

INTRODUCTION TO BAYESIAN PHYLOGENETIC SOFTWARE

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OUTLINE

Overview

Introduction to Bayesian software programs for phylogenetics

- MrBayes: history and current version
- Other programs: PhyloBayes, BEAST/*BEAST
- RevBayes: graphical models and Bayesian phylogenetics

break

Tutorial – **Conor Meehan** and Instructors

Phylogenetic reconstruction in MrBayes

- Basic phylogenetic inference and MCMC

dinner

OUTLINE

Overview

Convergence and MCMC diagnosis

- tools and metrics for evaluating MCMC samples

break

Tutorial – Conor Meehan and Instructors

Phylogenetic reconstruction in MrBayes

- MCMC diagnostics in Tracer
- Partitioned phylogenetic inference in MrBayes

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A Bayesian inference program for phylogenetic inference and model selection



John Huelsenbeck



Fredrik Ronquist

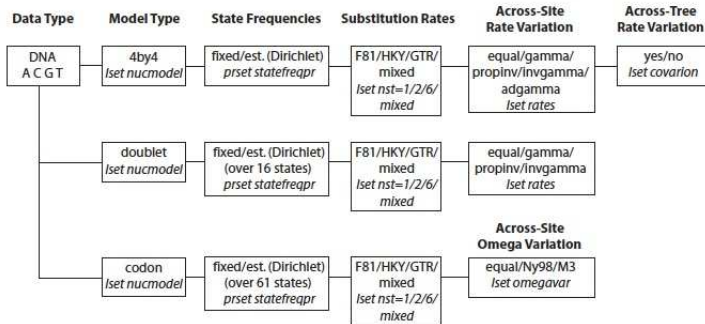
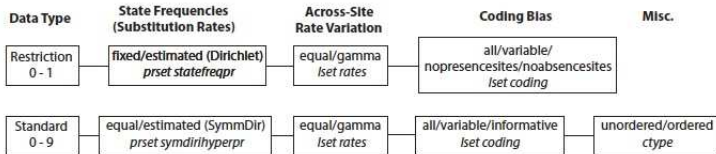
also Maxim Teslenko, Paul van der Mark, Daniel Ayres, Aaron Darling, Sebastian Höhna, Bret Larget, Liang Liu, Marc Suchard



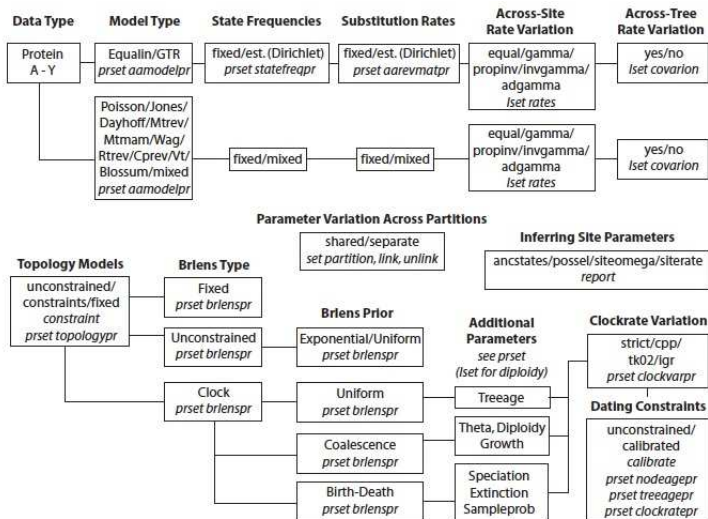
Phylogenetic inference under a wide range of models

- *Unrooted* trees
 - joint estimation of topology, branch length, and model parameters
- *Rooted* — time-calibrated trees
 - joint estimation of topology, branch rates, branch times, and model parameters, and gene-tree/ species-tree inference in BEST
- Data types
 - discrete characters — binary $(0, 1)$ or multi-state $(0, 1, \dots, 9)$
 - DNA — 4-state nucleotide, doublet, or codons
 - amino acid

MrBAYES — MODELS



MrBAYES — MODELS



PHYLOBAYES

Bayesian phylogenetic reconstruction under non-parametric mixture models

Lartillot, Philippe. 2004. **A Bayesian mixture model for across-site heterogeneities in the amino-acid replacement process.** *MBE* 21: :1095–1109.

Huelsenbeck, Suchard. 2007. **A nonparametric method for accommodating and testing across-site rate variation.** *Syst. Biol.* 56:975–987

Lartillot, Lepage, Blanquart. 2009. **PhyloBayes 3: a Bayesian software package for phylogenetic reconstruction and molecular dating.** *Bioinformatics* 25: 2286–2288.

BEAST/*BEAST

Joint Bayesian inference of tree topology (*rooted*) and divergence times

Bayesian **E**volutionary **A**nalysis **S**ampling **T**rees

- population size
- growth/decline in population
- bottlenecks/transition points
- gene trees/species trees
- virus transmission dynamics
- recombination
- migration
- founder effects
- epidemiological tracking
- phylogeography
- trait evolution
- dates of MRCA's
- lineage rates
- ancestral character state reconstruction
- times of bottlenecks/transitions

PROGRAM FEATURES

Method/Model/Feature	MrBayes v3.2	PhyloBayes	BEAST/ *BEAST
<i>Unrooted trees</i>	✓	✓	X
<i>Joint est. topology & times</i>	✓	X*	✓
<i>Gene-tree/species-tree</i>	✓	X	✓
<i>Dataset partitioning</i>	✓	✓	✓
<i>Bayes factors</i>	✓	✓	✓
<i>Morphological data</i>	✓	X	✓
<i>Demography/phylogeography</i>	X	X	✓
<i>DPP mixture on site-rates/models</i>	X	✓	X**
<i>Continuous traits</i>	X	✓***	✓
<i>Graphical-user-interface (GUI)</i>	X	X	✓

*divergence time estimation on fixed topology

**in BEAST2

***in companion program: Coevol

REV BAYES

A flexible programming environment
for model-based (primarily Bayesian)
phylogenetic inference



Sebastian Höhna



John Huelsenbeck



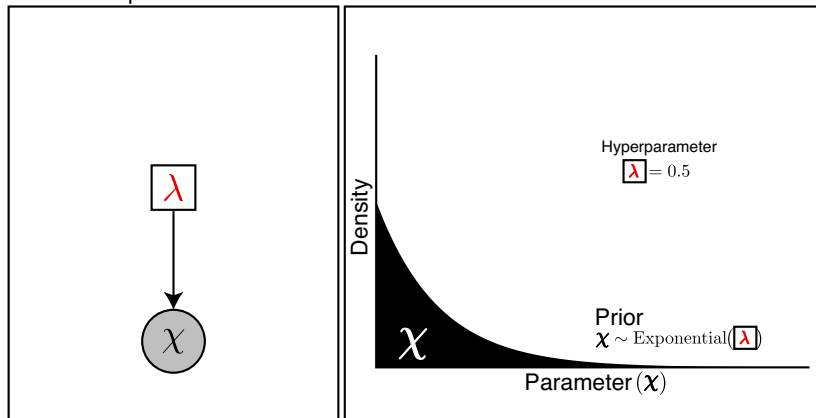
Fredrik Ronquist

also Bastien Boussau, Tracy Heath, Michael Landis, Brian Moore, Ben Redelings, Chi Zhang (and others)

GRAPHICAL MODELS IN REV BAYES

Models are represented by *directed acyclic graphs* (DAGs)

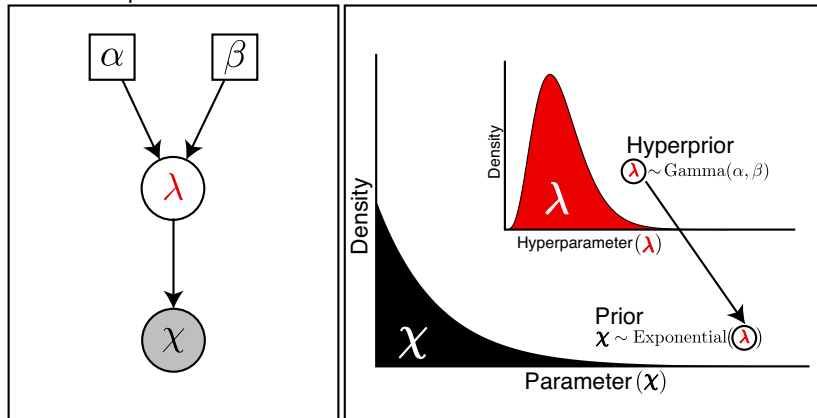
Graphical Model



GRAPHICAL MODELS IN REV BAYES

Models are represented by *directed acyclic graphs* (DAGs)

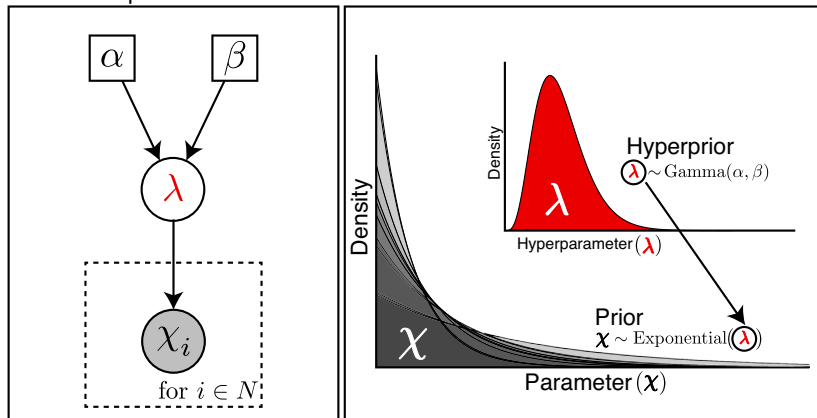
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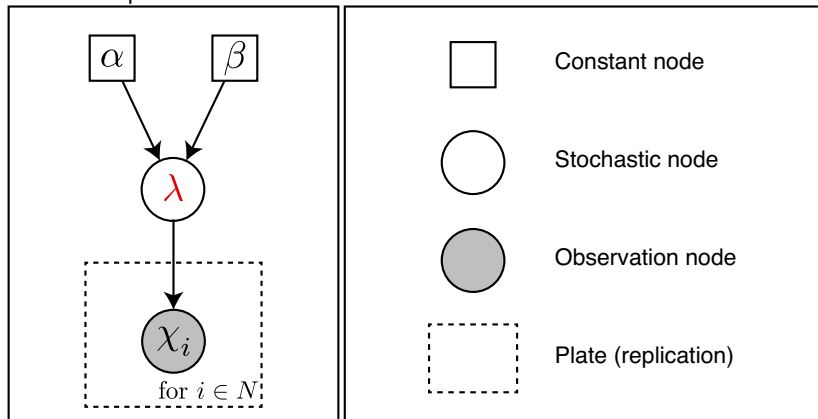
Graphical Model



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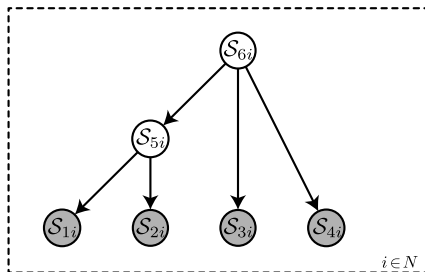
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Graphical Model



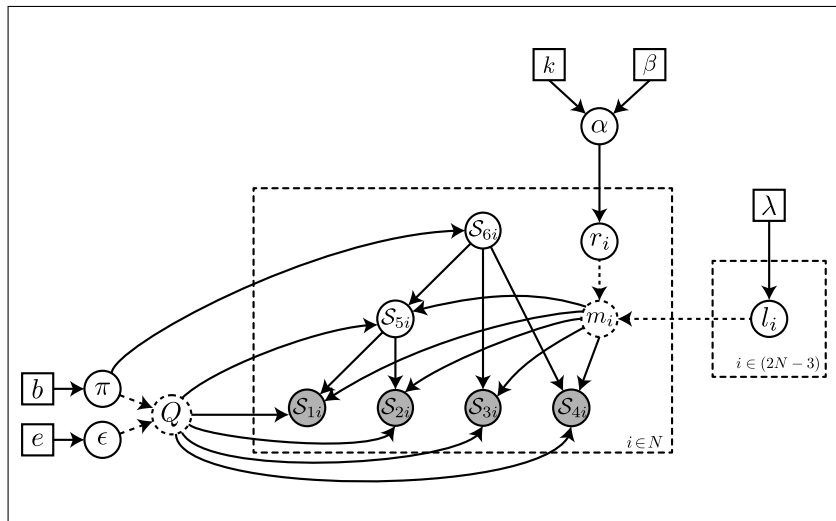
GRAPHICAL MODELS IN REV BAYES

A tree is a graphical model (DAG)



GRAPHICAL MODELS IN REVBayES

The GTR- Γ model



THE REV LANGUAGE

An R-like language for specifying models and MCMC analysis

```
# An example (partial)

# read the data
D <- readCharacterData("data/primates.nex")[1]

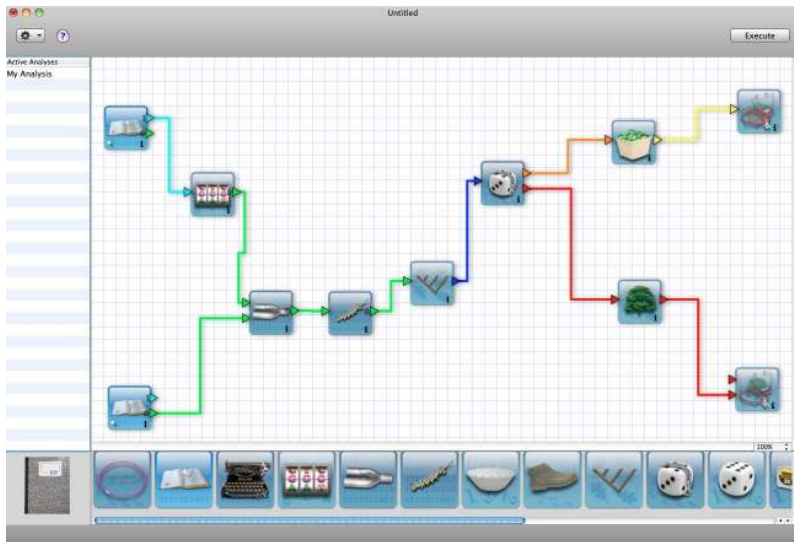
# substitution model priors
bf <- v(1,1,1,1)
e <- v(1,1,1,1,1,1)
pi ~ dirichlet(bf)
er ~ dirichlet(e)

# Moves on substitution model parameters
moves[1] <- mSimplex(pi, 10.0, 4, true, 2.0)
moves[2] <- mSimplex(er, 10.0, 6, true, 2.0)

...
```

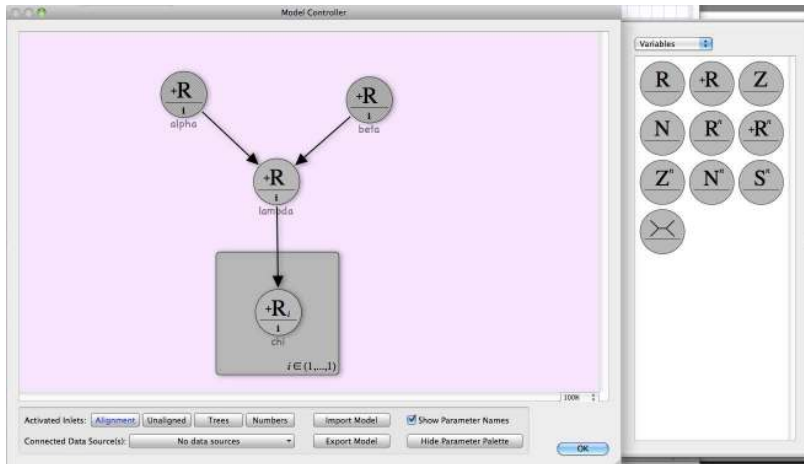
THE REVBayES GUI

Specifying the analysis work-flow



THE REVBayES GUI

Specifying the graphical model



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