Pore scale heterogeneity of porous media influencing the spatial and temporal distribution of microbial metabolic activity

KONSTANTIN STOLPOVSKY[1], MEHDI G. GHARASOO[2], MARTIN THULLNER[2]

[1] Department of Earth Sciences – Geochemistry, Utrecht University, the Netherlands, k.stolpovsky@uu.nl
[2] Department of Environmental Microbiology, UFZ – Helmholtz Centre for Environmental Research, Leipzig, Germany.

Introduction

Microbial activity plays a crucial and often dominant role in the cycling of carbon, nutrient elements and contaminants in the environment. Many of these reactive processes are taking place in porous environments like soils or aquifers. These environments are characterized by spatial heterogeneities at various scales down to the pore scale. Natural environment are also subject to temporal changes leading to periodic fluctuations of the microbial living conditions. Microorganisms can respond to such fluctuations by switching into a dormant state to endure unfavourable living conditions. In combination, spatial heterogeneities and fluctuating living conditions can have an important influence on the spatio-temporal distribution of microbial abundance and activity, and thus on their impact on reactive species.

Aim of the study

The aim of the present study is to explore the interaction between pore scale heterogeneities leading to different microhabitats within a porous medium and the dynamics of a microbial communities consisting of two bacterial species competing for an intermittently supplied substrate.

Pore network model approach

The applied reactive transport pore network model PNBRNS (Gharasoo et al., submitted) describes a porous medium as a two-dimensional network of interconnected pores assumed as cylindrical micro-tubes of identical length and individually assigned radii thus allowing for heterogeneous pore networks (Fig. 1).

In this study, we consider either a homogeneous medium with all pores having a constant pore radius of 160 μm and pore length of 1mm, or heterogeneous media with a normal distribution of the pore sizes defined by an average pore radius of 160 μm, with standard deviation of 70 μm. Pores are spatially arranged with a correlation lengths of 1 mm (i.e. no spatial correlation) and 5 mm (i.e. spatially correlated distribution).
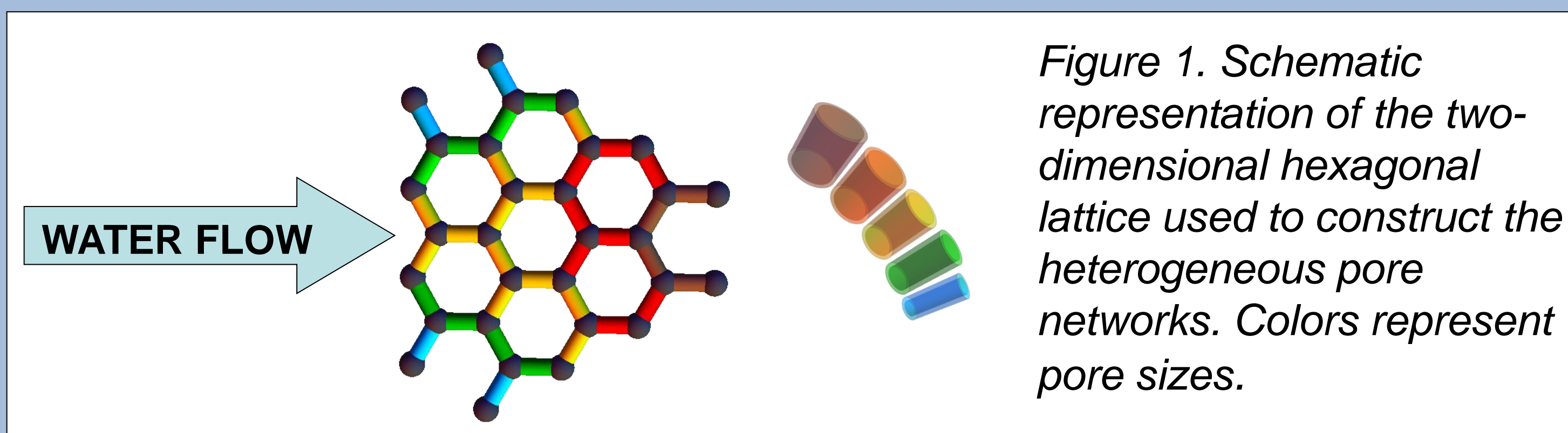

Figure 1. Schematic representation of the two-dimensional hexagonal lattice used to construct the heterogeneous pore networks. Colors represent pore sizes.

WATER FLOW

Dormancy approach

Microbial cells in each pore are represented by two different states: active and inactive (Fig. 2). Active cells are able to grow/divide, to consume available substrate (following Michaelis-Menten- or Monod-type kinetics) and are subject to decay/cell death. Inactive or dormant cells do not exhibit any growth or degradation activity while their decay/death rate is highly reduced compared to their active state. Depending on the environmental conditions (substrate availability) in a pore cells are assumed to switch between these two states (Stolpovsky et al., in press).
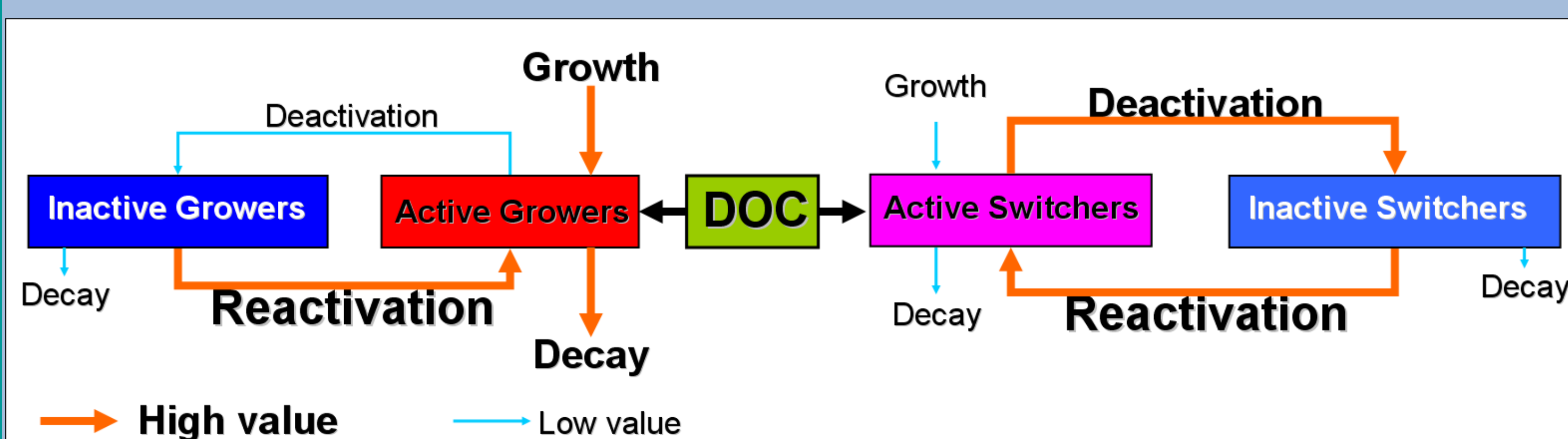

Figure 2. Schematic representation of the simulated microbial processes and involved bacterial species (Growers and Switchers).

Results

Figures 3 and 4 show simulated results for a single pore network realization example. While total biomass distribution and relative abundance of species is relatively stable in time (Fig. 3) the distribution of active bacteria is highly transient controlled by the dynamics of the substrate transport (Fig. 4).
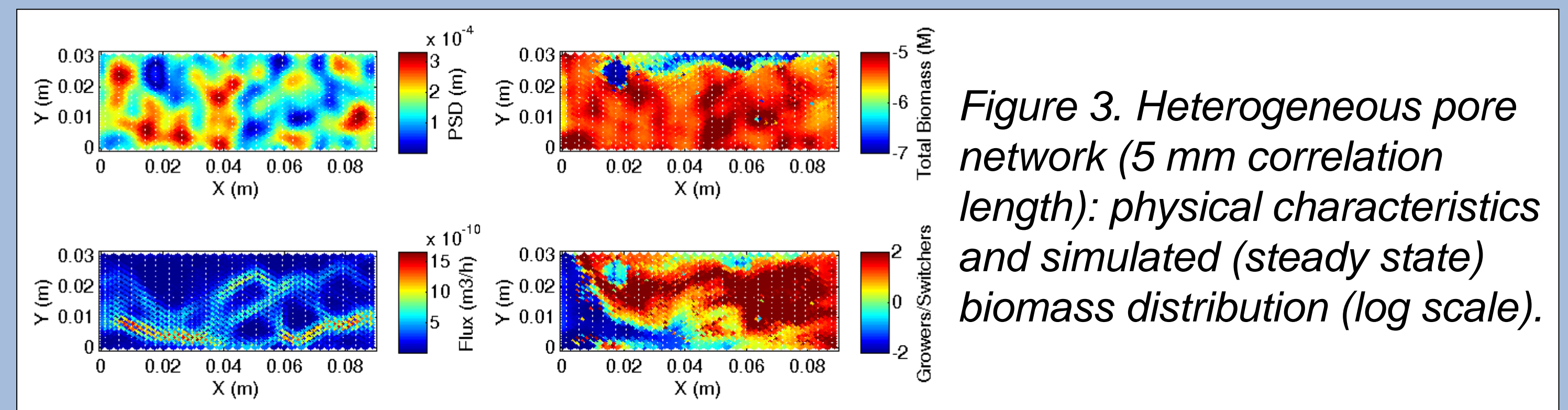

Figure 3. Heterogeneous pore network (5 mm correlation length): physical characteristics and simulated (steady state) biomass distribution (log scale).
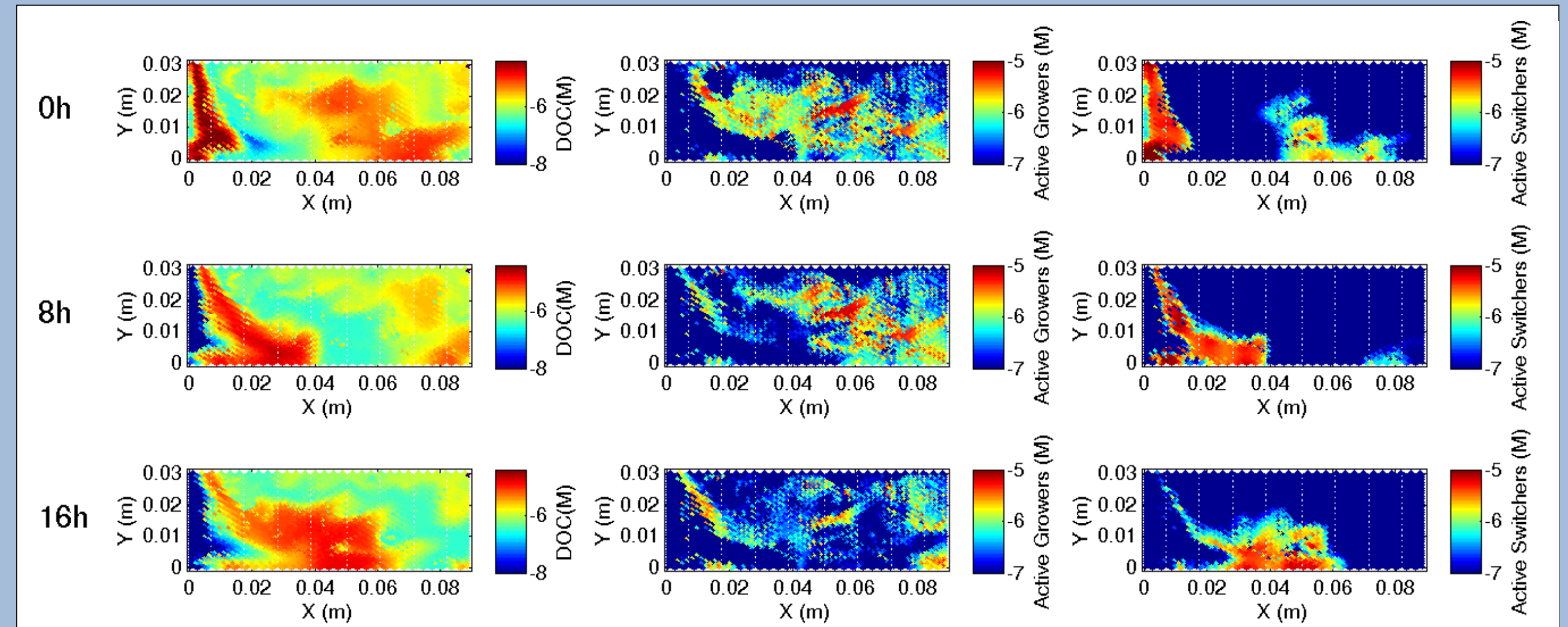

Figure 4. Heterogeneous pore network (5 mm correlation length): simulated concentration changes (log scale) during a single 24 hours feeding cycle.

Homogeneous media are mostly characterized by the dominance of a single species while heterogeneous media exhibit numerous pores with coexistence (Fig. 5).
The ratio between Growers and Switchers is strongest correlated with the average DOC concentration and its standard deviation (Fig. 6). The main driving factor for the competitive behavior of the microorganisms is the thus the DOC supply in each individual pore. Other parameters defining heterogeneity (pore radius, flow field) only having an indirect impact via their influence on DOC transport.
We also found that not only a single set of DOC conditions may be optimal for the competitive behavior of species (Fig. 6).
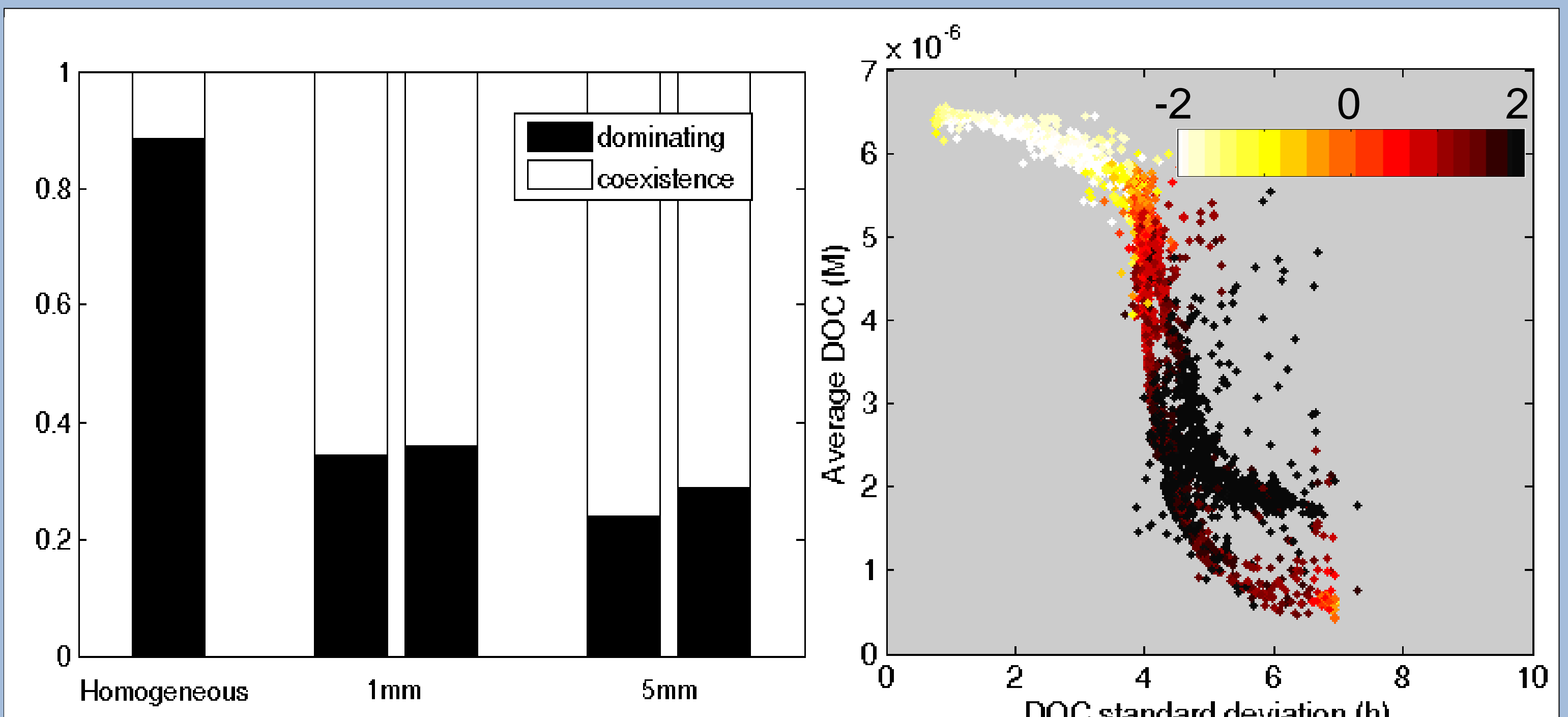

Figure 5. Fractions of pores dominated by a single species (either Growers or Switchers) or allowing coexistence of species. Each bar represents a single pore network realization

Figure 6. Dependency of the ratio (log scale) between Growers and Switchers (color of dots) on average and standard deviation of dissolved substrate (DOC) concentration.

Conclusions

- The observed spatial distribution patterns confirm results from earlier studies, showing the impact of heterogeneity and preferential flow patterns on microbial abundance and activity.
- Intermittently changing environmental conditions lead to strong fluctuations of bacterial activity but to stable distributions of bacterial abundance.
- Heterogeneity leads to a larger number of small niches dominated by a single species AND to an increased number of individual pores with species coexistence.
- Competitive advantage of single species not controlled by a single environmental factor but by a combination of different factors (characteristics of DOC dynamics).
- Not only a single set of environmental conditions might be optimal for the competitive behavior of species.

References

Gharasoo M., Centler F., Regnier P., Harms H. and Thullner M. A reactive transport modeling approach to evaluate the impact of pore scale heterogeneity on bioavailability in porous media. *Environmen. Modell. & Softw.* (submitted).

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Universiteit Utrecht

HELMHOLTZ CENTRE FOR ENVIRONMENTAL RESEARCH – UFZ