

## Variation in rates among lineages & through time

### Overview

- Overview of BAMM and BAMM mechanics
- Work through example dataset: BAMM run plus analysis with BAMMtools (together)
- Work in pairs to perform BAMM analysis of one of the example datasets (or your own dataset)

### Macroevolutionary rates

*Dynamics of an evolutionary process as measured on paleontological timescales*

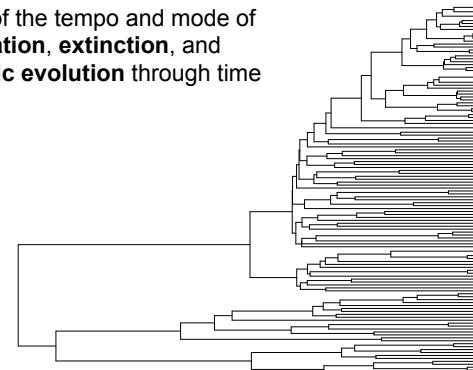
#### Diversification:

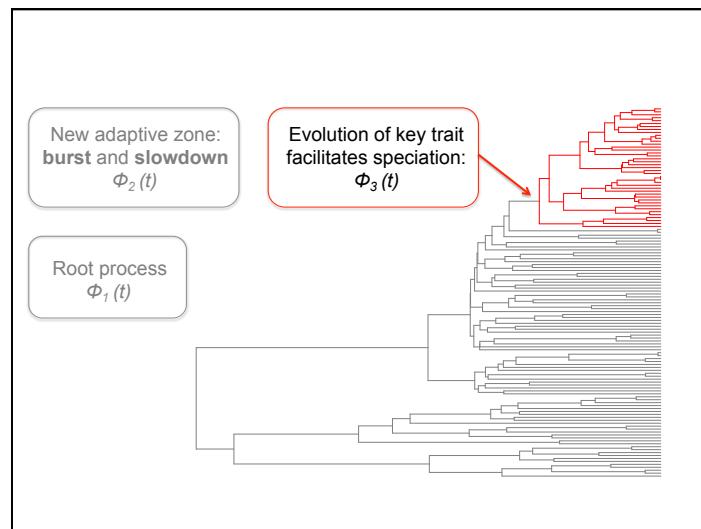
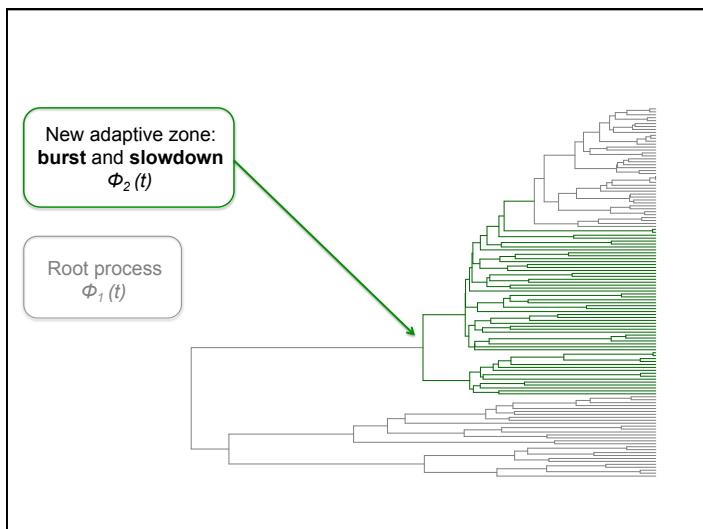
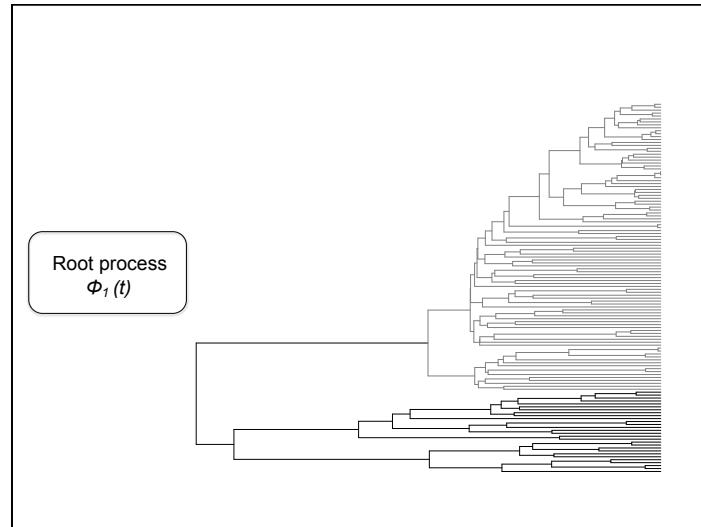
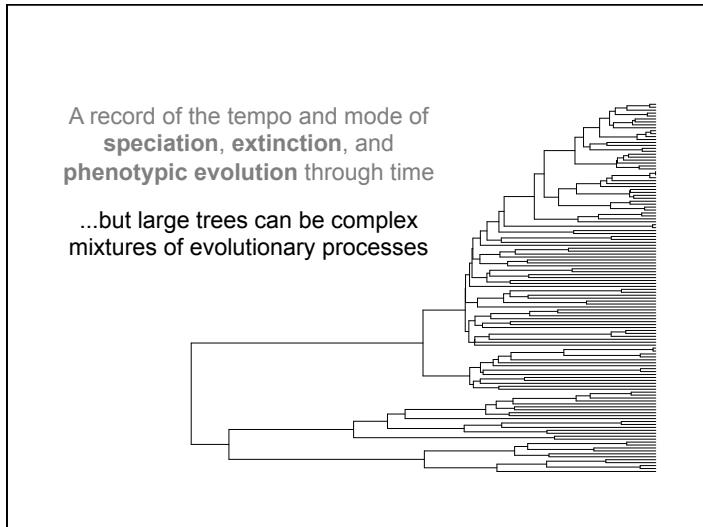
Speciation, Extinction  
Net diversification ( $S - E$ )

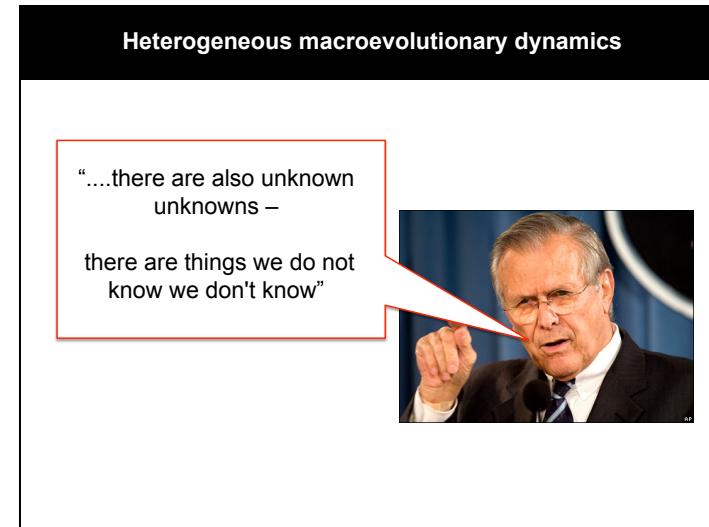
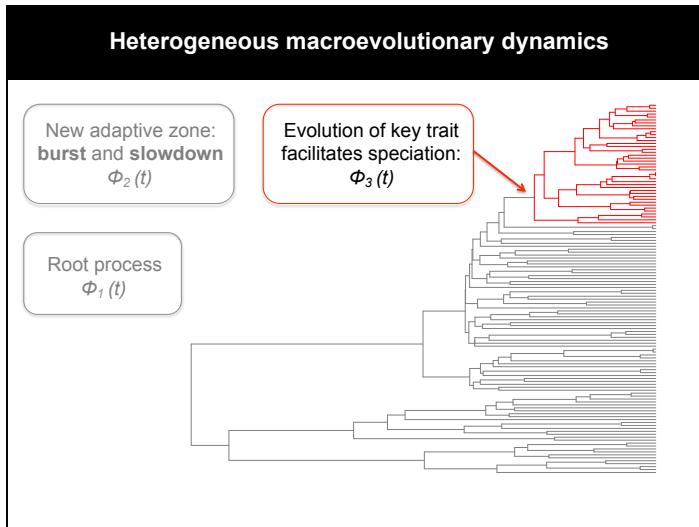
#### Phenotypic evolution:

Continuous characters  
Discrete characters  
Constraint regimes (e.g., OU process)

A record of the tempo and mode of **speciation, extinction, and phenotypic evolution** through time







### BAMM and BAMMtools

**Welcome**

BAMM (Bayesian Analysis of Macroevolutionary Mixtures) is a program for modeling complex dynamics of speciation, extinction, and trait evolution on phylogenetic trees.

BAMM is oriented entirely towards detecting and quantifying heterogeneity in evolutionary rates. It uses reversible jump Markov chain Monte Carlo to automatically explore a vast universe of candidate models of lineage diversification and trait evolution. It has been described and extended in several publications (Rabosky et al. 2013, Rabosky 2014). BAMM is a command line program written in C++. Post-run analysis and visualization is performed using the R package BAMMtools.

- Download BAMM and BAMMtools or go to our [Github](#) to get the development source code.
- Explore the [Graph Gallery](#) for a sample of analyses produced using BAMM and BAMMtools.
- Quickly start using and analyzing data with BAMM by reading the [Quick-start Guide to BAMM](#).
- Go to our [Frequently Asked Questions](#) page to see common questions and answers.

**Support**

The development of BAMM is funded by the National Science Foundation.

NSF

### BAMM help

**Welcome to the BAMM Google Groups page!**

BAMM (Bayesian Analysis of Macroevolutionary Mixtures) is a program for modeling complex dynamics of speciation, extinction, and trait evolution.

Please post any questions, comments, suggestions, possible bugs, etc. here. If you are reporting a problem, please include (if possible)

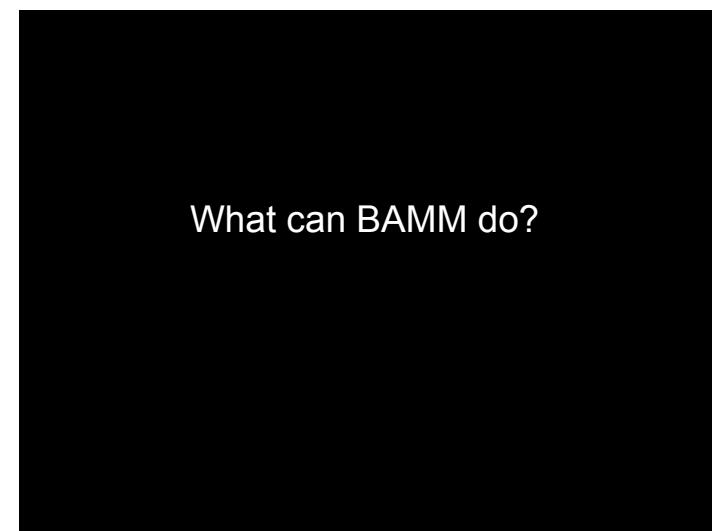
1. Data files that led to the problem
2. Control file
3. Operating system version and computer architecture
4. Compiler and version (if used)
5. run\_info.txt (if BAMM was able to run)

Possible bug with non-random incomplete sampling  
By Ben King - 5 posts - 16 views

sampling fractions  
By Eugenio Valderama - 3 posts - 20 views

Assumptions of current BAMM
- Ultrametric, resolved phylogenetic tree (all species extant)

Assumptions of current BAMM
- Ultrametric, resolved phylogenetic tree (all species extant)
<b>Speciation-extinction analyses only:</b>
- Either tree includes all species, or you can account for unsampled species (e.g., what percent are missing?)
- If taxa missing, taxon sampling should be random*
*not necessarily - see advanced...
<b>Phenotypic evolution only:</b>
- If phenotypic data: traits must be continuous

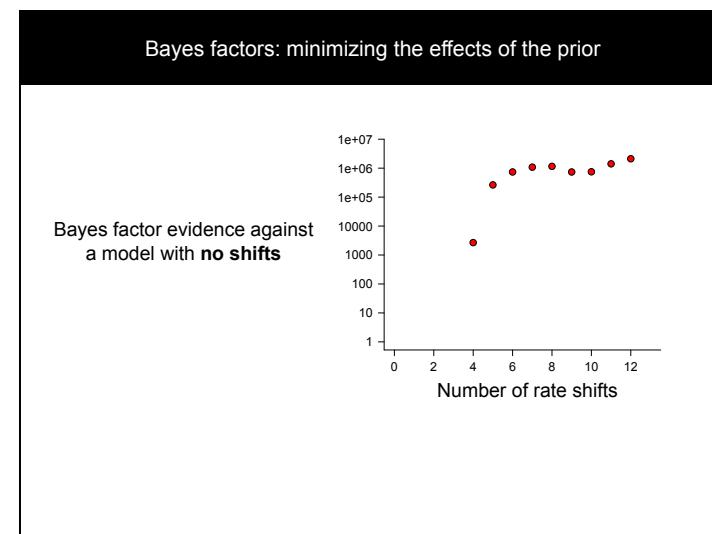
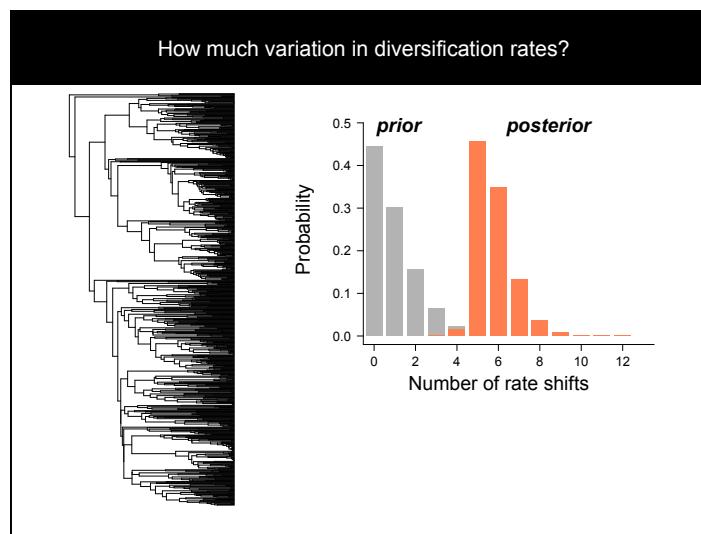
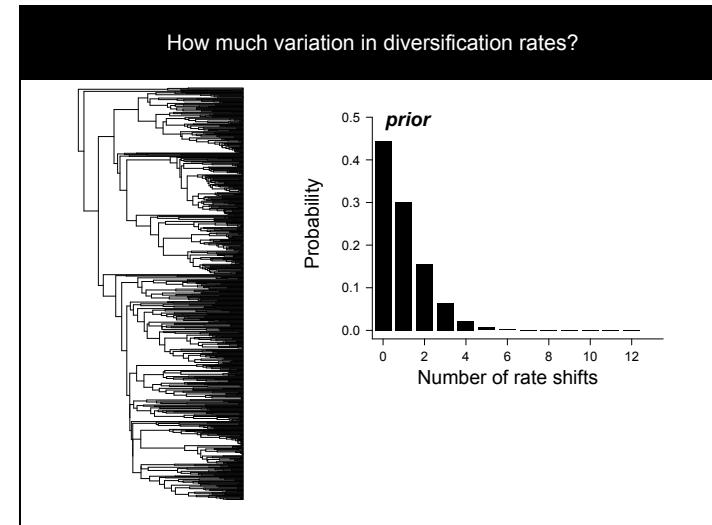


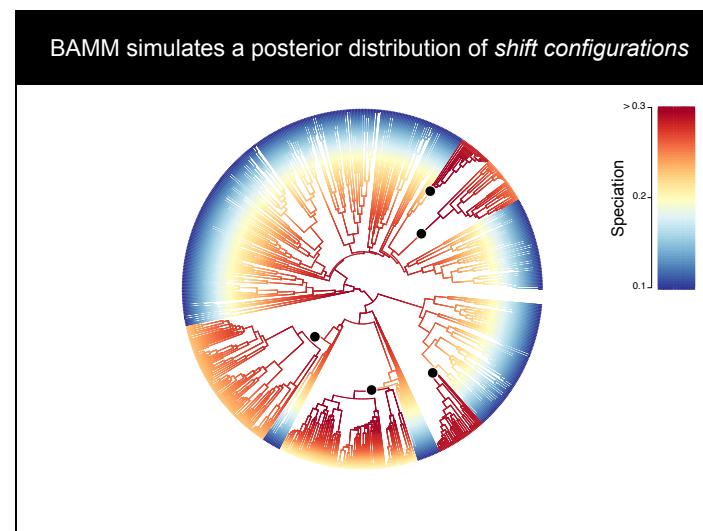
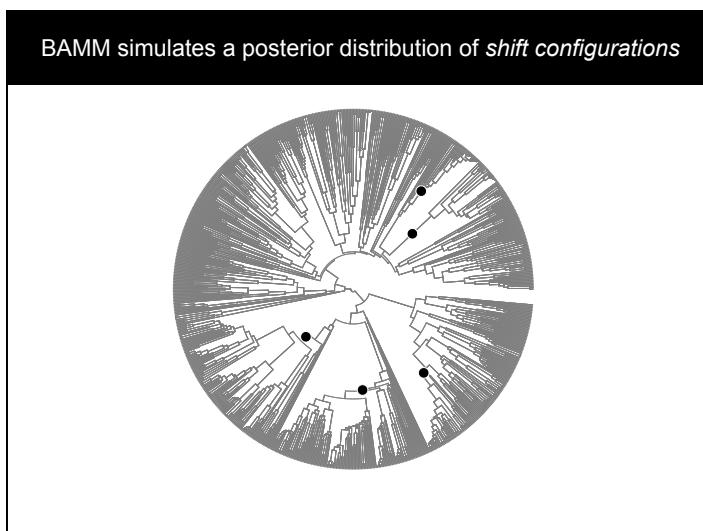
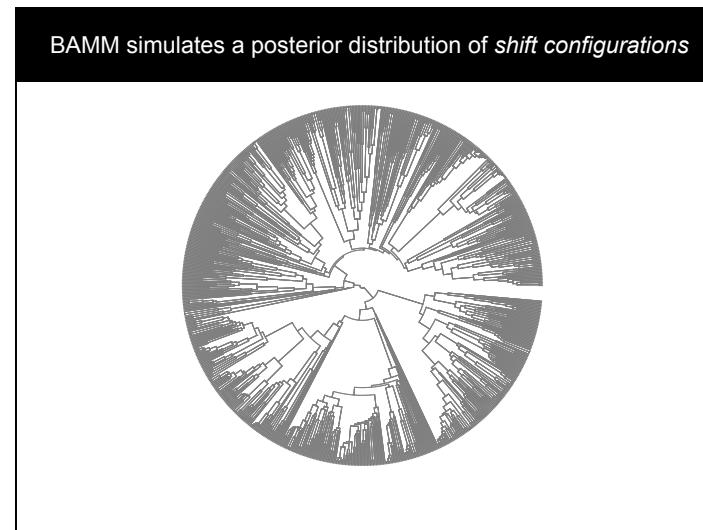
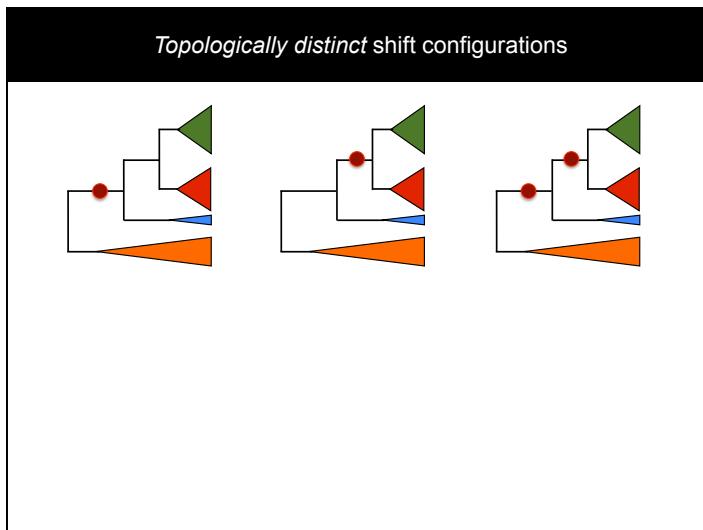
Analysis and visualization of complex dynamics on trees

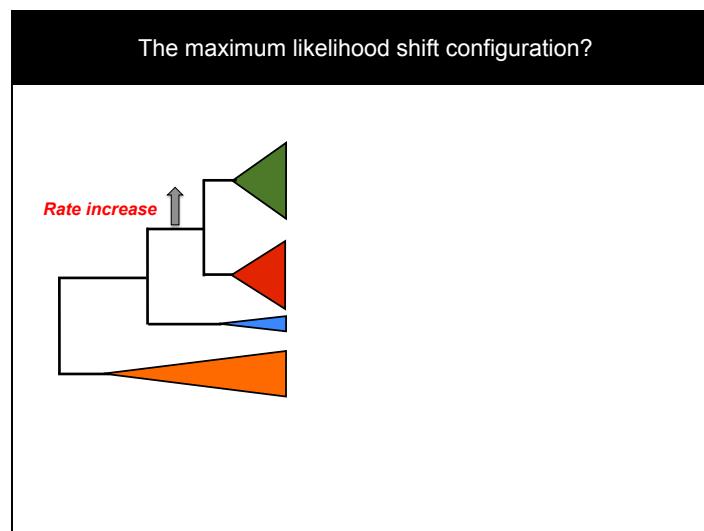
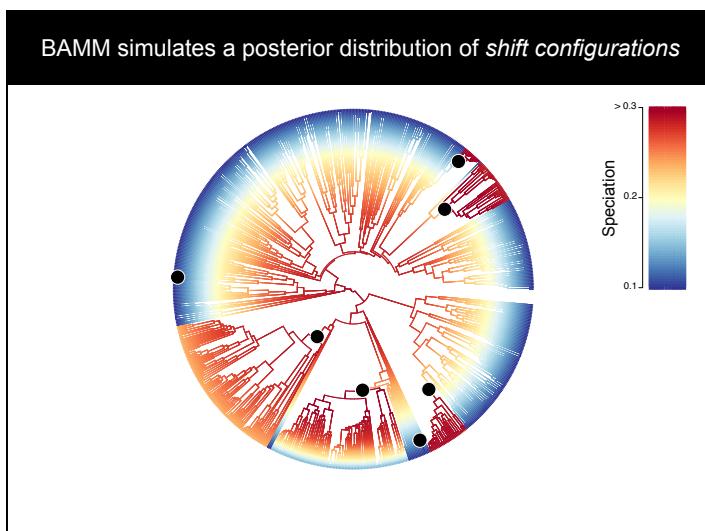
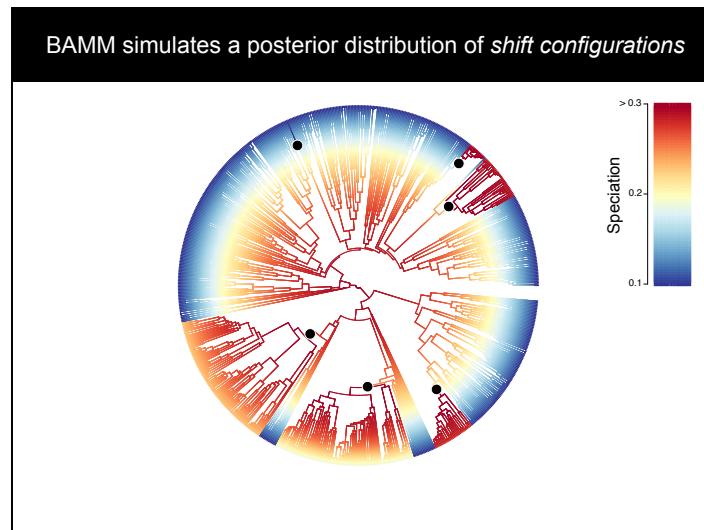
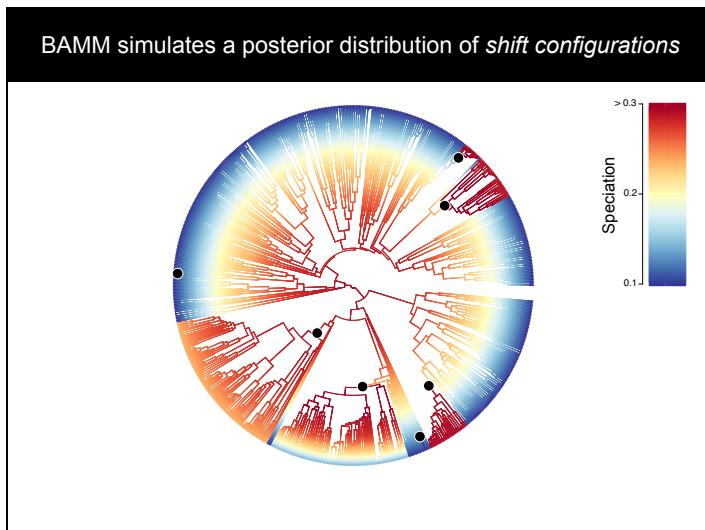
**Quantify and visualize rate heterogeneity**

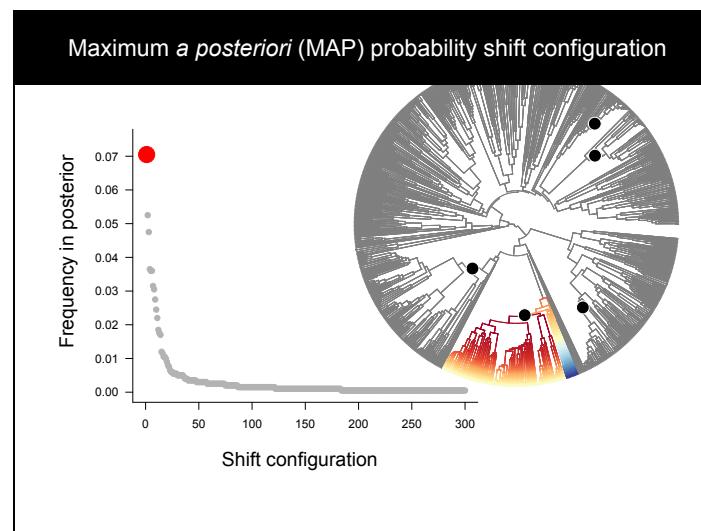
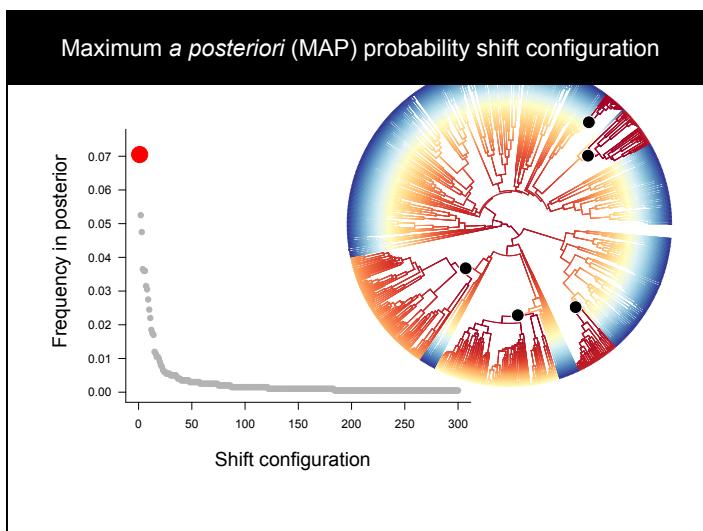
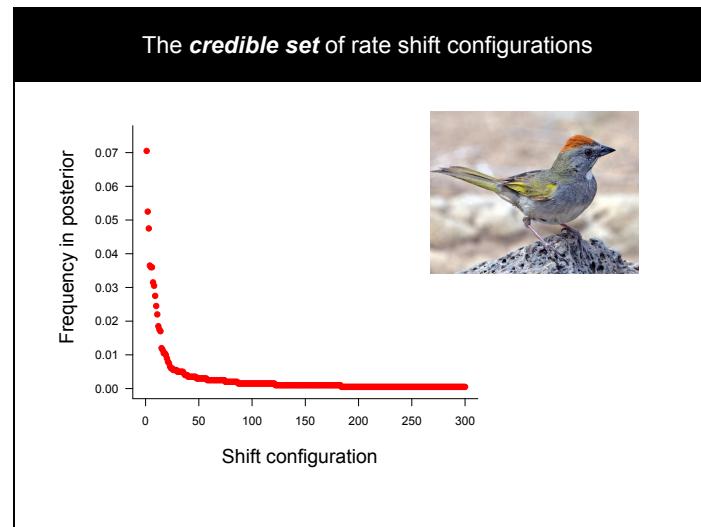
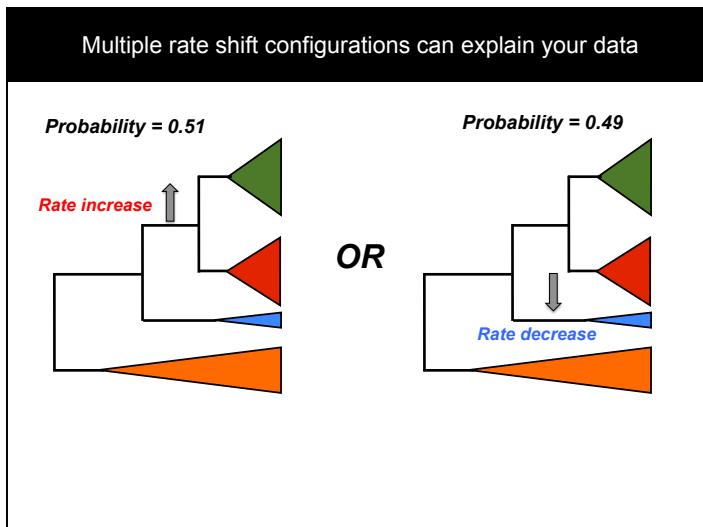
Identify lineages with similar rate dynamics

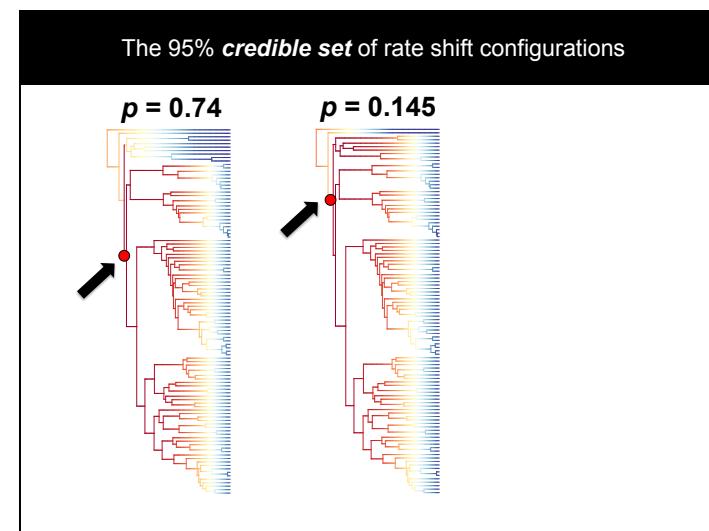
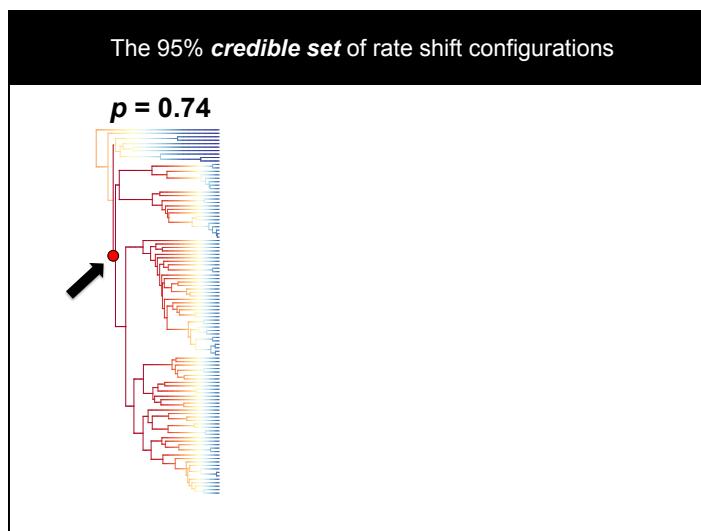
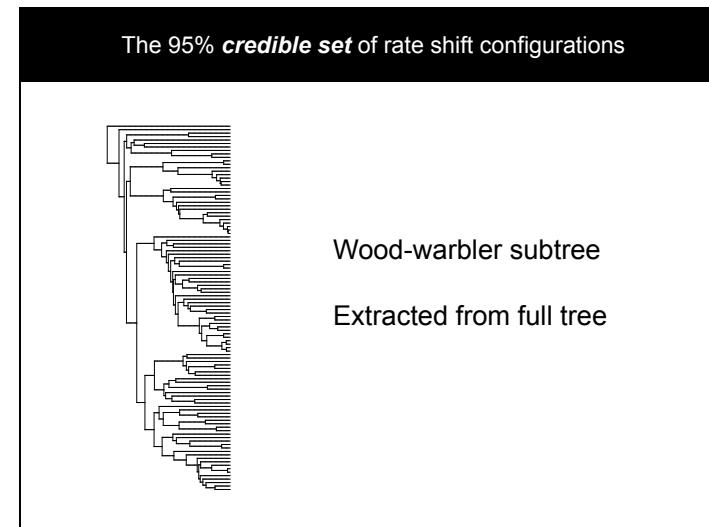
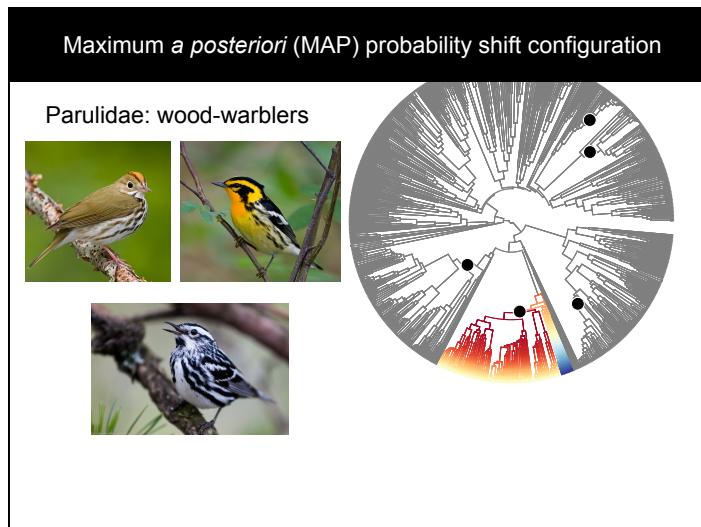
Trait-diversification correlations

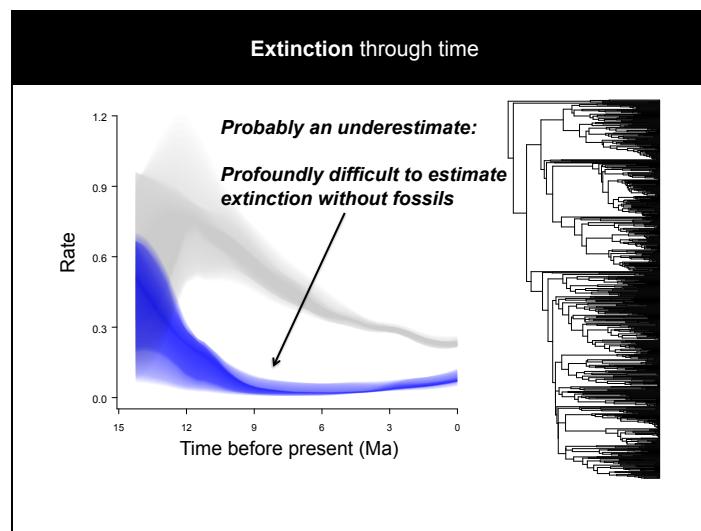
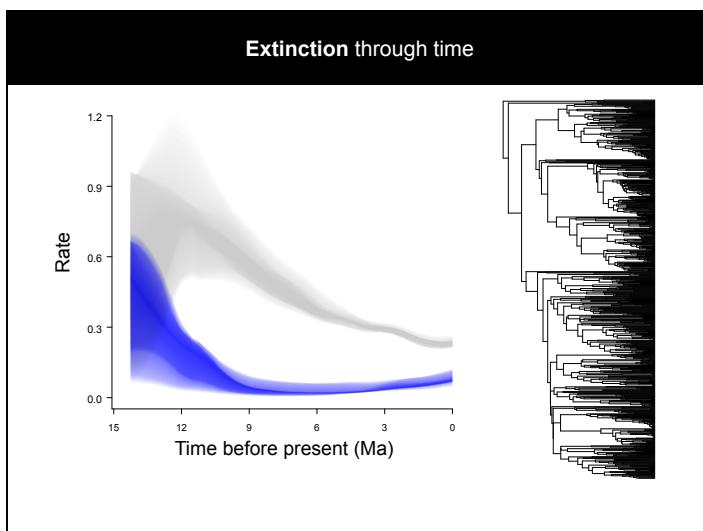
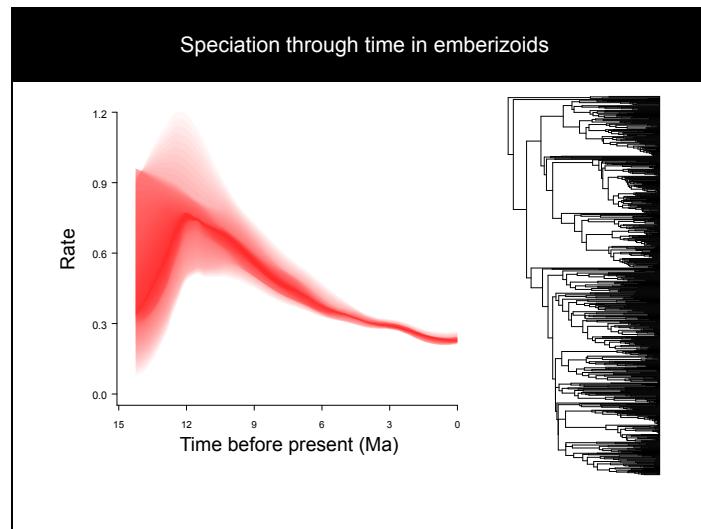
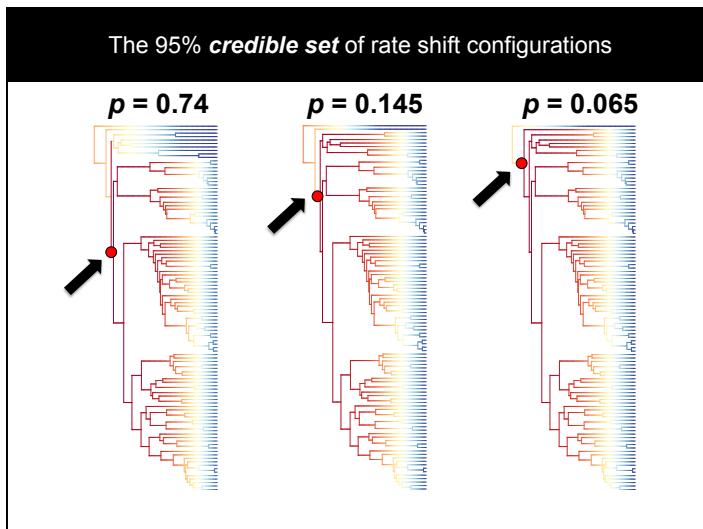


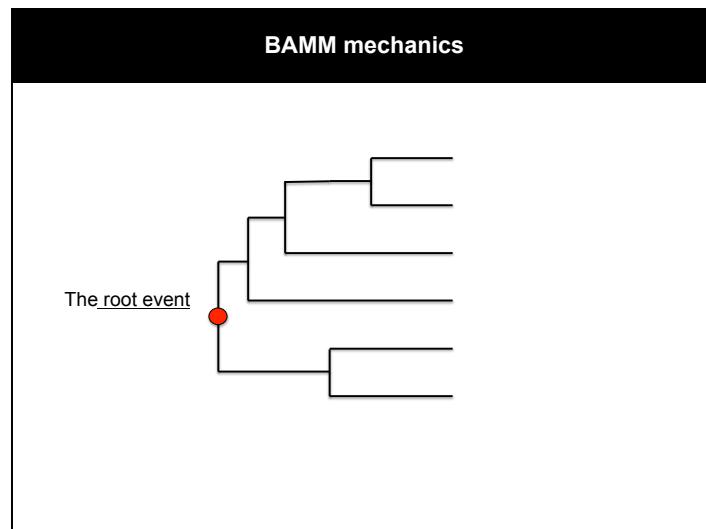
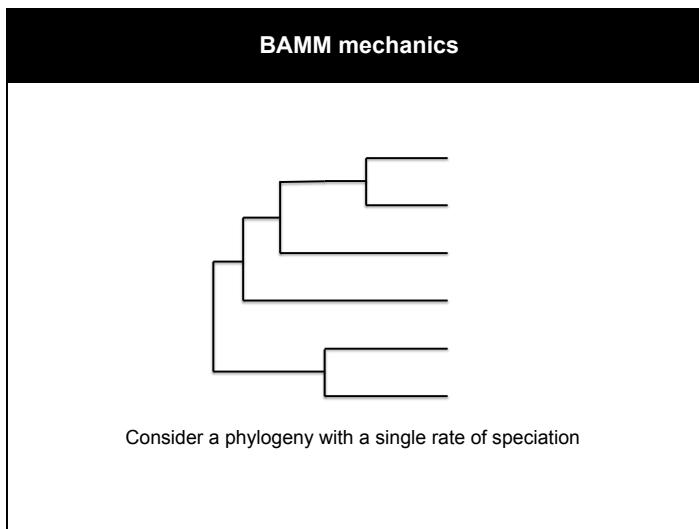
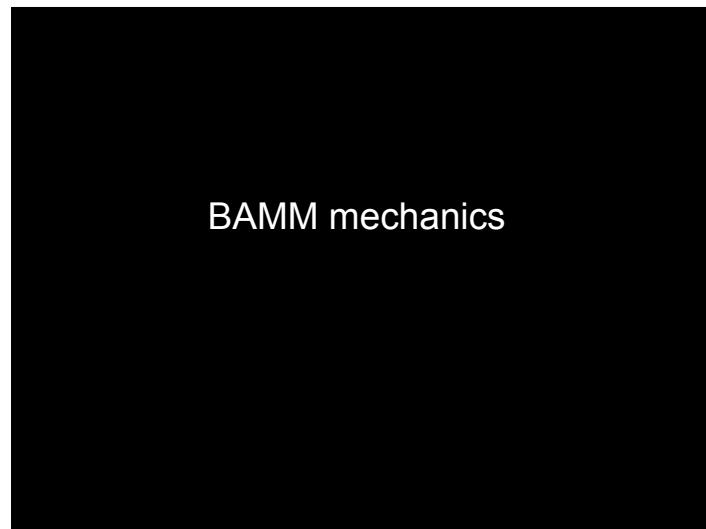
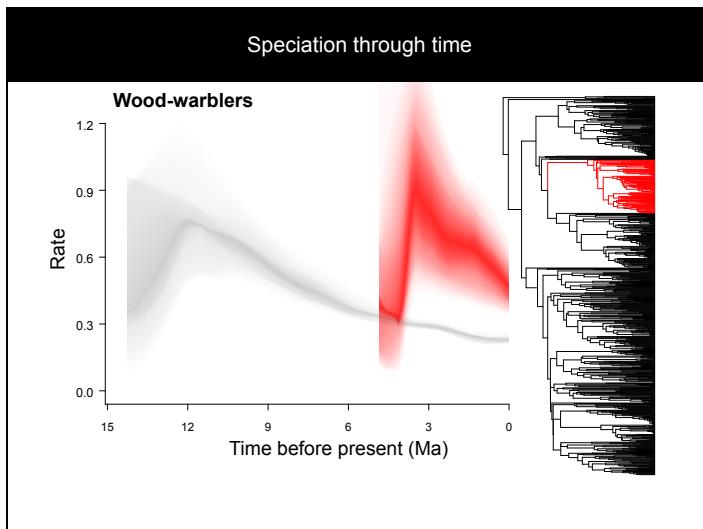


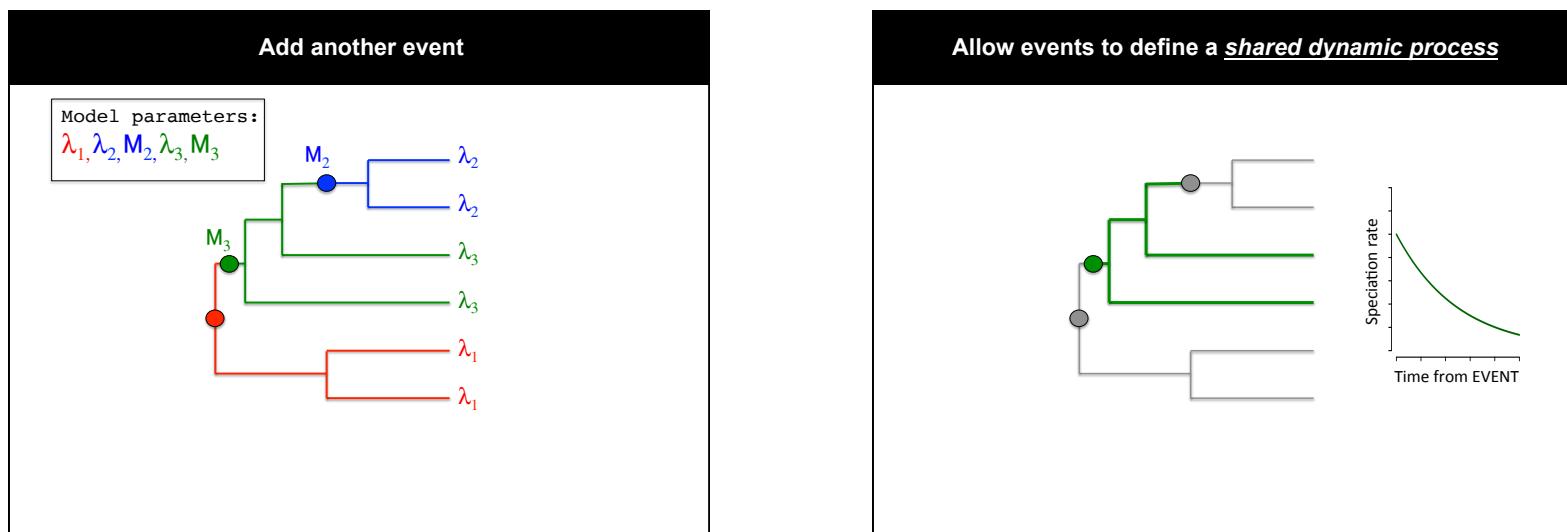
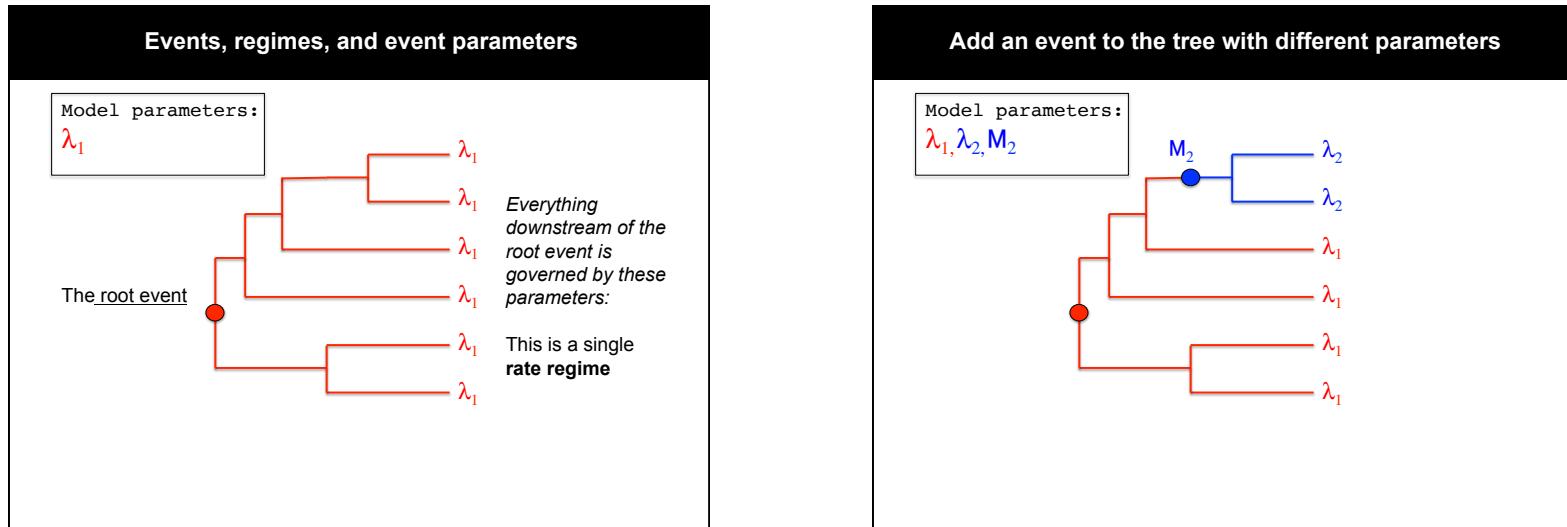


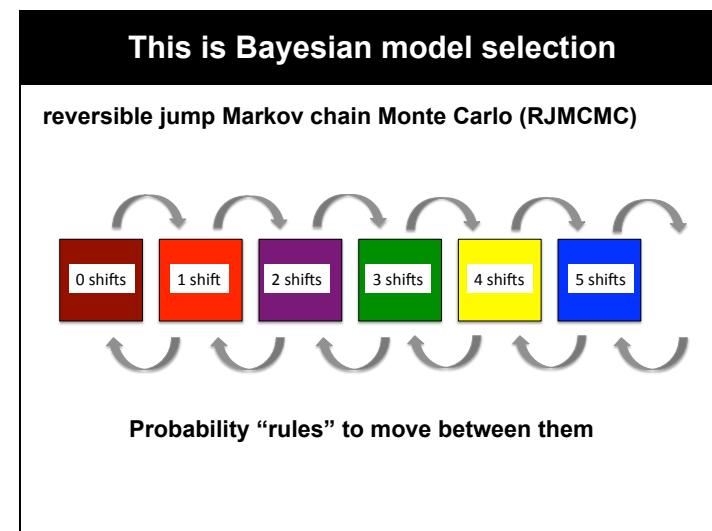
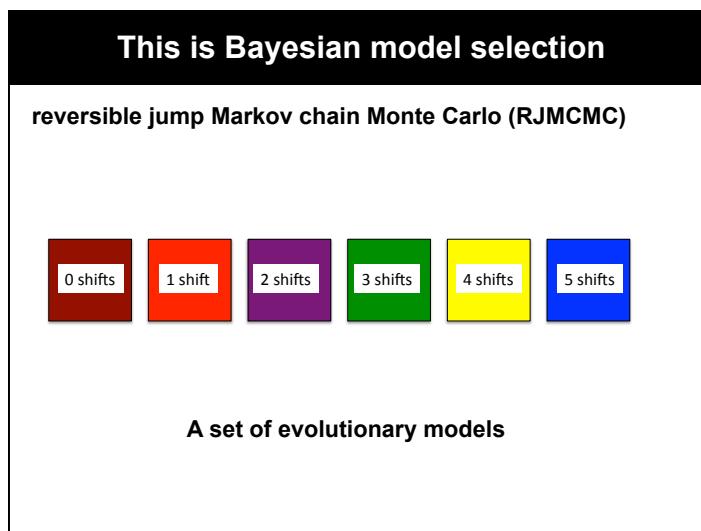
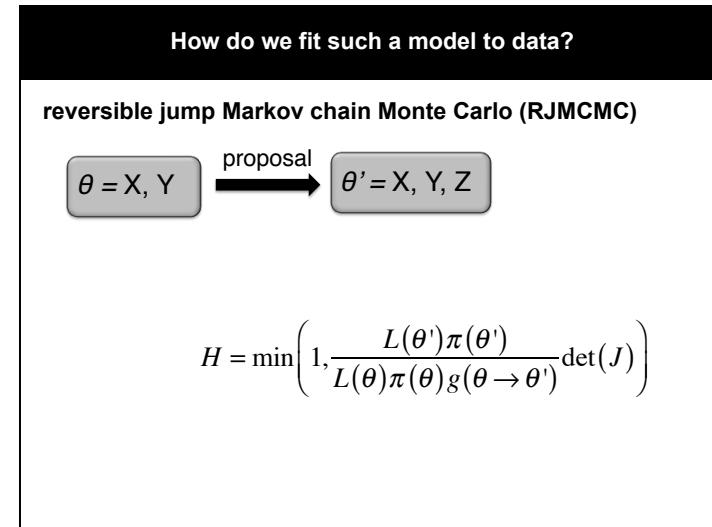
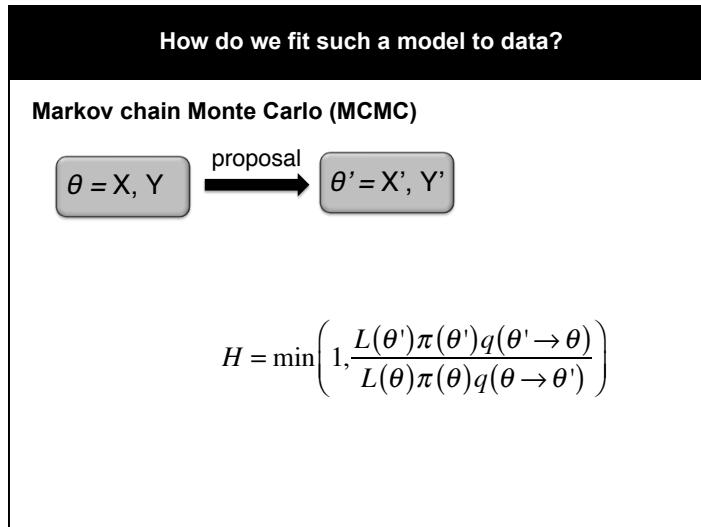


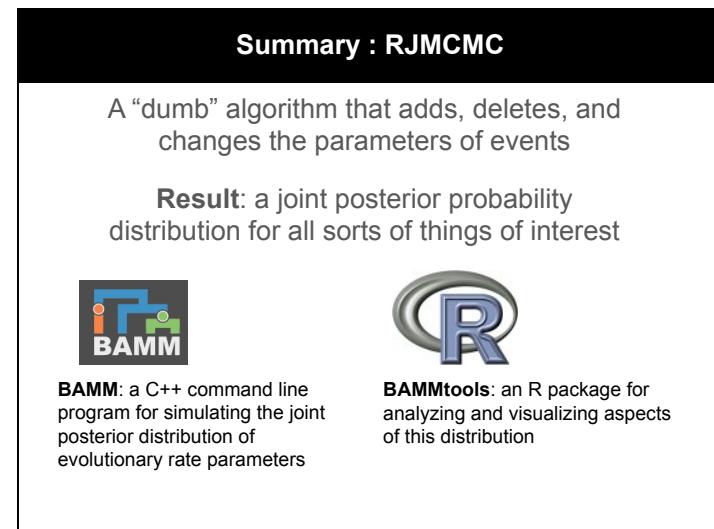
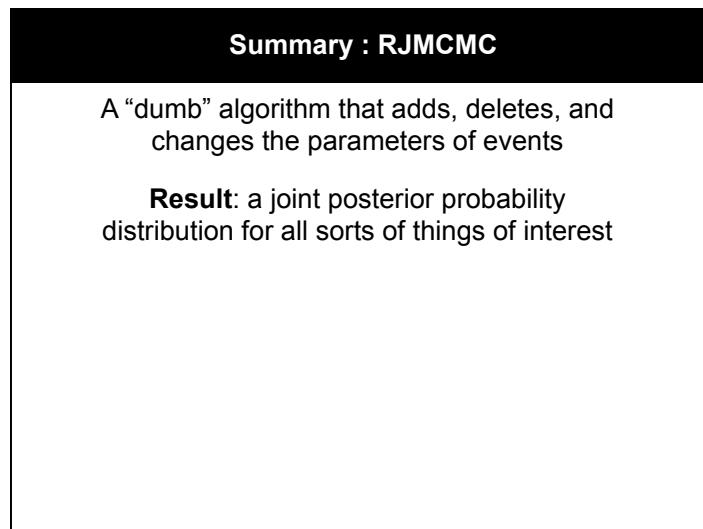
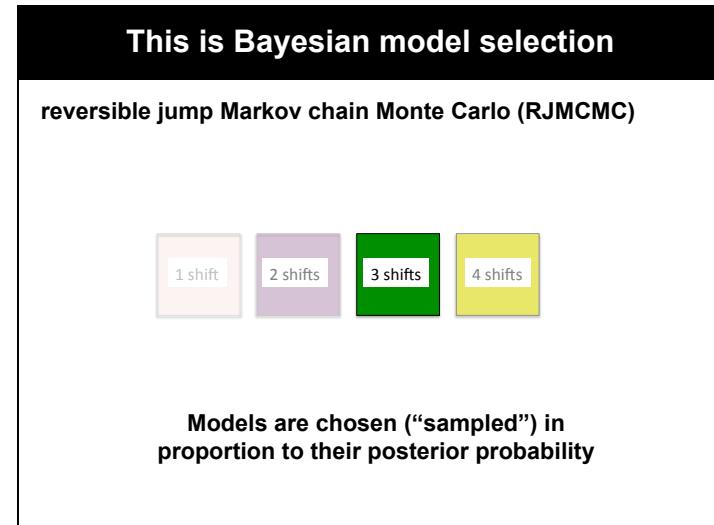
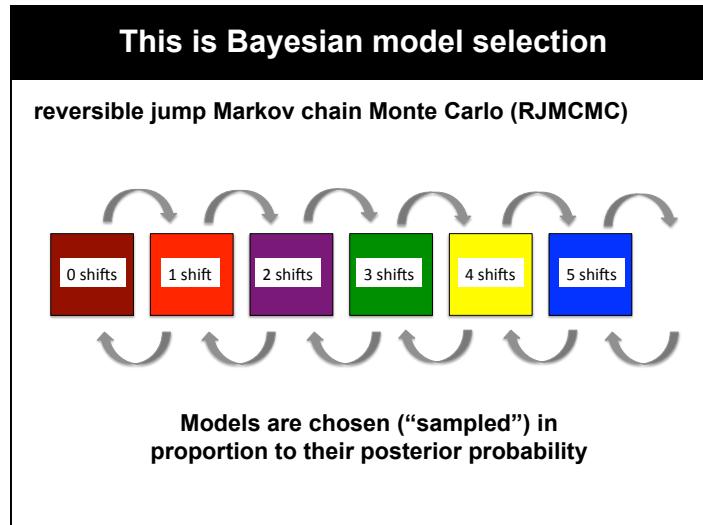












### Installation check

**BAMM** – *install from www.bamm-project.org*

**R**

**BAMMtools (R)** – *install from source*

**coda (R)** – *download from CRAN*

### BAMM analysis

### BAMM analysis

**BAMM:**

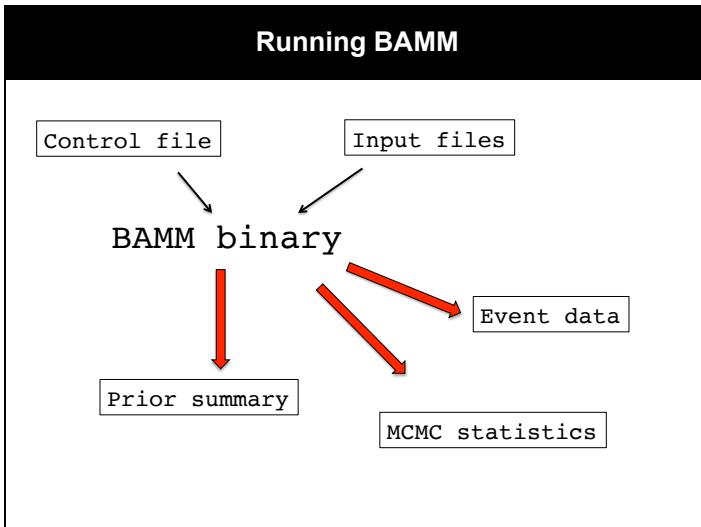
- Running BAMM
- Assessing convergence

**BAMMtools**

- Postrun processing, analysis, & visualization

### Running BAMM

```
graph TD; A[Control file] --> D[BAMM binary]; B[Input files] --> D;
```



### Control (configuration) file

```

modeltype = speciationextinction
# Specify speciationextinction or trait analysis

treefile = tanagers.tre
# Location of phylogenetic tree to be analyzed

runInfoFilename = run_info.txt
# File name to output general information about this run

runMCMC = 1
# perform an MCMC simulation? If runMCMC = 0, the program will
# check whether the data file can be read and whether
# an initial likelihood can be computed.
  
```

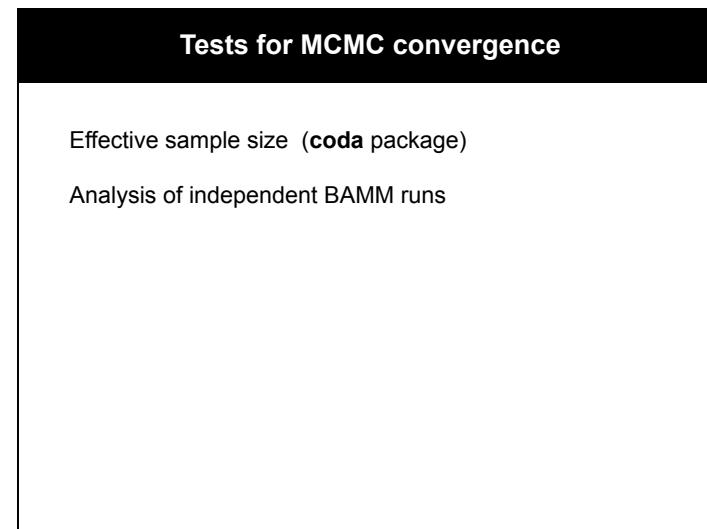
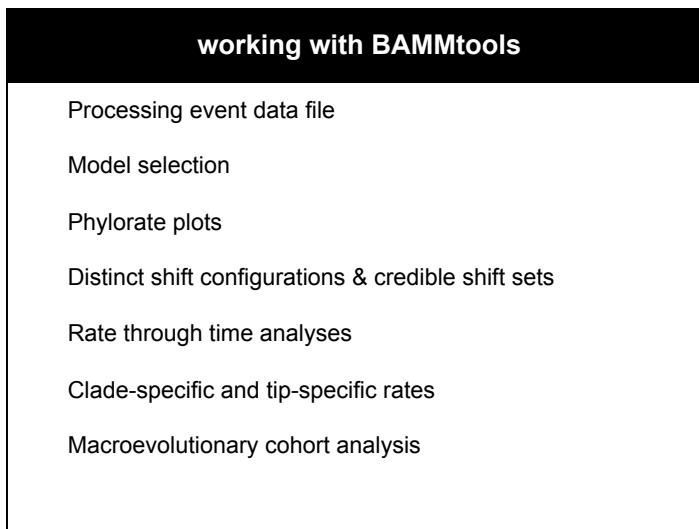
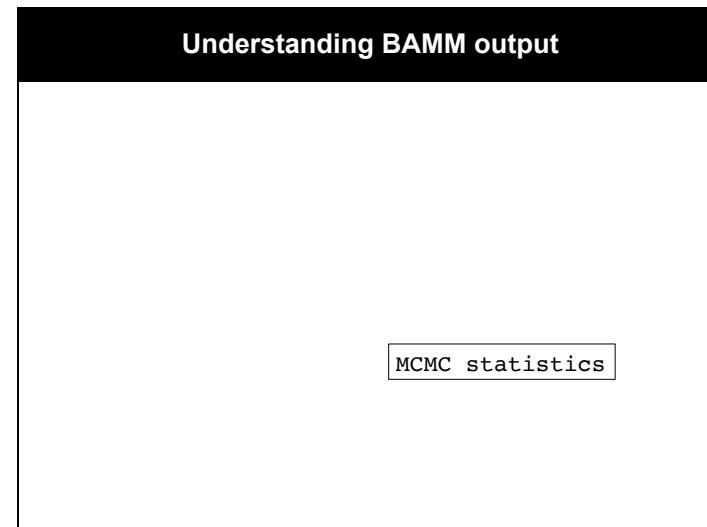
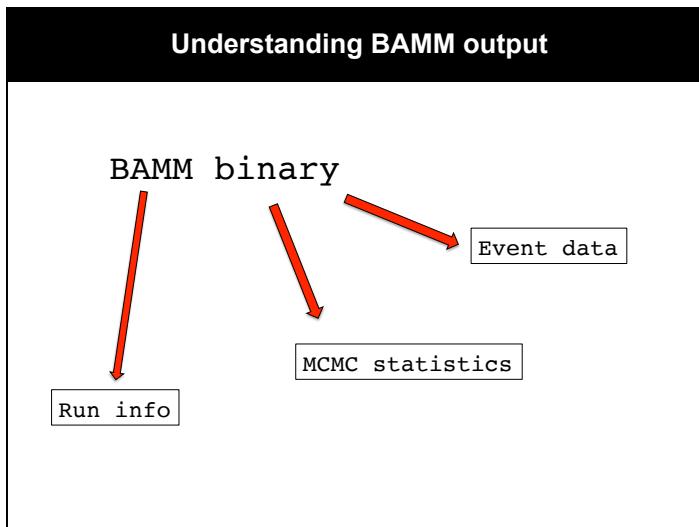
### Setting up configuration file

*Major parameter types in configuration file*

```

# GENERAL SETUP AND DATA INPUT
# PRIORS
# MCMC SIMULATION SETTINGS & OUTPUT OPTIONS
# OPERATORS: MCMC_SCALING_OPERATORS
# OPERATORS: MCMC_MOVE_FREQUENCIES
# INITIAL PARAMETER VALUES
# NUMERICAL AND OTHER PARAMETERS
  
```

### Running BAMM

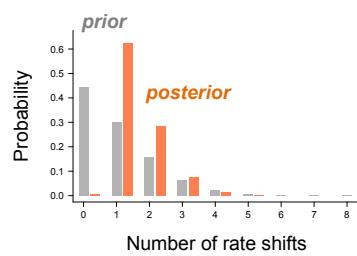


### General summary of diversification dynamics

loading event data & phylorate plots

### Bayesian model selection with BAMMtools

### The posterior and the prior

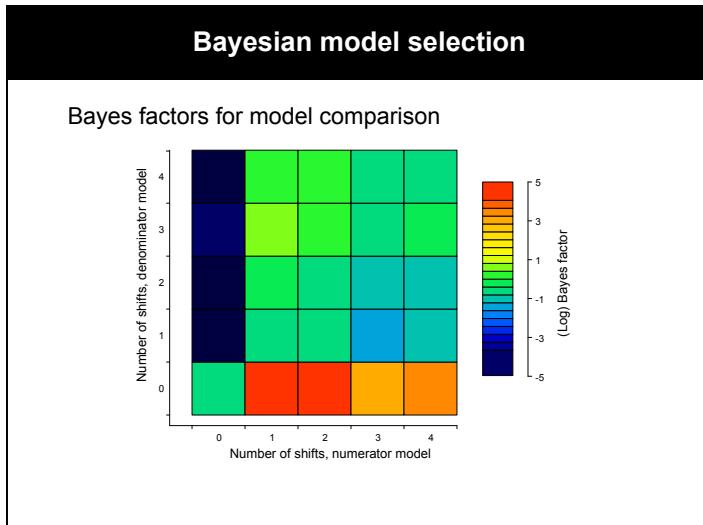


### Bayesian model selection

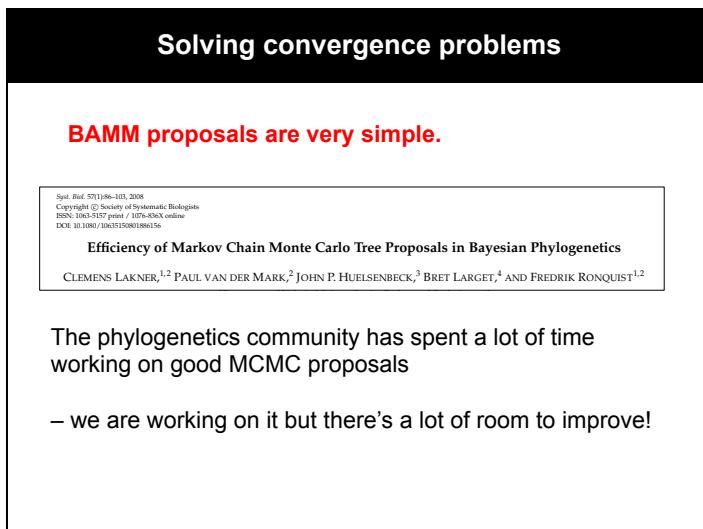
Bayes factors for model comparison

$$BF_{i,k} = \frac{post(M_i)}{prior(M_i)} / \frac{post(M_k)}{prior(M_k)}$$

(Exercise: compare Bayes factors of models versus the null model for 2 different Poisson rate priors)



- ### Fundamentals (on board)
- Topologically distinct shift configuration
  - Marginal shift probability
  - “core shift”
  - Bayesian *credible set* of shift configurations
  - Maximum *a posteriori* probability shift configuration



- ### Solving convergence problems
- Run for longer
  - Increase expected number of shifts (`poissonRatePrior`)
  - set `minCladeSizeForShift` greater than 1
  - Are your priors OK?
  - Partition data (last resort)