

Poster J-45
Assistant Research Fellow



Authors:

ChungYen Lin (*Institute of Information Science, Academia Sinica*)
Chi-Shiang Cho (*National Health Research Institutes*)
Chia-Ling Chen (*National Health Research Institutes*)
Fan-Kai Lin (*National Health Research Institutes*)
Chieh-Hua Lin (*National Health Research Institutes*)
Pao-Yang Chen (*National Health Research Institutes*)
Shu-Hwa Chen (*Institute of Zoology, Academia Sinica*)
Chen-Zen Lo (*National Health Research Institutes*)
Chao A. Hsiung (*National Health Research Institutes*)

Short Abstract: We used the fruit fly, as the target species to build protein networks integrated experimental and inferred interactions to form whole network under various scenarios. Based on the experimental Y2H interactions, we converted the protein interactions to domain interacting network to infer new protein interactions and perform the topology analysis.

Long Abstract:

Motivation:

In the era of proteomics, protein networks play a major role in expanding human knowledge towards biology. We used the fruit fly, *Drosophila melanogaster*, a widely studied model organism for eukaryotes, as the target species to build protein networks which are essential and important reflections of genomic function.

Result:

In this study, a mixed “hybrid model” of association and maximum likelihood estimation (MLE) methods is proposed for estimating the reliability of each experimental protein interaction derived from large-scale two-hybrid assays and to infer novel protein-protein interactions. Biological information from GO, KEGG, Uniprot, FlyBase, and Unigene was incorporated as biological filters under specific spatiotemporal scenarios, and protein annotation aided with depicting the network including experimental and predicted interactions with statistical estimation under a web interface. A ping-pong search was annexed for the putative path maps generated based on the shortest-path theory to decipher the complex relationships between any two proteins. Such a rewired database integrated with experimental and predicted interactomes was designed to provide a view of systems biology. From this interaction study, we expect that our work can be widely used to help proteomic-related laboratories carry out work across species.