

## Journal of Applied Bioinformatics & Computational Biology

A SciTechnol Journal

### Perspective

## **Computational Systems Biology** of Pathogen–Host Interactions

#### Gowthami Bainaboina<sup>1\*</sup>

#### Introduction

The Host-pathogen interaction is outlined as however microbes or viruses sustain themselves among host organisms on a molecular, cellular, system or population level. This term is most ordinarily accustomed see disease-causing microorganisms though they will not cause ill health all told hosts.

Infectious diseases square measure one in every of the preliminary causes of death worldwide annually. rising and reemerging diseases and drug resistant pathogens have created the matter a lot of serious for men. Therefore, novel therapeutic methods, referred to as theranostics, square measure more and more investigated to fight the biological threats.

Systems biology aims at understanding and modelling complicated biological systems as an entire. Systems biology approaches could concentrate on single or multiple levels, together with proteins, genes, tissues, cells, whole populations or organisms.

This space of analysis has emerged at the start of the twenty first century. It's characterized by a powerful association of wet research lab experiments and machine analysis, wherever the analysis and modelling of experimental information ends up in new hypotheses that cause new experiments

Typically systems biology approaches square measure categorised into bottom up and high down, wherever very cheap describes the interaction of molecules and also the high is that the holistic read on the system. bottom-up approaches aim for elucidating the interactions of cell parts by sub model aggregation. The read from the highest is made by genome-wide analysis and therefore by the supposed omics technologies (Transcriptomics, Genomics, Metabolomics, Proteomics).

Pathogens manipulate the cellular mechanisms of host organisms via pathogen-host interactions (PHIs) so as to require advantage of the capabilities of host cells, resulting in infections. The crucial role of those interspecific molecular interactions in initiating and sustaining infections necessitates a radical understanding of the corresponding mechanisms.

Citation: Bainaboina G (2020) Computational Systems Biology of Pathogen-Host Interactions. J Appl Bioinforma Comput Biol 10(1).191.

Received: December 28, 2020 Accepted: January 11, 2021Published:

In contrast to the normal approach of considering the host or infectious agent on an individual basis, a systems-level approach, considering the alphabetic character system as an entire is indispensable to elucidate the mechanisms of infection.

#### Systems Biology of Host-Pathogen Interactions

Pathogen-Host Interactions (PHIs) play a big role within the mechanisms of infections. Therefore, the investigation of infection mechanisms through PHIs may be a crucial step to develop novel and simpler solutions against drug-resistance and for customized medical aid. To the current aim, systems biology approach considers the entire alphabetic character system rather than focusing hosts or pathogens separately. Machine modeling and analysis encompasses a very important place among the entire systems biology progress.

#### **PHI-Based order and Transcriptome Information**

The genomic information from the host and the pathogen represents the basis for all further molecular analyses and bioinformatics investigations of PHI systems. Thus, genome sequencing is fundamental. It helps to boost identification, writing of infectious agent, virulence and antibiotic resistance detection, and development of recent vaccines and culture media. Single ester polymorphism (SNP) writing is very important for each identification and characterization of variants of pathogens (strains, clinical isolates) yet on study the susceptibleness of humans surely infections.

# PHI-Based genetic science and Transcriptome Information

Proteomics is that the comprehensive, integrative study of proteins and their biological functions. The goal of genetic science is usually to supply a whole and quantitative map of the protein of a species, together with shaping supermolecule cellular localization, reconstructing their interaction networks and complexes, and delineating communication pathways and regulative post-translational super molecule modification.

Author Affiliation

<sup>1</sup>Department of Pharmacy, QIS College of Pharmacy, Prakasam, AP, India

Тор



All articles published in Journal of Applied Bioinformatics & Computational Biology are the property of SciTechnol, and is protected by copyright laws. Copyright © 2021, SciTechnol, All Rights Reserved.

<sup>\*</sup>Corresponding authors: Gowthami Bainaboina, Department of Pharmacy, QIS College of Pharmacy, Prakasam, AP, India, Mobile:+918500024898; E-mail: gowthamibainaboina@gmail.com

January 18, 2021