Abstract
Deciphering Biomolecular Networks: Integrating Methods for Comprehensive Insights †

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Introduction: Recent advancements in biomolecular research have significantly enhanced our comprehension of the intricate interactions and networks governing cellular processes. This abstract introduces a review focused on biomolecular interactions and networks with a particular emphasis on comparing state-of-the-art methodologies, both experimental and computational, utilized in the study of protein–protein interactions.

Methods: Cutting-edge techniques in experimental and computational biology have been pivotal in unraveling biomolecular interactions. This review synthesizes the methodologies employed in studying protein–protein interactions, encompassing advanced experimental approaches such as X-ray crystallography and NMR spectroscopy. Moreover, it explores the integration of omics data, outlining the computational strategies used to construct comprehensive biomolecular networks.

Results: Exploring protein–protein interactions has revealed intricate binding interfaces and significant conformational changes, offering crucial insights into cellular function regulation. Through the integration of various data sources, including genomics, transcriptomics, proteomics, and metabolomics, a holistic view of biomolecular networks has emerged, elucidating the interconnectedness of molecular events within cells. These findings highlight the potential for targeted drug development and therapeutic approaches, driven by a deeper understanding of these networks.

Conclusions: This review underscores the collaborative efforts of researchers in advancing biomolecular science. By comparing different methodologies, including both experimental and computational approaches, significant progress has been made in deciphering the complexities of biomolecular networks. Clarification is provided regarding the inclusion of interactions on-chip, with surface characterization tools being considered where applicable.

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