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## Computational approaches for the analysis of protein interactomics

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Interactomics is the study of interactions, the whole set of molecular interaction in cells involving physical interaction and indirect interactions among molecules and genes. Protein interactome can provide more information about the functional links and the functional context of the proteins which are not apparent from protein sequence analysis or protein expression analysis. The significance of this information for systems biology and drug development rises with the increase in the size of protein interaction data and with the availability of protein interactomes. Domain-domain and protein-protein interactions are being analyzed from a biochemical and evolutionary perspective. Work involves developing computational methods, algorithms to understand protein interactions. Work is centered on the alignment of distantly related domains and the role of outliers (which are the extremely deviant members in a superfamily). Work focuses on the analysis of functional annotation and biological relevance of outliers using gene ontology and other resources. On-going work about a map or a network of domain interactions will be introduced for a better understanding of the structural interactome and in predicting the off-site interactions of drug candidates related to Mycobacterium tuberculosis. Also, the work focuses on the analysis of a protein superfamily and domains involved multiple biochemical functions.

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