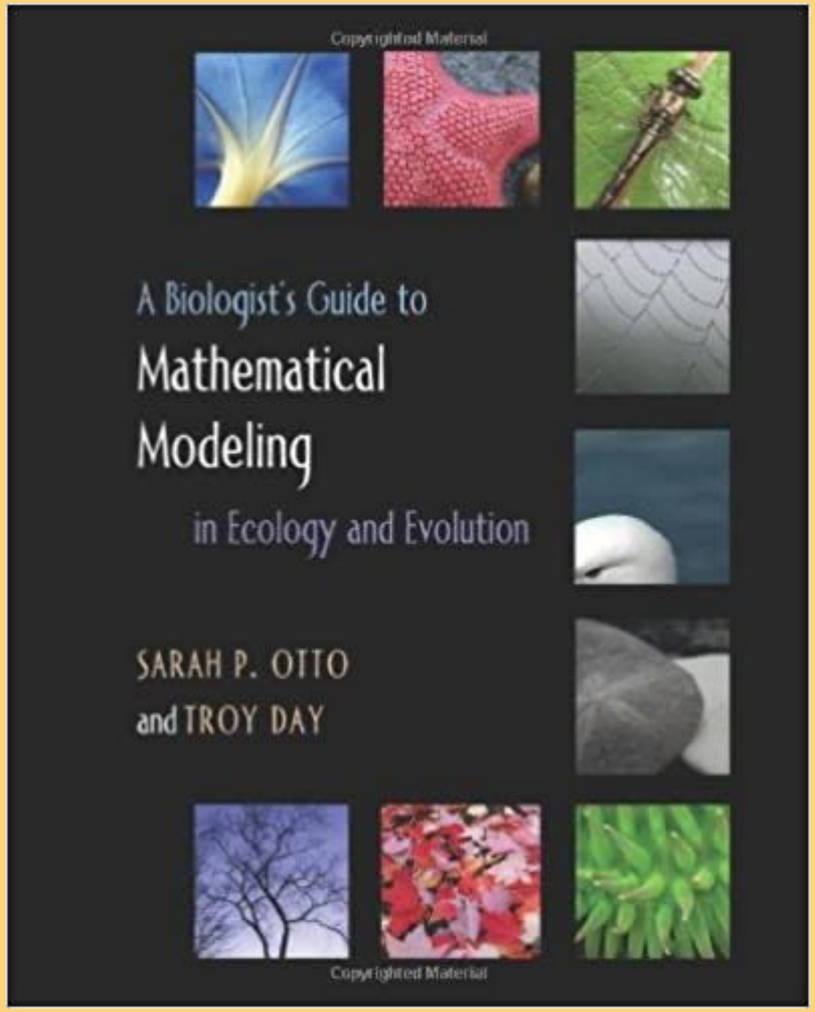
Thursday: first steps of your analysis

General structure:

Daily check in at 9:15 (or 8:15 on some days). Other check-ins as discussed & required. At least one of us will always be present at the lab during the practical hours. (Anyone working early?)

Lunch break from ~12:00-13:00

# 7 steps to modeling a biological problem




For more, check out Otto & Day: A Biologist's Guide to Mathematical Modeling in Ecology and Evolution: https://press.princeton.edu/books/hardcover/9780691123448/a-biologists-guide-to-mathematical-modeling-in-ecology-and-evolution

You find Chapter 2 in our shared folder; it provides the guideline to the 7 steps we will be going through in the practical.

# Evolutionary rescue - our “grand" topic of the year

A population that is doomed to extinction survives because of the spread of beneficial genetic change(s)

**Our suggestion:** we provide you with the basic code for a model and you modify, extend, and analyze it according to your interests

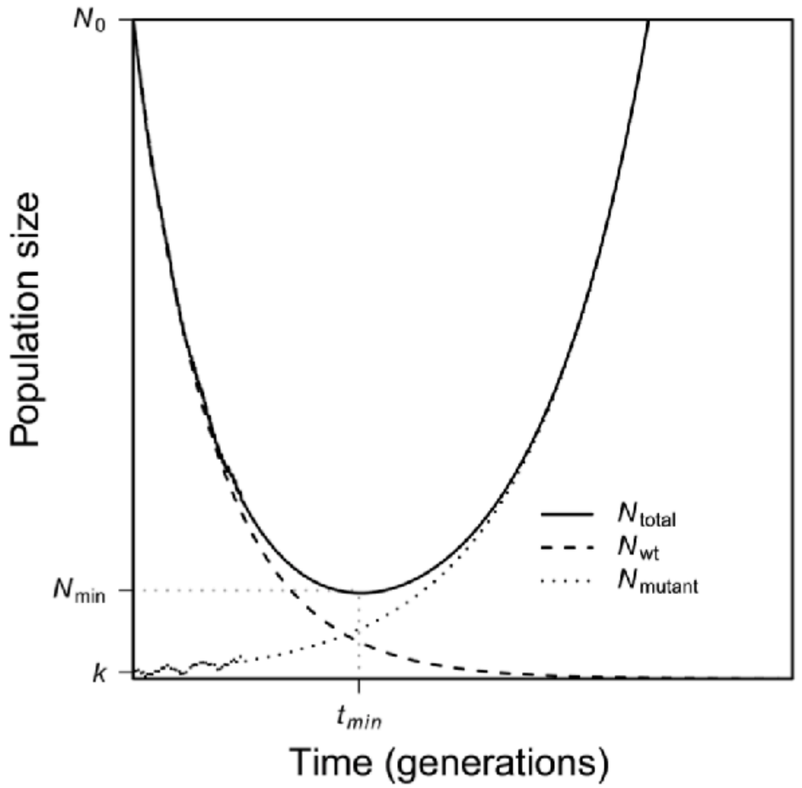
# Materials

Orr, H. A. & Unckless, R. L. The population genetics of evolutionary rescue. PLoS genetics 10, e1004551 (2014).

Orr, H. A. & Unckless, R. L. Population Extinction and the Genetics of Adaptation. The American Naturalist 172, 160–169 (2008).

Alexander, Helen K., Guillaume Martin, Oliver Y. Martin, and Sebastian Bonhoeffer. 2014. “Evolutionary Rescue: Linking Theory for Conservation and Medicine.” Evolutionary Applications 7 (10): 1161–79.

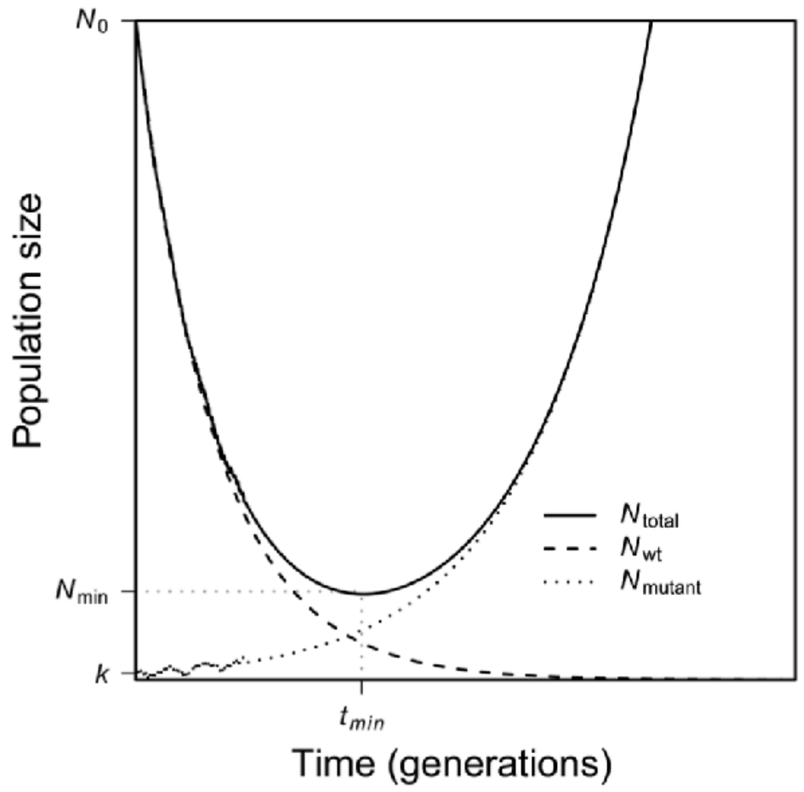
# What the dynamics of evolutionary rescue look like from a modeling point of view




Sudden environmental change at time 0 that leads to a negative mean fitness/growth rate

How likely is it that a new or existing beneficial mutation can rescue the population from extinction?

# Eco-evolutionary features of the model




The beneficial mutation has to establish before the population size is too small (eco-evo feedback # 1)

Genetic composition of the population changes growth rate (eco-evo feedback # 2)

We consider new mutations (i.e. the beneficial mutation appears after the environmental change) in comparison to existing mutations (“standing genetic variation”)

# Parameters of the model

Initial population size: $N_0$

Rate of population decline: $r$ (growth rate $R = 1 - r$)

Selection coefficient of the beneficial mutation: $s > r$

Mutation rate to the beneficial mutation: $u$

Initial frequency of the beneficial mutation: $p_0$

# The math coming out of this model

Probability of evolutionary rescue through a new mutation:

$$P_{\text{new}} = 1 - \exp\left(-\frac{2N_0u(s-r)}{r}\right)$$

Probability of evolutionary rescue through an existing mutation:

$$P_{\text{stand}} = 1 - \exp\left(-2N_0p_0(s-r)\right)$$

Total rescue probability: $P_{\text{total}} = P_{\text{new}} + P_{\text{stand}}$

When does standing variation rescue the population more likely than a new mutation? $p_0 > \frac{u}{r}$

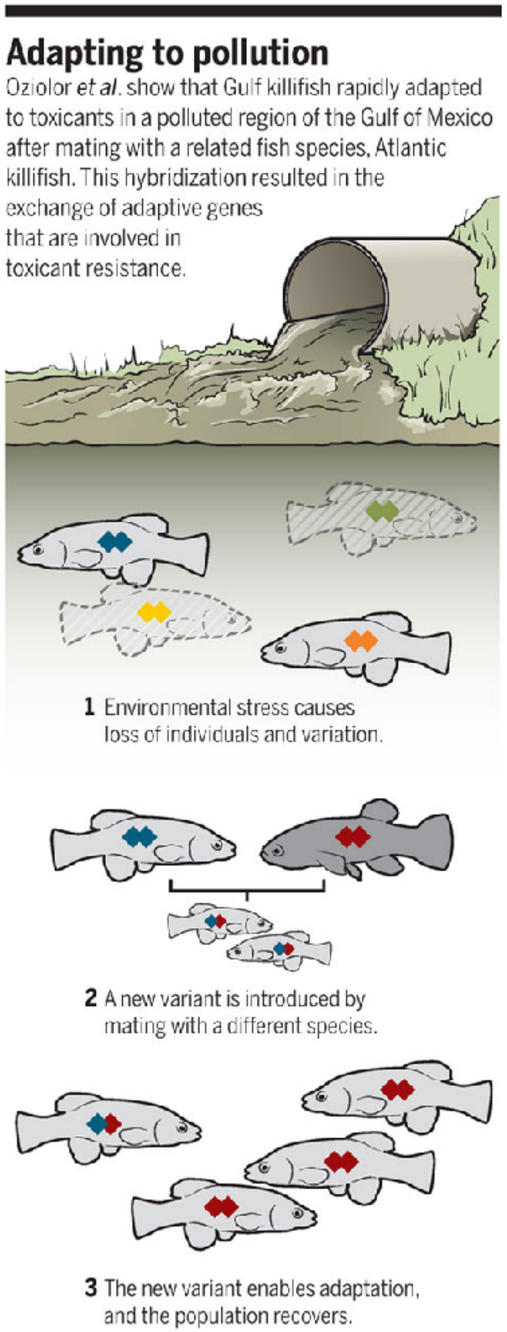
# Why evolutionary rescue matters in the face of climate change


https://www.youtube.com/watch?v=ZCKRjP_DMII

# Genetic rescue: human-facilitated evolutionary rescue

https://www.youtube.com/watch?v=IkMnpNu6IOI

# An example from the wild




Pfennig, K. S. How to survive in a human-dominated world. Science 364, 433–434 (2019).

Oziolor, E. M. et al. Adaptive introgression enables evolutionary rescue from extreme environmental pollution. Science 364, 455–457 (2019).

# Time for action

Download the file evolutionary-rescue-basic-discrete-time.Rmd from https://github.com/banklab/THEErp2025 and **save a copy under a new name** on your computer. Open the file in RStudio and “knit" the file to read the html output; this might require (automatic) installation of some packages.

Read the document and follow its instructions. We will continue there.