

Master thesis topics at the Lab of Environmental Change and Community Ecology

2026–2027 edition

General information

The team of Prof. Frederik De Laender at UNamur studies a deceptively simple question: **what happens to ecosystems when biodiversity changes?** We want to understand why some species disappear while others persist, how environmental change reshapes communities, and why these changes matter for the way ecosystems function. For example, our work has shown that biodiversity can alter how phytoplankton communities resist and recover from environmental stress [Baert et al. 2016](#), and that the effect of biodiversity on ecosystem functioning itself changes with environmental stress [Baert et al. 2018](#).

A particular strength of our lab is that we approach these questions from several directions. We use **controlled experiments**, especially with phytoplankton, to manipulate biodiversity and environmental conditions; **mathematical models and computer simulations** to uncover the mechanisms behind the patterns we observe; and **field data** to ask whether ideas developed in simplified systems also help us understand natural communities. For instance, recent work combined ecological theory, simulations, empirical information on temperature and pollution, and field data on stream invertebrates to show how average species responses can help predict effects of environmental change on coexistence [De Laender et al. 2023](#).

Our lab currently brings together **6 PhD students, 1 postdoctoral researcher, and 1 technician**, creating a small but active research environment with expertise ranging from experiments to ecological modelling and data analysis.

As a thesis student, you therefore join a group working at the intersection of **biodiversity, global change, ecosystem functioning, and ecological stability**. Depending on the project, you may grow organisms and run experiments, analyse ecological data, build and test models, or combine several of these approaches. You will meet regularly with the promoter and work closely with experienced researchers, while developing quantitative skills in R, experimental design, and ecological modelling that are useful well beyond ecology.

Both experimental topics below are carried out in collaboration with the **BCCM/DCG culture collection at Ghent University**, which maintains diatoms and other microalgae and provides biological material and culture expertise for these experiments.

Topic 1: Does environmental history matter? How stressor sequences shape phytoplankton communities

Description

Natural communities are increasingly exposed to multiple environmental stressors, including warming, pollution, changes in nutrient availability, salinity, and altered light conditions. These stressors are often studied by applying them simultaneously. In nature, however, environmental changes can also occur sequentially: a community may experience one stressor, recover partly, and then encounter another. Its response to the current environment may therefore depend on what it experienced before.

This thesis will investigate whether the **order of environmental stressors** affects the performance and composition of phytoplankton communities. Using controlled microcosm experiments, the student will expose synthetic algal communities to different sequences of environmental conditions. The central hypothesis is that identical stressors can have different effects depending on the preceding environmental history. Such history dependence may arise because previous exposure changes species abundances and community composition (**ecological memory**), but also because it leaves persistent changes in the phenotype or physiological state of individual strains (**phenotypic memory**).

The project will focus on a manageable subset of the larger experimental framework developed in our laboratory. Depending on the final design, the student can compare selected stressor sequences, quantify whether the response to a focal stressor depends on earlier exposures, and examine whether different histories leave detectable effects during recovery.

The experimental work will be conducted in collaboration with the **BCCM/DCG culture collection at Ghent University**, providing access to well-characterized diatoms and other microalgae and expertise in their cultivation.

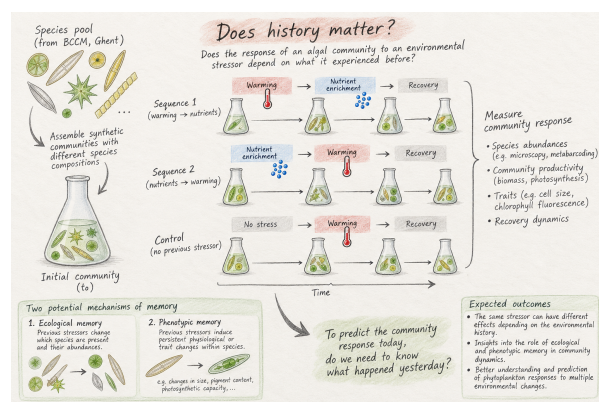


Figure 1: Does environmental history matter? Overview of the stressor-sequence experiment and the two potential mechanisms of ecological memory.

Methods

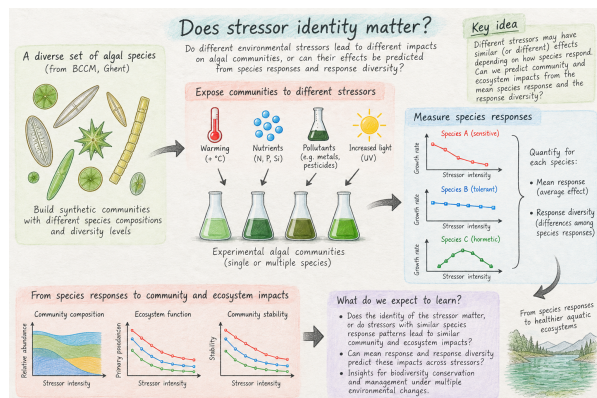
- **Experimental system:** synthetic phytoplankton communities assembled from laboratory algal strains.
- **Stressor sequences:** expose replicate communities to contrasting orders of selected environmental stressors under controlled conditions.
- **Measurements:** follow strain and community abundances through time using flow cytometry; complementary measurements can include cell size and chlorophyll fluorescence as indicators of phenotypic state.
- **Response variables:** quantify community performance, composition, responses to focal stressors, and recovery after stress release.
- **Data analysis:** use R to analyse time series and test whether current community responses depend on previous environmental conditions.
- **Extension:** if feasible, compare observed dynamics with predictions from a simple population-dynamic model that assumes responses depend only on current conditions.

This thesis provides training in experimental community ecology, phytoplankton culturing, flow cytometry, and quantitative analysis, while addressing a timely question: **can we predict ecological responses from present-day conditions alone, or do we also need to know an ecosystem's past?**

Topic 2: Does stressor identity matter? Predicting community responses from how species respond

Description

Ecologists usually classify environmental change by the **identity of the stressor**: warming, pollution, nutrient enrichment, harvesting, and so on. But does that identity actually tell us what will happen to a community? Two very different stressors might have similar ecological consequences if they affect the species in a community in similar ways. Conversely, the same stressor could have very different consequences in two communities whose species respond differently.



This project asks whether we can move beyond stressor identity and instead predict ecological impact from two properties of species responses. The **mean response** describes whether species are, on average, positively or negatively affected by a stressor. **Response diversity** describes how differently species respond: all species may react similarly, or some may decline while others are little affected or even benefit. Theory from our lab suggests that such relatively simple information can predict important effects of environmental change on species coexistence [De Laender et al. 2023](#), including effects of multiple stressors [Laloux & De Laender 2026](#).

The thesis will put this idea to an experimental test. First, single-species bioassays will quantify how algal species respond to contrasting stressors such as temperature change, nutrient pollution, and biomass extraction. These measurements will be used to make **a priori predictions** about the response of multispecies communities. Community microcosm experiments will then test whether stressors that generate similar mean responses and response diversity also generate similar ecological impacts – even when the stressors themselves are very different.

The central question is therefore: **does stressor identity matter once we know how the component species respond?** If it does not – or matters much less than expected – this could provide a more general way to understand environmental change without having to study every possible stressor separately.

This topic is connected to a larger **Marie Skłodowska-Curie research project on response diversity and ecological stability**, but the Master thesis is a focused project carried out at UNamur. The experimental work will be conducted in collaboration with

Figure 2: Does stressor identity matter? Species-level responses are used to predict community and ecosystem impacts across contrasting environmental stressors.

the **BCCM/DCG culture collection at Ghent University**, providing access to well-characterized diatoms and other microalgae and expertise in their cultivation.

Methods

- **Single-species bioassays:** measure responses of algal strains to selected environmental variables, potentially including temperature, nutrient pollution, and biomass extraction.
- **Response metrics:** calculate the mean response across species and their response diversity for each environmental change.
- **Community experiments:** assemble multispecies algal communities and expose them to selected environmental drivers.
- **Change regimes:** depending on the final experimental design, contrast sustained (**press**) and temporary (**pulse**) environmental changes.
- **Ecological responses:** quantify effects on population dynamics, community composition, temporal stability, and/or species coexistence.
- **Measurements:** use flow cytometry to track species abundances and community dynamics through time.
- **Data analysis:** use statistical models in R to test whether mean response and response diversity predict ecological impact across environmental contexts.

This project combines high-throughput experimental ecology with quantitative community ecology. It asks whether apparently different forms of environmental change can be understood through a common set of biological response properties, potentially providing a more general way to predict how ecological communities respond to a changing environment.

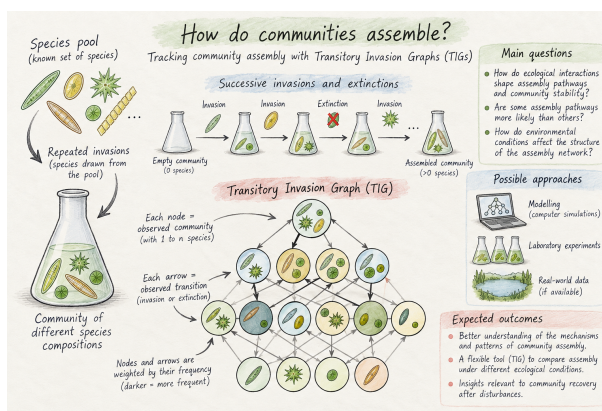
Topic 3: How do ecological communities assemble?

Mapping assembly pathways with Transitory Invasion Graphs

Description

How does an ecosystem go from an initially empty community to a community containing many interacting species? **Community assembly** emerges through successive species invasions and extinctions, and understanding these pathways is important both for fundamental ecology and for understanding how communities form or recover after disturbance.

A major difficulty is the enormous number of possible communities and transitions between them. We have recently developed a new approach, the **Transitory Invasion Graph (TIG)**, to summarize this complexity. A TIG follows an ecosystem exposed to repeated invasions from a known species pool and represents the resulting assembly process as a network. **Nodes are the communities that are actually observed, while edges are the observed transitions between them.** Weighting nodes and edges by how frequently they occur highlights the dominant community states and assembly pathways.



The method has already revealed different patterns of assembly, including effects of species interactions and community stability, variation in the diversity of possible assembly pathways, and distinct phases in which assembly is influenced by species arrival order or by species properties. However, TIGs are still a new approach and have so far been explored using simulated communities. This leaves considerable room for a Master thesis to help develop and test the framework.

Depending on the student's interests, the project can focus on **extending TIGs to broader ecological conditions**, using them to compare assembly under contrasting environmental scenarios, or using TIGs to investigate fundamental questions about why some assembly pathways are common while others are rarely observed. The work can be based primarily on ecological modelling and computer simulations, with the possibility of connecting the approach to laboratory data.

Methods

- **Ecological modelling:** simulate community assembly through repeated species invasions and extinctions.

- **Network analysis:** construct TIGs in which nodes represent observed communities and edges represent transitions between them.
- **Assembly dynamics:** quantify which communities and transitions dominate, how many alternative pathways occur, and how these patterns change through time.
- **Comparative scenarios:** test how species interactions, environmental conditions, or other ecological mechanisms alter assembly pathways.
- **Programming and data analysis:** implement simulations and analyses in R and/or other appropriate computational tools.
- **Possible extension:** explore how TIGs can be constructed from laboratory or real-world community data rather than simulations alone.

This topic is particularly suited to a student who enjoys **ecological theory, coding, and thinking about how complex community dynamics can be reduced to intuitive patterns**. The exact research question can be tailored within the broader TIG framework.

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Selected references

Baert, J. M., De Laender, F., Sabbe, K. & Janssen, C. R. (2016). Biodiversity increases functional and compositional resistance, but decreases resilience in phytoplankton communities. *Ecology*, 97, 3433–3440. <https://doi.org/10.1002/ecy.1601>

Baert, J. M., Eisenhauer, N., Janssen, C. R. & De Laender, F. (2018). Biodiversity effects on ecosystem functioning respond unimodally to environmental stress. *Ecology Letters*, 21, 1191–1199. <https://doi.org/10.1111/ele.13088>

De Laender, F., Carpentier, C., Carletti, T., Song, C., Rumschlag, S. L., Mahon, M. B. et al. (2023). Mean species responses predict effects of environmental change on coexistence. *Ecology Letters*, 26, 1535–1547. <https://doi.org/10.1111/ele.14278>

Laloux, B. & De Laender, F. (2026). Mean response and response diversity predict interactive stressor effects on coexistence in competitive communities. *Proceedings of the Royal Society B*, 293. <https://doi.org/10.1098/rspb.2025.3093>