

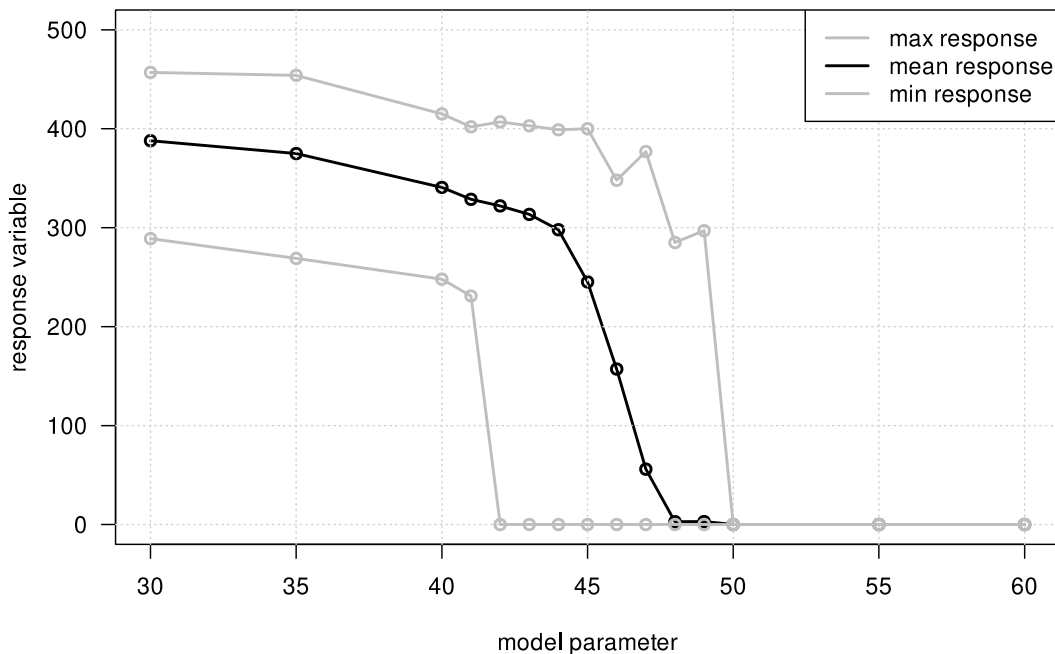
Project Syllabus

Time line

- 1) *baseline scenario:* *now – 04.12.2023*
finish baseline scenario by early December, ideally way before Christmas. The progress in the baseline scenario will vary between projects because some baseline scenarios are more demanding than the others. When you are done with the baseline scenario, I strongly recommend to show me your results. This will help to confirm your finding and biological understanding.
- 2) *your own research idea:* *04.12.2023 – January*
As soon as you are done with the baseline scenario, and you showed me your results, start to develop your own research idea. Here, it can make sense to show me your idea before starting to work on it. This is not a must, but recommended. Remember that those teams working on the same project must not develop the same research idea!
- 3) *presentation:* *29.01.2024 / 02.02.2024*
We will hold a “mini-symposium” over the course of two afternoons. You will present your results to the other course members, and potentially to interested people from the Plant Ecology Group. More details are provided below.
- 4) *report & R script:* *3-4 weeks after presentation*
After the presentation, you need to submit two things:
1) a short report on your research project (maximum three pages of text; a single PDF for the team).
2) one R script per team.
You will find more details on the report and the R script below.
- Grading*
Each team will get the same grade. This is mainly because it is nearly impossible for me to differentiate between your single contributions. You will win and loose as a team. If one team member however was *clearly* contributing less to the project, I will provide two separate grades.
- Questions & support:*
I am in the lecture hall during the lecture hours (Monday and Friday) to answer question, help with coding issues, etc. However, if nobody shows up within the first 20 minutes, I might leave again. If you want to show me your results on the baseline scenario, or discuss your research ideas, please send me a short note beforehand (to make sure that your slot is not colliding with that other teams).

1) Baseline scenario

Please make sure that you explore the behavior of the baseline scenario properly. It is not sufficient to run just a few simulations, for a couple of parameters, and explain your observations. Instead, you need to explore the parameter space systematically. Only such an exploration will allow you to obtain a solid understanding of how certain parameters affect the outcome of your model. At minimum, you need to obtain such kind of plot(s):



On the x-axis, you need to put a certain model parameter (e.g., dispersal probability, attack rate, ...). On the y-axis, you need to plot the response variable (e.g., total number of infected individuals, a measure of diversity, equilibrium population size, ...). It is furthermore essential that you run replicates for each parameter combination and plot the range of possible outcomes across the replicates (the gray lines in the plot above). This will illustrate by how much stochasticity determines the model outcome. Note that the population size in your simulations will have a considerable effect on the extent of stochasticity. The larger the population size, the smaller should be the variability among replicates. Ideally, you span the entire range of realistic parameter values (for instance, $0 < d < 1$ for survival). Most importantly, you should be able to provide a biological explanation for the underlying mechanism. Why is the response variable declining with parameter A?

The exact design of the plot is not important and you can easily pick dots with error bars instead of lines, use different colors, or plot the 90 percentile instead of the max- and min-values. You also do not need to provide such a plot for each parameter of your model, but for each parameter of interest! Some parameters are simply not important/interesting. There might also be additional kinds of plots that could provide interesting insights, but plots like this one above should build the core of your analysis. In most cases, I recommend to avoid bar plots (similar to histograms) or 3D diagrams, these are suited only for specific purposes (e.g., illustrating a trait value distribution). Make sure that your **Figure captions provide all the relevant information** (Which scenario is shown? Which parameter values have been used to create the plot?), that you **apply clear axis labels**, and that your **figure have a sufficient resolution** (e.g., exporting figures in vector-based formats like svg greatly improves the plot quality).

If your baseline scenario has several parameters of interest, you could even think about a fully factorial design (not a must, but useful). With a **fully factorial design**, you simulate all the possible parameter combinations. For instance, with 5 values of *parameter A* and 4 values of *parameter B*, a fully factorial design leads to $4 \times 5 = 20$ distinct parameter combinations. When further running 10 replicates per parameter combination, you need to run 200 simulations in this example. The great benefit of a fully factorial design is to test if certain model behaviors persist in all the possible conditions. For instance, does the response variable always decline with increasing value of parameter A, no matter of parameter value B?

2) Your own research idea (the fantastic scenario)

Developing your own research project is a challenging exercise, primarily because you need to develop a proper research hypothesis. This sounds easy, but it is not. A research hypothesis must be justified by a biological observation or fact and aims to solve a problem, to fill a research gap, or to answer an applied question. Please provide such a motivation in the presentation and the report. In addition, a hypothesis suggests an expected outcome. To check whether you developed a proper hypothesis, or not, you should be able to sketch the expected plot with pen and paper. In fact, one plot of your own project should look very similar to that one above (see section on the baseline scenario). The key questions for your specific hypothesis are: 1) What is the model parameter that you want to study systematically (what to put on the x-axis)? 2) What is the response variable (what to put on the y-axis)? 3) What kind of pattern do you expect, and why?

3) Presentation

You need to prepare a presentation of ~15 minutes, that will be followed by ~15 minutes of questions and feedback. All the group members should contribute equally to the presentation.

If your baseline scenario is rather simple and you managed to achieve plenty of new findings in your own project, you could present the results of the baseline scenario in the introduction, and use them as a starting point to introduce your own ideas. Note however that some baseline scenarios are quite complicated on their own and are not suited for such kind of strategy.

In your presentation, make sure to develop a clear and easy-to-follow story line. This should help to guide the attention of your audience carefully from one step to the next. That means that you should avoid any “side stories” that distract the attention from the main story line. All your arguments should follow a linear logic where each step nicely connects to the previous step.

Introduction:

The introduction should direct your audience from the broad-scale topic (the 10,000 feet perspective) to a specific problem or open question that justifies/motivate your project. Ideally, you lead the audience to a “research gap” that you want to answer.

The model:

In this part, you need to illustrate the ecological scenario of your study and provide a clear understanding of your simulation scenario. How does the population/community look like? What events take place each day/year? What is happening during these events? What is your study design? What quantities do you track over time, and when? **Important:** Do not dive too much into technical

details of your simulations. Focus on the biological questions and address your talk to biologist (including empiricists that work on other topics).

Results:

Do not necessarily show us all your results and “bomb” us with too many plots, but focus on a small number of key findings. Use a handful of wisely chosen plots that illustrate the fundamental biological mechanisms. Importantly, show “good” plots with clear and concise color schemes, large font sizes, well chosen axes titles, and legends whenever necessary.

Conclusions:

Head back to the 10,000 feet perspective and summarize what you have learned. Ideally, connect your findings to some of the questions, examples, or ideas that you raised in the introduction, or to previous publications.

To those teams working on the same topic:

Check if you can coordinate your talks. For instance, it does not make sense to hold the same introduction on disease dynamics multiple times in a row. Instead, all teams might contribute to a single (slightly longer) introduction on this topic. Similarly, all teams hopefully obtain similar result on the baseline scenario and it is not necessary to present these findings several times in a row.

4) Report & R script

The project report should not exceed 3 pages of text (figures and captions can be put on top) and should be written in a short and concise manner with a clear “story line” that guides the reader carefully through your findings. The report must have the same structure as described for your presentation (see the information above on introduction, the model, ...). Make sure that your plots are of high quality (e.g., export as vector-based format from R). The axis titles and labels of the plots must be readable (large enough font size), the figures should have a good resolution (scalable vector formats help a lot here, e.g., export your graphs from R as svg-files). The figure captions must contain all information that is necessary to understand the content (parameter values of the simulations) and you must add Figure references in the main text. The submission date after your talk might allow you to incorporate some of the feedback on your presentation.

In addition, each team should submit a single R script. The R script should contain all the simulations of your baseline scenario and your own research idea. In fact, the script should allow me to reproduce all your findings and all your plots (presentation and report). Please indicate in the script if a plot is used in the presentation or report. Apply a good structure to your script and use *code folding* wisely! In addition, *comment your code* extensively. This does not mean that you need to write long comments (!), but a few key words every other line should be enough. The main purpose of code folding and commenting is to help me to navigate your code and to help you to establish a good coding practice. Try to keep your code as tidy and as “minimalistic” as possible.