A major challenge in Systems Biology is to uncover the causal mechanisms through which complex cell behaviors emerge from a multitude of low-level molecular interactions. Understanding these causal mechanisms is critical for medical research as it enables the identification of potential targets for drugs.

In this spirit, biologists have been building models of the cell chemistry that aggregate known interactions between proteins. In this talk, we introduce a technique to analyze the causal structure of simulation traces generated from such models. Concretely, our method leverages simulation to produce causal diagrams that explain outcomes of interest in terms of enablement and prevention relations between molecular events.

A key contribution of our work is an algorithm to simulate counterfactual scenarios efficiently. Given a reference trace, it provides an answer to questions such as: What would have happened had a particular event not happened? Doing so, it generalizes Pearls standard treatment of counterfactuals to complex dynamical systems.

(Based on joint work with Jean Yang and Walter Fontana, published at IJCAI-18.)

This talk will be given in the context of the "AI seminar series":
http://www.cs.cmu.edu/~aiseminar/

Presented in Partial Fulfillment of the CSD Speaking Skills Requirement.