DETERMINATION AND ANALYSIS OF PROTEIN INTERACTION NETWORKS

F. Pazos [(1)]

[(1)] Computational Systems Biology Group (Centro Nacional de Biotecnología-CSIC, Madrid, Spain)

Modern Biology is characterized by the determination of the molecular repertories of living systems in a massive (high-throughput) way. This "-omics" approach to biological phenomena is providing new insights into the functioning of cells by allowing their study from a global and systemic perspective. The whole set of interactions between members of the protein repertory of a cell is known as the "interactome". Accurate and comprehensive determination of interactomes is crucial for understanding the functioning of biological systems since protein interactions are in the basis of most cellular processes. Several experimental techniques were developed for this task of determining interactomes. These fall into two main families, those based on complementation assays (e.g. "yeast two hybrid system") and those based on purification of complexes (e.g. "tandem affinity purification followed by identification by mass spectrometry"). In parallel, a number of computational techniques were developed for complementing these experimental approaches. These are based on genomic and sequence features of the proteins intuitively related to interactions and functional relationships. Interactomes obtained with these methods were the first subjects of study of "network biology". Important biological information was obtained from the topological properties and connectivity patterns of these protein interaction networks. Not only basic biological knowledge is being obtained from these interactomes. Sub-networks of protein interactions are also being used as markers of diseases and possible targets for therapeutic intervention performing better than individual proteins for these tasks.