Thesis topics 23-24

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General information

The team of Frederik De Laender is a dynamic, supportive, and productive environment where you will learn a lot and have lots of fun. What we have to offer in particular are: (1) top-notch supervision (weekly meetings with the promoter, more frequent meetings with technical supervisors); (2) internationally recognized expertise on theoretical ecology and population and community ecology; and (3) a solid training of your quantitative skills.

1 Topic 1: Interactions between functional traits and population growth in *Synechococcus* sp.

Understanding how populations grow and respond to ongoing global change is important to predict impacts on biodiversity. A central concept in population ecology is that of “traits”: morphological, phenological, or physiological characteristics measured at the individual level. Traits are often thought to determine population growth under a variety of environmental conditions. However, not all traits are important for population growth. Similarly, not all traits predict the response of populations to global change drivers such as temperature change or pollution.

Measuring the influence of traits on population growth and on the impact of global change on population growth is very hard. In this thesis, we will carry out a series of original experiments with microcosms (“mini-ecosystems”) that will make this possible. Our study system will consist of strains from the globally prevalent marine phytoplankton genus *Synechococcus*. The strains of this genus display a rich variety of pigmentation (two examples in Fig. 1). We will expose them to heat waves, and monitor their population growth (; examples in Fig. 3) and traits (pigmentation, complexity, and size; examples for pigmentation in Fig. 2) using flow cytometry and state of the art analytical tools.

2 Topic 2: Patch occupancy in metacommunities.

A metacommunity is a spatial network inhabited by interacting species. Patches are connected via dispersal, which permit individuals to move from one patch to the next. Understanding how metacommunities work is of prime importance for conservation and environmental planning. In this thesis, we want to contribute to this understanding.

A main challenge is to understand how this type of metacommunity persists through time. By persistence we mean: the number of sites in which all species coexist (Fig. 4). Persistence is important

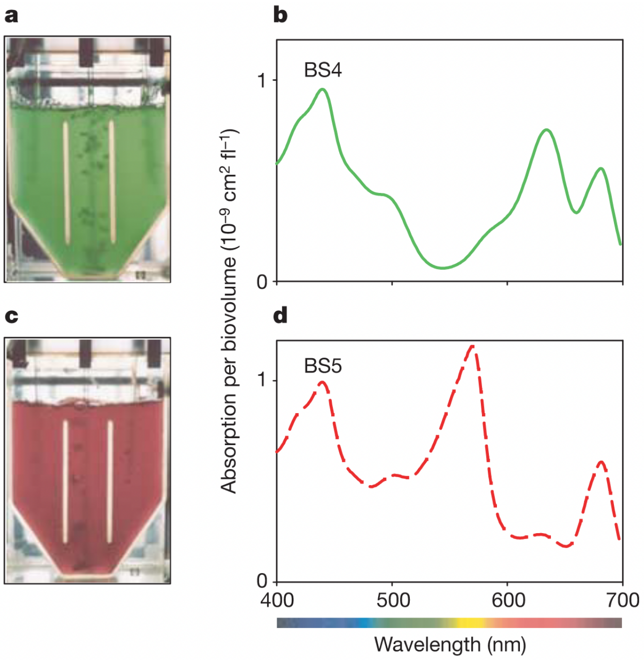

Figure 1: (From Stomp et al. 2004, Nature) Pigmentation traits of two strains of the phytoplankton genus *Synechococcus*: left: appearance in lab conditions; right: absorption spectra. These traits are not stable, however, and we expect they determine population growth.

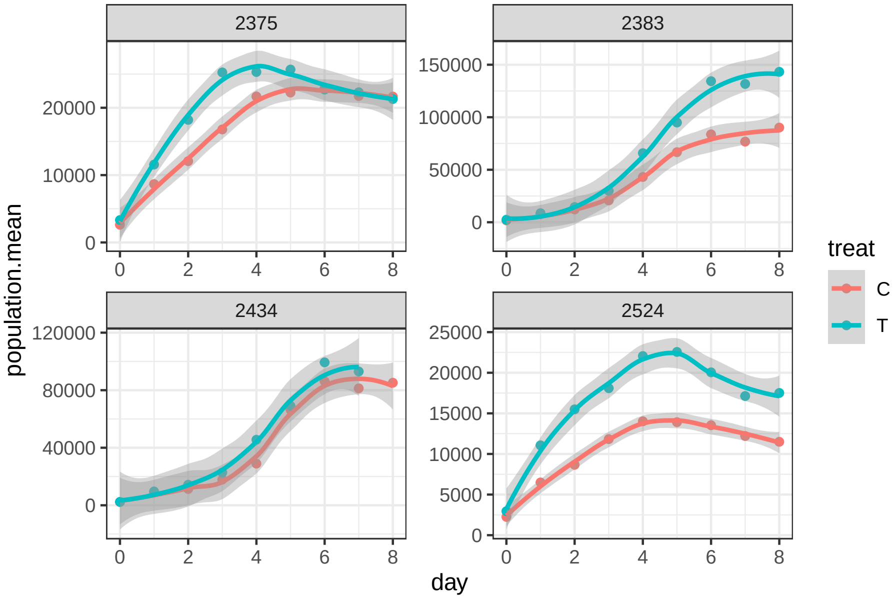

Figure 2: Four strains of the phytoplankton genus *Synechococcus* grown at reference temperature (20 °C) or at high temperature (22 °C). Note that some strains respond more strongly to temperature than others.

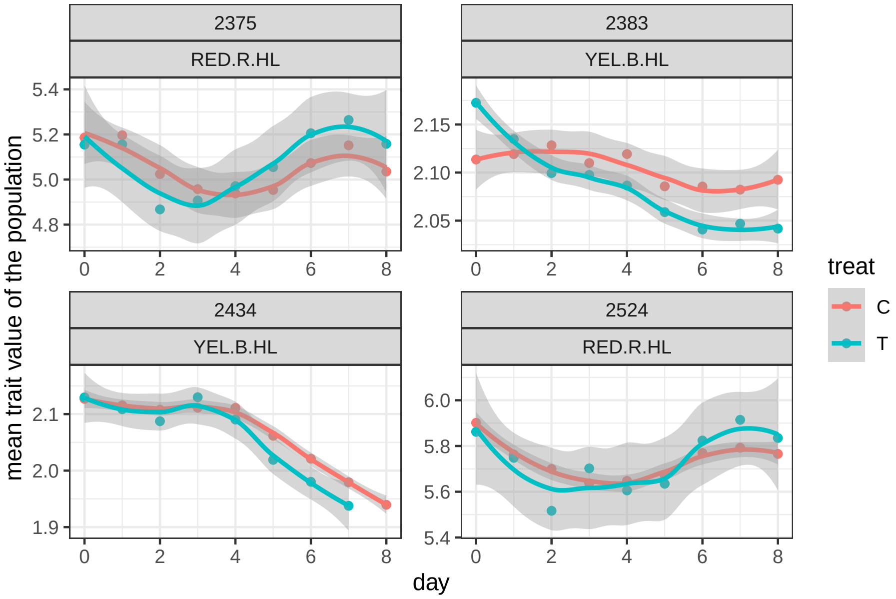

Figure 3: The change of a single relevant trait for each of the four strains from Fig. 2: “RED” and “YEL” denote red and yellow-ish pigmentation, respectively. Colours are as in Fig.2.

because when it is large, it means that all species are almost everywhere and thus the loss of a patch is unlikely to change overall biodiversity of the metacommunity.

The main difficulty in predicting persistence is the influence of dispersal. When we ignore dispersal, predicting persistence is easy as it just depends on species interactions (Fig. 5, lines). Numerical results from mathematical models show that this prediction fails even at modest dispersal rates (Fig. 5, dots). More precisely, dispersal greatly facilitates persistence. At the moment, we are building theory to explain this phenomenon. The proposed thesis can consist of the following options: (1) model simulations with several community types (Fig. 5 just represents competitive communities, but not for example food webs of plant-pollinator networks); (2) an experiment with cyanobacteria where we will construct spatial networks of microcosms to test the influence of dispersal on persistence.

3 Topic 3: How do community assembly graphs look like?

Communities don’t compose overnight. Instead, the composition of a community we observe in nature is the result of a process called “community assembly”. An empty environment gradually evolves towards a fully shaped after multiple successive invasion attempts.

Assembly graphs are a way to depict the process of community assembly (Fig. 6). Nodes of this graph represent combinations of species that can coexist, and links signify successful invasion attempts. The structure of this graph matters because it tells us how easily a community (re)assembles and therefore predicts the genesis of biodiversity. For example, a well-connected graph with more nodes will more readily allow (re)assembly than a poorly connected one with fewer nodes.

A main challenge is that it is computationally intensive (and therefore often impossible) to know the structure of an assembly graph. That is because one needs to evaluate if coexistence is possible for 2^n subcommunities (where n is the number of species in the pool), because the graph only

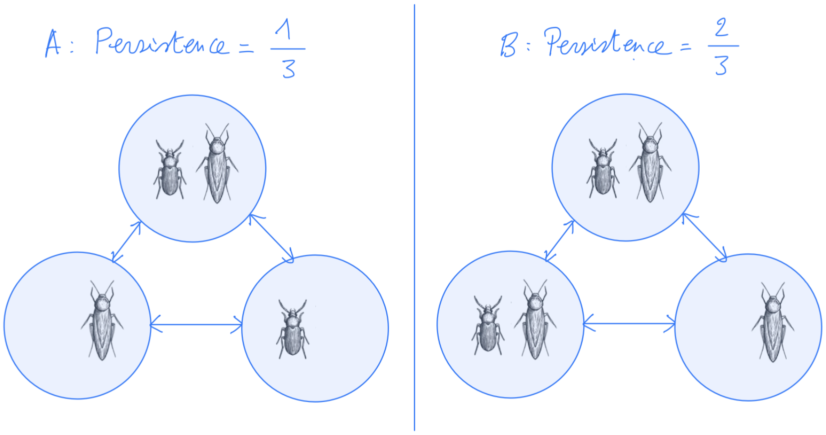

Figure 4: Persistence in a metacommunity, consisting of two insect species competing across three patches. A: The two species coexist in 1 patch only; hence persistence is 1/3. B: The two species coexist in 2 patches out of three; hence persistence is 2/3.

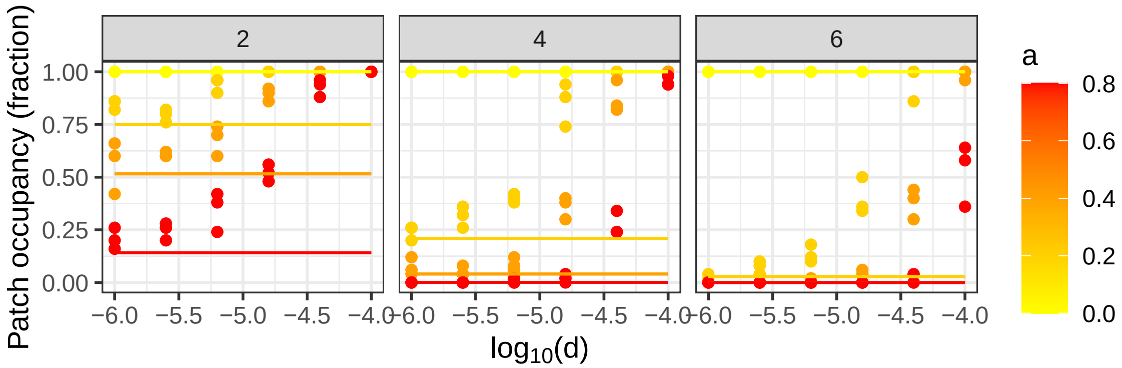

Figure 5: Even small dispersal rates promote persistence. Shown are simulation results of patch occupancy (=persistence) for a competitive metacommunity of *n* species (2, 4, or 6 species, see panel labels) in a spatial network of 50 patches as a function of the dispersal rate. Colors are different strengths of species interactions, where yellow is weak and red is strong. Lines are predictions when there is no dispersal.

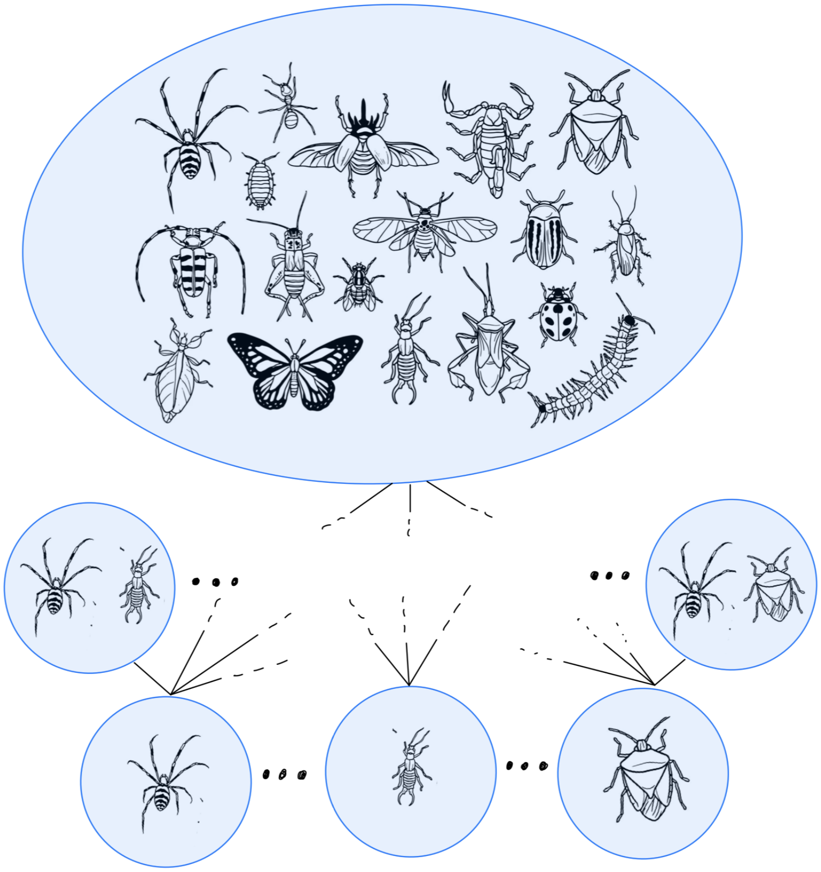

Figure 6: A small piece of an assembly graph, where nodes represent subcommunities of the full community (on top). Links represent species invasion.

contains those subcommunities for which all species coexist. For example, in order to identify the real assembly graph in Fig. 6, we would need to test if 2^18 species combinations can coexist or not. Even when using a model this is going to be not possible or at least will take a very long time.

In an ongoing project, we attempt at finding a solution to this problem by looking for general patterns of assembly graphs. The thesis topic associated to this project can either be computational, where we would carry out simulations with small networks, or experimental, where we would experimentally reconstruct the assembly process in cyanobacteria communities.