

# Mathematical & Computational Biology Seminar

Organizer: Valerie Hower

Wednesday, 2:00–3:00pm, 939 Evans

---

Sept. 30    **Kristina Crona**, UC Merced

*Bayesian networks and resistance conferring mutations*

It is well known that resistance conferring mutations for viruses and bacteria may be restricted in the order of occurrence. A central problem is to derive from the data the constraints on the orders in which the mutations have accumulated. We consider a Bayesian network model for mutations conferring resistance to antibiotics where both conjunctions and disjunctions are allowed as logical constraints. Clinically found TEM variants associated with antibiotic resistance suggest that disjunctions (as well as conjunctions) occur. More precisely, the mutation E240K is never present without the occurrence of other mutations. However, four different mutant variants with a combination of E240K and another mutation have been found clinically. Laboratory results (joint work with Miriam Barlow and Stephen Jacobs) confirm that disjunction may occur for TEM variants and some antibiotics. In light of these findings we suggest a Bayesian network model where the constraints are statements generated by conjunctions and disjunctions (but no negations). Our laboratory results also show that the adaptive landscapes associated with the clinically important TEM-85 are very complex with multiple peaks, reversed mutations, fewer mutational trajectories and prolonged mutational trajectories, as compared to a classical model. The result is a considerably less efficient Darwinian process where existing models do not seem to apply, and we suggest a model where interactions between subpopulations are central.