Cologne Evolution Colloquium

CRC 1310   Predictability in Evolution

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Mathematical modeling of microbial ecosystems: fundamental insights and practical applications

Microbial ecosystems offer an ideal platform to study fundamental mechanisms of life, and engineered microbial communities are also extremely relevant to tackle some of today's grand societal challenges. An ecosystem is a complex network of dynamic spatio-temporal interactions among organisms as well as between organisms and the environment. Mathematical models with their abstraction capability are essential to capture the underlying phenomena and connect the different scales at which these systems act. I will present two works addressing very distinct questions using two different deterministic methods: constraint based stoichiometric models and differential equation models. In the first example, I discuss how we used an extension of dynamic flux balance analysis to investigate the diauxic shift from glucose to acetate consumption in *Escherichia coli.* Approaching this problem from a different perspective, we show that this still extensively studied phenomenon can be described as an emergent property of population dynamics rather than a coordinated and uniform metabolic switch. In the second example I present a work where, using limited time-serie metagenomic data, we reconstructed a qualitative ordinary differential equations model of the dynamic microbial community associated to an industrially relevant microalga, the diatom *Phaeodactylum tricornutum*. Such model, even if not yet quantitative, can offer insights on community stability and key one-to-one interactions.

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University of Cologne
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Hosted by Tobias Bollenbach