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Biography

I received a B.S. degree from Istanbul Technical University, Turkey (Chemical Engineering) and a Master's (Computational Sciences and Engineering) and Ph.D. (Computational Sciences and Engineering) from Koc University, Turkey (advisors: Prof Ozlem Keskin and Prof. Attila Gursoy). During my Ph.D, I closely collaborated with Prof. Ruth Nussinov from National Cancer Institute (NCI). My Ph.D. work focused on structural modeling of protein interactions and incorporating them into the protein interaction networks. We developed an algorithm for large-scale prediction of protein-protein interactions and assembly of protein complex structures which integrates structural and evolutionary similarity with flexible refinement and energy calculations. Then, I joined Ernest Fraenkel's group at Massachusetts Institute of Technology as a Postdoctoral Associate and began working on revealing how the networks of interactions among proteins and genome are altered in cells during disease.

Abstract of Current Work

Signaling and regulatory networks are essential for cells to control processes such as growth, differentiation and response to stimuli. Although a variety of "omic" data sources are available to probe signaling pathways, these data are typically sparse and noisy. My work has been focused on formulating an approach for using "omic" data to reconstruct multiple pathways that are altered in a particular condition. Previously, we have shown that these data could be efficiently analyzed by solving the prize collecting Steiner tree (PCST) problem to reveal a biologically relevant signaling pathway composed of a subset of the detected proteins through other undetected proteins present in the interactome. I modified this approach to simultaneously discover multiple pathways searching for "forests" consisting of multiple trees, and using directed edges in the interactome. I used the approach to examine changes in signaling that occur in glioblastoma multiforme (GBM). This approach discovered both overlapping and independent signaling pathways. Although the algorithm was not provided with any information about the phosphorylation status of cell surface receptors, it identifies a small set of clinically relevant receptors among hundreds present in the interactome. The method can be applied efficiently to "omic" data and is able to reconstruct networks that are enriched in functionally and clinically relevant proteins. Currently, I am working on incorporating existing pharmaceutical or biological agents into this algorithm to suggest possible combined therapy to treat specific diseases.