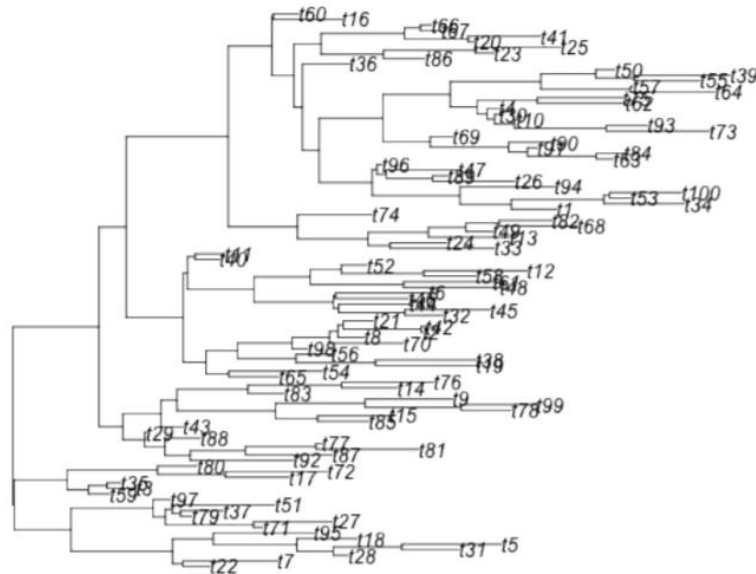


# Dating Phylogenetic Trees

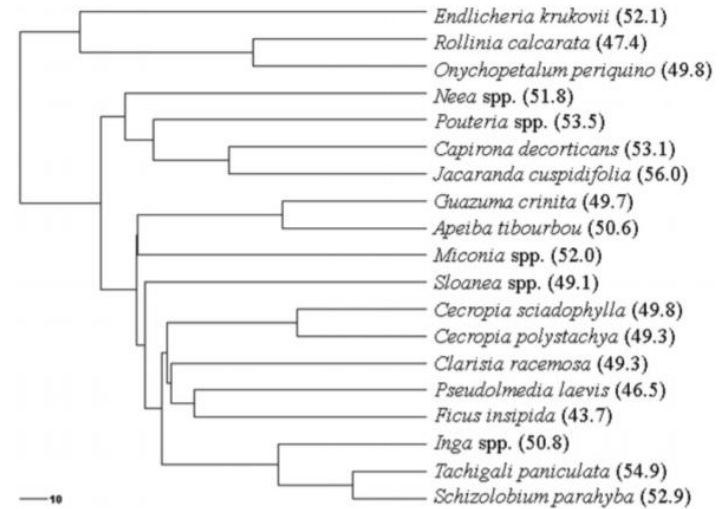
What are the units of branch lengths from a statistical phylogenetics analysis?

Distance = Expected # of substitutions per site

Time x Rate = Distance



Non-ultrametric



Ultrametric tree

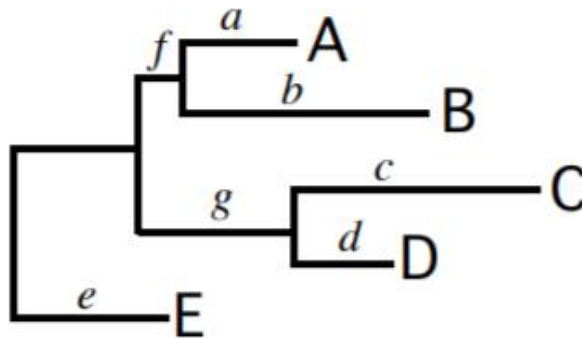
# Why do we want an ultrametric tree?

# How do you get rate?

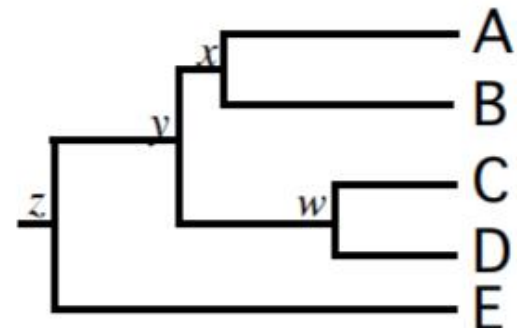
One option: Assume a universal or strict “molecular clock”

Why do real lineages often not evolve in a clock-like manner?

Non-clock Tree



Clock-like Tree



# How we go from non-ultrametric tree to a chronogram in real units of time (e.g. millions of years)

Need to specify:

- How the rates vary across branches  
(clock model)

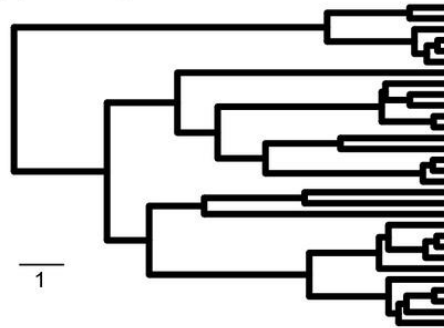
- How branch lengths are distributed across the tree (Timetree models)

- Fossil calibrations (or biogeographic, ancient DNA/sampled ancestors, etc)

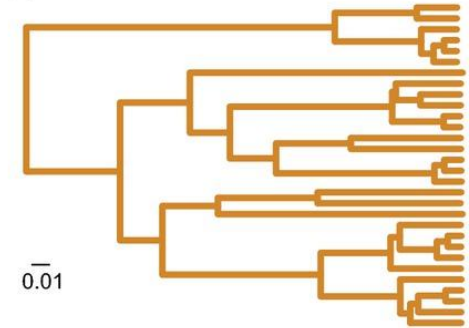
# Clock Models

How do rates vary across the tree?

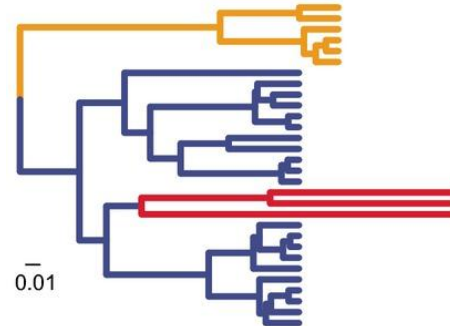
(a) Chronogram



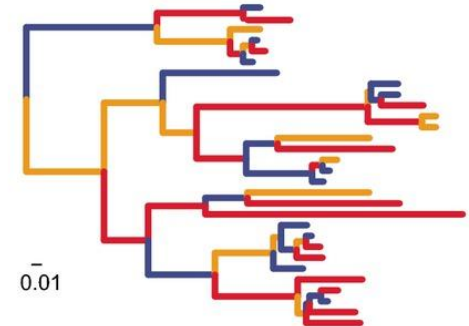
(b) Strict clock



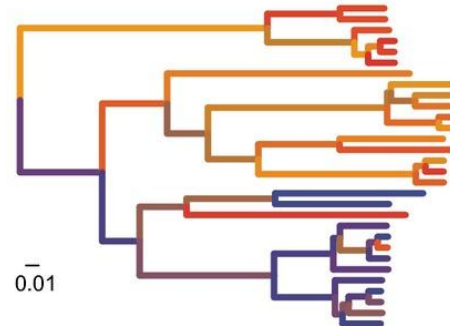
(c) Local multi-rate clock



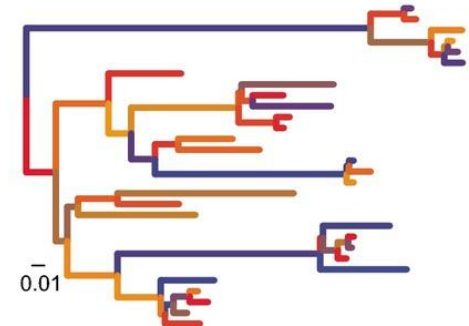
(d) Discrete multi-rate clock



(e) Autocorrelated relaxed clock



(f) Uncorrelated relaxed clock



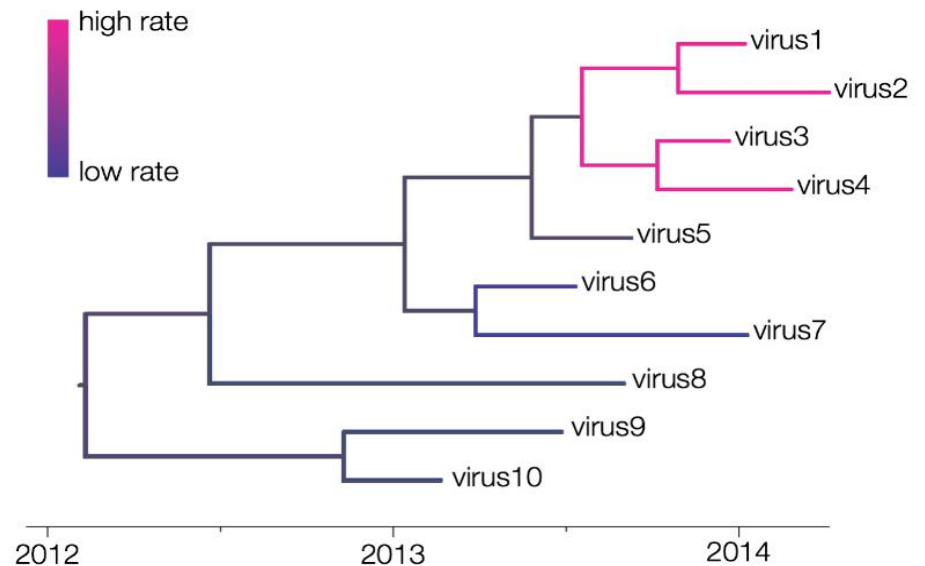
Ho & Duchene, 2014;  
Molecular Ecology

# Clock Models

Local clocks

Fixed: User supplied clades

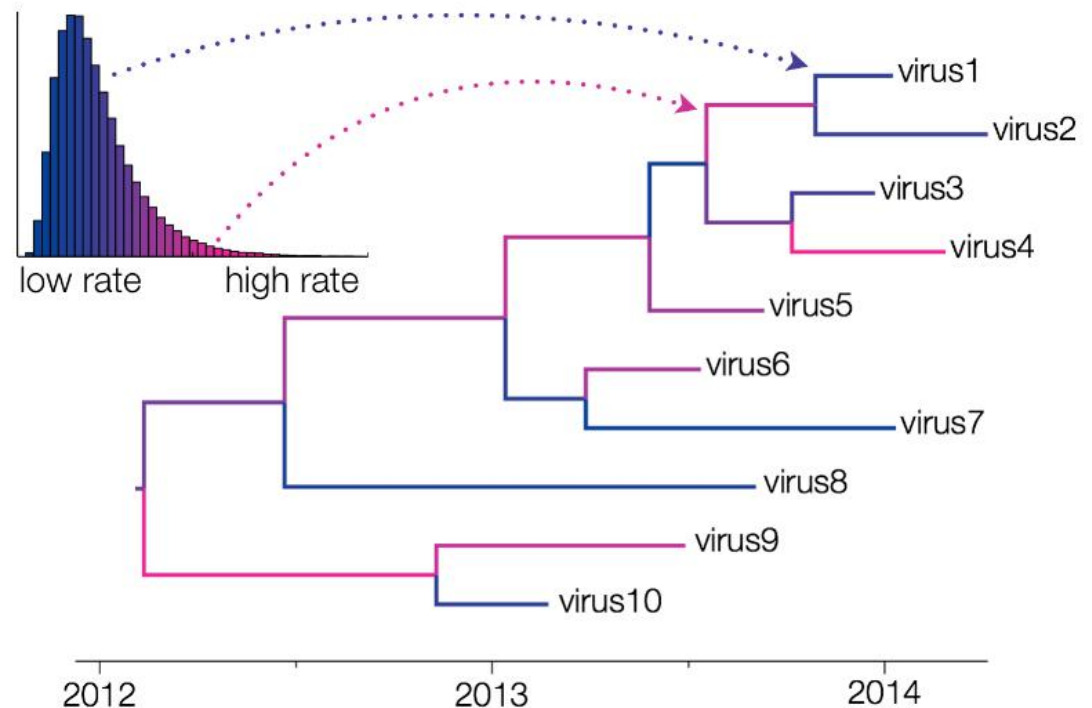
Random: Algorithm finds small number of clades



*Under the fixed local clock model, a shift in evolutionary rate occurs at the TMRCA of each defined taxon set.*

# uncorrelated relaxed clock

(often lognormal distribution, kind of like gamma rates, but across branches, not sites)

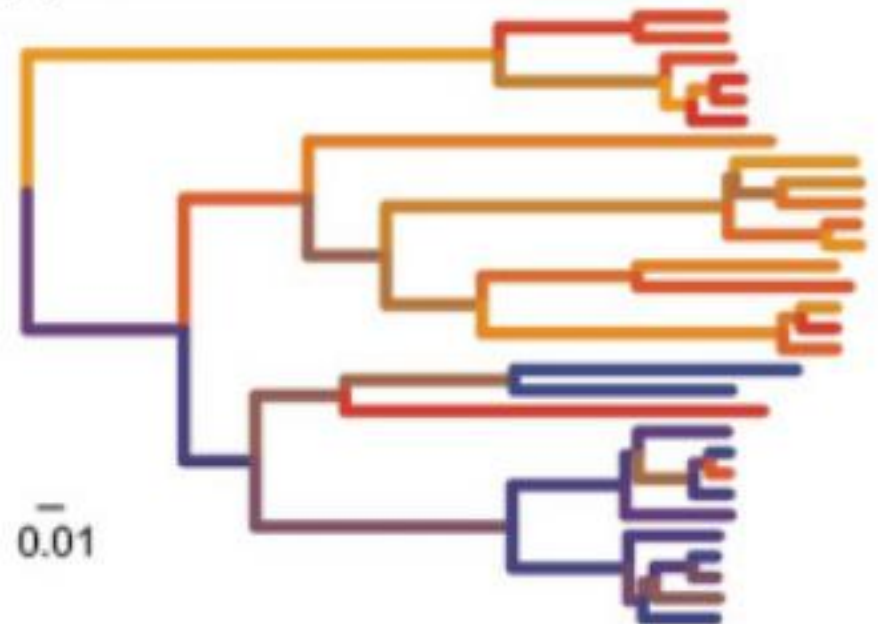


*Under the uncorrelated relaxed clock model, the evolutionary rate at each branch is drawn from an underlying distribution.*

# autocorrelated relaxed clocks

Rates have “memory” from previous branch

(e) Autocorrelated relaxed clock



Non-parametric “smoothing” approaches assume autocorrelated rates, and try to minimize the change across branches Sanderson (1997. *Mol. Biol. Evol.*, 14:1218); r8s, treePL, chronoPL. Fast and efficient for large trees. Assumes branch lengths are estimated without error. Quick and dirty approach.



# Timetree models

## Birth-death model

speciation rate,  $\lambda$   
extinction rate,  $\mu$

Diversification rate:  
 $\lambda - \mu$

Turnover:  
 $\lambda + \mu$

Yule/pure-birth model  
if  $\mu = 0$

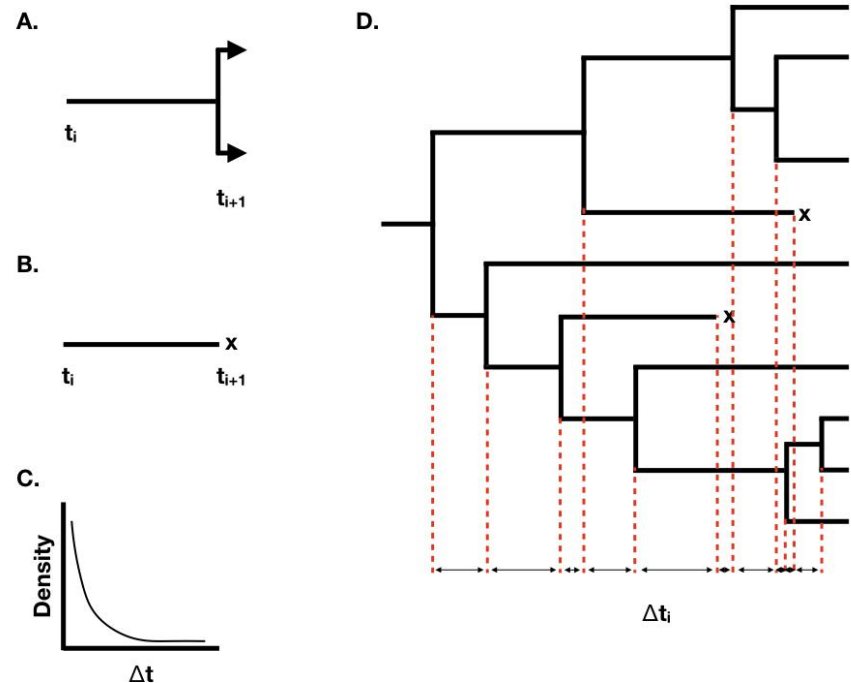


Image from Harmon textbook

(Will cover this a bunch more  
studying diversification)

# Phylodynamics

Other timetree models: Coalescent priors

Often used for viral dynamics

Include “population size” as a parameter and allow inference on past demography



Tanja Stadler

## Bayesian Coalescent Inference of Past Population Dynamics from Molecular Sequences

A. J. Drummond, A. Rambaut, B. Shapiro, and O. G. Pybus

Department of Zoology, University of Oxford, Oxford, United Kingdom

*Syst. Biol.* 62(5):674–688, 2013  
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DOI:10.1093/sysbio/syt030  
Advance Access publication April 28, 2013

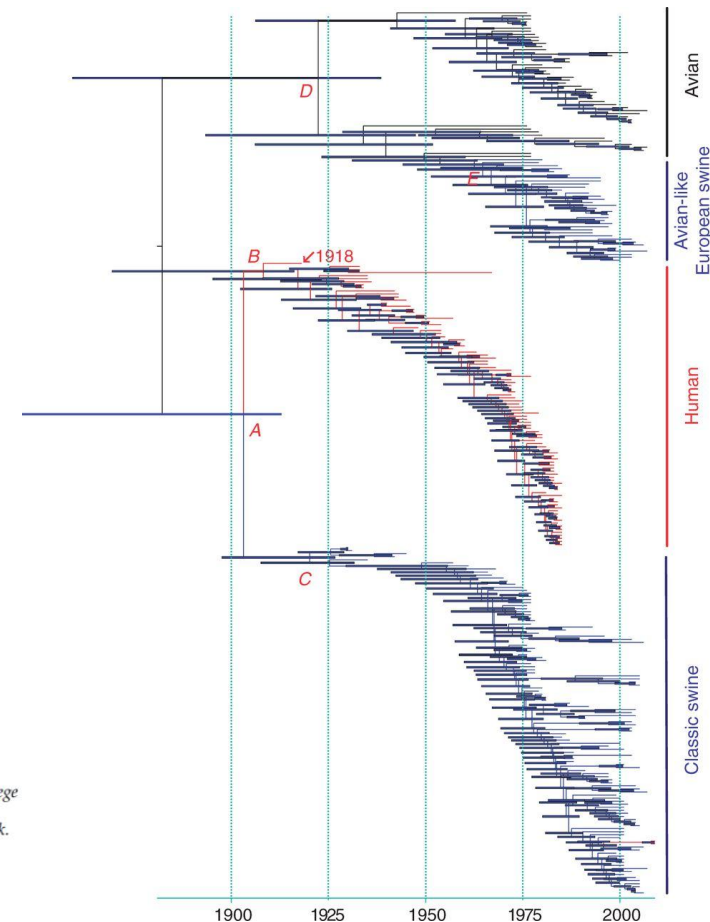
## Dating Phylogenies with Sequentially Sampled Tips

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<sup>1</sup>Institut für Integrative Biologie, Eidgenössische Technische Hochschule Zürich, 8092 Zürich, Switzerland; and <sup>2</sup>Department of Biology, University College London, London WC1E 6BT, UK

\*Correspondence to be sent to Department of Biology, Darwin Building, University College London, London WC1E 6BT, UK; E-mail: z.yang@ucl.ac.uk.

Received 21 November 2012; reviews returned 15 February 2013; accepted 23 April 2013  
Associate Editor: Laura Kubatko



# Calibrating nodes

Incorporates  
uncertainty

Drawback...Only  
the oldest fossil in  
a crown group is  
used to set the  
prior

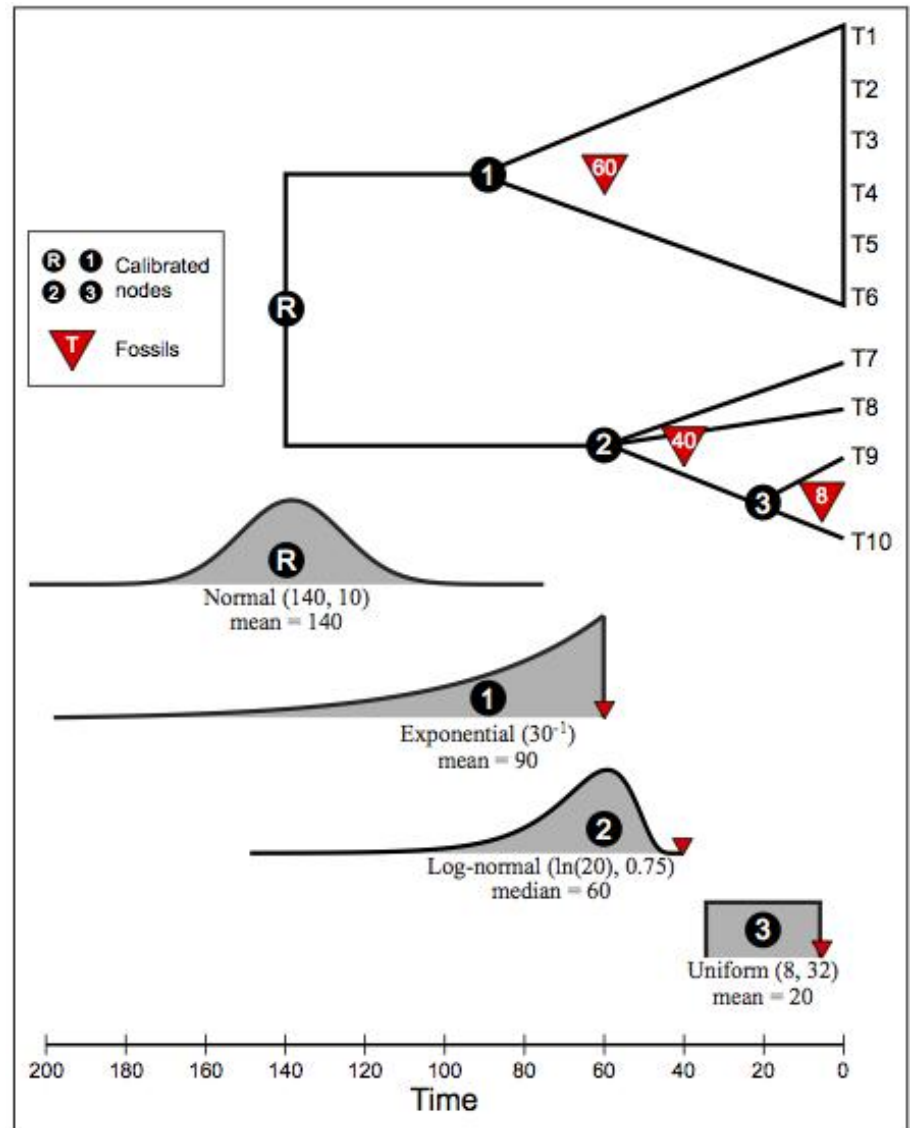


Figure from Dennis Lavrov,  
<https://sites.google.com/site/eeob563/computer-labs/lab-7>

# Another drawback...

Setting complicated, interacting priors

Sometimes the prior you think you're setting isn't what you're actually setting...

*Syst. Biol.* 67(2):340–353, 2018

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DOI:10.1093/sysbio/syx074

Advance Access publication September 7, 2017

## **The Past Sure is Tense: On Interpreting Phylogenetic Divergence Time Estimates**

JOSEPH W. BROWN\* AND STEPHEN A. SMITH

*Department of Ecology & Evolutionary Biology, University of Michigan, 830 North University Avenue, Ann Arbor, MI 48109, USA*

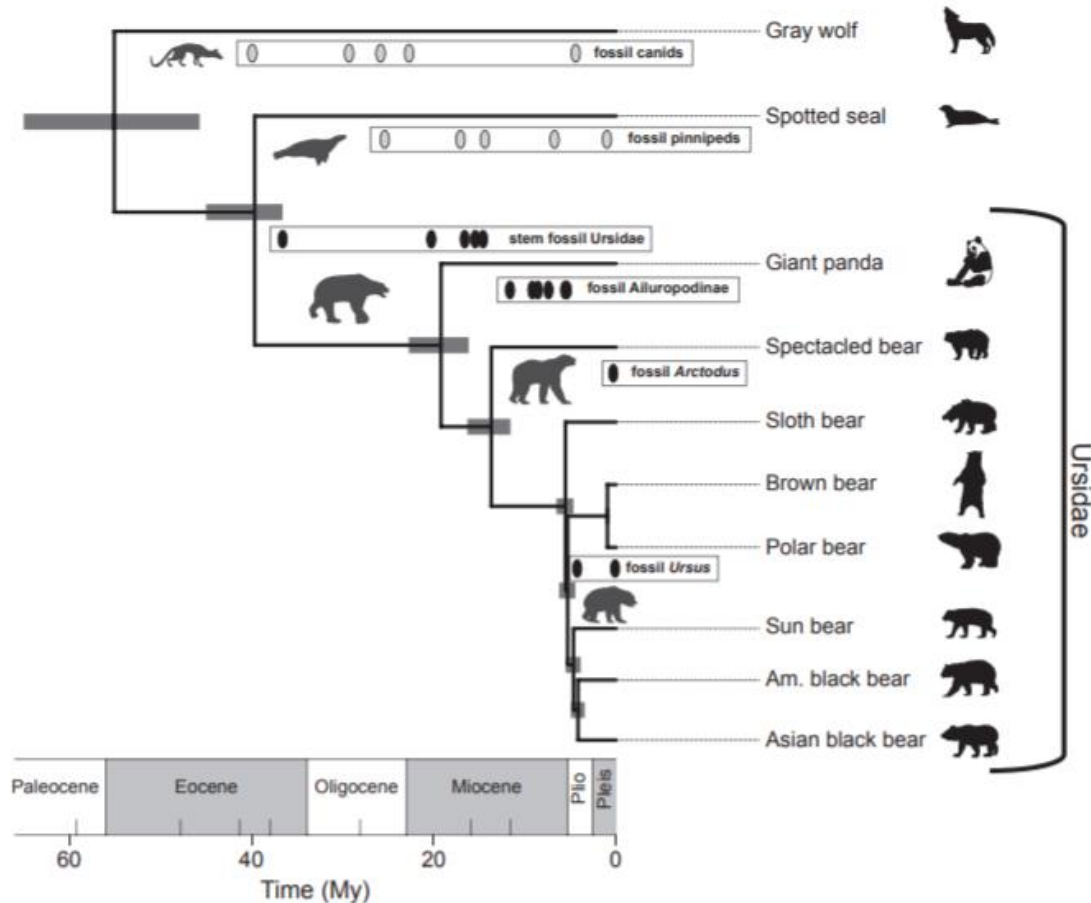
*\*Correspondence to be sent to: Department of Ecology & Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109, USA;*

*E-mail: josephwb@umich.edu.*

*Received 7 March 2017; reviews returned 29 August 2017; accepted 4 September 2017*

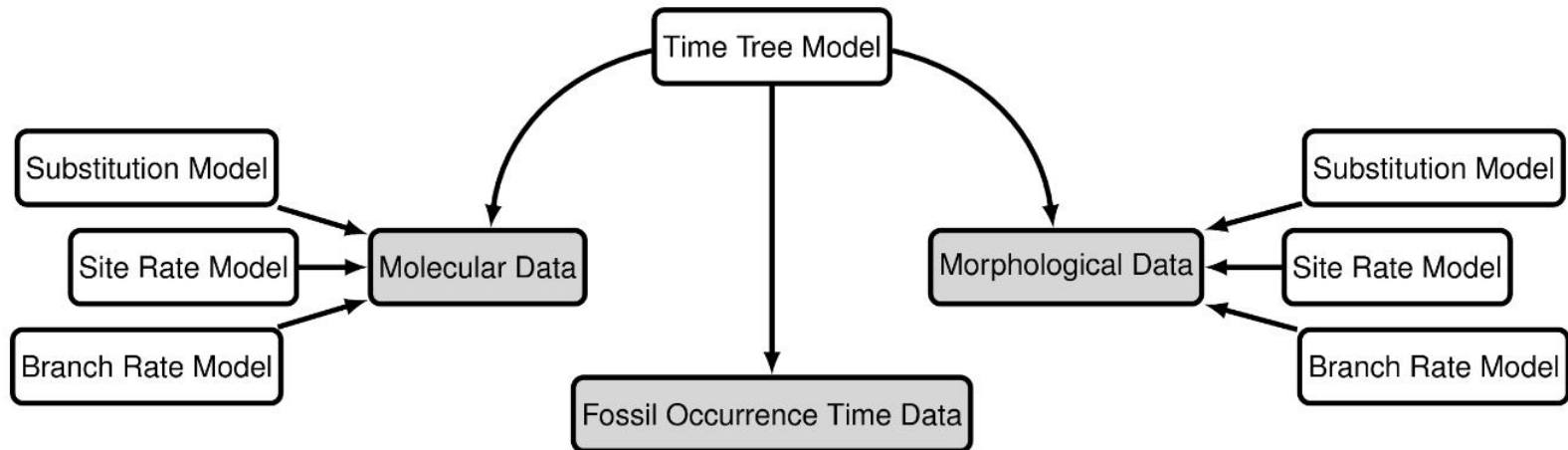
*Associate Editor: Simone Ho*

# Tip-Dating



**Fig. 4.** The divergence times of extant bears and two caniform out-groups estimated under the FBD model. The branch lengths are in proportion to the mean branch time in millions of years. Horizontal node bars represent the 95% CI for node ages. In each labeled box, the ovals indicate the fossil occurrence times. The fossils in the family Ursidae are all indicated with black ovals, whereas the out-group fossils are shaded light gray. *Ursus* (including *Melursus* and *Helarctos*) species include the sloth bear, brown bear, polar bear, sun bear, American black bear, and Asian black bear. (Silhouette images available at <http://phylopic.org/>.)

# Fossilized Birth-Death Process & Total evidence analyses

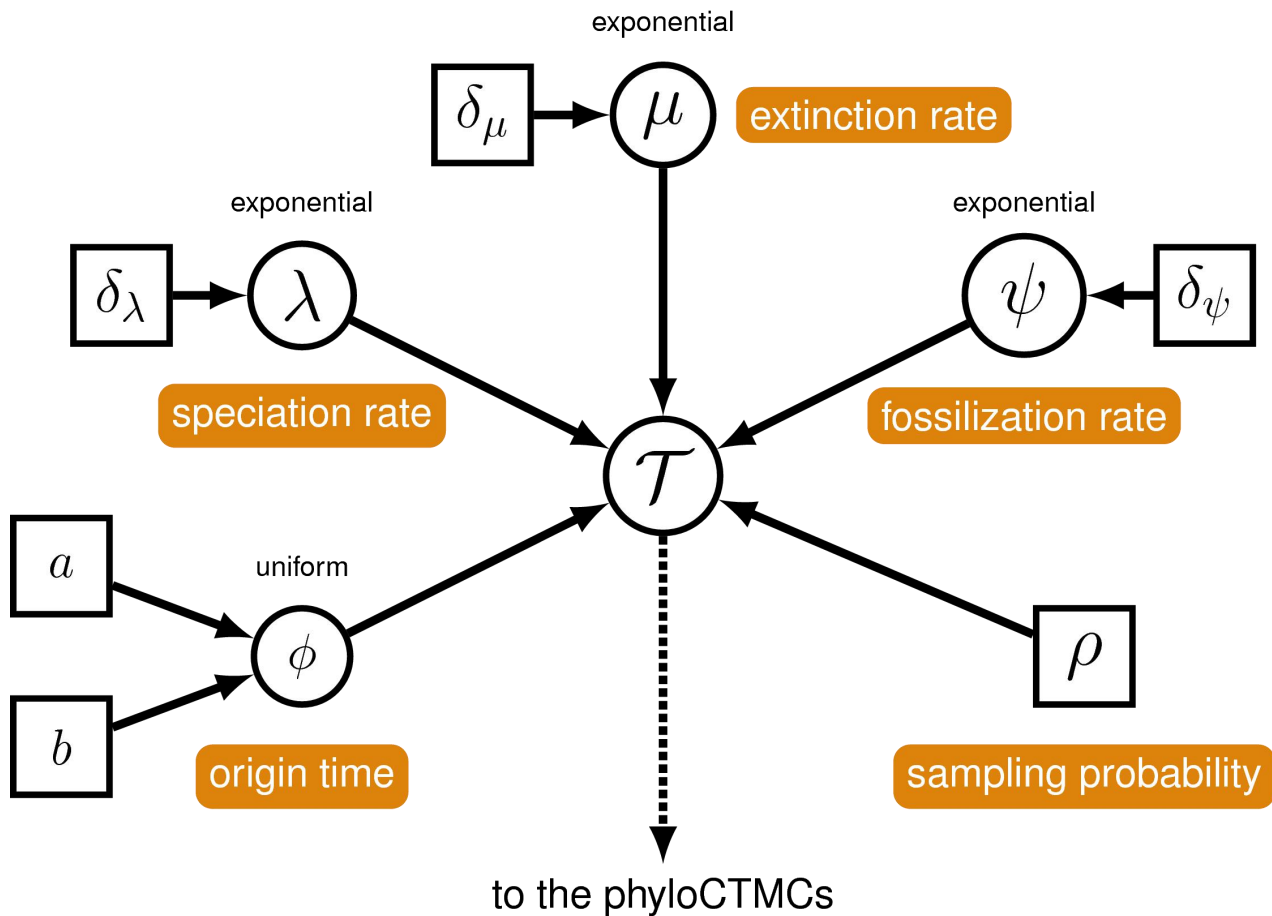


**Figure 1.** Modular components of the graphical model used in the “combined-evidence” analysis described in this tutorial.



Tracy Heath  
Iowa State U.

# Timetree model: FBBDP



# Sampling ancestors

We usually assume we can't directly sample ancestors

But what does this depend on?

What if we sample closer to the present?

What if we sample



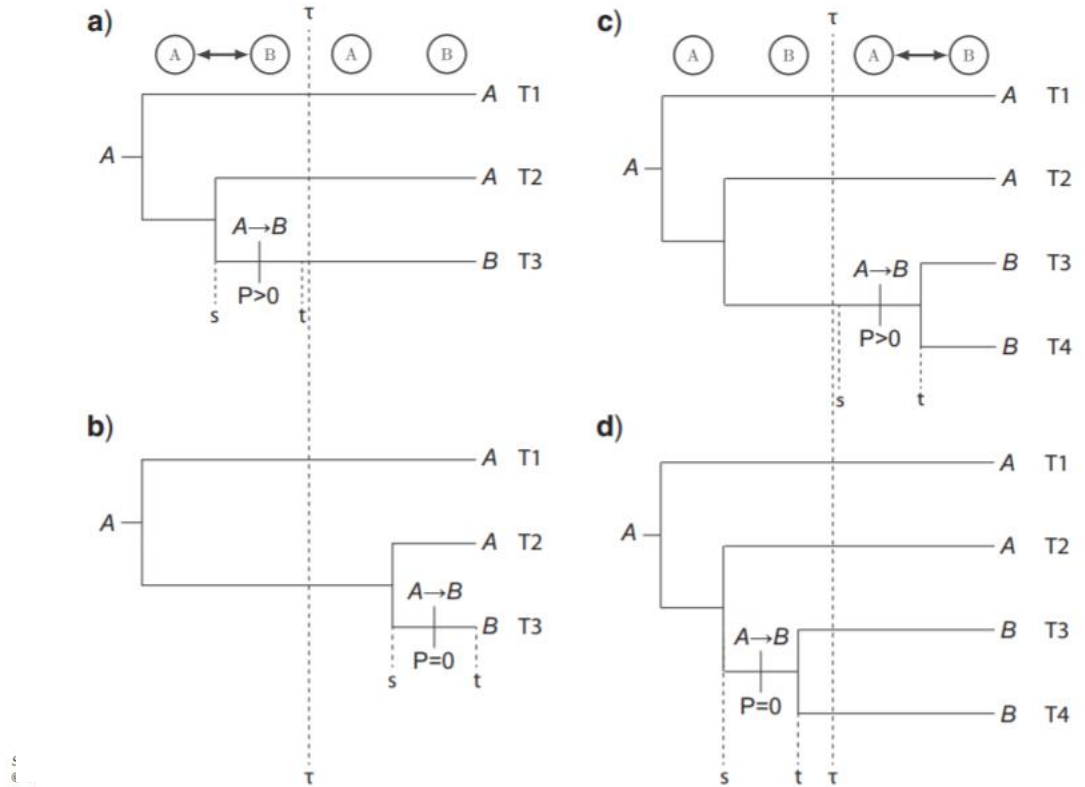
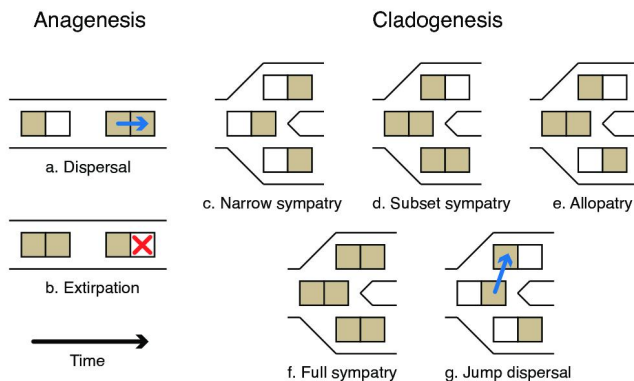
# Dating with biogeography

DEC model

Dispersal +  
Extinction +  
Cladogenesis

(Ree & Smith 2008)

(This is the model I  
showed on the exam)



For:  
DOI: 10.1073/syso.10.10.1000  
Advance Access publication May 6, 2016

## Biogeographic Dating of Speciation Times Using Paleogeographically Informed Processes

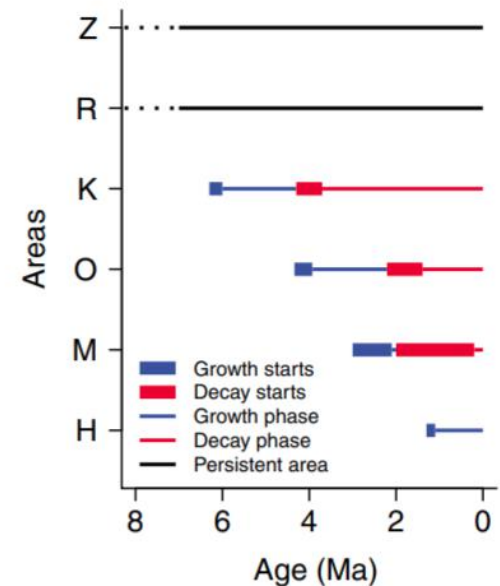
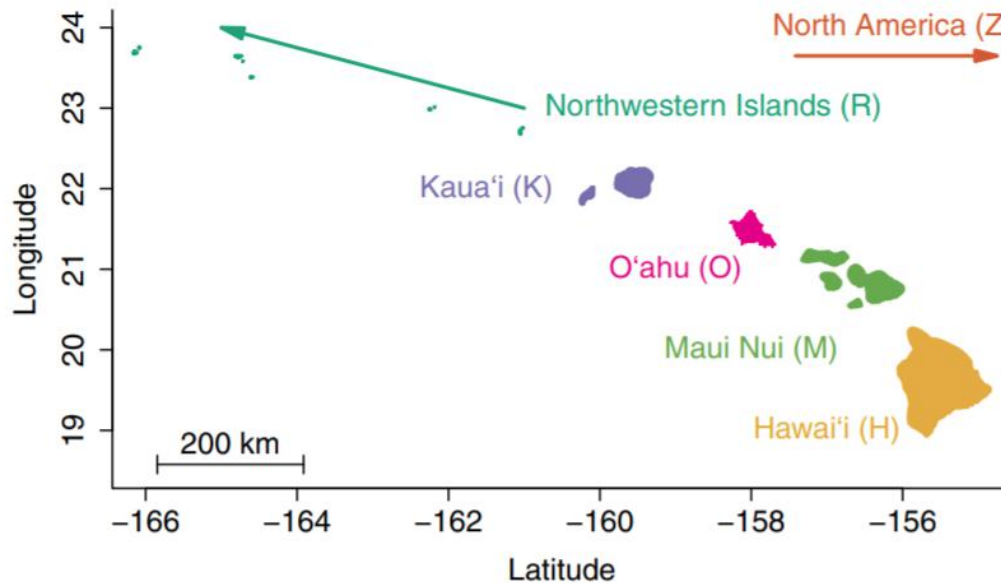
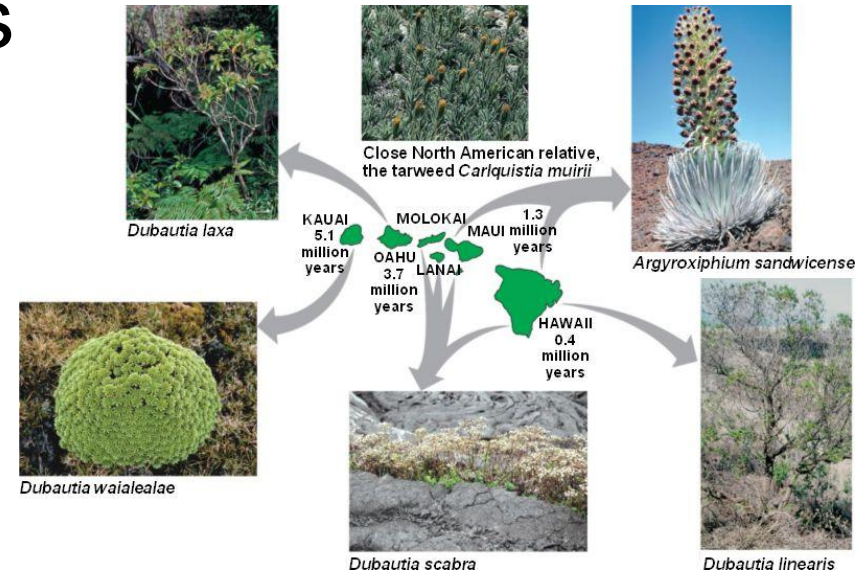
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<sup>1</sup>Department of Integrative Biology, University of California, Berkeley, CA 94720, USA; <sup>2</sup>Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520, USA;

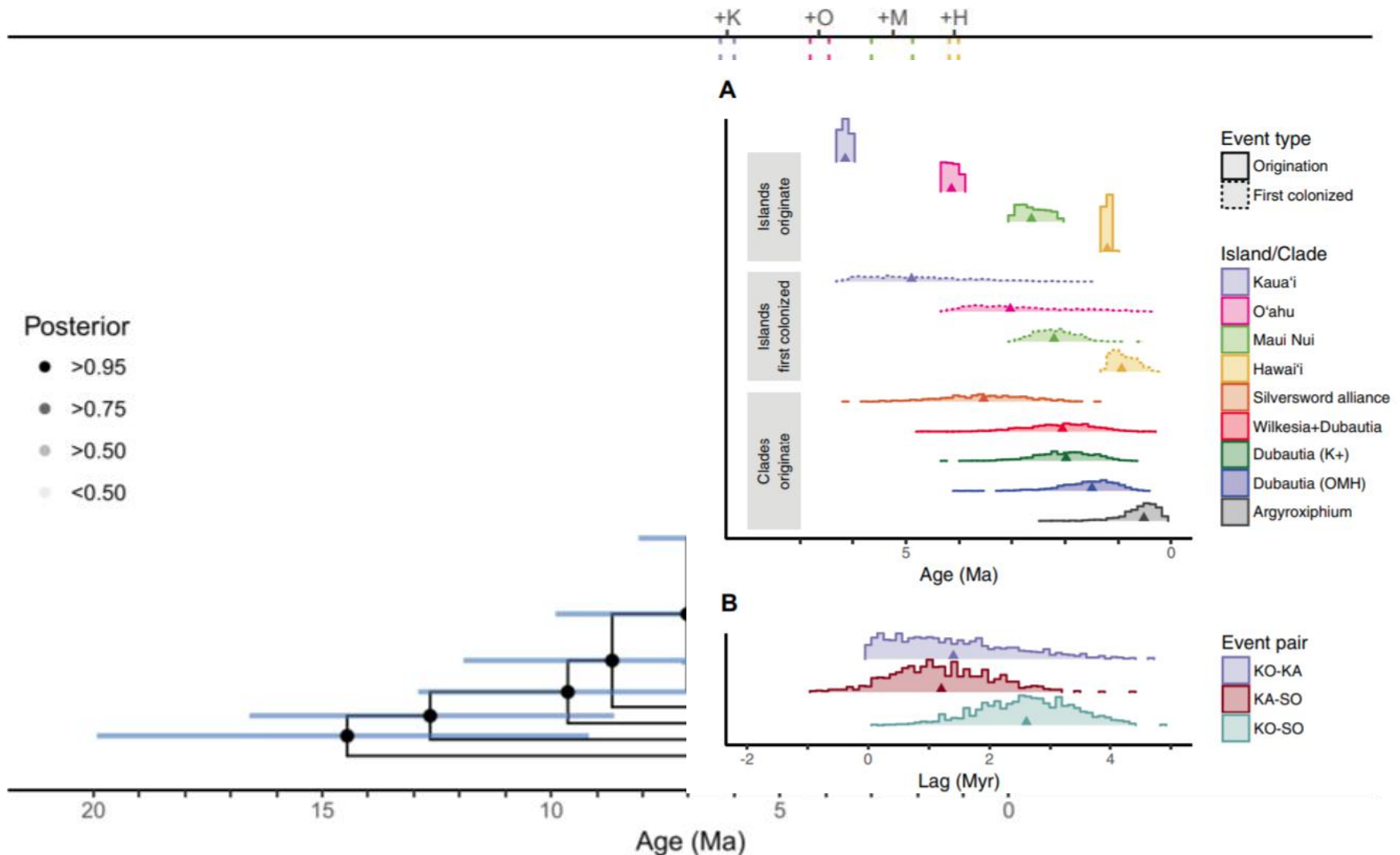
\*Correspondence to be sent to: Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520, USA;  
E-mail: michael.landis@yale.edu

Received 8 October 2015; reviews returned 26 April 2016; accepted 28 April 2016  
Associate Editor: Emma Goldberg

# Hawaiian Silverswords (Landis, et al. 2018)



# Hawaiian Silverswords (Landis, et al. 2018)



# Summary

In order to convert phylogenies to timetrees, we need additional data and/or assumptions (non-identifiability of rate/time).

Clock models model heterogeneity in rate across branches, timetree models make assumptions about how the tree is shaped/formed

Calibrations can be placed as constraints or priors at nodes, or in tip-dating analyses

Total-evidence/integrated analyses are extremely promising for building our knowledge of evolutionary history