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Computational Biology Applied to Host-Pathogen Interactions

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Deadline for manuscript submissions:
closed (31 December 2022)

Message from the Guest Editors

Dear Colleagues,

Attempting to understand immune protection or to identify a new drug target is a challenge, as well as the identification of pathogen proteins that control host cell signaling and metabolism (host reprogramming), computational approaches provide a rapid solution to study host and pathogen interactions at the system level, to mine and exploit network biology insights. Through the integration of multi-omics data to molecular networks, studies in recent years have identified new potential host and pathogen factors involved in pathogenicity. One of the most important types of molecular networks is host-pathogen interaction (HPI) networks in the study of infectious diseases, which shed light on the concepts of mechanisms of infections. Meticulous validation by experimental data is similarly important and with the advent of large-scale omics data, analysis pipelines become increasingly important. Infection happens and can come from bacteria, viruses, parasites and fungi. From all these domains of life articles involving computational approaches and their validation are invited.

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Special Issue

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Editor-in-Chief

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Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

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