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Virtual Brown Bag Research Discussion Series

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Network Reconstruction of Dynamic Biological Systems: Doubly Penalized LASSO

Reconstruction of biological networks is a crucial step in extracting information from a large volume of experimental data. Various methods have been developed to reconstruct networks from data, each of which possesses its own strength and disadvantages. In this talk, I will first describe examples of network reconstruction techniques including classic optimization-based approaches (e.g., least-squares methods), dimensionality reduction methods (e.g., statistical significance tests combined with either principal components regressions (PCR), or partial least squares (PLS), Bayesian networks and hybrid methods (e.g., Linear Matrix Inequalities (LMI) and Least Absolute Shrinkage and Selection Operator (LASSO). Next, I will introduce our most recent method, called Doubly Penalized Linear Absolute Shrinkage and Selection Operator (DPLASSO) for network reconstruction with the intent to combine the beneficial features of a regression and statistical significance testing-based method and a penalized optimization method. I will present results from applications to simulated data from synthetic random networks as well as from a biological system, namely the cell cycle in budding yeast.

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