

Time: Monday May 2nd, 2011 3:00pm

Location: Buchanan A203

**Parametric inference of ancestral protein interaction networks**

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Protein interaction networks can be represented as graphs. The evolution of these networks is modelled by probabilistic graphical models on a rooted tree. Sturmfels and Pachter laid out a general framework to study such models as algebraic objects (Algebraic Statistics for Computational Biology, Cambridge Univ. Press). We use the concepts developed by them to study the evolution of protein interaction networks, and apply the techniques on simulated and real data (Pinney et al. PNAS vol. 104 no. 51).