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Sommario/riassunto	A thorough understanding of pathogenic microorganisms and their interactions with host organisms is crucial to prevent infectious threats due to the fact that Pathogen-Host Interactions (PHIs) have critical roles in initiating and sustaining infections. Therefore, the analysis of infection mechanisms through PHIs is indispensable to identify diagnostic biomarkers and next-generation drug targets and then to develop strategic novel solutions against drug-resistance and for personalized therapy. Traditional approaches are limited in capturing mechanisms of infection since they investigate hosts or pathogens individually. On the other hand, the systems biology approach focuses on the whole PHI system, and is more promising in capturing infection mechanisms. Here, we bring together studies on the below listed sections to present the current picture of the research on Computational Systems Biology of Pathogen-Host Interactions: - Computational Inference of PHI Networks using Omics Data - Computational Prediction of PHIs - Text Mining of PHI Data from the Literature - Mathematical Modeling and Bioinformatic Analysis of PHIs Computational Inference of PHI Networks using Omics Data Gene regulatory, metabolic and protein-protein networks of PHI systems are crucial for a thorough understanding of infection mechanisms. Great advances in molecular biology and biotechnology have allowed the production of related omics data experimentally. Many computational methods are emerging to infer molecular interaction networks of PHI

systems from the corresponding omics data. Computational Prediction of PHIs Due to the lack of experimentally-found PHI data, many computational methods have been developed for the prediction of pathogen-host protein-protein interactions. Despite being emerging, currently available experimental PHI data are far from complete for a systems view of infection mechanisms through PHIs. Therefore, computational methods are the main tools to predict new PHIs. To this end, the development of new computational methods is of great interest. Text Mining of PHI Data from Literature Despite the recent development of many PHI-specific databases, most data relevant to PHIs are still buried in the biomedical literature, which demands for the use of text mining techniques to unravel PHIs hidden in the literature. Only some rare efforts have been performed to achieve this aim. Therefore, the development of novel text mining methods specific for PHI data retrieval is of key importance for efficient use of the available literature. Mathematical Modeling and Bioinformatic Analysis of PHIs After the reconstruction of PHI networks experimentally and/or computationally, their mathematical modeling and detailed computational analysis is required using bioinformatics tools to get insights on infection mechanisms. Bioinformatics methods are increasingly applied to analyze the increasing amount of experimentally-found and computationally-predicted PHI data. Acknowledgements: We, editors of this e-book, acknowledge Emrah Nikerel (Yeditepe University, Turkey) and Arzucan Ozgur (Bogaazici University, Turkey) for their contributions during the initiation of the Research Topic.

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