



INTEGRATING METABOLIC NETWORK INFORMATION INTO AN INDIVIDUAL-BASED FRAMEWORK

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BACKGROUND

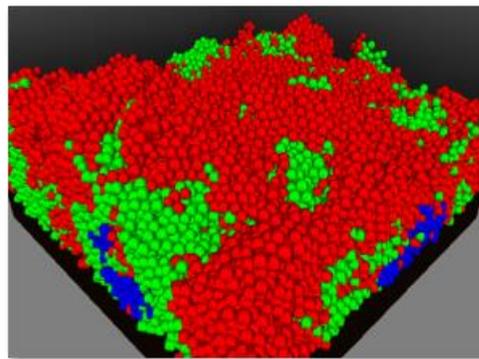
B&N, C&G, L, L&W, M

MORE INFO

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Background

Recent technological advances have resulted in an enormous increase in the amount of data describing microbial communities, such as large-scale “-omics” information. Despite the colossal collection of such data, there is still a lack of true understanding of the fundamental mechanisms that allow microbial communities to function and interact with their environment. Hence there is an important need to move beyond a descriptive approach, and towards more functional, predictive models of microbial community and their functioning.



One tool that can help in this regard is metabolic network modelling, which breaks down metabolic pathways into their constituent reactions and enzymes, permitting the analysis of their role in the network. Such models provide a more complete survey of the metabolic processes and interactions taking place within a microbial community, therefore providing important information about its functioning and dynamics.

Scope of the thesis

There are currently few attempts to synthesize metabolic network models and individual-based models (IBMs), although such an approach could represent a powerful tool for understanding the mechanisms driving community functioning.

The goal of this thesis is therefore to make a first step in this direction: to integrate a small-scale metabolic network with an existing IBM of a microbial community. The latter captures the fundamental processes underlying the interactions between individuals and with their environment: reproduction, mobility and competition.

By converting the metabolic network information into rules that can be implemented in the IBM, a more realistic and detailed representation of the community functioning can be obtained. *In silico* experiments will be conducted to investigate the effects of changes or breakdowns in the network, for example in the case of invasion of the community. For that purpose, we will resort to the high-performance computing infrastructure of Ghent University.

