From Genomics to Functional Proteomics: *In silico* Approach

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Recent advances in genome sequencing projects are shifting the focus of high-throughput biological science from DNA (genomics) to proteins (proteomics). While genomic data provide a necessary knowledge base, they are often insufficient for understanding the biological function of proteins and protein machines. Protein machines often perform their function(s) via interactions with other biomolecular machines (e.g., ligands, proteins, or nucleotides). Thus, a comprehensive understanding of protein functionality will require information at various levels including structures, protein interactions, metabolic and regulatory pathways, and cellular networks. In this talk we present several computational challenges towards such understanding and ways to approach them. We will specifically focus on addressing basic questions, such as what interacting partners each protein has, where such interactions occur, and how site-specific mutations affect a protein function(s).

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