Introduction:
Markov state models for molecular dynamics simulations

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Many biochemical events we’d like to capture by molecular dynamics (MD) simulations take place on timescales longer than we can simulate. Simulation of β$_2$-adrenergic receptor transitioning spontaneously from its active state to its inactive state occurs after 11 µs (weeks of simulation time).

Simulation of β$_2$-adrenergic receptor transitioning spontaneously from its active state to its inactive state

Rosenbaum et al., *Nature* 2010; Dror et al., *PNAS* 2011
What if instead of running one long simulation, we run many short simulations?

- Can we use many short simulations to predict what would have happened in a longer simulation?
- We need a way to summarize the information from many short simulations.
- One way to do this involves Markov State Models.
A Markov model for predicting tomorrow’s weather given today’s weather

https://dzone.com/articles/markov-models-and-hidden
Markov state models for MD simulations

- Each node represents a conformational state (that is, a group of similar conformations)
- Each edge represents a transition from one state to another and has an associated probability

How can these Markov State Models be useful?

• Running many short simulations instead of one long simulation
  – E.g., Folding@Home
  – Need to decide initial conditions for each short simulation
• Potentially: reduce total amount of simulation time necessary
• Human interpretation/summarization of simulation data
Background material

• A basic introduction to Markov models

• Molecular dynamics slides from CS/CME/BioE/Biophys/BMI 279:

• Question: how is this connected to PageRank?