Cancer Systems Biology Services Section Home

History

The roots of Cancer Systems Biology can be traced back to the mid-20th century when scientists began to appreciate the complexity of cancer beyond simplistic genetic explanations. The concept of systems thinking gained momentum with the advent of high-throughput technologies, allowing for the analysis of large-scale biological data. In the 1990s, the Human Genome Project provided a pivotal foundation, and the field gained further prominence with the introduction of high-throughput screening techniques and computational modeling.

Evolution till Date

Cancer Systems Biology has evolved from studying isolated genetic mutations to comprehending the intricate networks of signaling pathways, genetic alterations, and microenvironmental interactions that drive cancer progression. Integrative approaches, such as genomics, transcriptomics, proteomics, and metabolomics, have been combined with advanced computational methods to construct detailed models of cancer systems. These models provide insights into the dynamic behavior of cancer cells and have led to the identification of potential therapeutic targets.

Industrial Applications

1. Drug target identification using network-based analyses.
2. Predicting drug response and resistance mechanisms.
3. Personalized medicine approaches for cancer treatment.
4. Biomarker discovery for early cancer detection.
5. Development of combination therapy strategies.
6. Virtual screening of compound libraries for drug discovery.
7. Simulation of tumor growth and response to treatment.
8. Identification of key driver mutations and pathways.
9. Analysis of tumor heterogeneity and clonal evolution.
10. Functional analysis of non-coding RNA in cancer.
11. Understanding the role of the tumor microenvironment.
12. Modeling immune system interactions in cancer.
13. Integration of multi-omics data for comprehensive analysis.
14. Network-based analysis of cancer signaling pathways.
15. Uncovering synthetic lethality interactions for therapy.

16. Identification of potential repurposable drugs.
17. Characterization of metastatic processes.
18. Analysis of epigenetic modifications in cancer.
19. Prediction of patient prognosis based on omics data.
20. Exploration of the role of non-genetic factors in cancer.