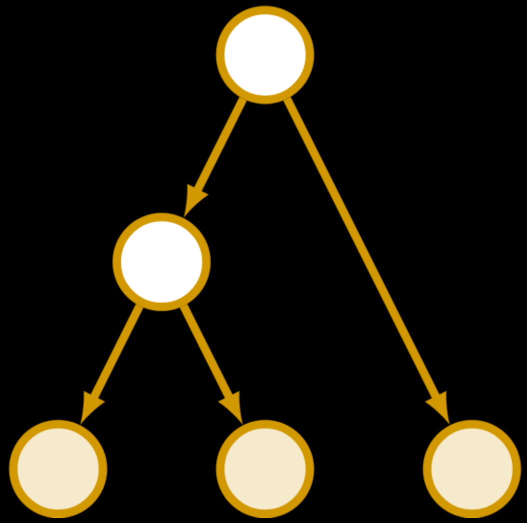


BCB 503:
RevBayes Intro

Second session: Trait Evolution, MCMC

Orlando Schwery, 31. Aug. 2021, University of Idaho

Course Plan and Schedule

- 3:30pm Pacific, on Zoom

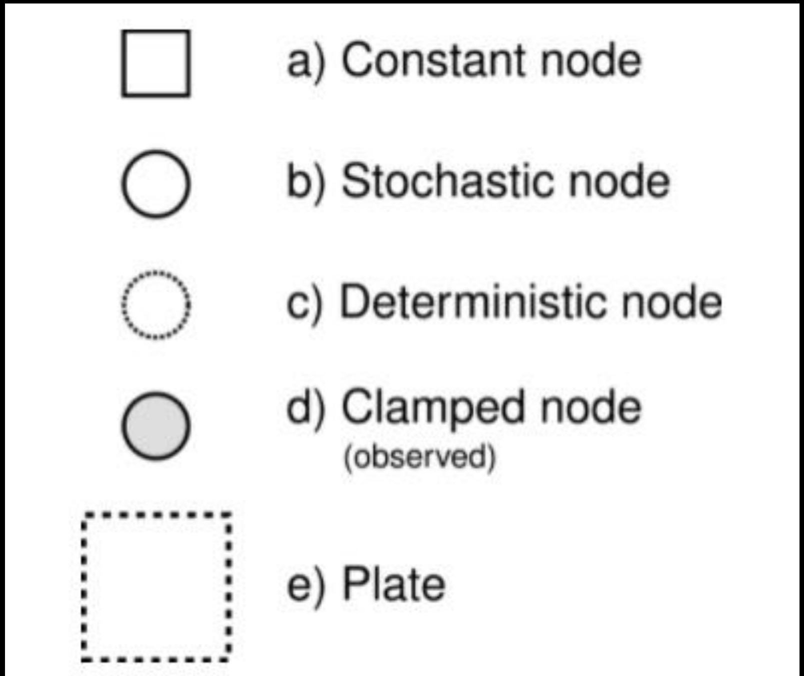
- **24. Aug.:** Intro
- **31. Aug.:** Trait Evolution
- **07. Sep.:** Biogeography
- **14. Sep.:** Diversification
- **21. Sep.:** [Model Testing/Adequacy]
- **28. Sep.:** [Hierarchical Models, FBD, …?]

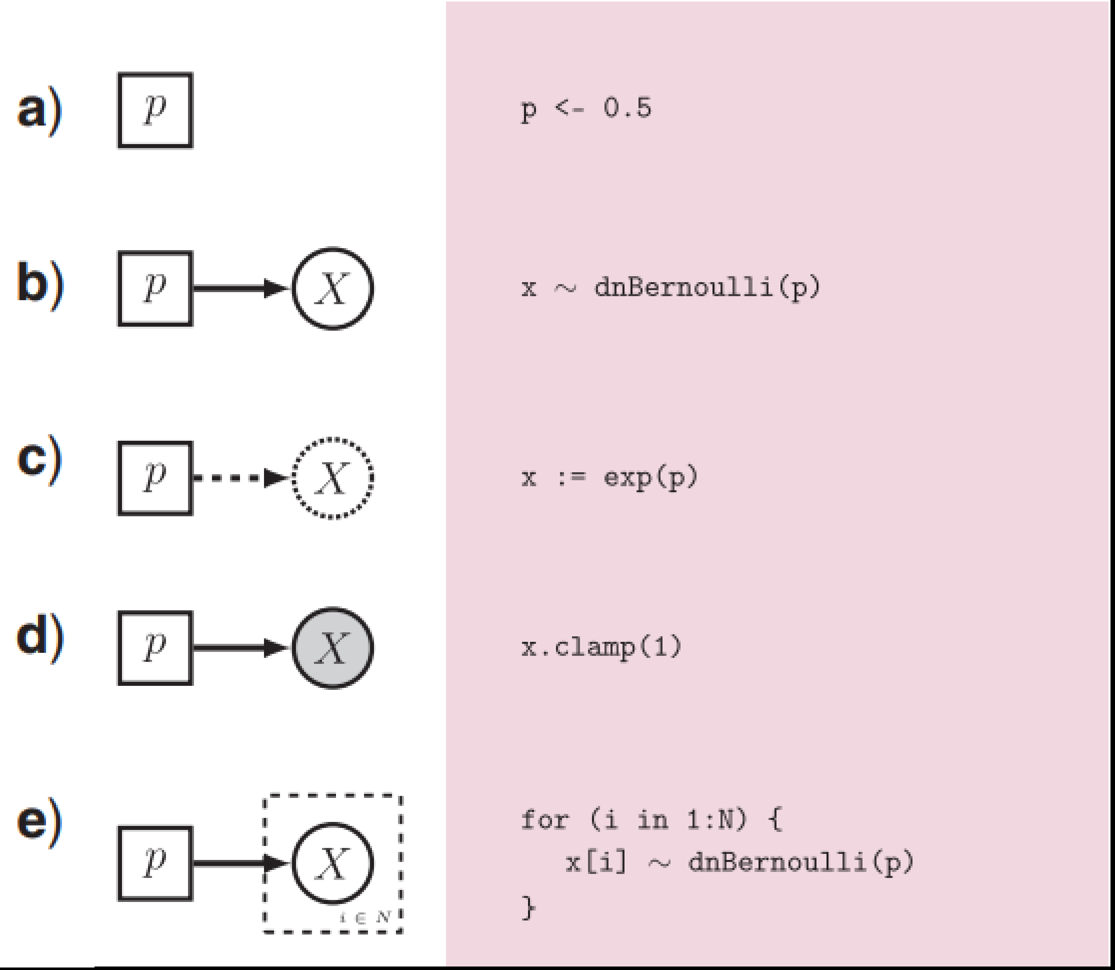
→ Absences: Recording, Remote, Add-On, …

Briefest recap from last time:

- Use from command-line
- Possibility to use RStudio or Jupyter as GUI…

Graphical Models



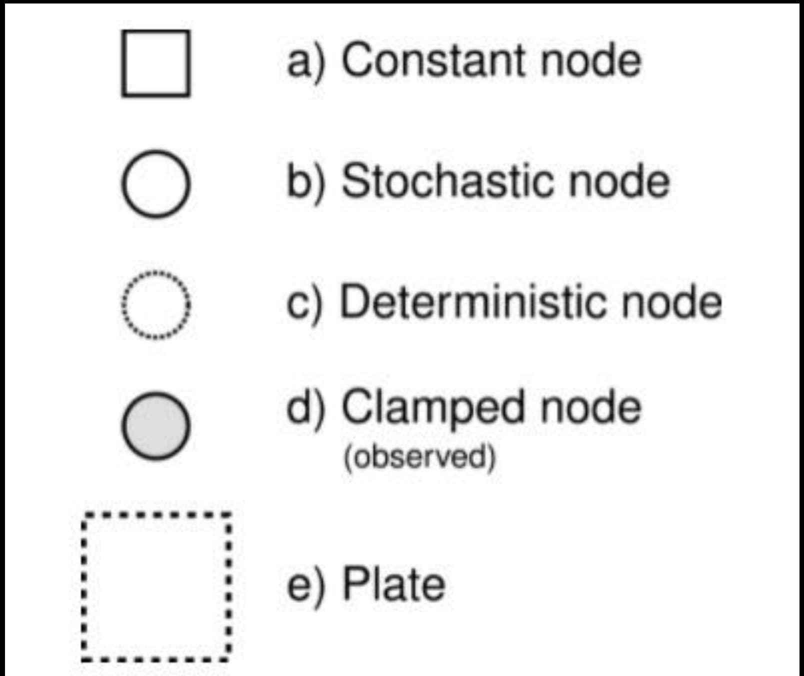


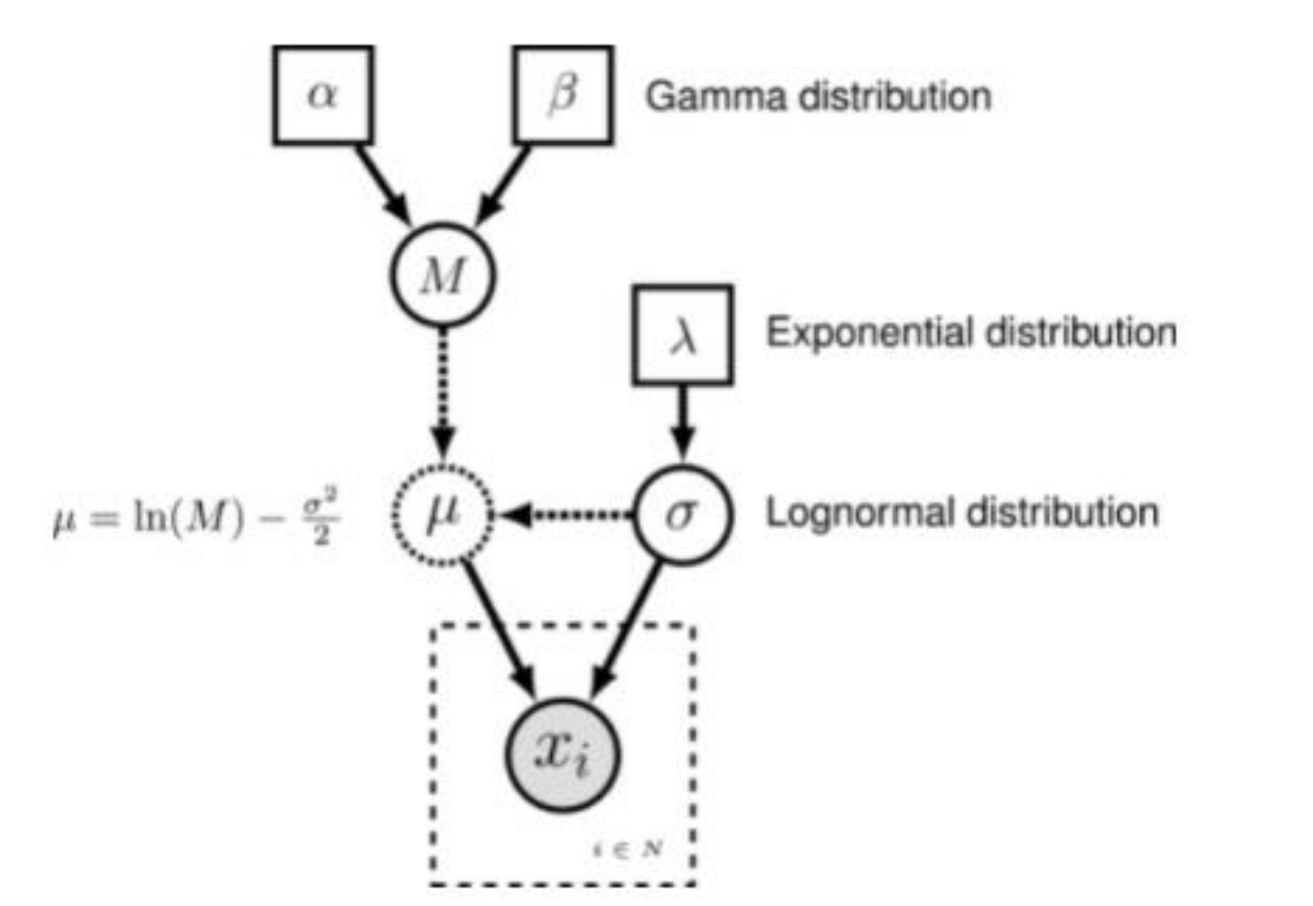
Directed Acyclic Graph (DAG)

→ Nodes (vertices) and Edges (circles/squares and arrows)

Höhna *et al.* 2016 Syst. Biol.

Graphical Models





Lognormal Model/Distribution:

$X = e^{\mu+\sigma z}$ [μ: location parameter (log mean); σ: standard deviation]

Trait Evolution in RevBayes - Overview

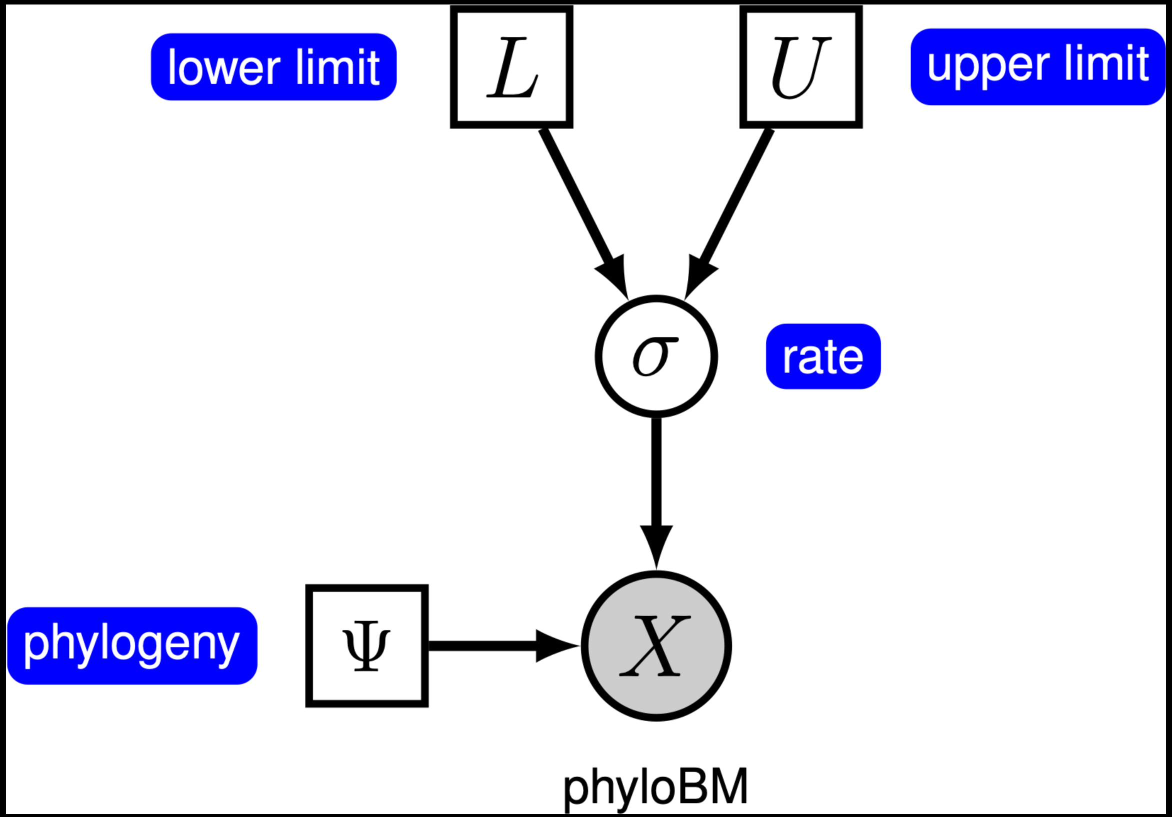
- Continuous Characters
  - Brownian Motion models
    - Simple BM (rates of evolution)
    - Relaxed BM (with rate shifts)
    - Multivariate BM (correlated evo)
    - State-Dependent BM (combines
  - Ornstein-Uhlenbeck models
    - Simple OU (trait optima)
    - Relaxed OU (with rate shifts)
- Discrete Characters
- Host Repertoire Evolution

Additional contents therein:

- Model selection using reversible-jump MCMC
- Reversible vs. irreversible trait evo
- Background-rate variation
- Results plotting using RevGadgets

Simple Brownian-Motion

- Single rate parameter sigma^2
  - Drawn from loguniform distribution
  - Lower bound L
  - Upper bound U
- The phylogeny is assumed to be fixed, thus added as a constant node
- The node X contains the BM model for trait data based on tree and rate, with observed data clamped to it



Simple Brownian-Motion

- Put data in subfolder “data” for good practice

- Off to the code!

MCMC in RevBayes - Overview

- Introductions to MCMC
  - Poisson (airline and coalmine accidents)
  - Binomial (coin flipping) [with video links]
  - Gamma (archery)

- Convergence Assessment [in R]

Additional contents therein:

- Coding up an MCMC from scratch
- Running analyses in batch mode
- More on the Metropolis-Hastings Algorithm
- Visualizing the samples (traces, posterior distributions)
- Different moves, their tuning and weights
- Using ESS to evaluate how different moves perform
- Exploring prior sensitivity

Running an MCMC

- The other tutorials are doing a pretty good job at looking more in-depth at the inner workings of the MCMC, different options etc.
- We’ll use it out of the box, focusing on the ‘how to run’ for now.
- Background:
  - Bayesian analyses: we’re interested in the posterior distribution of our parameters, often can’t be calculated directly, so we do it numerically using MCMC
  - ‘robot on landscape’ analogy
    - Move through parameter space
    - Evaluate likelihood of parameter combinations at proposed move
    - Move towards improvement to get to peak(s)

Running an MCMC

- Off to the code!