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Editorial

Editorial Note on Cancer Biology

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EDITORIAL

Cancer systems biology is the study of cancer as a dynamic adaptive mechanism with evolving properties at multiple biological scales using systems biology approaches. Cancer systems biology is the study of how the intracellular networks of normal cells are disrupted during carcinogenesis using systems biology methods in order to create successful predictive models that can aid scientists and clinicians in the validation of new therapies and drugs. Tumours are distinguished by genomic and epigenetic instability, which changes the roles of a wide range of molecules and networks within a single cell, as well as the interactions with the surrounding environment. To decode the dynamics of tumor genesis as well as cancer heterogeneity, cancer systems biology approaches rely on the use of computational and mathematical methods.

The need for improved methods to distil information from large-scale networks, the importance of combining multiple data types in the construction of more practical models, and the difficulties in converting insights about tumorigenic pathways into therapeutic strategies are all examples of cancer systems biology. As a result, cancer systems biology takes a systemic approach to the disease, incorporating genetics, signalling networks, epigenetics, cellular activity, mechanical properties, histology, clinical manifestations, and epidemiology. Finally, properties on one scale, such as histology, are clarified by properties on a lower scale, such as cell activity. Traditional basic and clinical cancer research is combined with “exact” sciences such as applied mathematics, engineering, and physics in cancer systems biology. It uses a variety of “omics” technologies.

Cancer systems biology's applications include, but are not limited to, elucidating essential cellular and molecular networks underlying cancer risk, initiation, and progression, thus fostering an alternative perspective to the conventional reductionist approach, which has traditionally focused on characterizing single molecular aberrations. Cancer systems biology has its origins in a variety of biomedical research events and realizations’, as well as technical advancements. Cancer was once thought to be a single illness that could be detected, recognized, and treated. It was regarded as an "alien" component that developed into a homogeneous mass and should be removed. The discovery of essential oncogenes or tumour suppressor genes in the etiology of cancer was the subject of cancer research. These discoveries transformed our understanding of the molecular events that drive cancer progression. Targeted therapy is the latest peak of advancements spawned by such discoveries.

Comprehensive genomic studies of mutations, rearrangements, copy number variations, and methylation at the cellular and tissue levels, as well as robust analysis of RNA and microRNA expression data, protein levels, and metabolite levels, are all possible with high-throughput technologies. New mathematical and computational algorithms that demonstrate the complex interplay between experimental biology and the quantitative sciences are used in cancer systems biology computational approaches. A cancer systems biology approach can be used at various levels, ranging from a single cell to a tissue, a patient with a primary tumour and potential metastases, or some combination of these situations.

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