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***Modeling protein-protein interactions with  
HMMs and BNs***

**Abstract**

HMMs (Hidden Markov Models) and BNs (Bayes Nets) are two graph-based formalisms used in machine learning to model and assign probabilities to events given past information. HMMs are well-suited to modeling sequence information; Bayes Nets naturally model features such as pH, location, or temperature. We have combined HMMs and BNs in several architectures and applied them to prediction of binding affinities of SH3 domains to peptide ligands.

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**Tuesday, January 21<sup>st</sup>  
4:00 p.m.**

Room 1221  
Computer Sciences / Statistics Building  
1210 West Dayton Street