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The relation between pore-scale heterogeneity, bioavailability and bacterial mobility: a numerical modelling approach

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Abstract Desirable reactive subsurface processes, e.g. nutrient cycling or degradation of organic contaminants, are driven by microorganisms populating the soil matrix. These environments are characterized by heterogeneities at various scales which influence the transport of chemical species and the spatial distribution of microorganisms. As a result, the biodegradation rate of contaminants at large scales does not only depend on the degradation capacity of the indigenous microbial population, but also on their distribution patterns and the heterogeneities of the hosting media. Many of these organisms are motile and exhibit a chemotactic behaviour driven by gradients of substrate and fellow organisms. In this study, we developed a reactive transport pore-network model to study the bioavailability effects resulting from structural heterogeneity of the pore space. Then, we included an individual-based modelling approach to simulate the bacterial pattern conformation in heterogeneous porous media. By varying the degree of structural heterogeneities or the chemotactic sensitivities of the bacteria, we explored how the degradation performance is affected and what population distributions emerge.

Key words individual-based modelling; pore network model; bioavailability; reactive transport model; spatial distributions; pore-scale heterogeneity; microbial patterns