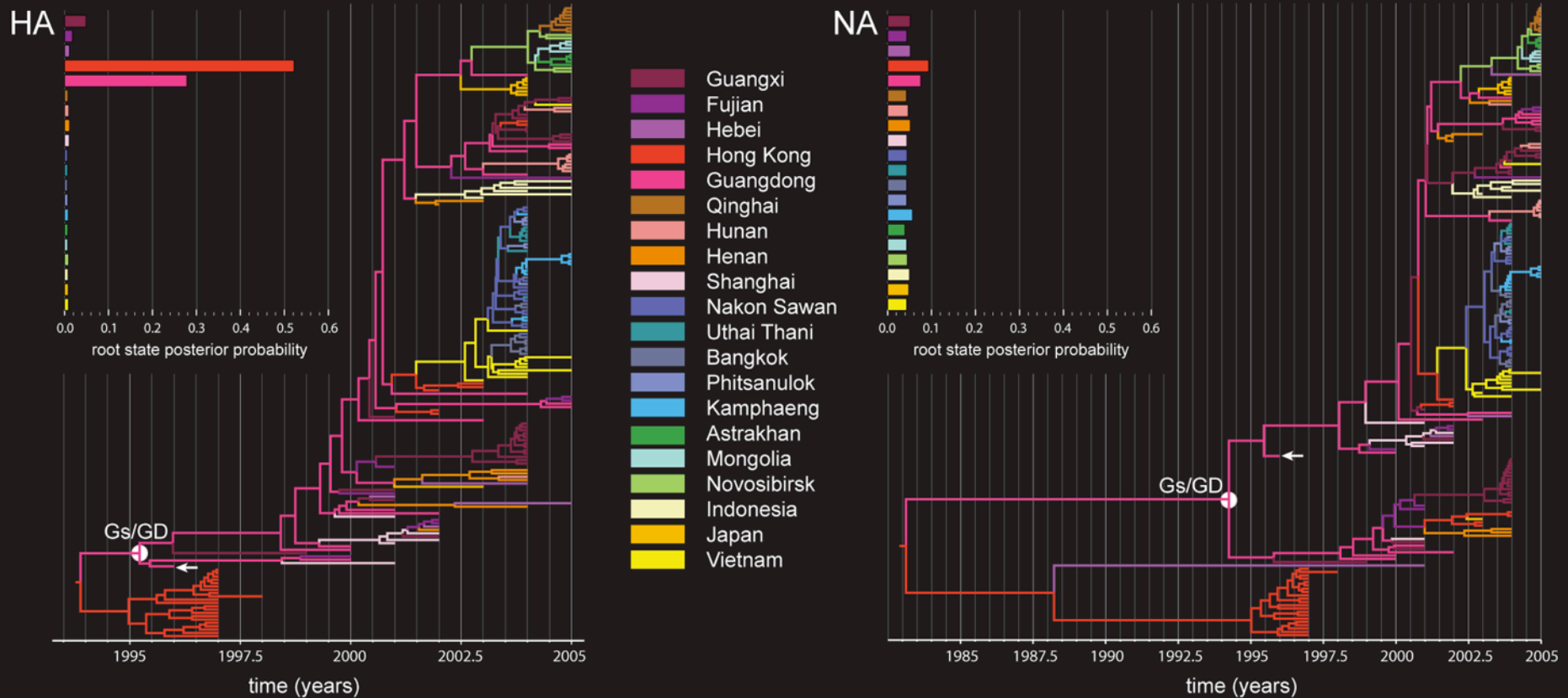


A primer on phylogenetic biogeography and DEC models

Jan 08, 2017
Michael Landis
SSB Meeting
Baton Rouge, LA

Epidemiology

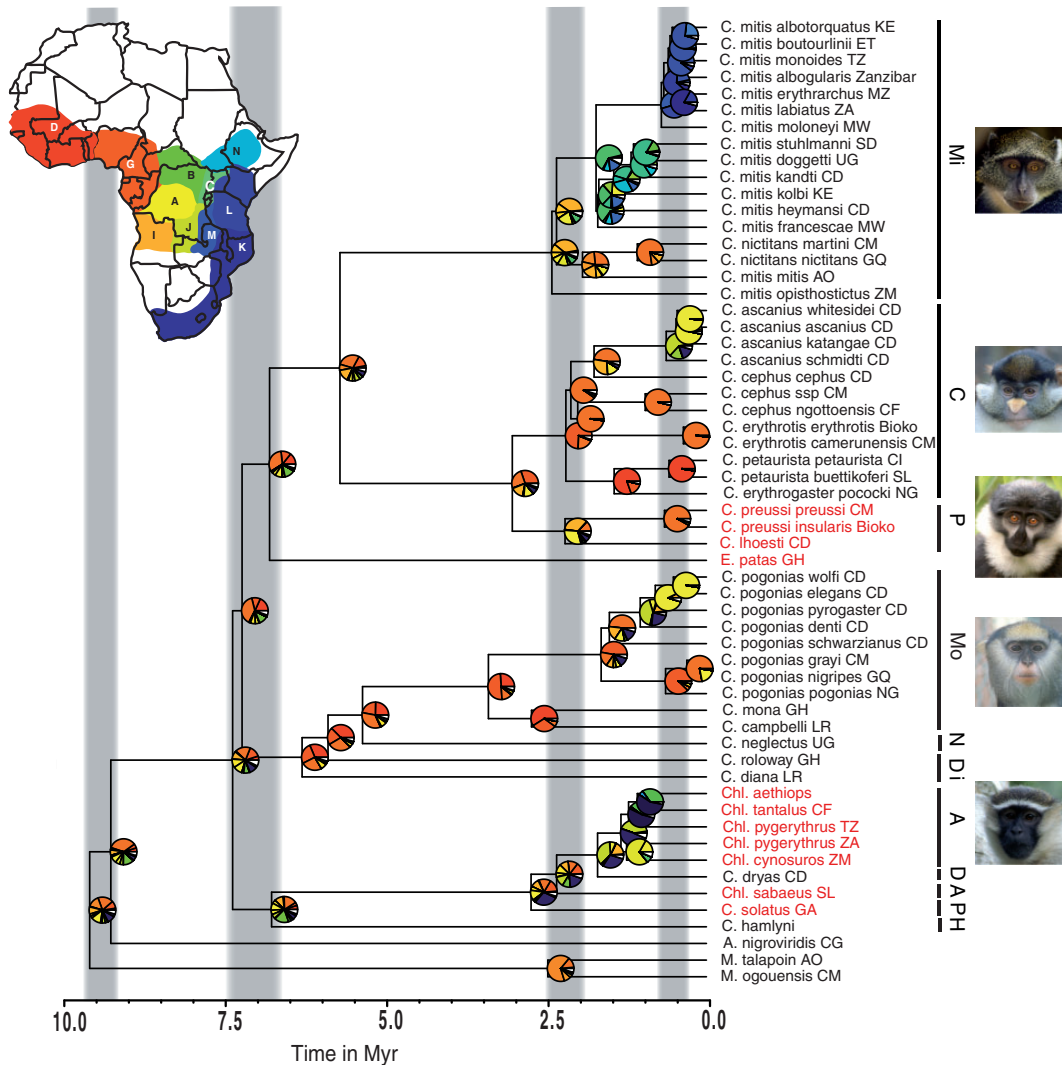


Hemagglutinin (HA)

H5N1
(Avian Flu)

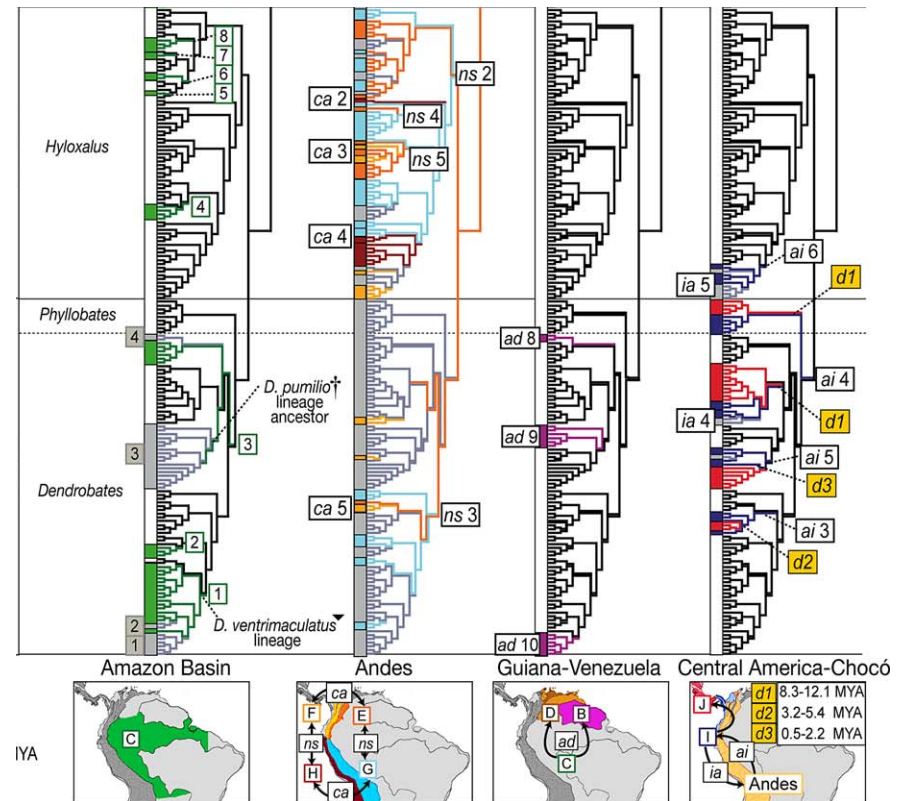
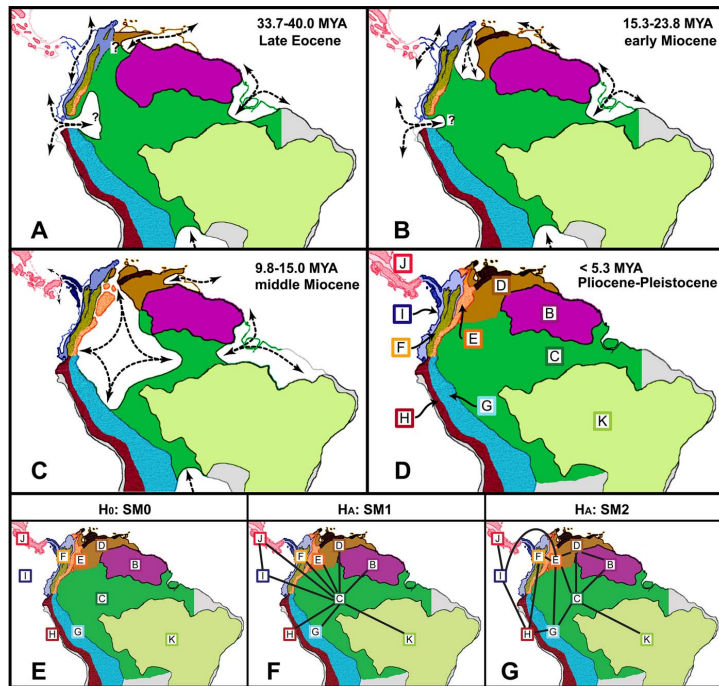
Neuraminidase (NA)

Conservation



Cercopithecidae (Primates)

Historical biogeography



Testing connectivity hypotheses

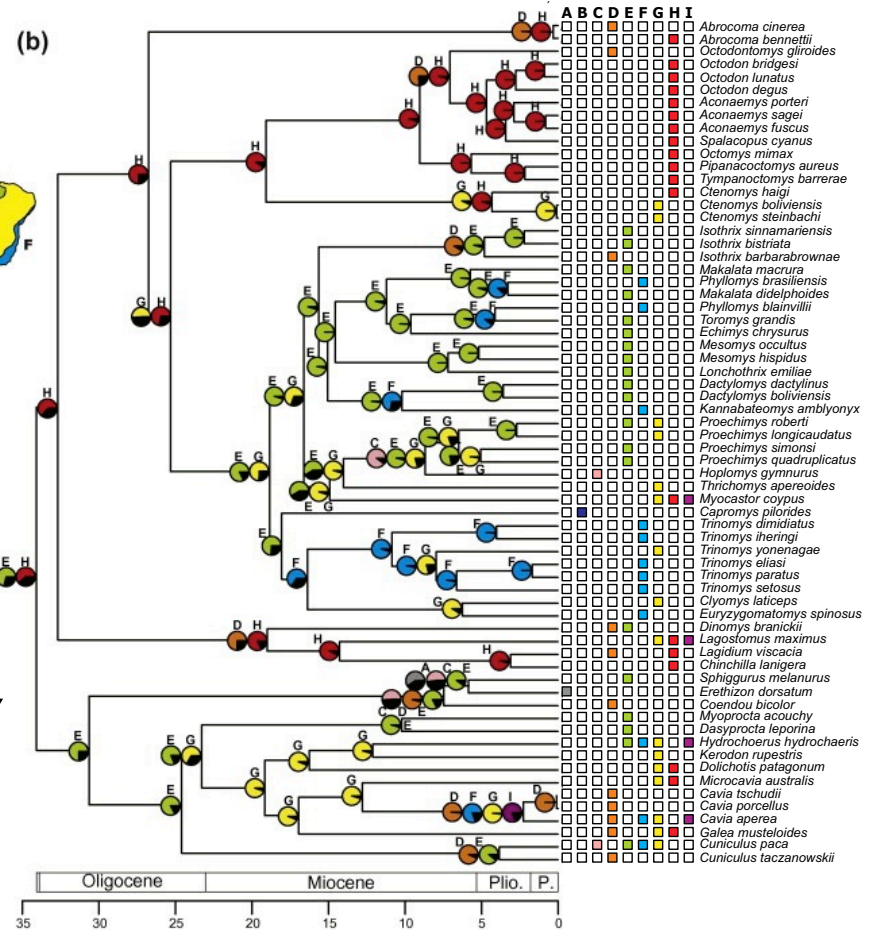
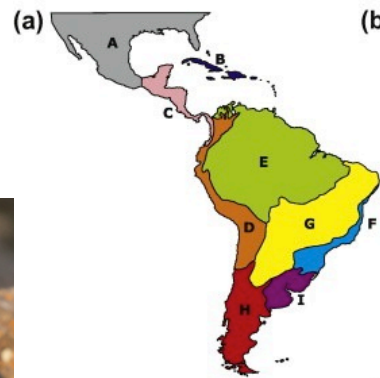
Discrete areas
(character states)

Time-calibrated
phylogeny

Data matrix



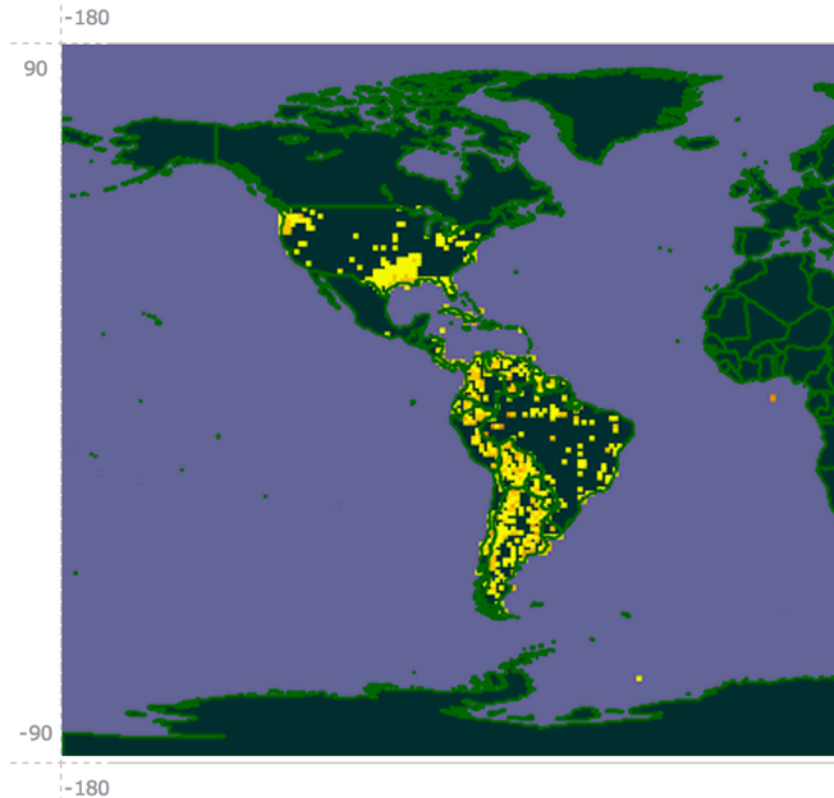
Octodon degus



Ancestral state
estimates

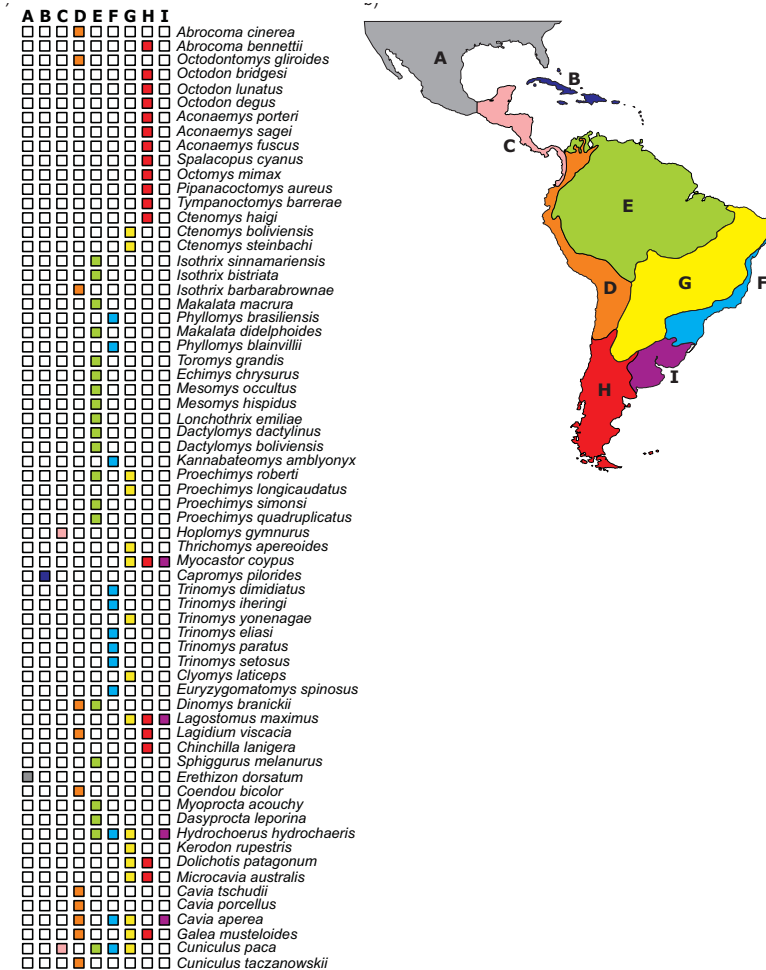
Species occurrence data (gbif.org, 2013)

Map of results



► Your search returned **13,264** occurrences with coordinates.

Discrete presence-absence (Upham & Patterson, 2012)



DEC

Dispersal-(Local) Extinction-Cladogenesis (DEC)

Many areas per taxon (range)

D,E as parameterized event types

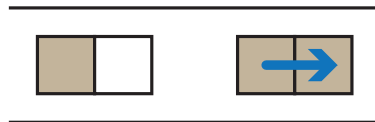
Work by:

Ree *et al.*, 2005 (Evolution)

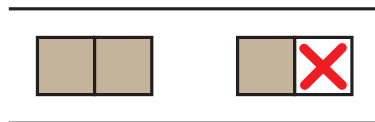
Ree & Smith, 2008 (Syst Biol)

DEC event types

Anagenesis



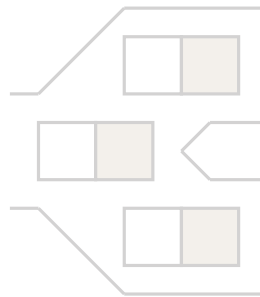
a. Dispersal



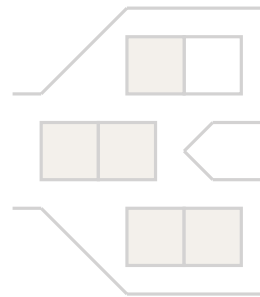
b. Extirpation



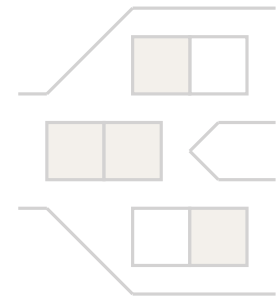
Cladogenesis



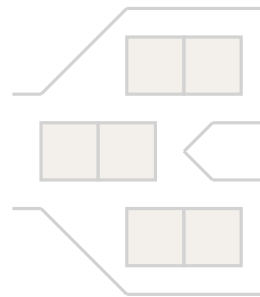
c. Narrow sympatry



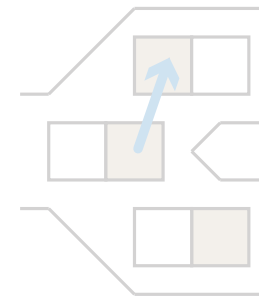
d. Subset sympatry



e. Allopatry



f. Full sympatry



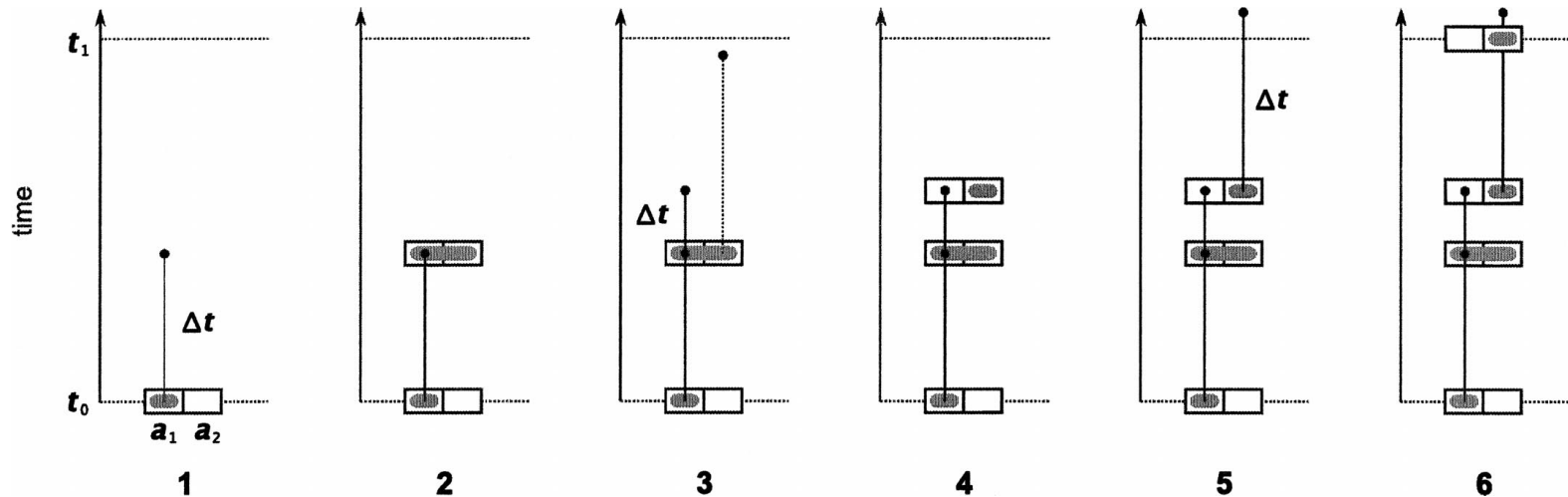
g. Jump dispersal

Rate matrix for anagenesis

$$Q = \begin{array}{c|cccccccc} & \emptyset & 1 & 2 & 3 & 12 & 13 & 23 & 123 \\ \hline \emptyset & — & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & E_1 & — & 0 & 0 & D_{12} & D_{13} & 0 & 0 \\ 2 & E_2 & 0 & — & 0 & D_{21} & 0 & D_{23} & 0 \\ 3 & E_3 & 0 & 0 & — & 0 & D_{31} & D_{32} & 0 \\ 12 & 0 & E_2 & E_1 & 0 & — & 0 & 0 & D_{13} + D_{23} \\ 13 & 0 & E_3 & 0 & E_1 & 0 & — & 0 & D_{12} + D_{32} \\ 23 & 0 & 0 & E_3 & E_2 & 0 & 0 & — & D_{21} + D_{31} \\ 123 & 0 & 0 & 0 & 0 & E_3 & E_2 & E_1 & — \end{array}$$

$$\mathbf{P}_{ij}(t) = [\exp \{ \mathbf{Q}t \}]_{ij}$$

Dispersal & Extirpation



Exponentially-distributed times between events

DEC event types

Anagenesis



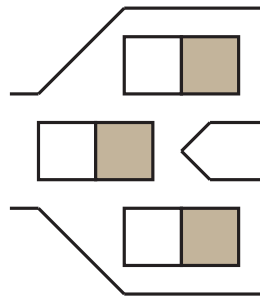
a. Dispersal



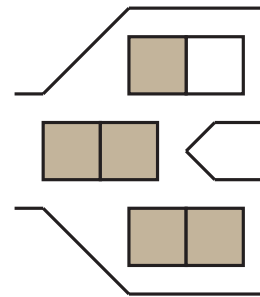
b. Extirpation



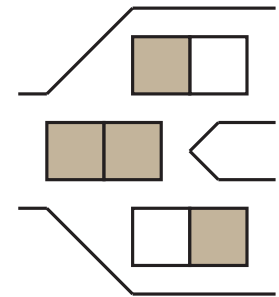
Cladogenesis



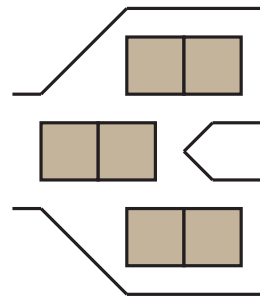
c. Narrow sympatry



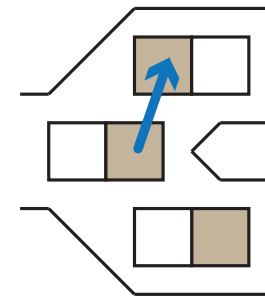
d. Subset sympatry





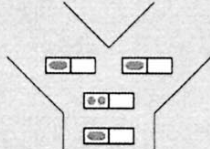


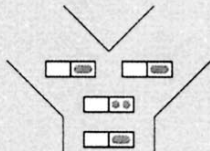


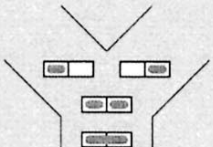
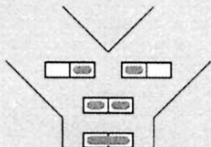

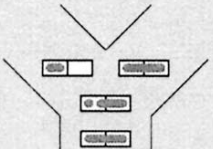


e. Allopatry



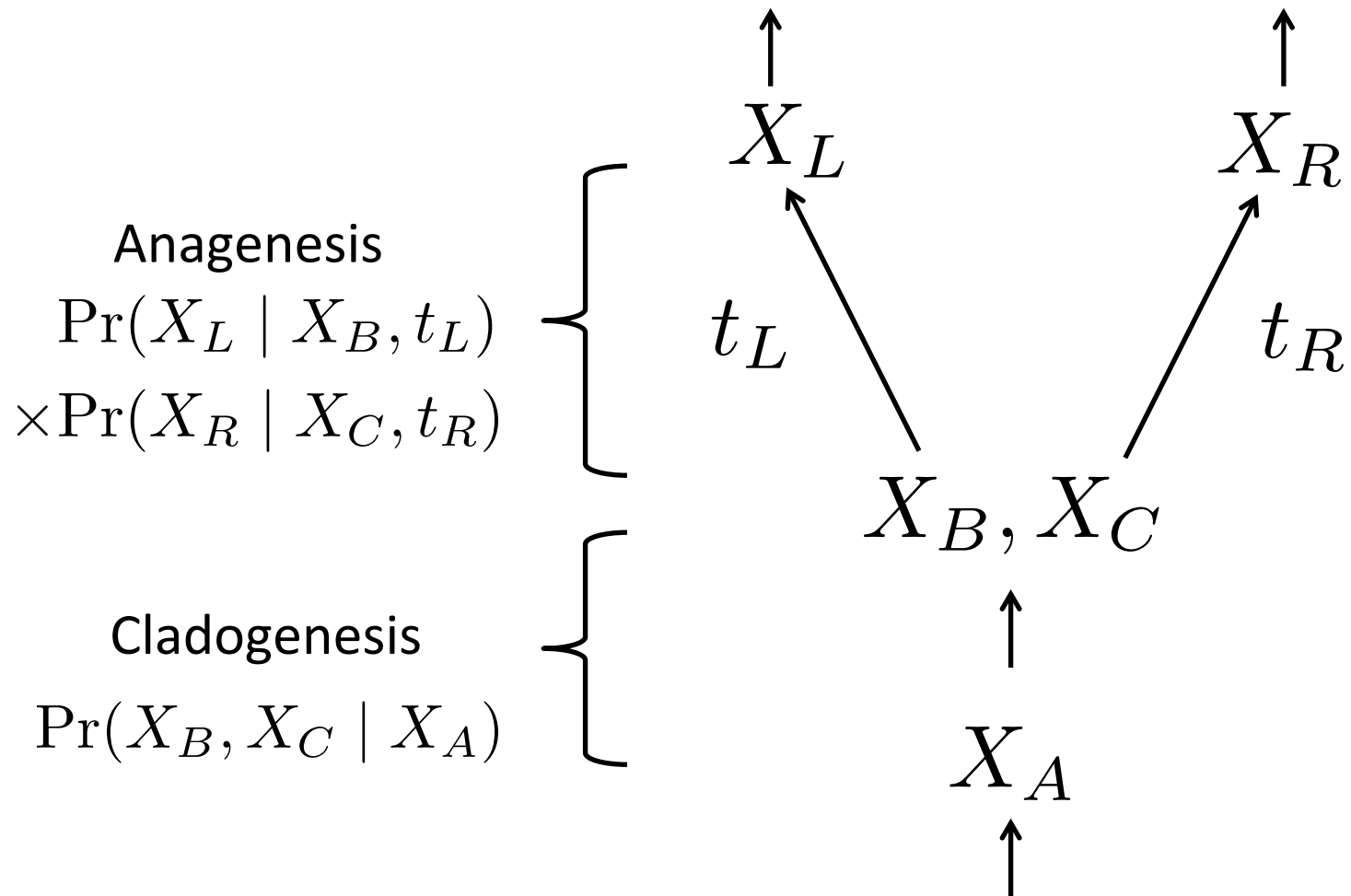
f. Full sympatry




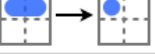
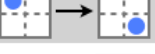
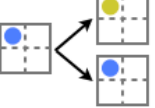
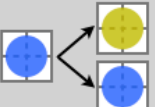
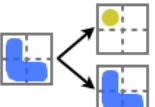
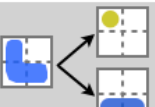
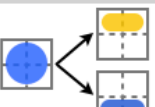
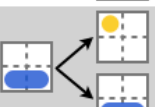
g. Jump dispersal

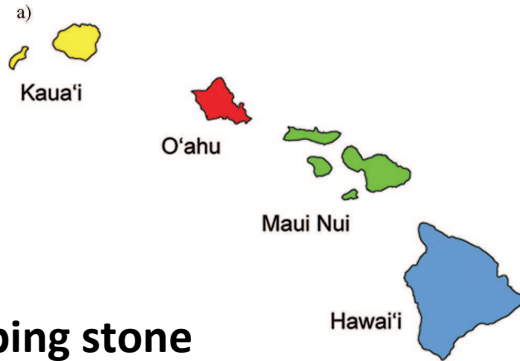
		Ancestral range	Subdivided range after speciation	Inheritance scenarios for subdivided range	Prob	
Sympatry (narrow)	[	Scenario 1 		1/1	
					1/1	
Allopatry	[	Scenario 2 		1/6, 1/6	
						
Sympatry (subset)	[Scenario 3 			1/6, 1/6
						

DEC likelihood

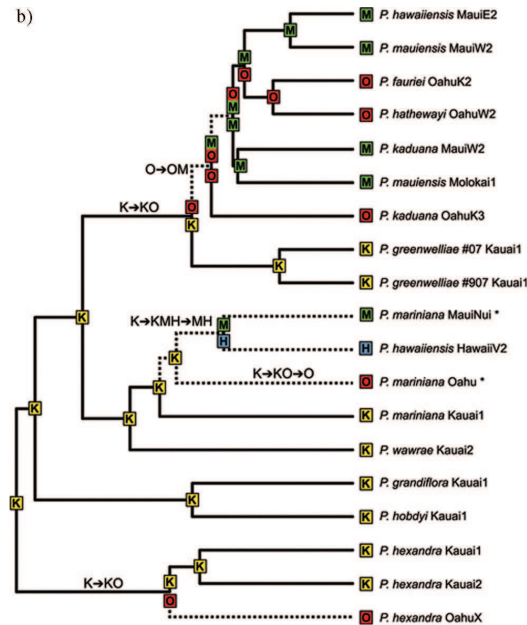
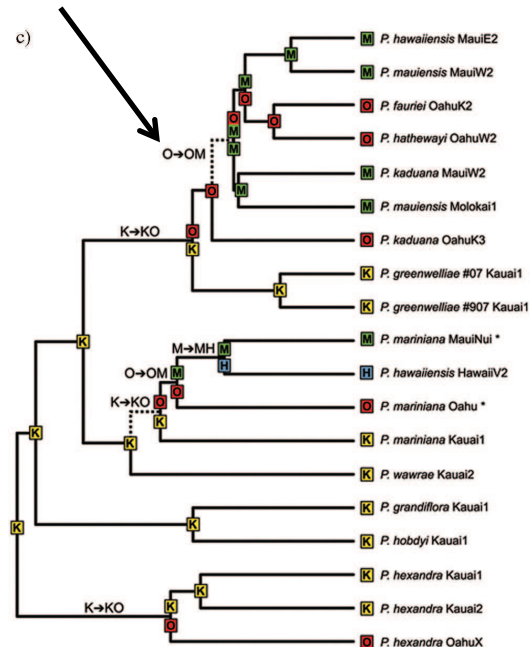


Generalized DEC model

	Process	Ranges Before After	Character mapping	DIVA	DEC (GeoSSE, LAGRANGE)	BayArea, BBM (RASP)	Parameter of BioGeoBEARS Supermodel
Anagenetic	Dispersal			✓	✓	✓	d (& x, b)
	Extinction			✓	✓	✓	e (& u, b)
	Range-switching		✓				a (& x, b)
Cladogenetic	Sympatry (narrow)		✓	✓	✓	✓	y (& $mx01y$)
	Sympatry (widespread)					✓	y (& $mx01y$)
	Sympatry (subset)				✓		s (& $mx01s$)
	Vicariance (narrow)			✓	✓		v (& $mx01v$)
	Vicariance (widespread)			✓			v (& $mx01v$)
	Founder						j (& $x, mx01j$)



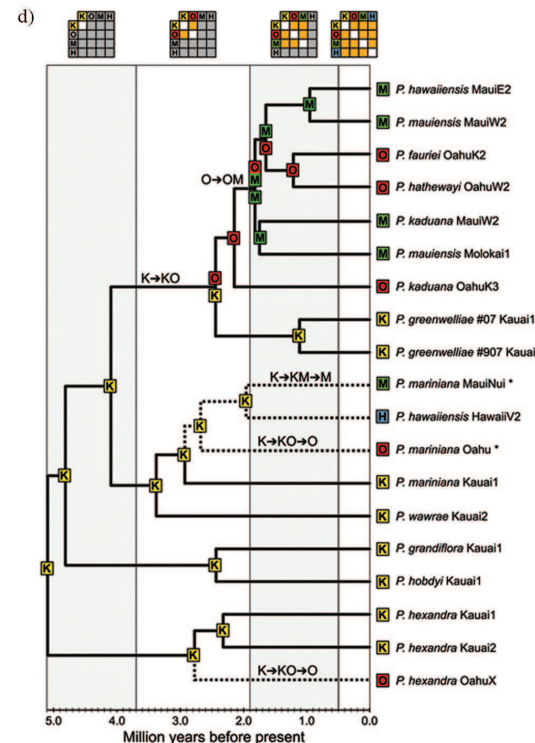
Stepping stone
(Small adjacent ranges:
K, O, M, H, KO, OM, MH)



Unconstrained
(constant,
equal rates)



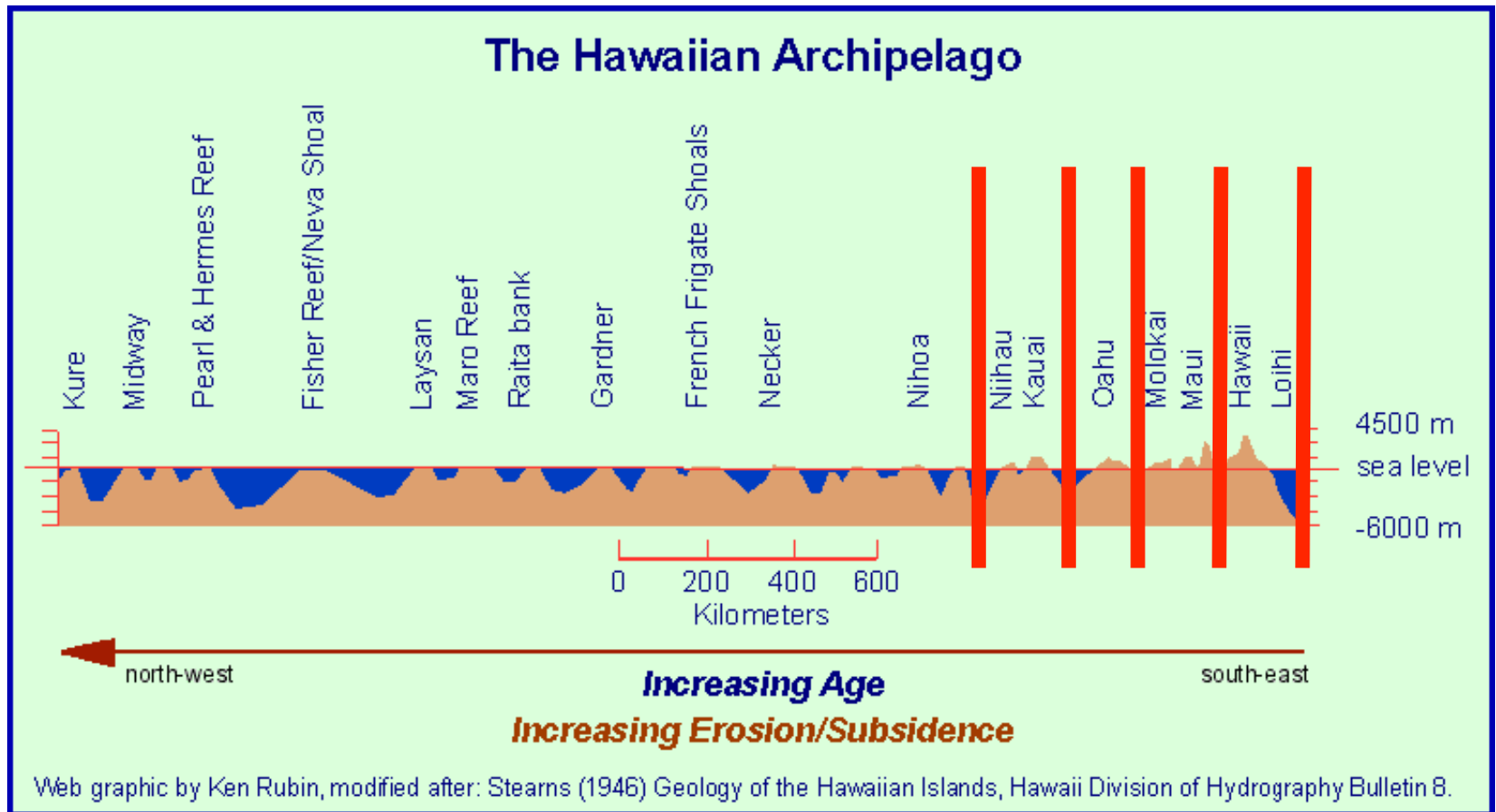
Psychotria mariniana



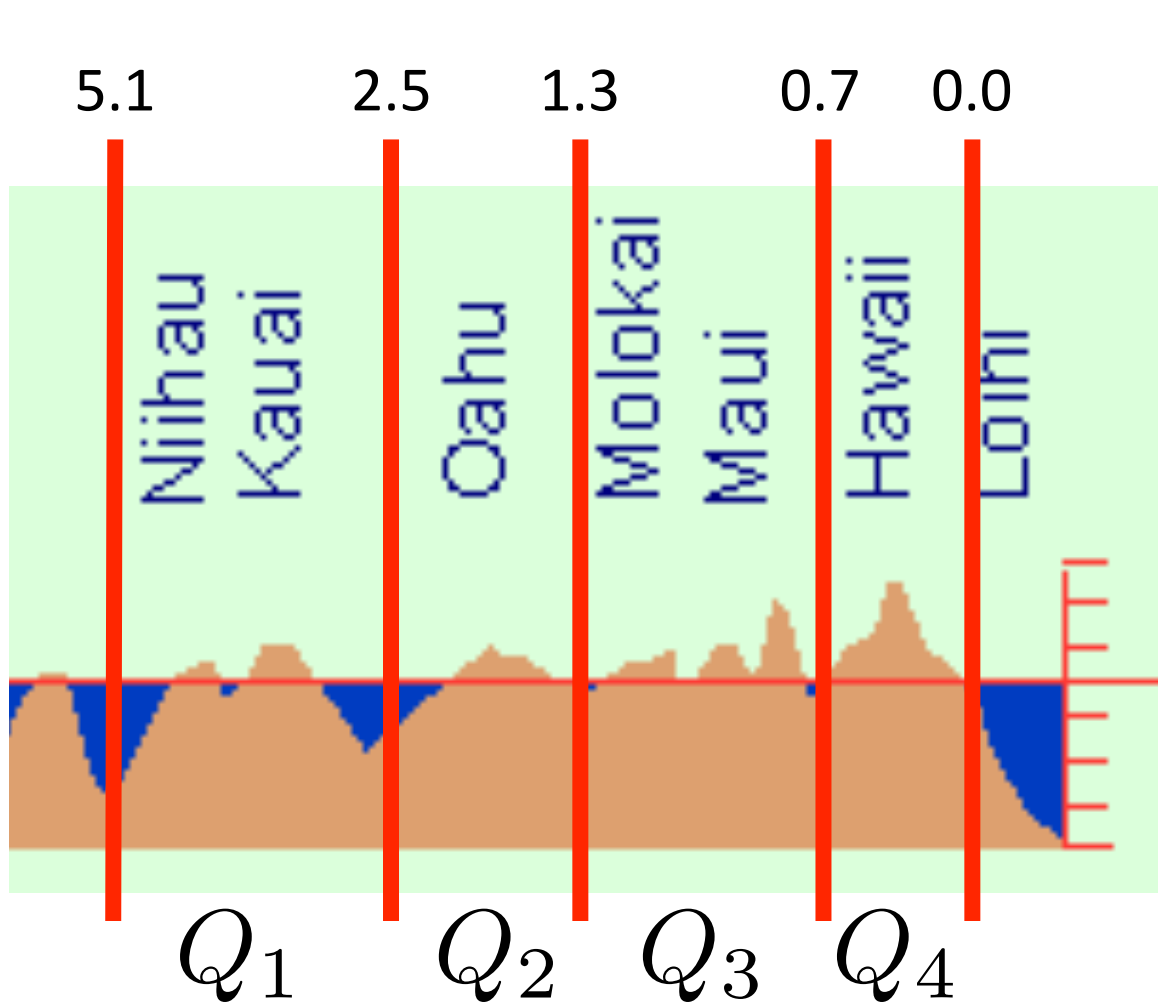
Stratified
(time-dependent probs)

Ree and Smith, 2008 (Syst Biol)

Stratified model



Island
origin
times
(Ma)



Q_i varies
over time!

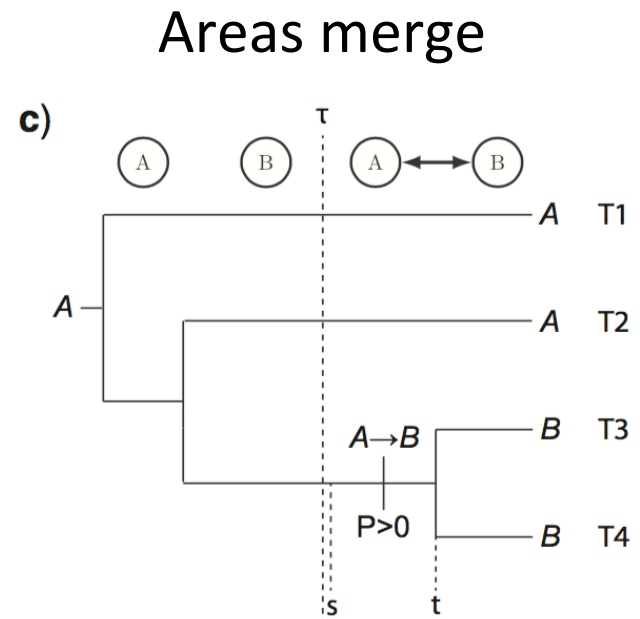
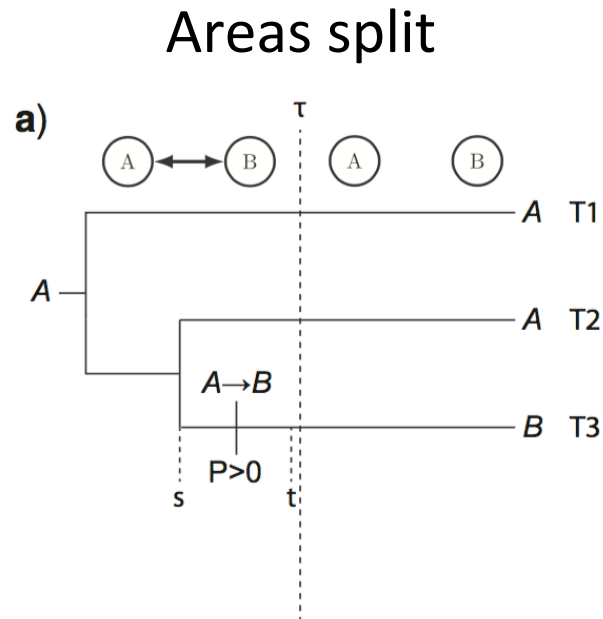
Transition probability
over epochs

$$P(x \rightarrow y; t) = \left[\prod e^{Q_i \delta t_i} \right]_{x,y}$$

Dating with biogeographic processes

Probable
speciation
time

Prob > 0



Dating with biogeographic processes

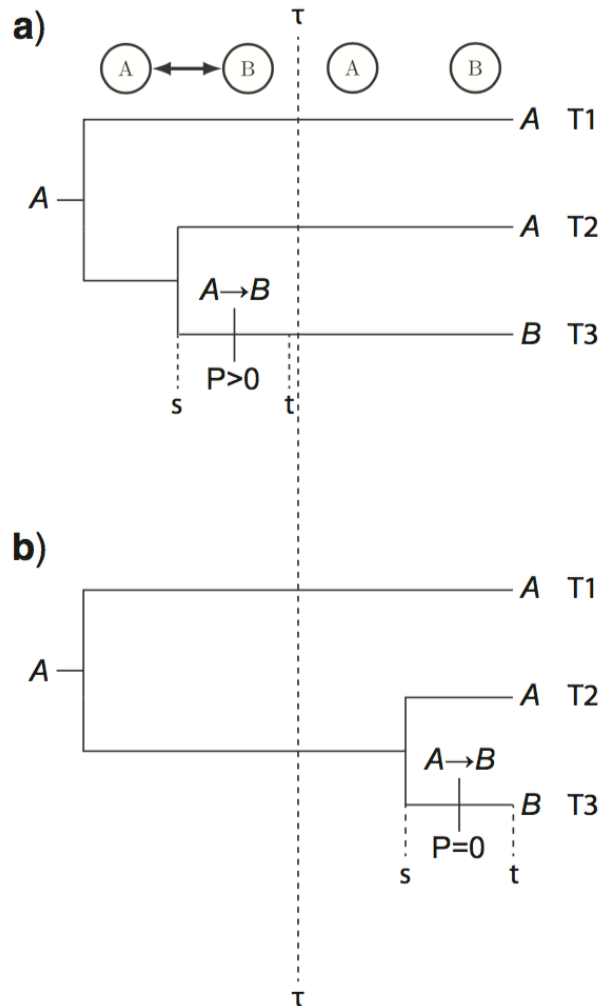
Probable
speciation
time

Prob > 0

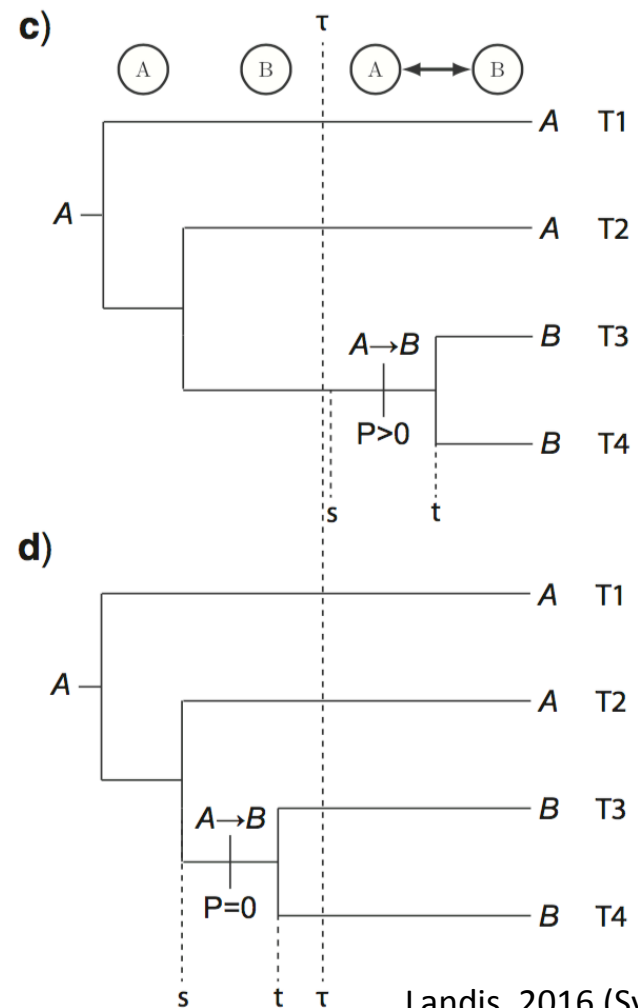
Improbable
speciation
time

Prob = 0

Areas split



Areas merge



RevBayes

Flexible model specification

Graphical models

Easy and intuitive to use

Rev language interface

Fast computation and efficient inference

C++ backend

Bayesian terminology

D	data, observations
θ	model parameters
$P(D \mid \theta)$	model likelihood
$P(\theta)$	prior probability
$P(\theta \mid D)$	posterior probability

Bayes rule
$$P(\theta \mid D) = \frac{P(D \mid \theta)P(\theta)}{P(D)}$$

Model equations

How are variables interrelated?

$$D \sim \text{Exponential}(Y)$$

$$Y = (\theta_1 - \theta_2)^2$$

$$\theta_1 \sim \text{Exponential}(1)$$

$$\theta_2 \sim \text{Exponential}(1)$$

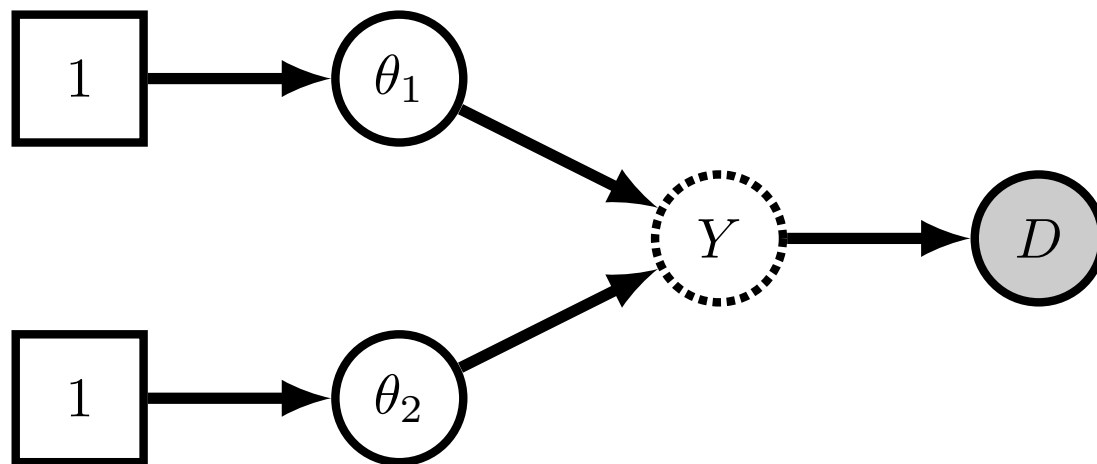
Model graph

$$D \sim \text{Exponential}(Y)$$

$$Y = (\theta_1 - \theta_2)^2$$

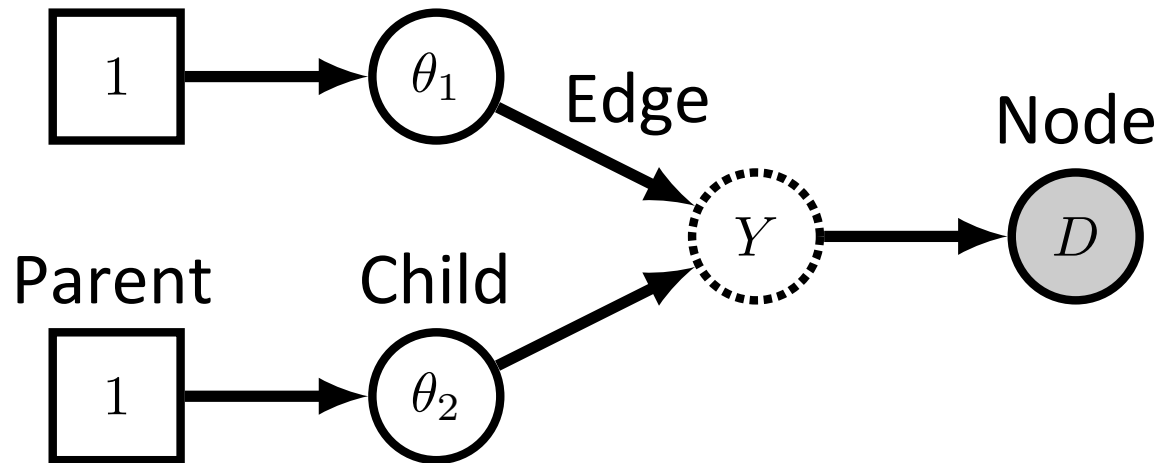
$$\theta_1 \sim \text{Exponential}(1)$$

$$\theta_2 \sim \text{Exponential}(1)$$



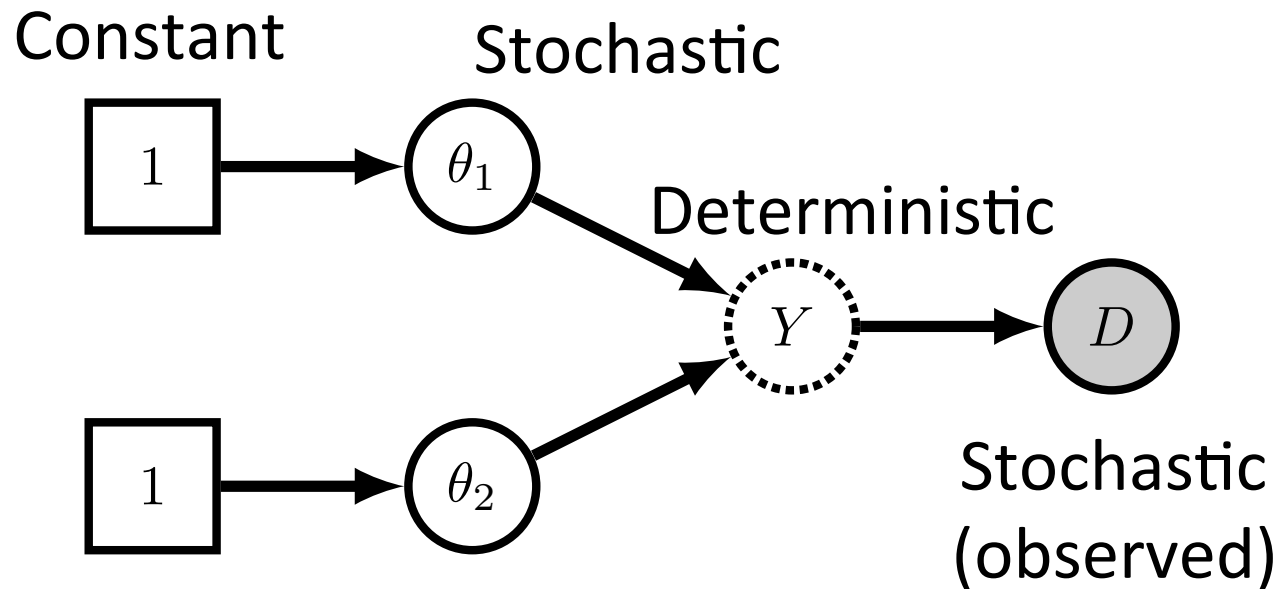
Model variable relationships

Edges indicate how child variables depend on parent variables



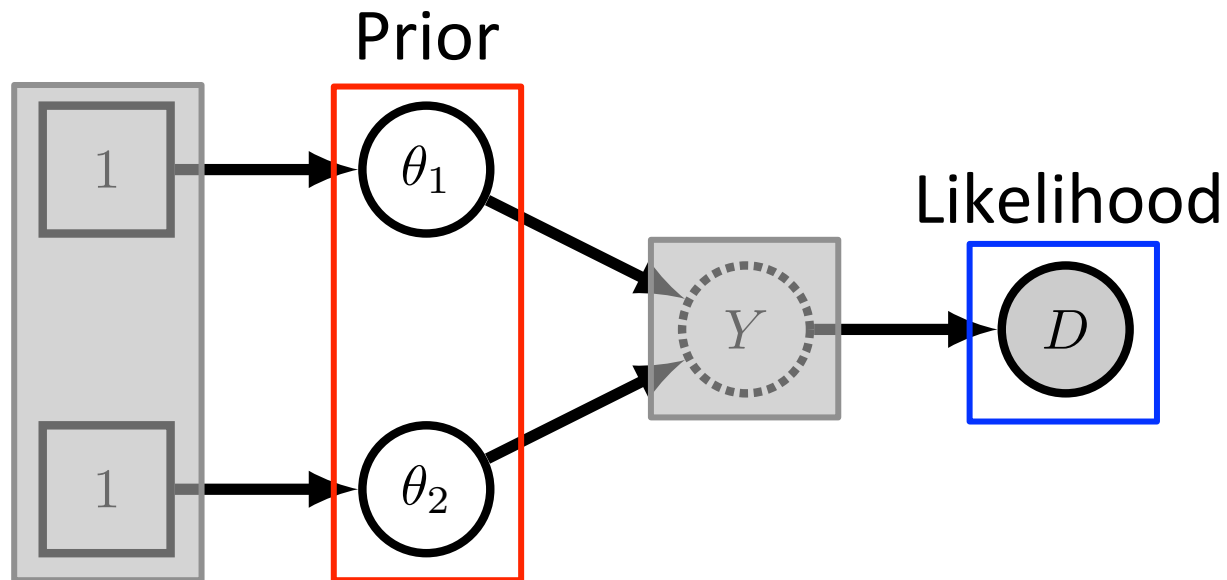
Model variable types

Nodes have different properties



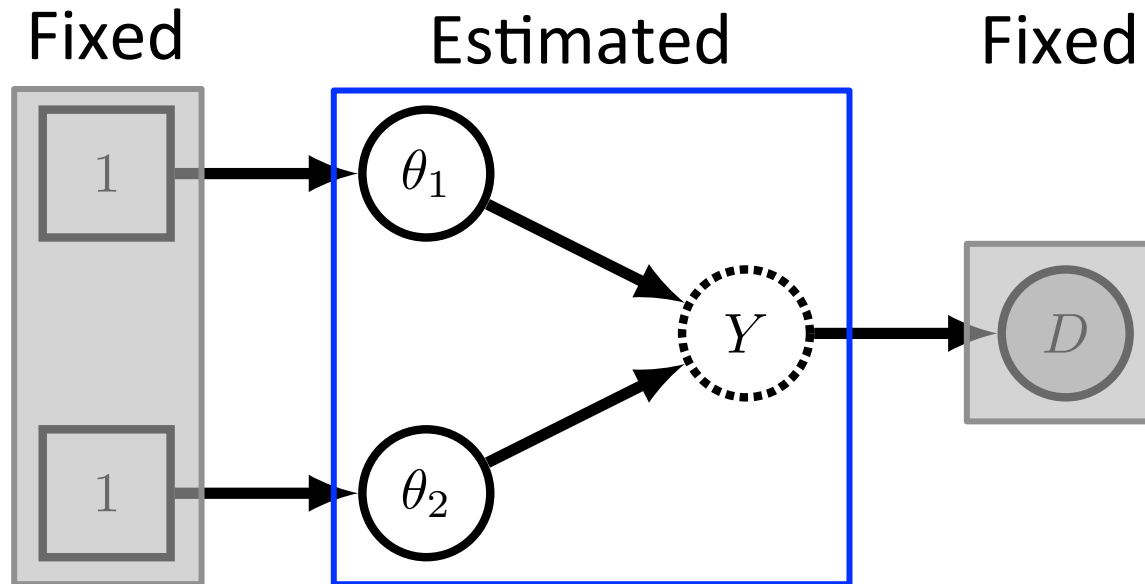
Model probabilities

Stochastic nodes contribute to model posterior



Parameter estimation

Estimate the values of deterministic and (unobserved) stochastic nodes



Model in Rev

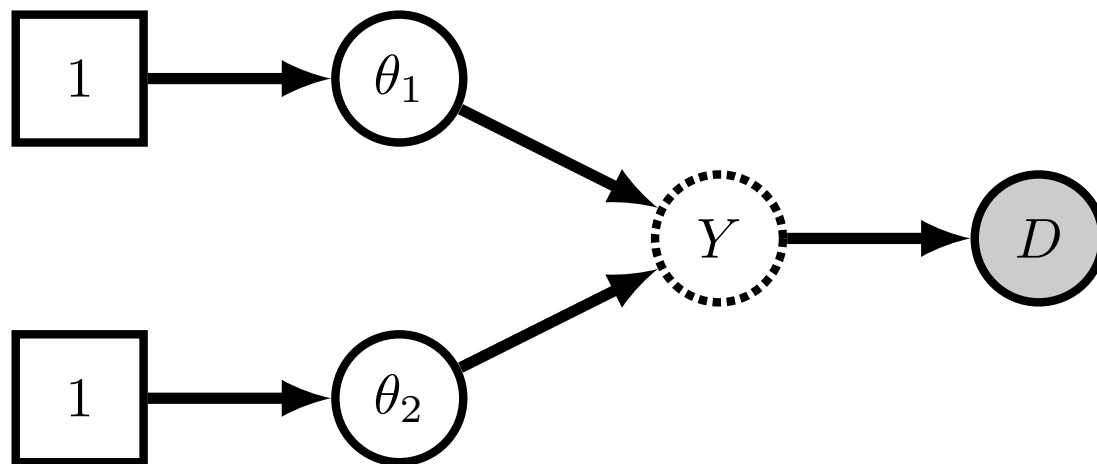
$D \sim \text{Exponential}(Y)$

$Y = (\theta_1 - \theta_2)^2$

$\theta_1 \sim \text{Exponential}(1)$

$\theta_2 \sim \text{Exponential}(1)$

```
for (i in 1:2) {  
  theta[i] ~ dnExp(1)  
}  
Y := (theta[1]-theta[2])^2  
D ~ dnExp(Y)  
D.clamp(3.14159)
```



Let's build some models!!