Thesis topics 2025-2026

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General information

The team of Prof. Frederik De Laender at UNamur offers an inspiring environment for ambitious students eager to grow as scientists. We are a dynamic, supportive, and productive group where you will not only learn a lot, but also enjoy the process. What makes our lab special?

- Top-notch supervision: you'll meet weekly with the promoter for guidance, and even more frequently with experienced technical supervisors who provide hands-on support.
- Internationally recognized expertise: our group is at the forefront of theoretical ecology and population and community ecology, giving you the chance to contribute to cutting-edge questions in biodiversity, ecosystem functioning, and global change.
- Strong quantitative training: from ecological modeling to advanced data juggling, you will develop a skillset that is highly transferable — whether you pursue a career in science, data analysis, or beyond.

Joining us means you will work on innovative ecological projects (such as forest carbon dynamics or biodiversity under multiple stressors), collaborate within a friendly and motivated team, and benefit from our extensive international network of collaborators.

If you are curious, motivated, and ready to challenge yourself, we will provide the tools, mentoring, and atmosphere to help you succeed — and have fun along the way.

1 Topic 1: Productivity across space: How patch number and dispersal shape plankton productivity.

1.1 Description

Biodiversity and productivity are not only determined by local conditions but also by how ecosystems are connected in space. In nature, species live in metacommunities — networks of patches linked by dispersal. Dispersal can allow species to colonize new habitats, maintain diversity, and rescue declining populations in stressful conditions. Recent theory and work in our lab suggest that species coexistence becomes easier in larger metacommunities, but how this translates into ecosystem productivity in stressed landscapes is still poorly understood.

This project will focus on measuring how productivity of highly diverse plankton communities depends on the number of patches and the rate of dispersal across stressed landscapes. By creating

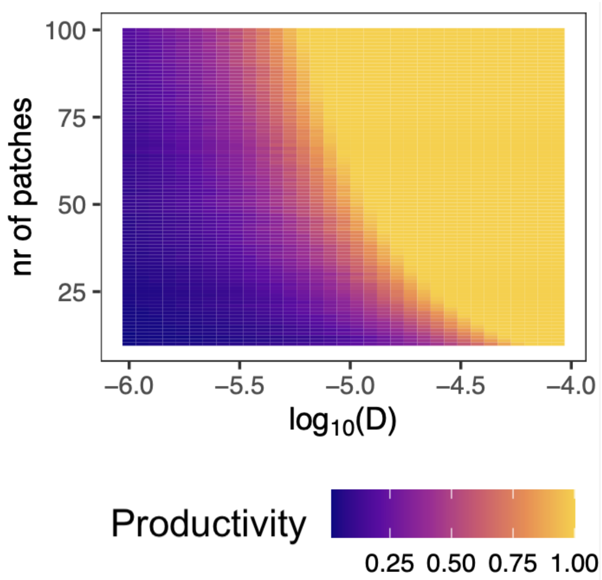

Figure 1: You will test the hypothesis that mean productivity across patches in a metacommunity is larger when there are more patches, or when patches are better connected (p is the number of patches, D is the dispersal rate among those patches).

simple but realistic networks of connected microcosms, the student will test how spatial structure influences productivity and stability in multispecies communities (Fig. 1). The results will contribute to a better understanding of how landscape fragmentation, local environmental stress, connectivity, and dispersal shape ecosystem functioning — with implications for conservation and spatial planning.

1.2 Methods

- Experimental setup: Construct spatial networks of microcosms (e.g., flasks or multi-well plates) inhabited by diverse plankton communities. Vary the number of patches (small vs. large networks) and dispersal rates (from isolated to highly connected).
- Measurements: Use flow cytometry and fluorescence to quantify cell abundance, biomass, and light capture as proxies for ecosystem productivity. Track communities over time to estimate growth rates and stability.
- Modeling extension (if interested): Develop simple numerical models of metacommunities to simulate productivity under varying patch numbers and dispersal rates, and compare with experimental data.
- Analysis tools: R or Python for time series modeling, mixed-effects models, and network visualization.

This thesis will provide hands-on training in experimental ecology, quantitative modeling, and spatial theory, using cutting-edge methods to test fundamental principles of biodiversity and ecosystem functioning.

2 Topic 2: Is biodiversity an insurance against stressor diversity? A microcosm test with phytoplankton communities.

2.1 Description

Global ecosystems are increasingly subject to multiple interacting stressors, such as warming, eutrophication, and pollution. Predicting responses is difficult because stressors may interact synergistically or antagonistically, while biodiversity can buffer ecosystem function through compensatory dynamics. However, it is unclear if this insurance effect holds when stressor richness increases and the ecosystem is put under untenable pressure.

This thesis will test biodiversity–stressor interactions in a simplified laboratory system. Using phytoplankton microcosms, the student will expose a subset of 3–4 algal strains (e.g. *Synechococcus*, *Chlorella*, *Chlamydomonas*) to 2–3 stressors (e.g. warming, nutrient enrichment, shading, pollution), both individually and in combination. Communities of different richness (monocultures vs. mixtures) will be compared in terms of growth, biomass, and light capture. The main hypotheses are that (i) biodiversity reduces functional loss under stress, (ii) stressor interactions amplify or dampen biodiversity effects, and (iii) stressor similarity modulates response diversity and resilience. If time permits, we will also investigate the influence of stressor interactions on these hypotheses (Fig. 2).

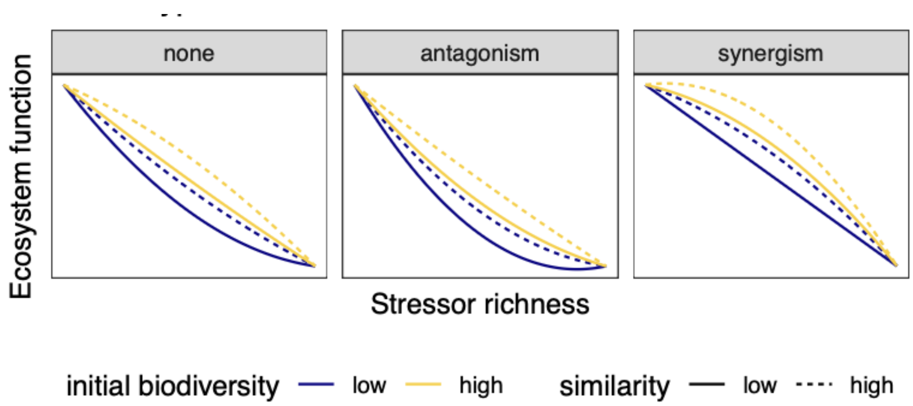

Figure 2: You will test the hypothesis that the negative effect of stressor richness (on the x-axis) on ecosystem function (on the y-axis) is smaller when initial biodiversity is higher, but that this benefit is lost at high stressor richness. When stressors are more similar (see legend) we expect that biodiversity has a higher buffering effect. You will further test the hypothesis that antagonistic stressor interactions shift these trends down, while synergistic stressor interactions have the opposite effect.

2.2 Methods

- Culturing & experimental design: Microcosms in well plates under controlled light/temperature; biodiversity levels (1 vs. mixtures) crossed with single and combined stressors.
- Measurements: Flow cytometry for cell abundance, size proxies, and fluorescence (chlorophyll, accessory pigments); biomass estimates from biovolume calculations.

- Data analysis: Growth curves fitted with generalized additive or logistic models; mixed-effects models testing effects of biodiversity, stressor richness, and interactions.
- Tools: R.
- Extensions: If time permits, functional partitioning (selection vs. complementarity) could be applied to community outcomes.

This project trains the student in experimental ecology, flow cytometry, and advanced data analysis, while contributing insights into biodiversity's role under global change.

3 Topic 3: Chaos in the forest(?)

3.1 Description

Forest soils regulate carbon fluxes through complex interactions among organic matter, microbes, and soil fauna. Network models of carbon pools and fluxes suggest that such systems may exhibit nonlinear dynamics, including multiple attractors, tipping points, and chaotic regimes. Detecting such behavior is critical for predicting soil carbon stability and resilience under changing forest composition and environmental conditions.

This thesis will analyze and model forest soil carbon dynamics to test for nonlinear behavior. The student will use an existing soil carbon model, and parameterize it with empirical data on carbon pools, microbial traits, isotopes, and faunal contributions. Hypotheses are that (i) forest soil systems can sustain alternative attractors corresponding to distinct carbon cycling regimes, (ii) chaotic dynamics emerge under certain parameter values, and (iii) tree composition and soil conditions influence the likelihood of nonlinear shifts (Fig. 3).

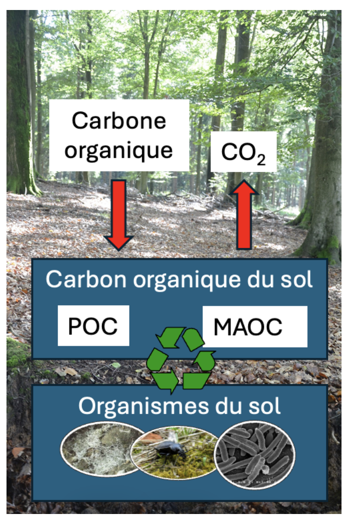

Figure 3: You will test the hypothesis that the negative effect of stressor richness (on the x-axis) on ecosystem function (on the y-axis) is smaller when initial biodiversity is higher and when stressors are more similar (see legend). I will further test the hypothesis that antagonistic stressor interactions shift these trends down, while synergistic stressor interactions have the opposite effect.

3.2 Methods

- Modeling framework: Dynamical systems model representing carbon pools (e.g. litter, microbes, fauna, dissolved organic matter) and fluxes between them.
- Data inputs: Field-calibrated carbon budgets and functional traits (in collaboration with UCLouvain and ULiège).
- Analysis: Phase-space reconstruction and attractor visualization.
- Sensitivity analysis on key drivers (e.g. microbial turnover, litter input, soil pH).
- Software tools: R.
- Validation: Compare modeled patterns with observed variability and thresholds in field data.

This thesis combines ecological theory, dynamic modeling, and nonlinear analysis to explore how resilience and tipping points shape soil carbon cycling in temperate forests.

4 Topic 4: Roadmaps of Life: How Species Properties Shape Community Assembly Pathways

4.1 Description

Ecological communities are never static — they are constantly reshaped by the arrival and establishment of new species. An invading species may succeed without displacing others (increasing richness), replace one or more established species (altering composition), or fail to establish at all. Which outcome occurs depends on the biological traits and ecological interactions of both invaders and residents.

To capture these dynamics, ecologists use assembly graphs, where each node represents a possible community configuration and each edge corresponds to an invasion event. These graphs reveal the "roadmaps" by which communities assemble, showing whether all pathways converge to the same endpoint, diverge into alternative stable states, or cycle indefinitely without stabilizing. This thesis explores how species properties — such as growth rates, abundances, and interaction strengths — shape the structure of assembly graphs and, in turn, influence the outcomes of community assembly. Questions may include: under what conditions do alternative stable communities arise? What patterns emerge in assembly graphs as the diversity of invaders increases? When does community composition cycle instead of stabilize (Fig. 4)?

4.2 Methods

- Modeling framework: Computer simulations of multi-species communities using population dynamic models (e.g. Lotka–Volterra or resource competition).
- Assembly graph construction: Map invasion outcomes into graph structures and quantify their properties (e.g. connectivity, convergence, cycles, number of stable endpoints).
- Analysis tools: R for network analysis (igraph, networkx), dynamical systems modeling (deSolve, SciPy), and visualization.
- Extensions: If time allows, small-scale laboratory experiments with planktonic algae could complement the modeling, testing specific predictions on invasion and coexistence.

- Note: this topic can also be transformed into an experimental topic.

This project offers hands-on training in theoretical ecology, modeling, and network analysis, while addressing fundamental questions about how biodiversity emerges and persists.

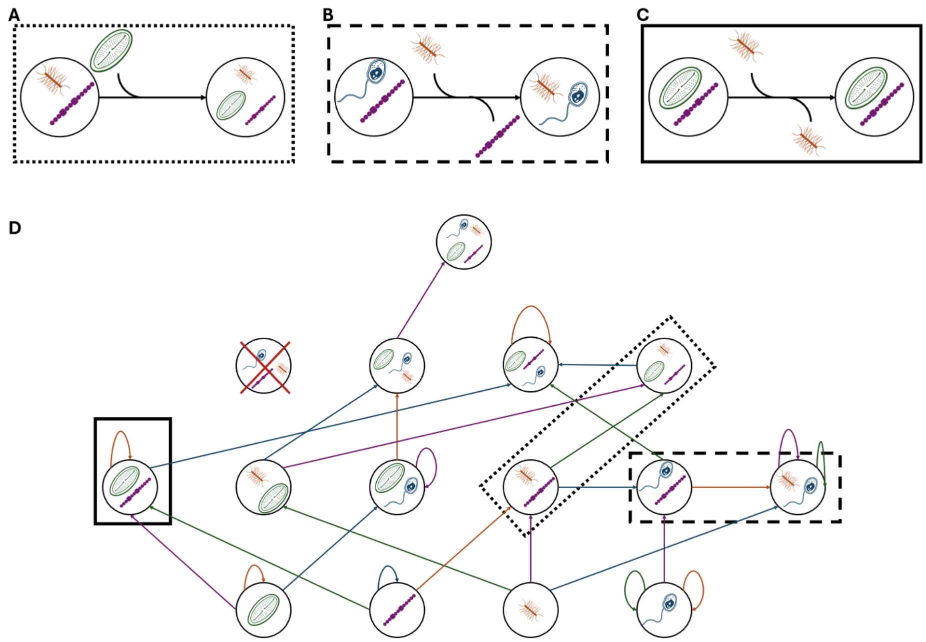

Figure 4: Illustration of the possible outcomes of species invasions, represented through the assembly graph of a pool of four species. Panels A–C depict three distinct invasion scenarios. (A) the invading species successfully establishes without displacing pre-established species, which increases overall species richness, (B) the invader establishes but drives the extinction of one or more pre-established species, so that species richness remains unchanged or decreases, and (C) the invader fails to establish, and the community composition remains the same. All of these are represented in (D) the corresponding assembly graph, which summarizes all possible assembly pathways for the four-species pool. Nodes represent potential community states, while edges represent invasion events. Edge colors indicate the identity of the invading species.