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Sommario/riassunto	<p>The identification and mapping of protein-protein interactions (PPIs) is a major goal in systems biology. Experimental data are currently produced in large scale using a variety of high-throughput assays in yeast or mammalian systems. Analysis of these data using computational tools leads to the construction of large protein interaction networks, which help researchers identify novel protein functions. However, our current view of protein interaction networks is still limited and there is an active field of research trying to further develop this concept to include important processes: the topology of interactions and their changes in real time, the effects of competition for binding to the same protein region, PPI variation due to alternative splicing or post-translational modifications, etc. In particular, a clinically relevant topic for development of the concept of protein interactions networks is the consideration of mutant isoforms, which may be responsible for a pathological condition. Mutations in proteins may result in loss of normal interactions and appearance of novel abnormal interactions that may affect a protein's function and biological cycle. This Research Topic presents novel findings and recent achievements in the field of protein interaction networks with a focus on disease. Authors describe methods for the identification and quantification of PPIs, the annotation and analysis of networks, considering PPIs and protein complexes formed by mutant proteins associated with pathological conditions or genetic diseases.</p>

