

Facing the challenges of multiscale modelling of bacterial and fungal pathogen-host interactions

Schleicher J(+), Conrad T(+), Gustafsson M, Cedersund G, Guthke R, Linde J (2015) Facing the challenges of multiscale modelling of bacterial and fungal pathogen-host interactions *Briefings in Functional Genomics* 2016, pii: elv064. (Review)

[Details](#)



Abstract

Recent and rapidly evolving progress on high-throughput measurement techniques and computational performance has led to the emergence of new disciplines, such as systems medicine and translational systems biology. At the core of these disciplines lies the desire to produce multiscale models: mathematical models that integrate multiple scales of biological organization, ranging from molecular, cellular, and tissue models to organ, whole-organism, and population scale models. Using such models, hypotheses can systematically be tested. In this review, we present state-of-the-art multiscale modelling of bacterial and fungal infections, considering both the pathogen and host as well as their interaction. Multiscale modelling of the interactions of bacteria, especially *Mycobacterium tuberculosis*, with the human host is quite advanced. In contrast, models for fungal infections are still in their infancy, in particular regarding infections with the most important human pathogenic fungi, *Candida albicans* and *Aspergillus fumigatus*. We reflect on the current availability of computational approaches for multiscale

modelling of host–pathogen interactions and point out current challenges. Finally, we provide an outlook for future requirements of multiscale modelling.

Beteiligte Forschungseinheiten

[Microbiome Dynamics](#) [Gianni Panagiotou](#) [Mehr erfahren](#)

Leibniz-HKI-Autor*innen



Theresia Conrad

[Details](#)



Reinhard Guthke

[Details](#)



Jörg Linde

[Details](#)



Jana Schleicher

[Details](#)

Themenfelder

[Netzwerke der Wirt-Pilz-Pathogen Interaktion](#)

Identifizier

doi: 10.1093/bfgp/elv064

PMID: 26857943