

# A review on Computational Systems Biology of Pathogen-Host Interactions

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## Abstract

Pathogens manipulate the cellular mechanisms of host organisms via Pathogen-Host Interactions (PHIs) in order to take advantage of the capabilities of host cells, leading to infections. The crucial role of these interspecies molecular interactions in initiating and sustaining infections necessitates a thorough understanding of the corresponding mechanisms. Unlike the traditional approach of considering the host or pathogen separately, a systems-level approach, considering the PHI system as a whole is indispensable to elucidate the mechanisms of infection. Following the technological advances in the post-genomic era, PHI data have been produced in large-scale within the last decade. Systems biology-based methods for the inference and analysis of PHI regulatory, metabolic, and protein-protein networks to shed light on infection mechanisms are gaining increasing demand thanks to the availability of omics data. The knowledge derived from the PHIs may largely contribute to the identification of new and more efficient therapeutics to prevent or cure infections. There are recent efforts for the detailed documentation of these experimentally verified PHI data through Web-based databases and platforms. Despite these advances in data archiving, there are still large amounts of PHI data in the biomedical literature yet

to be discovered and novel text mining methods are in development to unearth such hidden data. Here, we review a collection of recent studies on computational systems biology of PHIs with a special focus on the methods for the inference and analysis of PHI networks, covering also the Web-based databases and text-mining efforts to unravel the data hidden in the literature.

## Involved units

[Microbiome Dynamics](#) [Gianni Panagiotou](#) [Read more](#)

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## Topics

[Networks of host- fungal pathogen interaction](#)

## Identifier

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