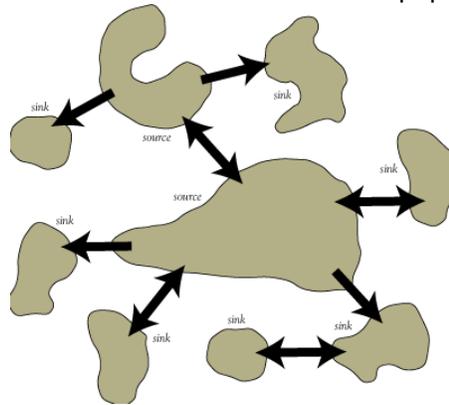




MODELLING THE INTERACTIONS BETWEEN SEAWEED POPULATIONS AT EUROPEAN SCALE

Background

When trying to describe the dynamics of a living organisms, one typically focuses on one particular population of the organism under study, thereby neglecting the interactions that are commonplace between spatially separated populations of the same organism (metapopulations). This is, however, an unrealistic simplifying assumption because, for instance, spatially separated marine populations can mutually interact through ocean and sea currents. In particular, this holds true for seaweed metapopulations.



The dynamics of the populations in the different patches occupied by the metapopulation can be described by so-called spatially implicit models that simulate the demographic processes within every patch and the mutual interaction between the patches. Typically, these models are based on a network whose nodes represent the different patches and an edge is drawn between two nodes if there exists interaction between them (e.g. migration or gene flow).



Scope of the thesis

The aim of this thesis is to develop a model that simulates the dynamics of a metapopulation of brown seaweeds and to parametrize and validate this model using data (e.g. population size, gene flow, fitness) available at the Phycology Research Group of Ghent University. Ultimately, this model should allow for simulating the metapopulation dynamics of seaweeds under varying environmental conditions at a European scale.

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BACKGROUND

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