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Advances in Multi-scale Systems Biology Applications: An Editorial Overview

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Introduction

Systems biologists apply techniques from experimental biology, computer science, informatics, mathematics, and statistics to integrate data across several platforms and time and space scales in order to build computational and mathematical models of living systems' integrative, holistic processes. Endocrine-related cancers are well suited to study from a systems perspective due to the signalling complexities caused by the roles of growth factors, hormones, and their receptors as critical regulators of cancer cell biology, as well as the interactions between cancer cells, normal cells, and signalling molecules in the tumour microenvironment. Furthermore, growth factors, hormones, and their receptors, such as oestrogen biosynthesis in breast cancer, oestrogen receptors or HER2 in prostate cancer, and androgen receptors in prostate cancer, are usually beneficial therapeutic targets [1].

Description

Given the underlying complexities, Systems biology provides an alternate framework for studying and treating these malignancies. To appropriately interpret the results of systems-based investigations, some understanding of how in silico models are generated and utilised to characterise a system and anticipate the impacts of perturbations on system function is required. In this review, we present an overview of the subject of cancer systems biology and discuss some of the benefits, limitations, and hazards of utilising predictive multiscale modelling to research endocrine-related tumours. Many improvements in endocrine-related tumours have emerged from the experimental domains of cellular and molecular biology, as well as their translation into clinical applications throughout the last few decades. In general, cellular and molecular investigations have taken a reductionist approach [2-3].

A systems-based approach expands on this important work by providing a more comprehensive account of the complex networks of interacting genes, proteins, and metabolites that determine how a cancer cell survives and thrives in the tumour microenvironment, as well as how the host responds to the tumour. According to this perspective, molecular networks and the subcellular processes they regulate interact with activity within the tumour cell, its microenvironment, and the cancer-bearing organism. Endocrinologists and experts in other domains are used to taking a holistic approach, where interactions can have both local and distant consequences. However, in the 'post-genomic era,' the tools and technologies available to adequately investigate any cancer as a systems-disease have evolved considerably. With these advancements has come improved understanding of the extraordinary intricacy of signalling, its integration, and the coordination shown in directing and executing cellular operations.

We hope that this review paper will introduce a wide audience to the potentials and limitations of a systems approach to improving our understanding and treatment of endocrine-related malignancies [4]. The topic of endocrine-related cancer systems biology is vast and complex, and we recognise that several aspects in this field are handled at a rather simple level here. Nonetheless, we feel that a systems approach, incorporating computational and mathematical modelling, will be beneficial. depicts an overview of the organisation of this review. We begin with a discussion of why models are required, how modellers commonly approach developing their models, and some considerations for modelling unique purposes.

Then, as a result of the dynamical features of signalling networks, we demonstrate how models can be built with a modular structure and how modularity can lead to emergent behaviours. We address deterministic, stochastic, and Bayesian models, as well as how their parameters are derived from data and error bounds are presented [5]. We next go through model performance, potential sources of inaccuracy, the significance of independently checking model predictions, and drug interaction modelling. Following sections describe instances of a knowledge-guided computational tool for network construction, a mathematical model of the oestrogen receptor landscape, and some insights into model interpretation.

Conclusion

A system, for the purposes of this review, is a collection of interacting components that produces a defined biological output in response to certain inputs. Such input–output models must sufficiently describe the system's complexity in order to be useful. Complexity does not always imply 'largeness' many nodes and edges. Due to inherent feedforward and feedback loops and non-linear kinetic rate laws, relatively tiny networks can demonstrate non-intuitive signal-processing capabilities, with little changes in input producing disproportionately big changes in output.

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