

# Department Seminars

## Bayesian Models for Genetic Pathways



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### Abstract:

We define a class of Bayesian graphical models for the inference of molecular pathways based on expression data. Under a Bayesian framework, our models update a prior consensus pathway using expression profiles and provide posterior estimates of protein-protein interactions that are specific to the study population. We introduce a set of discrete prior models that are specific to the dependence structure in the prior pathway. For inference, the posterior network is presented with directionality and strength for the each protein-protein interaction. We demonstrate the models using a novel type of proteomics data based on reverse phase protein arrays (RPPA).

Bio: Yuan Ji received his PhD degree at the University of Wisconsin in 2003. His current research focus is in bioinformatics and computational biology. [http://faculty.mdanderson.org/Yuan\\_Ji/](http://faculty.mdanderson.org/Yuan_Ji/)

**Friday,**  
**October 30, 2009**

**G5/113 CSC**

**12:00-1:00 p.m.**