

Computational systems biology of pathogen-host interactions

Durmus S, Cakir T, Guthke R (2016) Computational systems biology of pathogen-host interactions *Front. Microbiol.* 7, 21. (Review)

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Abstract

Pathogen-Host Interactions (PHIs) play a significant role in the mechanisms of infections. Therefore, the investigation of infection mechanisms through PHIs is a crucial step to develop novel and more effective solutions against drug-resistance and for personalized therapy. To this aim, systems biology approach considers the whole PHI system instead of focusing hosts or pathogens individually. Computational modeling and analysis has a vital place within the whole systems biology workflow (Cyclic operation of experimental and modeling work). Multi-scale modeling provides the holistic view needed in the investigation of pathogen-host molecular interactions. However, it is usually very difficult to identify the model structure and parameters for complex multi-scale models. On the other hand, focused modeling types require more stringent and advanced feature selection approaches.

This research topic aims to provide examples from the current picture of the research on computational systems biology of PHIs. The papers included here review recent studies or present

original research on computational inference of PHI networks, computational prediction of PHIs, text mining of PHI data from the literature, and mathematical modeling and computational analysis of PHI networks. This research topic presents three review papers, 10 original research articles, and one technology report.

Opening this research topic, we provide a comprehensive review of the studies on computational systems biology of PHIs ([Durmuş et al.](#)). We focus on the computational methods for the inference of molecular interaction networks of PHI systems, bioinformatic analysis of PHI networks, the Web-based PHI databases, and text-mining efforts to extract PHI data hidden in the literature. In this sense, this review provides a systems perspective on which the other articles covered in this research topic are based.

Involved units

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Leibniz-HKI-Authors



Reinhard Guthke

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Identifier

doi: 10.3389/fmicb.2016.00021

PMID: 26870002