



Network-based analysis and multi-omics approaches for biology and medicine

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Over the last decades, the rapid advancement of high-throughput technologies has led to an unprecedented accumulation of biological data across multiple molecular layers, including genomics, transcriptomics, proteomics, and epigenomics [1,2]. While these data offer extraordinary opportunities to investigate the molecular basis of human diseases, their complexity and heterogeneity pose significant analytical challenges. In this context, network-based approaches have emerged as powerful frameworks to model biological systems and to interpret the intricate web of molecular interactions underlying cellular functions.

Traditional reductionist approaches have primarily focused on identifying individual genes or molecules associated with specific phenotypes. However, complex diseases are rarely driven by single factors; rather, they arise from perturbations affecting interconnected molecular networks [3]. Network medicine provides a conceptual and methodological framework to address this complexity by representing biological systems as networks of interacting components and by interpreting diseases as perturbations of specific network regions, commonly referred to as disease modules [4,5]. Foundational studies in the field have highlighted how the network organization of the interactome constrains disease mechanisms and therapeutic interventions [4,5].

The integration of multi-omics data within network models has further strengthened this paradigm. Multi-layered network representations enable the simultaneous analysis of heterogeneous datasets, capturing interactions across different biological scales. Such integrative approaches have proven effective in uncovering disease-associated mechanisms and molecular determinants, as demonstrated in studies combining transcriptomic and epigenomic data in complex disorders such as chronic obstructive pulmonary disease [6,7]. These strategies allow the identification of regulatory patterns and biomarkers that remain undetected in single-layer analyses.

Methodological advances in network analysis have also played a central role in the evolution of the field. A variety of computational tools have been developed to identify key nodes and regulatory elements within biological networks. Algorithms such as SWIM and its extensions have enabled the detection of crucial nodes associated with disease processes [8,9], with successful applications in cancer and other

complex diseases [10]. In parallel, network-based approaches to drug repurposing have gained increasing attention. Tools such as SAvE-UNNER exploit network topology to identify novel therapeutic uses for existing drugs, including applications to emerging conditions such as COVID-19 [11,12]. Moreover, integrative frameworks that combine therapeutic efficacy with side-effect profiles have been proposed to improve drug repositioning strategies [13].

Network medicine has also contributed to a deeper understanding of complex disease mechanisms. For example, network-based analyses have been applied to neurodegenerative disorders such as Alzheimer's disease, revealing the interplay between multiple molecular pathways involved in disease progression [14]. These findings further support the view that a systems-level perspective is essential to capture the multifactorial nature of human diseases.

This Special Issue, entitled “*Network-based analysis and multi-omics approaches for biology and medicine*”, aims to highlight recent advances in this rapidly evolving field. It brings together contributions from computational biology, systems biology, bioinformatics, and biomedical research, reflecting the inherently interdisciplinary nature of network medicine.

The articles collected in this Special Issue cover a broad range of topics, including novel computational methods for biological network analysis, multi-omics data integration, and applications to precision medicine. Several contributions propose innovative algorithms for network construction, clustering, and module detection, aimed at identifying key regulatory components and functional pathways. Other studies focus on integrative frameworks that combine heterogeneous omics datasets to improve disease characterization and biomarker discovery. In addition, a number of articles explore network-based strategies for drug discovery and repurposing, as well as approaches for patient stratification and personalized therapeutic interventions. Together, these contributions provide a comprehensive overview of current trends and emerging directions in network-based biomedical research.

Despite the significant progress achieved, important challenges remain. The integration of large-scale multi-omics datasets is still

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hindered by issues such as data heterogeneity, noise, and incomplete knowledge of molecular interactions. Furthermore, the translation of network-based findings into clinical applications requires robust validation and stronger integration between computational and experimental approaches.

Looking forward, the convergence of network medicine with artificial intelligence, longitudinal patient data, and digital health technologies is expected to further enhance our ability to model disease complexity and predict clinical outcomes. These developments may pave the way for more accurate and personalized approaches to diagnosis, prognosis, and therapy.

In conclusion, this Special Issue underscores the growing importance of network-based and multi-omics approaches in biology and medicine. By integrating methodological innovation with real-world applications, it highlights the potential of network medicine to advance our understanding of complex diseases and to support the development of precision medicine strategies.

Declaration of competing interest

The author has no conflicts of interest to declare.

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