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Sommario/riassunto	<p>Scientists today have access to an unprecedented arsenal of high-tech tools that can be used to thoroughly characterize biological systems of interest. High-throughput "omics" technologies enable to generate enormous quantities of data at the DNA, RNA, epigenetic and proteomic levels. One of the major challenges of the post-genomic era is to extract functional information by integrating such heterogeneous high-throughput genomic data. This is not a trivial task as we are increasingly coming to understand that it is not individual genes, but rather biological pathways and networks that drive an organism's response to environmental factors and the development of its particular phenotype. In order to fully understand the way in which these networks interact (or fail to do so) in specific states (disease for instance), we must learn both, the structure of the underlying networks and the rules that govern their behavior. In recent years there has been an increasing interest in methods that aim to infer biological networks. These methods enable the opportunity for better understanding the interactions between genomic features and the overall structure and behavior of the underlying networks. So far, such network models have been mainly used to identify and validate new interactions between genes of interest. But ultimately, one could use these networks to predict large-scale effects of perturbations, such as treatment by multiple targeted drugs. However, currently, we are still at an early stage of comprehending methods and approaches providing a robust</p>

statistical framework to quantitatively assess the quality of network inference and its predictive potential. The scope of this Research Topic in Bioinformatics and Computational Biology aims at addressing these issues by investigating the various, complementary approaches to quantify the quality of network models. These "validation" techniques could focus on assessing quality of specific interactions, global and local structures, and predictive ability of network models. These methods could rely exclusively on in silico evaluation procedures or they could be coupled with novel experimental designs to generate the biological data necessary to properly validate inferred networks.

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