

## **Comparative Genomics: Sequence, Structure and Networks**

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In this talk, I will describe my group's recent work in the area of comparative genomics. Comparative genomics comprises the class of methods where one compares like biological data across different species with the hope of discovering isomorphic regions that will lead to insights into biological function. We have found this approach to be successful in several areas of interest, including gene and regulatory motif recognition and discovery, RNA secondary structure prediction, protein structure alignment and threading, and gene orthology detection. I will especially focus on a novel algorithm we have developed, ISORANK, for global alignment of multiple protein-protein interaction (PPI) networks. The guiding intuition here is that a protein in one PPI network is a good match for a protein in another network if their respective sequences and neighborhood topologies are a good match. We encode this intuition as an eigenvalue problem, in a manner analogous to Google's PageRank method. Using ISORANK, we compute the first known global alignment of the yeast, fly, worm, mouse, and human PPI networks. Akin to the complete sequencing of genomes and their comparative analysis, complete descriptions of interactomes and their comparative analysis is fundamental to a deeper understanding of biological processes. This talk will be introductory in nature. No background in biology will be assumed.