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**Modeling and Numerical Simulation of Biological Systems  
by Multigrid Methods**

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A typical feature of biological systems is their high complexity and variability. This makes modelling and computation very difficult, in particular for detailed models based on first principles. The problem starts with modelling geometry, which has to extract the essential features from those highly complex and variable phenotypes and at the same time has to take in to account the stochastic variability. Moreover, models of the highly complex processes which are going on these geometries are far from being well established, since those are highly complex too and often couple on a hierarchy of scales in space and time. Simulating such systems always puts the whole approach to test, including modeling, numerical methods and software implementations. In combination with validation based on experimental data, all components have to be enhanced to reach a reliable solving strategy.

To handle problems of this complexity, new mathematical methods and software tools are required. In recent years, new approaches such as parallel adaptive multigrid methods and corresponding software tools have been developed allowing to treat problems of huge complexity. In the lecture we report on the numerical simulation of the diffusion of xenobiotics through human skin. First computations for this problem were made in the last decade, yielding new insight into permeation pathways through human skin, which were confirmed experimentally ten years later.