Structural Bioinformatics and Genomic Profiling of Advanced Cancer: Enabling Translational Research

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Abstract

Cancer represents a genetically complex and heterogeneous disease, driven by diverse genomic and molecular alterations that disrupt critical signalling pathways controlling cell growth, differentiation, and survival. Recent advances in structural bioinformatics and integrative genomic profiling have transformed our understanding of tumour biology, providing insights into the molecular mechanisms that underlie cancer initiation, progression, and therapeutic response.

Our study highlights an integrated approach combining high-throughput sequencing with computational structural analysis to interpret the functional and conformational consequences of genetic alterations in advanced cancers. A comprehensive bioinformatics pipeline was developed to process exome, transcriptome, and copy number data, enabling the identification of somatic and germline variants, structural rearrangements and gene expression signatures. By mapping these alterations onto three-dimensional protein structures and biological pathways, structural bioinformatics provides a mechanistic framework for understanding, how specific mutations alter protein stability, signalling interactions, and drug-binding potential.

The integration of genomic and structural data facilitates the discovery of key driver mutations, pathway perturbations, and novel therapeutic targets. Collectively, these multidimensional analyses bridge the gap between basic genomic discoveries and clinical applications, supporting translational oncology through data-driven biomarker development and precision medicine.