Model-Based Inference of Phylogeny: Overview

Brian R. Moore Department of Evolution & Ecology University of California, Davis Bodega Phylogenetic Workshop, 2019

Statistical Estimation of Phylogeny: An Outline

Generic statistical paradigm

pose a substantive question

develop a stochastic model with parameters that, if known, would answer the question

collect observations that are informative about model parameters

find the best estimate of model parameters (by some means) conditioned on (*i.e.*, given) the data at hand

Statistical phylogenetic paradigm

what is the phylogeny of my study group?

develop a phylogenetic model with a tree (and branch lengths) and a Markov model describing how traits change over the tree

assemble a data matrix (*e.g.*, of DNA sequences) sampled from members of your study group

find the best estimate of phylogeny (and other model parameters) using a likelihoodbased method (maximum-likelihood or Bayesian inference)

Statistical Estimation of Phylogeny: An Outline



Statistical Estimation of Phylogeny: Course Goals

Why we are here

Develop a strong intuition for the theory of statistical phylogenetic methods demystify principles of statistical inference and phylogenetic models

Develop skills to apply phylogenetic methods

how to perform common analyses under common phylogenetic models how to specify models that are well suited to your specific questions



Sunday: Introduction to phylogenetic models and RevBayes



John Huelsenbeck

Basic probability concepts CTMC Likelihood computation

Sunday: Introduction to phylogenetic models and RevBayes



Sebastian Hohna

Graphical models Introduction to RevBayes How to specify models using Rev

Sunday: Introduction to phylogenetic models and RevBayes



MCMC assessing MCMC performance

Brian Moore

Monday: Model specification



Model selection/hypothesis testing Model adequacy

Bob Thomson

Tuesday: Divergence-time estimation



Relaxed-clock models

Brian & Mike May

Tuesday: Divergence-time estimation



John Huelsenbeck

Calibrating divergence times



Sebastian Hohna

Wednesday: Evolution of continuous characters



Diffusion models

Peter Wainwright



Mike May

Thursday: Evolution of discrete characters



CTMCs

Michael Landis

Thursday: Evolution of geographic range



Biogeographic models

Michael Landis

Friday: Lineage diversification



Sebastian Hohna

Branching-process models State-dependent models



Mike May

Saturday: Project presentations!



You!

Statistical Estimation of Phylogeny: RevBayes

Why RevBayes?



Transparency Flexibility Modularity Nice features *But please ask if you are interested in other software

RevBayes!