

Chapter XXIII

Systems Biology and Infectious Diseases

Alia Benkahla

Institut Pasteur de Tunis, Tunisia

Lamia Guizani-Tabbane

Institut Pasteur de Tunis, Tunisia

Ines Abdeljaoued-Tej

ESSAI-UR Algorithmes et Structures, Tunisia

Slimane Ben Miled

*Institut Pasteur de Tunis, Tunisia and
ENIT-LAMSIN, Tunisia*

Koussay Dellagi

Institut Pasteur de Tunis, Tunisia

ABSTRACT

This chapter reports a variety of molecular biology informatics and mathematical methods that model the cell response to pathogens. The authors first outline the main steps of the immune response, then list the high throughput biotechnologies, generating a wealth of information on the infected cell and some of the immune-related databases; and finally explain how to extract meaningful information from these sources. The modelling aspect is divided into modelling molecular interaction and regulatory networks, through dynamic Boolean and Bayesian models, and modelling biochemical networks and regulatory networks, through Differential/Difference Equations. The interdisciplinary approach explains how to construct a model that mimics the cell's dynamics and can predict the evolution and the outcome of infection.

INTRODUCTION

Systems biology is an emerging interdisciplinary field in life science research which purpose is to study the dynamic interactions and the network structure in cells or tissues or whole organisms. It is commonly accepted that the design of research in this field, encompasses the following six steps (Ng, Bursteinas, Gao, Mollison, & Zvelebil, 2006; Philippi & Kohler, 2006): (i) generation of suitable biological data sampled from a population; (ii) enrichment of the collected data by publicly available data; (iii) curation

of this data; (iv) exhaustive integration of the curated data; (v) modelling of the mechanism(s) of interest; and (vi) validation of the predicted model. Knowing the complexity of systems biology considered at the tissue or organism level, we will focus in our review on systems biology at the cell level.

Systems biology research aims at understanding the mechanisms that shape the biological functions of a cell. It is achieved through the integration of biological information about the cell of interest (Box 1), then the extraction of mathematical models that mimic the behaviour of this cell under different conditions. These models should then guide biologists to design the appropriate experiments to be tested on the bench, which hopefully will yield decisive results.

The biological function of the cell is determined by the dynamic interactions between different components or molecules involved in a given pathway. Pathways are not isolated but highly intricate and interconnected, and constitute a large, single, coherent but complex cellular network. The study of the cellular process modulated in response to an external stimulus is a phenomenon that depends not only on the number but also on the diversity and the dynamic of intracellular interactions.

The response of host cells to pathogens has been extensively investigated as a model of cellular response to external *stimuli*. Such model takes systems biology a step further as it integrates data that are generated from two interacting/conflicting living organisms: the host and the pathogen. The specificity of this system should be taken into account during the modelling process and advanced strategies that capture this cohabitation and its consequences are required for modelling (Forst, 2006). Numerous host's and pathogen's proteins are usually involved in these interactions and trigger various biochemical reactions regulated in cascade. The outcome of the infection will depend on this complex network of cellular interactions.

Another level of complexity is introduced by the interactions/exchanges between the host's cells and the infectious agent (parasite, virus, bacteria). Especially as high throughput technologies, dedicated to the characterisation of these interactions/exchanges and their effects on the biological function of the two organisms, are still missing. However the use of organism's oriented biotechnologies (i.e.: transcriptome) allowed a coherent and understandable view of the studied system. Even though these experiments fail to unveil the crosstalk between host and pathogen, they give separate insights into the host or pathogen responses. Developing tools that could integrate and process this data is a major task in infectious systems biology research.

Box 1. The modelling of the mechanisms that shape the biological functions of an infected cell is achieved through the integration of information concerning the complexity of the system.



24 more pages are available in the full version of this document, which may be purchased using the "Add to Cart" button on the publisher's webpage:
www.igi-global.com/chapter/systems-biology-infectious-diseases/21545

Related Content

Fluorescence Imaging of Mitochondrial Long-Term Depolarization in Cancer Cells Exposed to Heat-Stress

Cathrin Dressler, Olaf Minet, Urszula Zabaryloand Jürgen Beuthan (2009). *Handbook of Research on Systems Biology Applications in Medicine* (pp. 673-692).

www.irma-international.org/chapter/fluorescence-imaging-mitochondrial-long-term/21560

Integrating Telehealth into the Organization's Work System

Joachim Jean-Julesand Alain O. Villeneuve (2011). *E-Health, Assistive Technologies and Applications for Assisted Living: Challenges and Solutions* (pp. 161-194).

www.irma-international.org/chapter/integrating-telehealth-into-organization-work/51388

Monitoring of Patients with Neurological Diseases: Development of a Motion Tracking Application Using Image Processing Techniques

Tiago Rafael dos Santos Martins Pereira Rodrigues, Vítor Carvalhoand Filomena Soares (2013). *International Journal of Biomedical and Clinical Engineering* (pp. 37-55).

www.irma-international.org/article/monitoring-of-patients-with-neurological-diseases/101928

Detection of Rarefaction of Capillaries and Avascular Region in Nailfold Capillary Images

Suma K. V.and Bheemsain Rao (2016). *International Journal of Biomedical and Clinical Engineering* (pp. 73-86).

www.irma-international.org/article/detection-of-rarefaction-of-capillaries-and-avascular-region-in-nailfold-capillary-images/170463

Computer Aided Modeling and Finite Element Analysis of Human Elbow

Arpan Guptaand O.P. Singh (2016). *International Journal of Biomedical and Clinical Engineering* (pp. 31-38).

www.irma-international.org/article/computer-aided-modeling-and-finite-element-analysis-of-human-elbow/145165