Geophysical Research Abstracts
Vol. 12, EGU2010-10753, 2010
EGU General Assembly 2010

Simulated Population Patterns of Migrating Bacteria in Structured Environments

Florian Centler, Ingo Fetzer, and Martin Thullner

UFZ - Helmholtz Centre for Environmental Research, Department of Environmental Microbiology, Permoserstr. 15, D-04318 Leipzig, Germany (florian.centler@ufz.de)

Many desirable reactive subsurface processes, for example nutrient cycling or the degradation of organic contaminants, are driven by microorganisms populating the soil matrix. Due to the high spatial and temporal complexity of the soil matrix, microbial life is not evenly distributed in the soil matrix but rather concentrated in distinct hot spots. Bacteria are capable of detecting gradients of nutrients or other chemical signals in their environment and direct their movement along such gradients, a process known as chemotaxis. In this theoretical study, we consider two chemotactically mediated movement incentives for bacteria: (i) affinity to nutrients and (ii) affinity to fellow organisms. The first incentive ensures efficient usage of available resources, while the second incentive leads to bacterial accumulation, providing shelter from adverse environments and allowing for synchronized behaviour. Using an individual-based modelling approach we analyse the population patterns that can develop as a consequence of these movement incentives in a hypothetical environment: a linear array of microhabitats in which microorganisms can migrate between adjacent habitats. A preliminary analytical analysis is performed to investigate the steady states of the system and their stability. Each microhabitat is characterized by nutrient level and bacterial occupation level. For an isolated microhabitat, three states are possible: extinction, space limited growth, and nutrient limited growth. These three states can also be observed in the full model of linearly connected microhabitats, leading to uniform population distributions within the array. An analytical analysis reveals that non-uniform spatio-temporal population patterns can develop, if a precondition involving the carrying capacity of the microhabitats, the steady state occupation level, the strength of the bacterial random motility, and the strength of the affinity to fellow organisms is fulfilled. The individual-based computational model is used to explore these non-uniform population patterns. Parameter constellations are identified that give rise to a variety of population patterns, from static non-uniform patterns to migrating waves and chaotic behavior.