



The University of Chicago  
Department of Statistics

Master's Seminar

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**Graphical Models for Phospholipid/Phosphoprotein  
Coexpression Data**

**THURSDAY, August 7, 2008 at 11:00 AM**  
**110 Eckhart Hall, 5734 S. University Avenue**

**ABSTRACT**

In a graphical model, each node corresponds to a variable, and edges are drawn from covariate to response, where each variable is, in turn, treated as the response while the remaining variables are possible covariates. Graphs are constrained to be acyclic. Recently, directed acyclic graphs have been applied to the study of cell signaling networks, which allow information to be transmitted within a cell via the interaction of proteins and lipids. Given coexpression data consisting of both observational and interventional measurements (Sachs et al., 2005), we search for the optimal graph of relationships among 11 proteins and lipids in the human immune system. We apply the algorithm of Silander and Myllymäki (2006) and, for comparison, a multiple-restart stepwise search in the space of graphs.