

Phylogenetics

Introduction to
phylodynamics

RL-V3 MPP

Rachel Warnock

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Today

- **Recap:** total-evidence dating
- Intro to phylodynamics and diversification rate estimation

Recap: Bayesian phylogenetic dating

We use a Bayesian framework

$$P(\text{model} \mid \text{data}) = \frac{P(\text{data} \mid \text{model}) P(\text{model})}{P(\text{data})}$$

likelihood

priors

posterior

marginal probability of the data

Bayesian divergence time estimation

The data

and / or

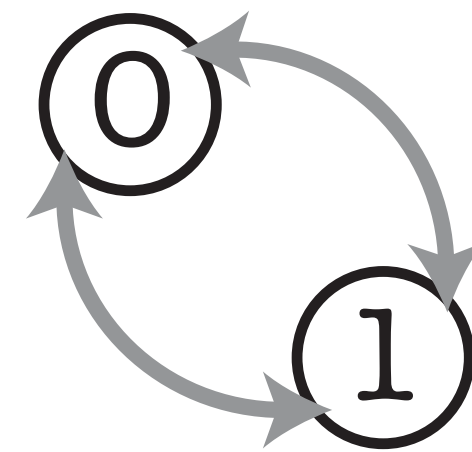
0101... ATTG...
1101... TTGC...
0100... ATTC...



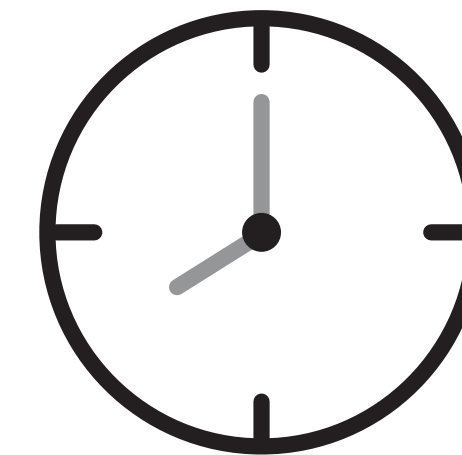
phylogenetics
characters

sample
ages

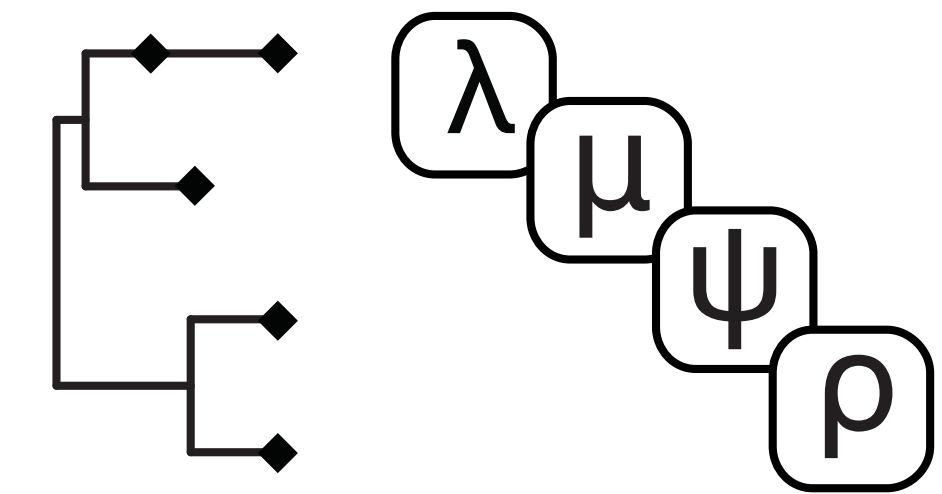
3 model components



substitution
model



clock
model



tree and tree
model

Bayesian divergence time estimation

posterior

$$P(\text{tree, } \lambda, \mu, \psi, \rho, \text{clock} \mid \text{data}) =$$

likelihood

probability of the
time tree

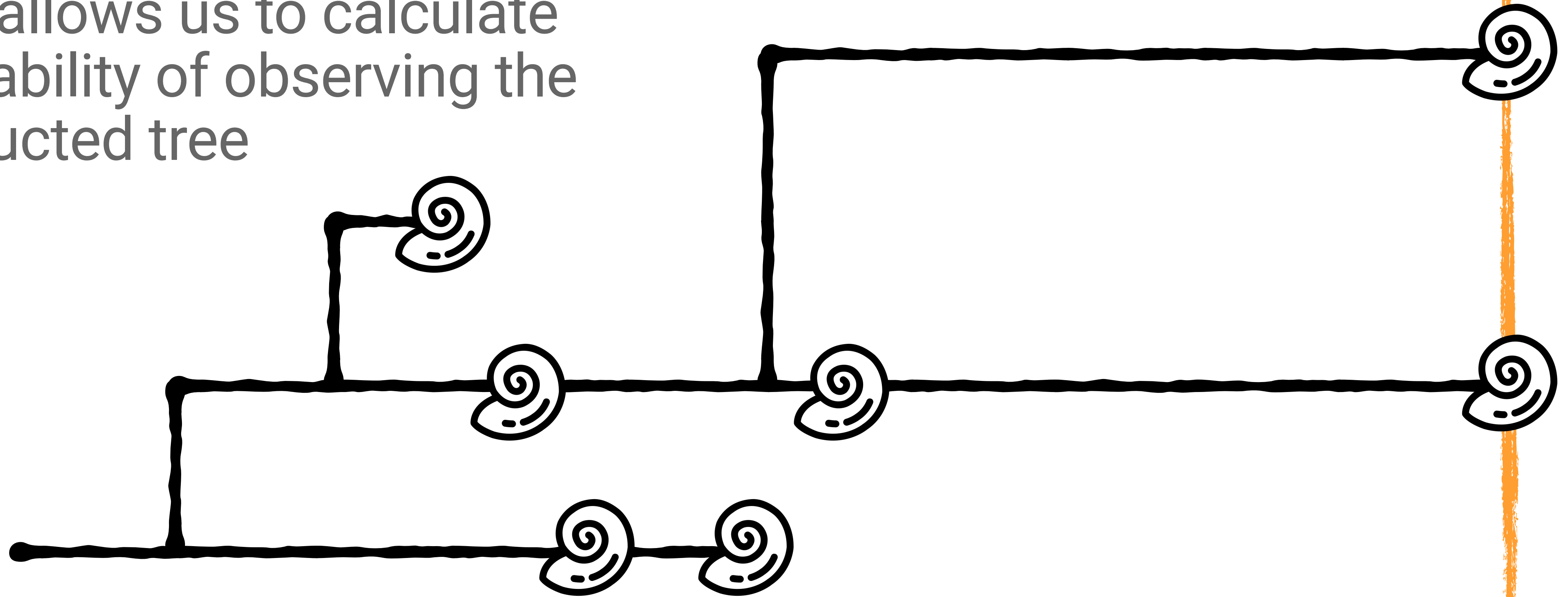
priors

$$P(\text{data} \mid \text{tree, } \lambda, \mu, \psi, \rho, \text{clock}) P(\text{tree} \mid \lambda, \mu, \psi, \rho) P(\lambda) P(\mu) P(\psi) P(\rho) P(\text{clock})$$

$$P(\text{data})$$

marginal pr of the data

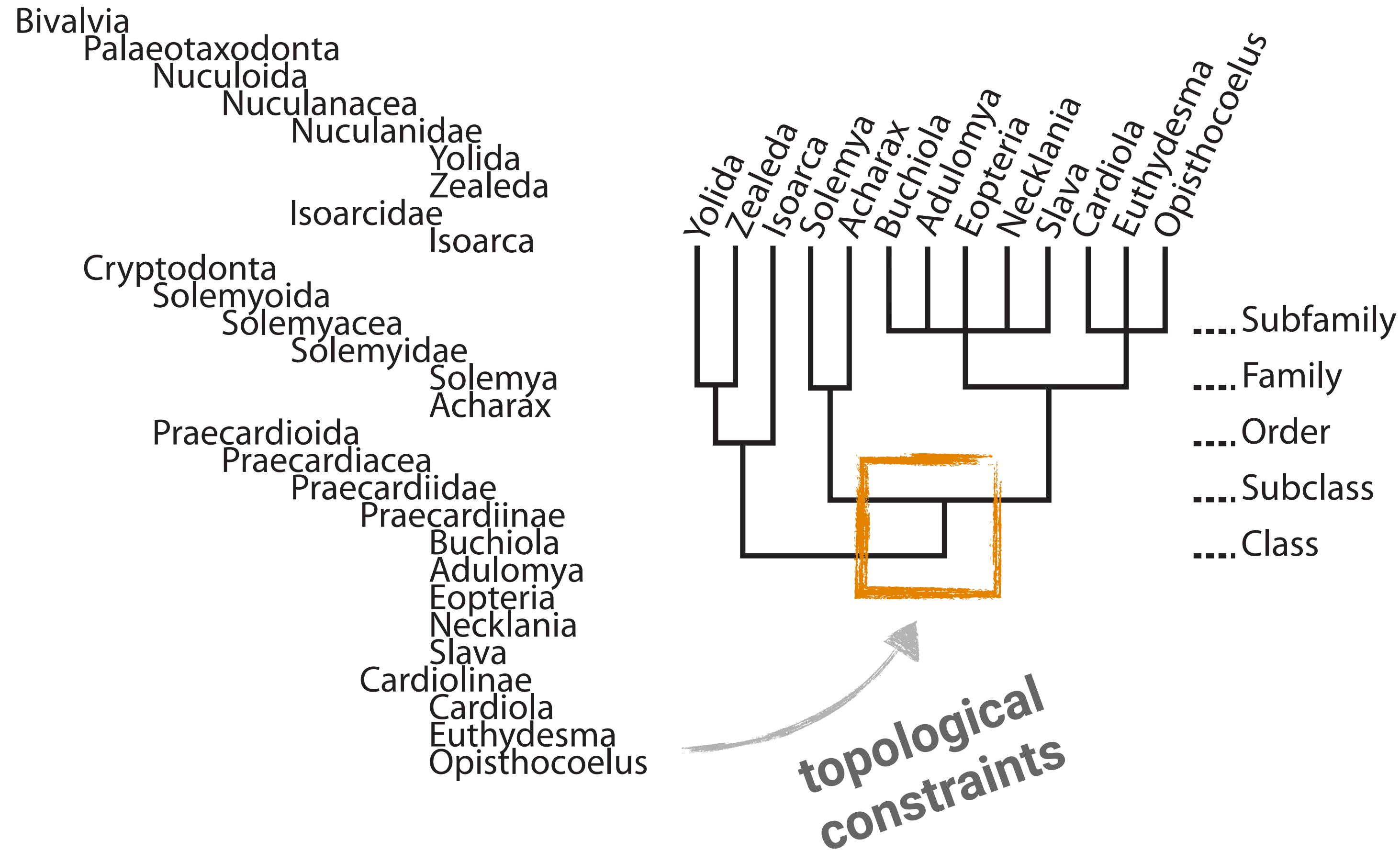
The **fossilised birth-death (FBD) process** allows us to calculate the probability of observing the reconstructed tree



$$P \left(\text{Tree} \mid \text{Fossil}^{\lambda, \mu, \psi, \rho} \right)$$

*Sampling-through-time in birth-death trees. Stadler. (2010)
First implemented: Heath et al. (2014) and Gavryushkina et al. (2014)*

Fossils can be incorporated via **taxonomy** or **character data** (total-evidence)



ATAT...

TCAC...

?????

OR

1001...

1101...

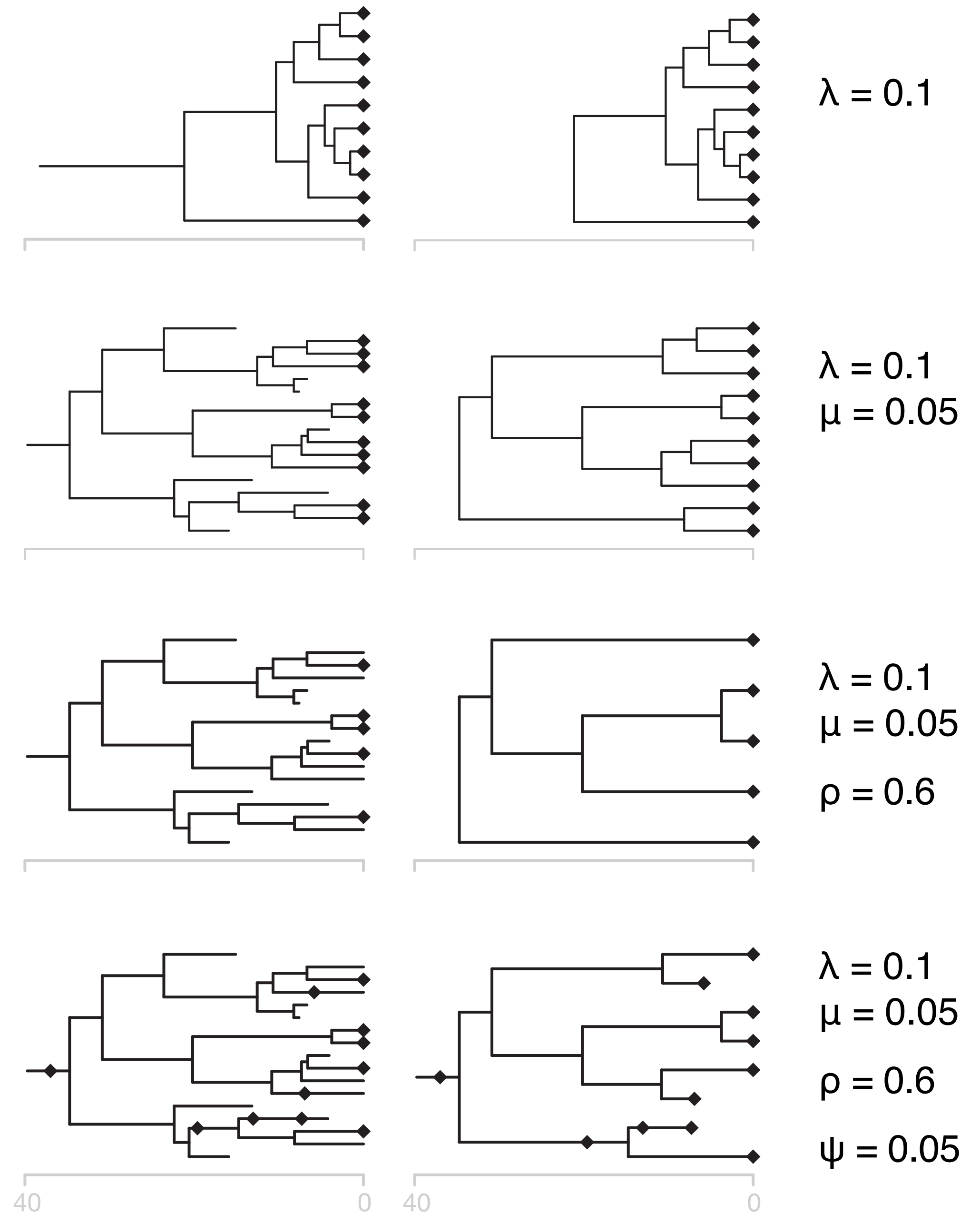
0100...

Relationship to (some) other birth-death process models

These models are special cases of the FBD process, with fossil sampling (ψ) = zero

For epidemiology: *Stadler et al.* ([2012](#))
 See also: *Stadler and Yang* ([2013](#))
 Review: *MacPherson et al.* ([2022](#))

complete vs. reconstructed trees



Yang and Rannala ([1997](#))
Stadler ([2009](#))

Stadler ([2010](#))

Exercise

- molecular sequences for living ferns
- fossil ages
- morphology for living and fossil species



PALE MOUNTAIN POLYPODY,
Polypodium phegopteris.

Phylodynamics

Diversification rate estimation

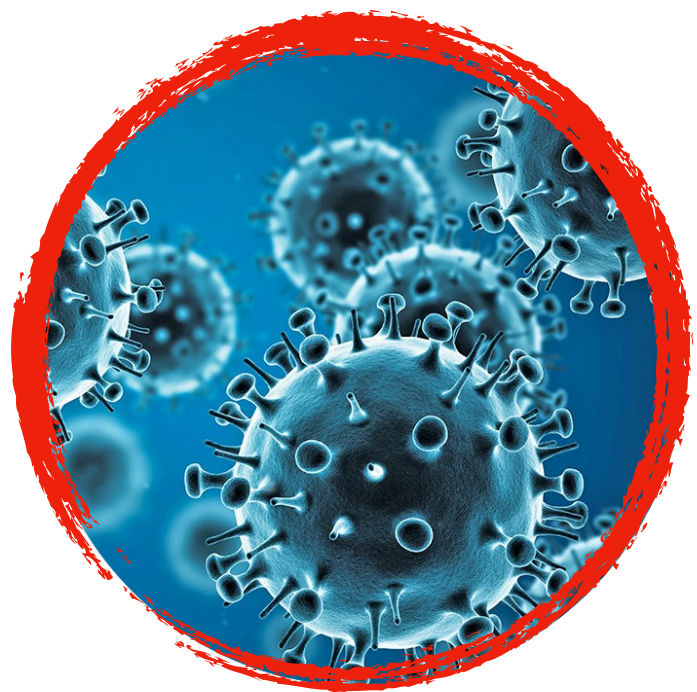
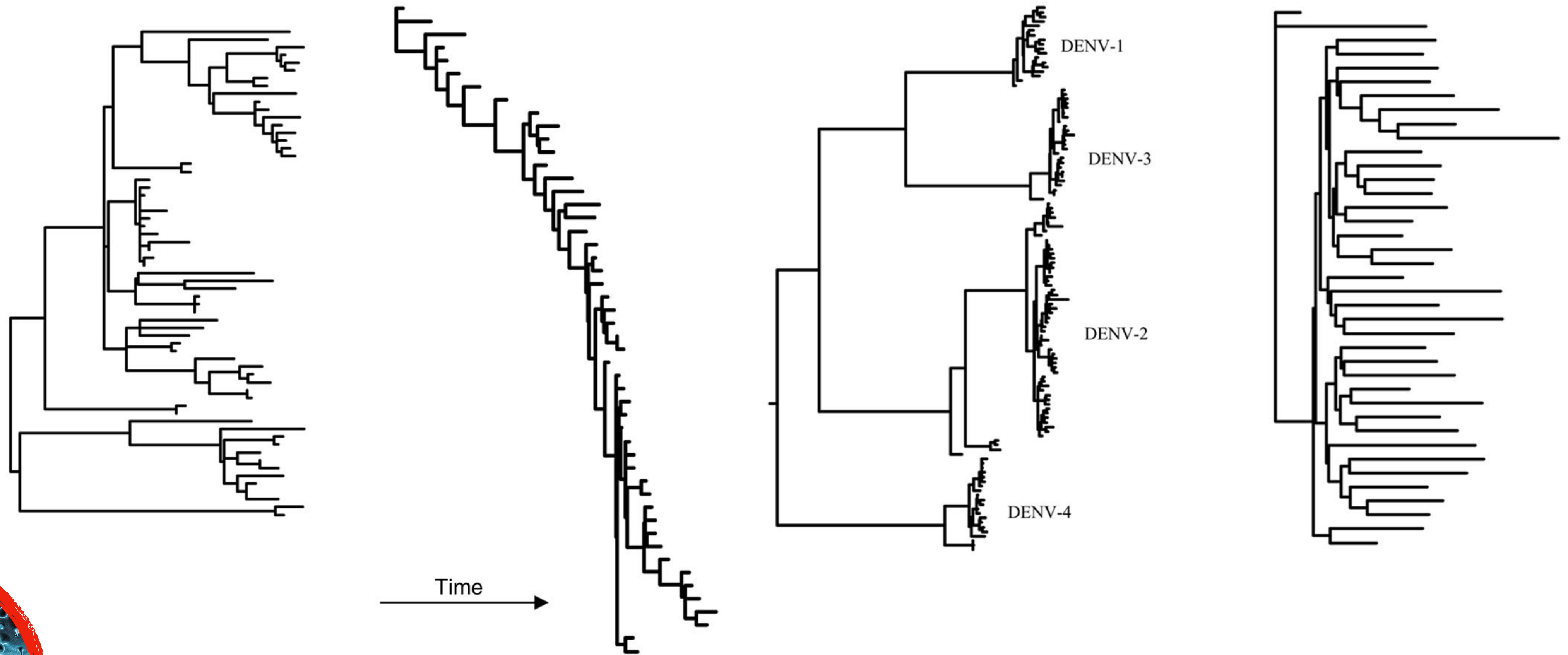
Bayesian divergence time estimation

$$P \left(\begin{array}{c} \text{Tree} \\ \lambda, \mu, \psi, \rho \\ \text{Clock} \end{array} \mid \begin{array}{c} 0101\dots \\ 1101\dots \\ 0100\dots \end{array} \text{Data} \right) =$$

probability of the
time tree

$$\frac{P \left(\begin{array}{c} 0101\dots \\ 1101\dots \\ 0100\dots \end{array} \mid \begin{array}{c} \text{Tree} \\ \lambda, \mu, \psi, \rho \\ \text{Clock} \end{array} \right) P \left(\begin{array}{c} \text{Tree} \\ \lambda, \mu, \psi, \rho \end{array} \mid \text{Data} \right) P \left(\begin{array}{c} \lambda, \mu, \psi, \rho \end{array} \right) P \left(\begin{array}{c} \text{Clock} \end{array} \right) P \left(\begin{array}{c} \text{Clock} \end{array} \right)}{P \left(\begin{array}{c} 0101\dots \\ 1101\dots \\ 0100\dots \end{array} \mid \text{Data} \right)}$$

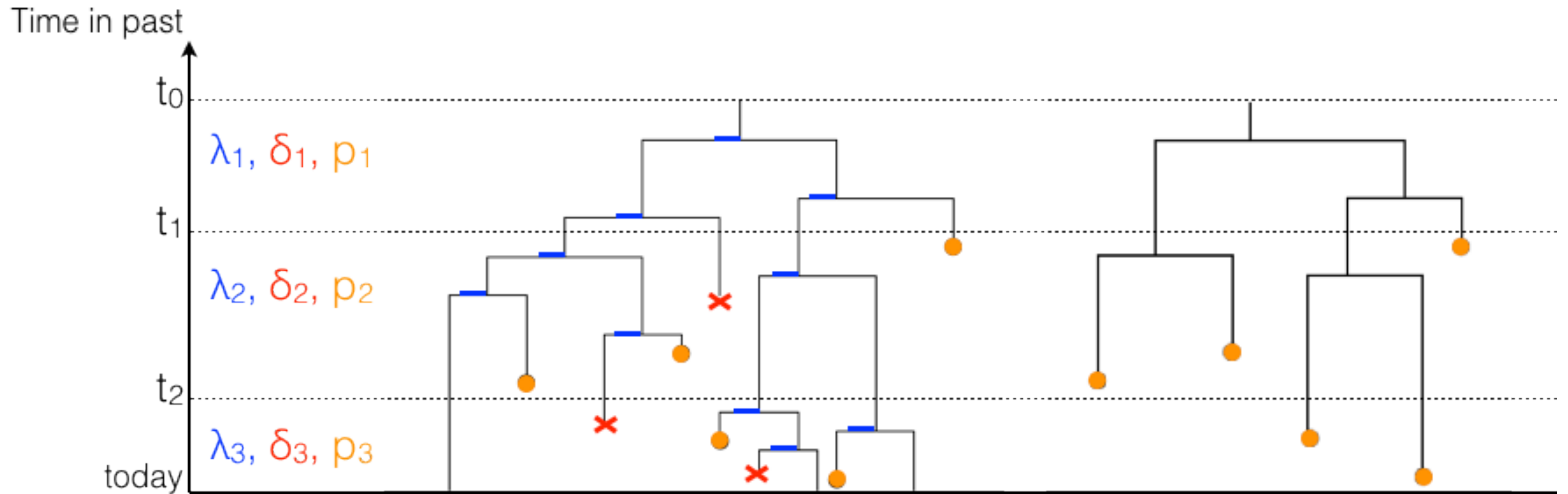
Tree shape is informative about underlying dynamics



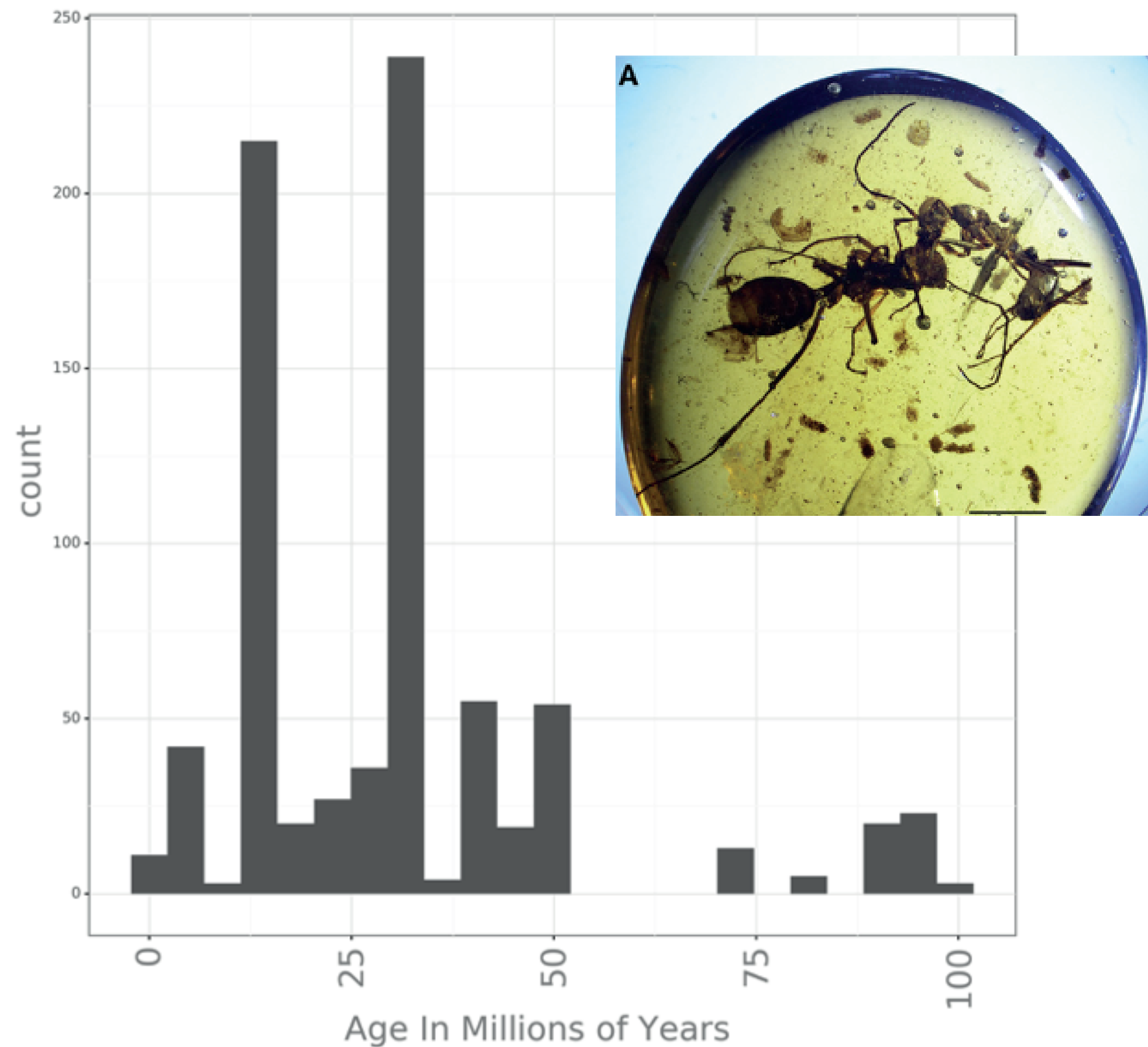
This paper coined the term phylodynamics
Grenfell et al. 2004. Science

The skyline birth-death process

First used for tracking the spread of infectious diseases



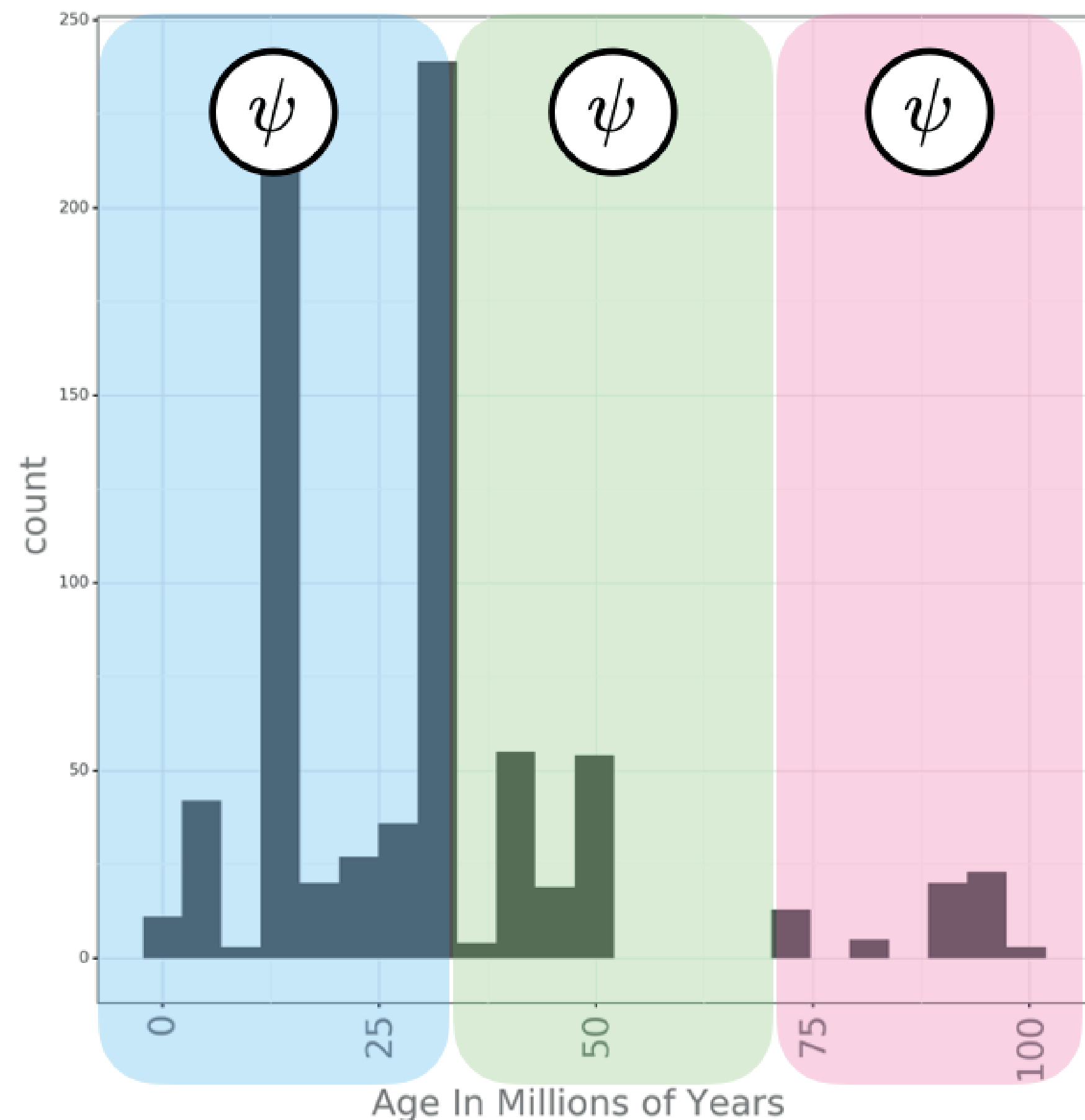
Estimating parameters in macroevolution



Ants have very variable fossil sampling over time

→ We can take this into account using the FBD skyline model

Estimating parameters in macroevolution



The oldest fossils are around 100 Ma

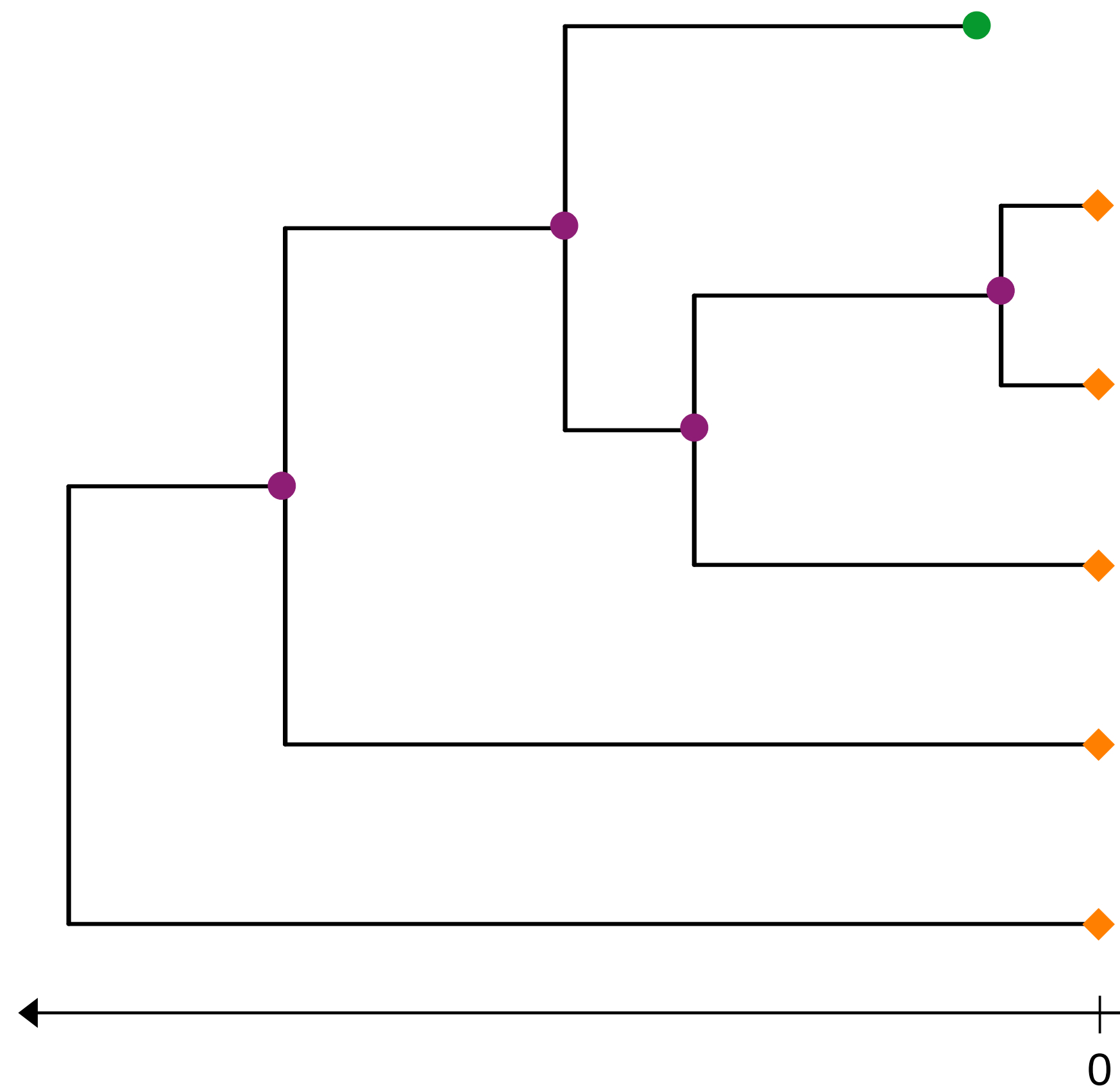
Different assumptions about the fossil sampling process produce different results

Skyline models recover an older age estimate for the origin of ants (= 140 Ma)

The multi-type birth-death process

Simple birth-death process

Extant species only



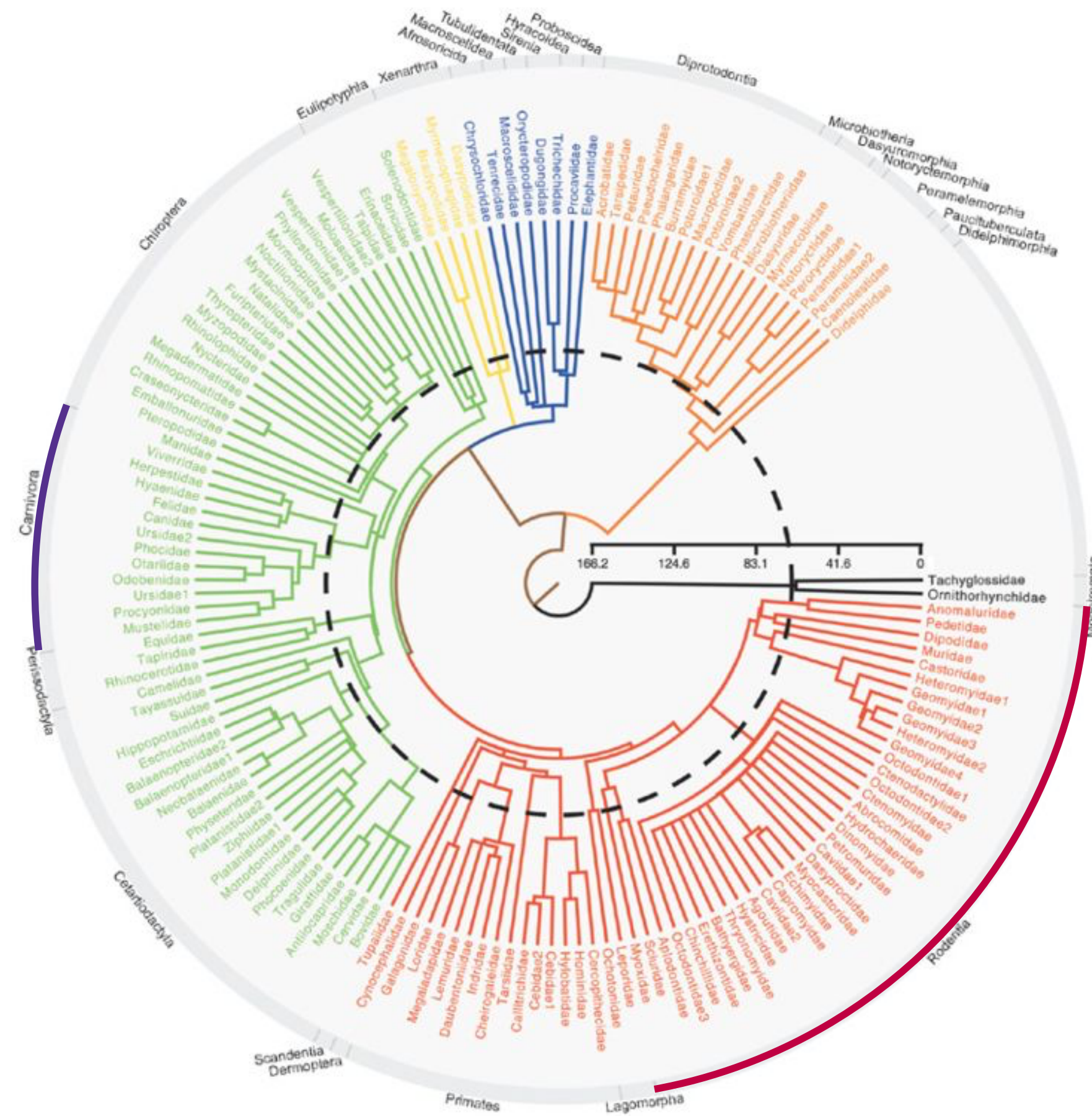
Parameters:

λ – birth rate

μ – death rate

ρ – extant species sampling probability

Rate heterogeneity in evolution

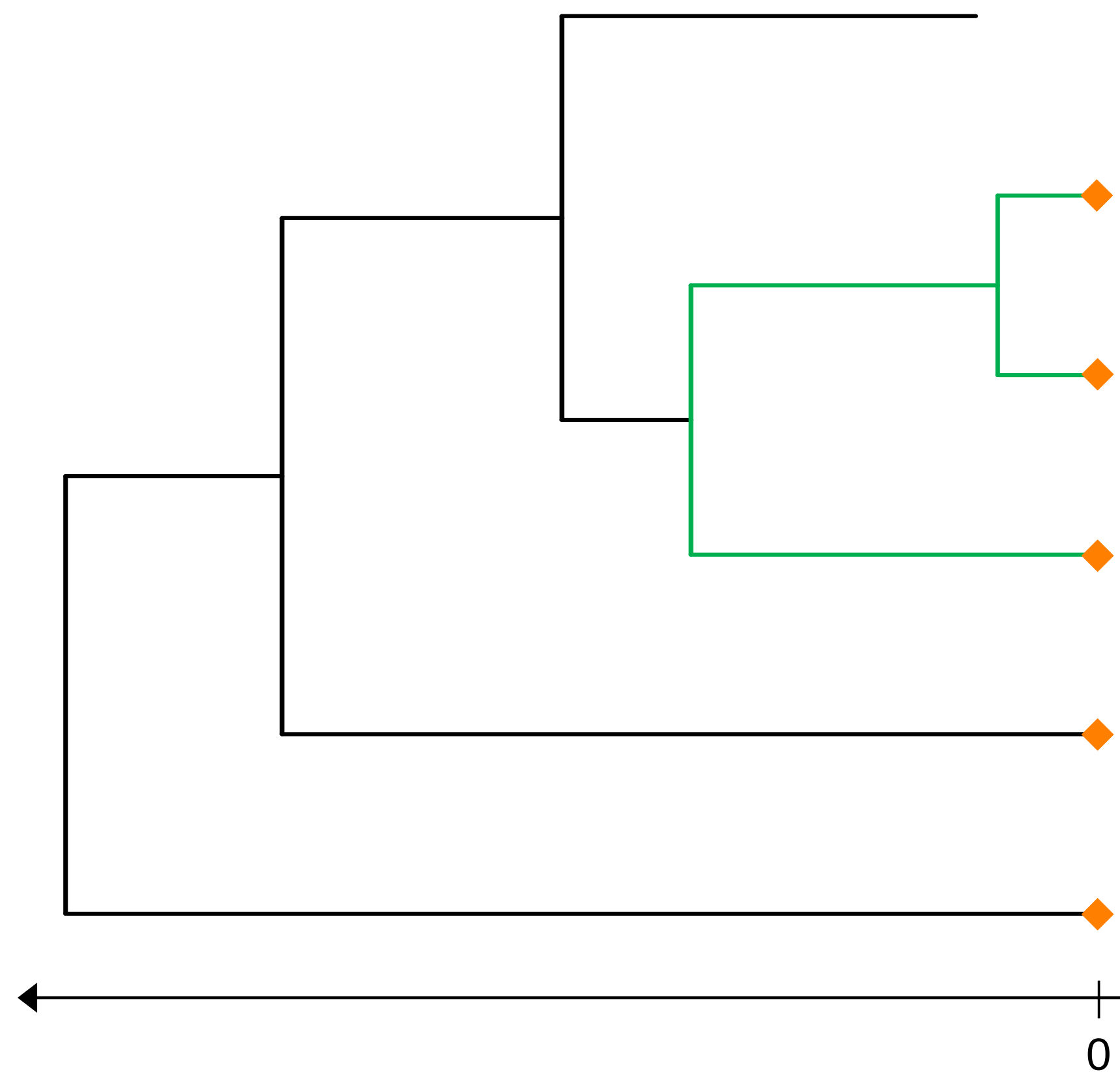


Bininda-Emonds *et al.* Nature 2007

Size discrepancies across clades are evidence of variations in evolutionary processes

Many traits are proposed to drive variation: e.g., body size, mating systems, environment

Multi-type birth-death (MTBD) process



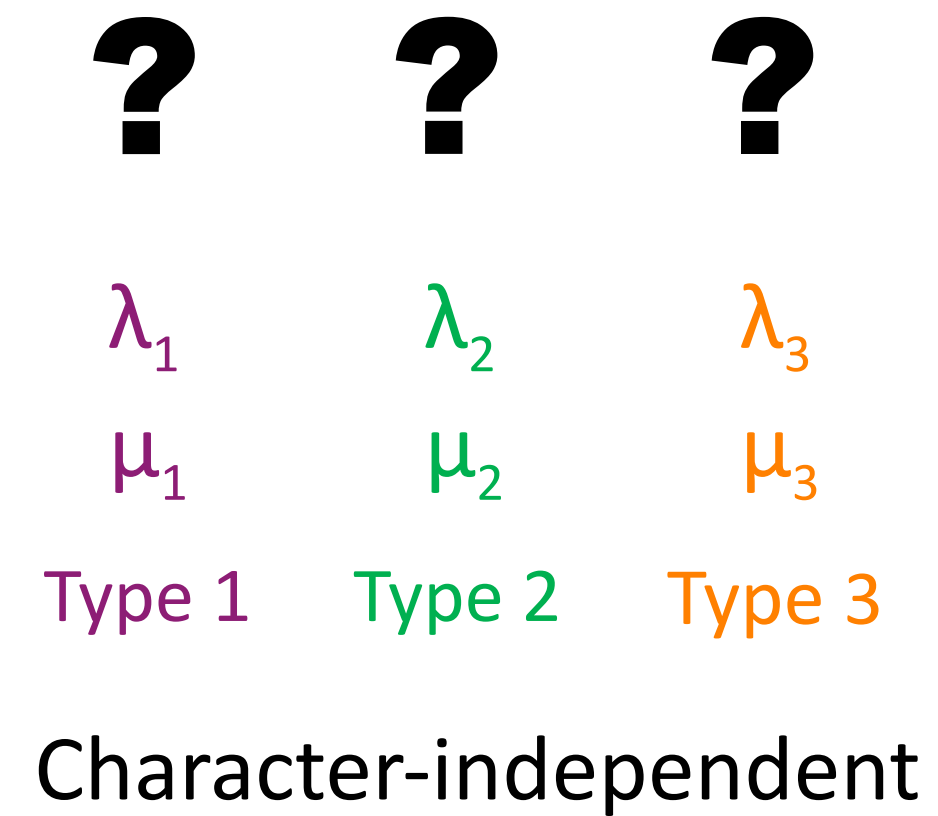
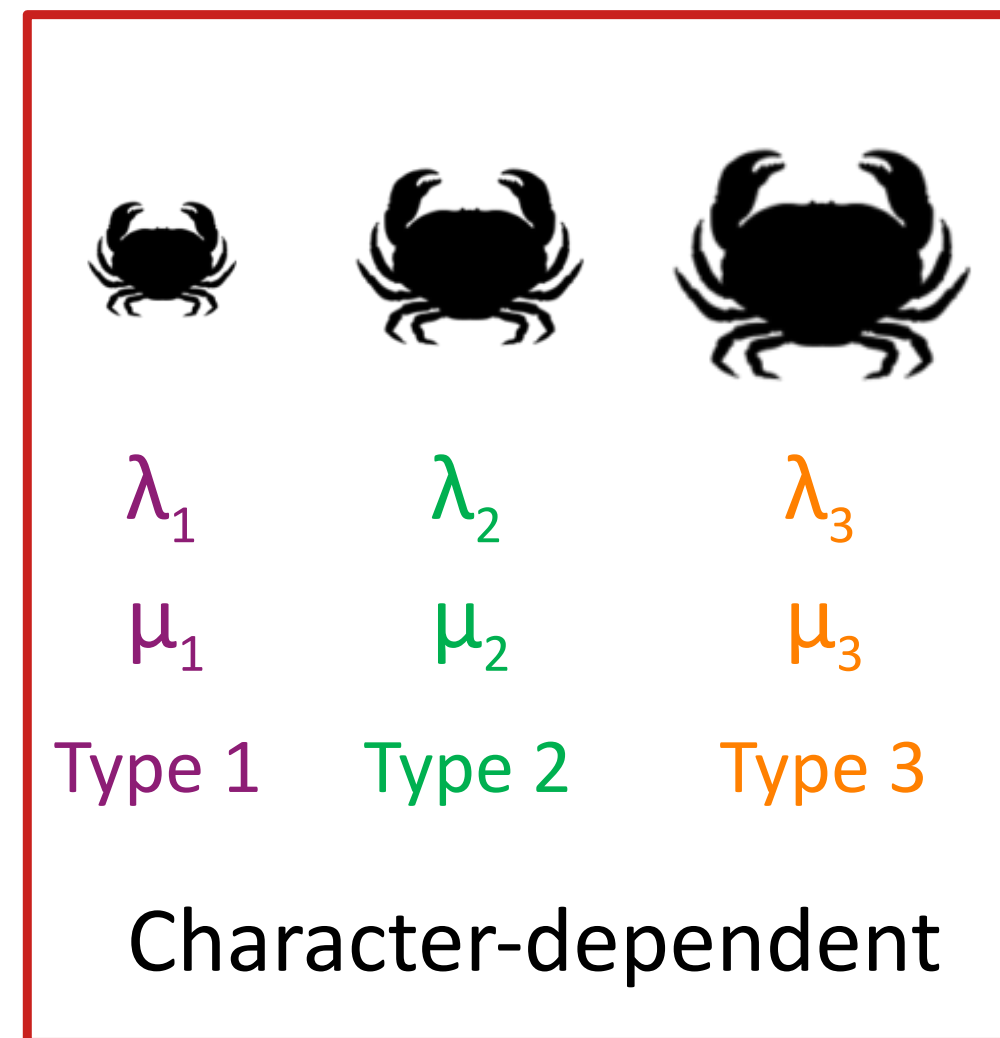
2 types, type 1 & **type 2**

λ_1 & λ_2 – birth rates

μ_1 & μ_2 – death rates

ρ – extant species sampling probability

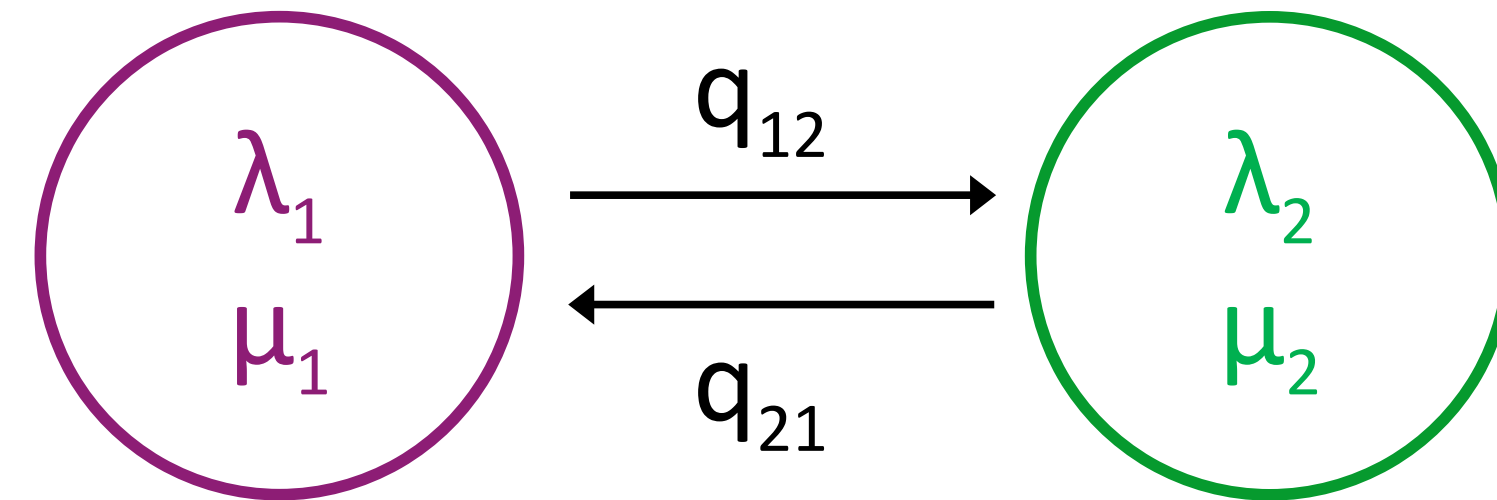
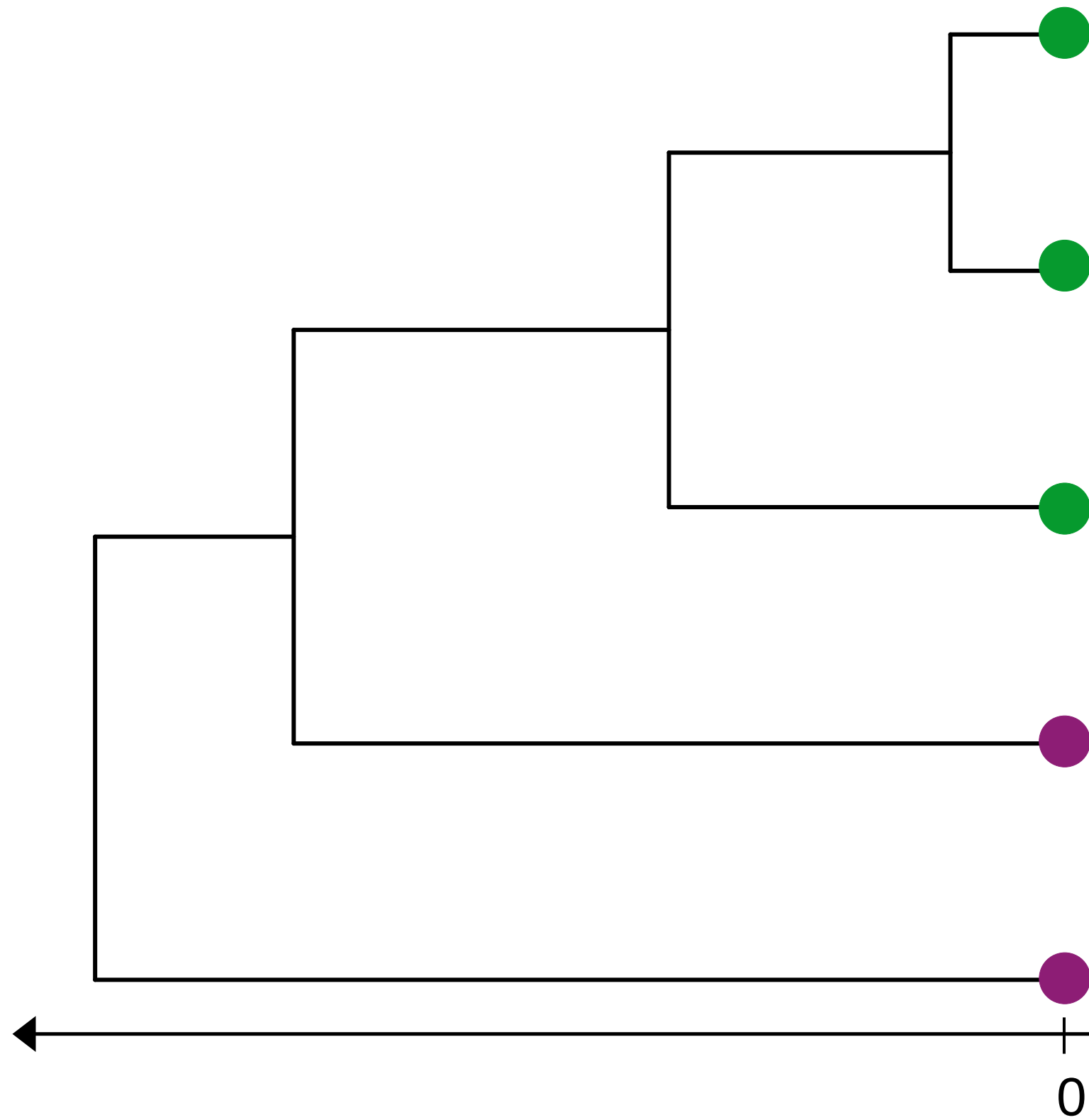
Character-dependent or independent?



In a character-dependent model:

The **number of types** is known and the **type at the tips** is known

The BiSSE/MuSSE/BDMM model



Parameters of the model:

λ_i – birth rates

μ_i – death rates

q_{ij} – transition rates

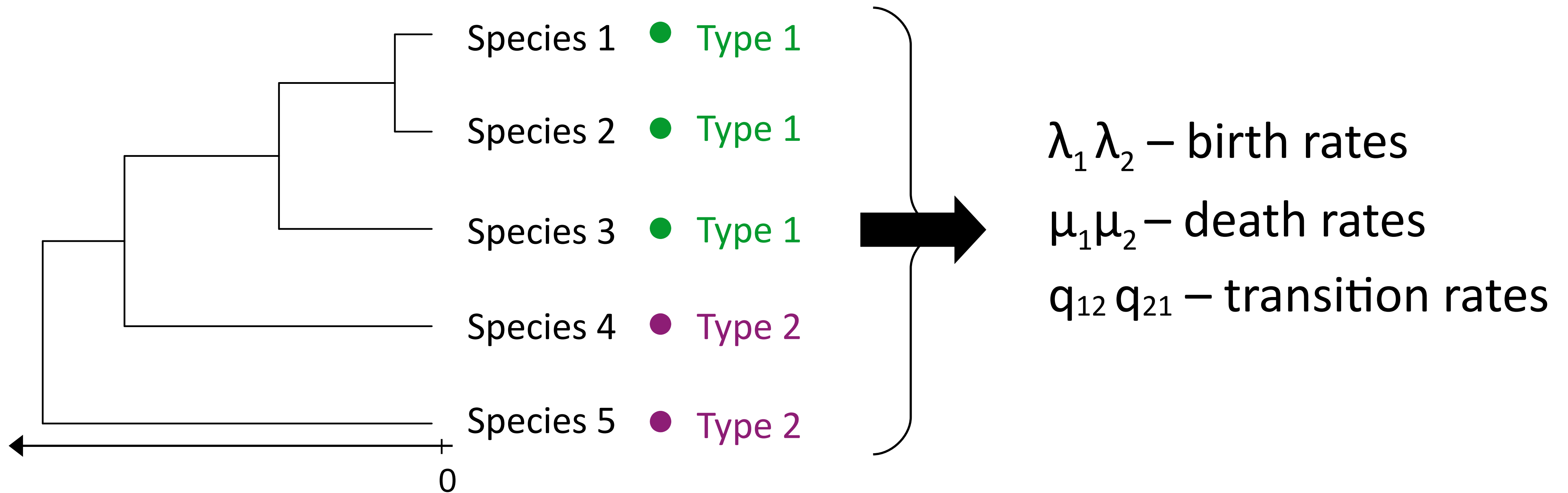
ρ/p – sampling probability

Maddison *et al.* **Sys. Bio.** 2007

Fitzjohn *et al.* **Sys. Bio.** 2009

Kühnert *et al.* **MBE** 2016

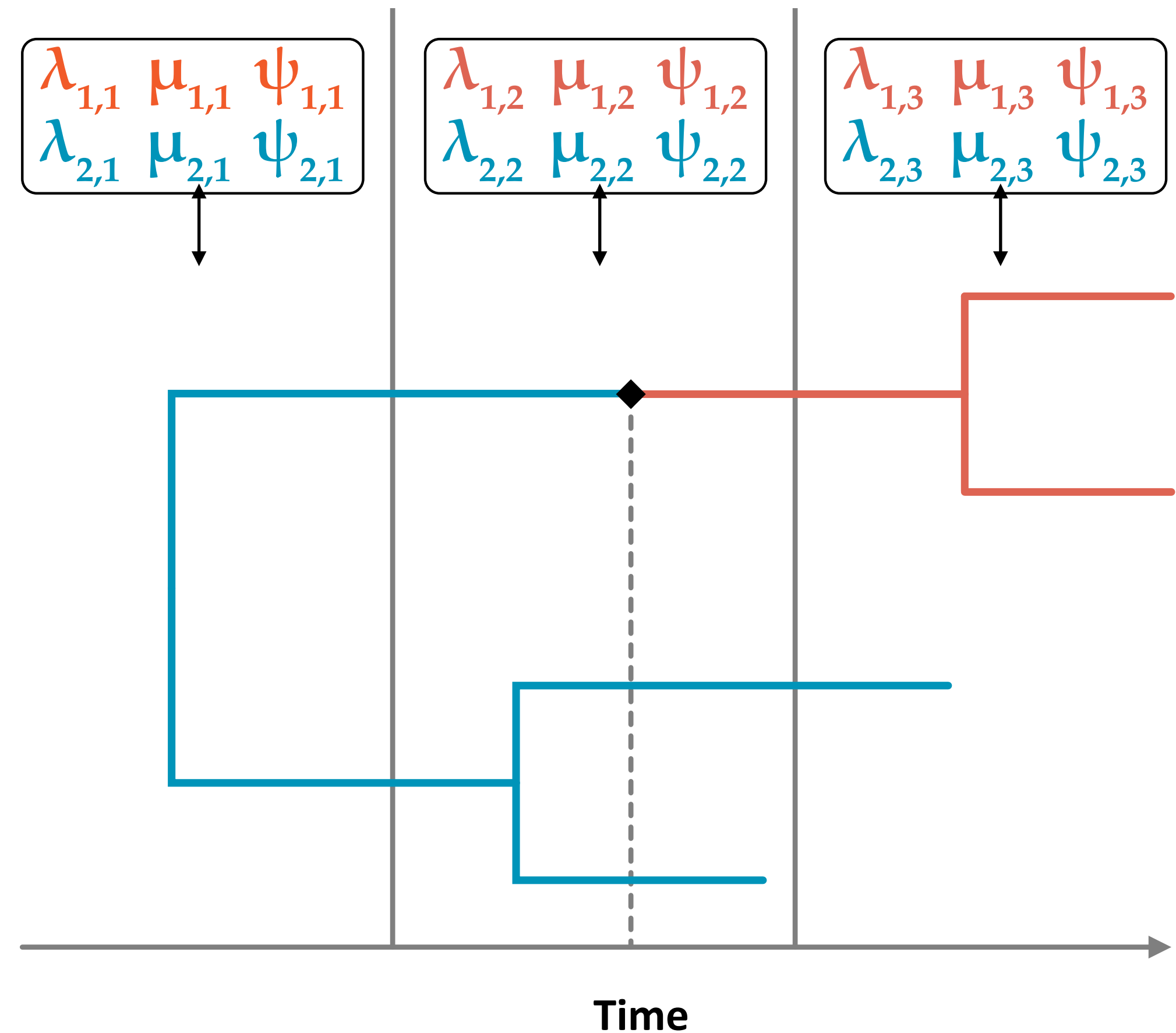
SSE/BDMM inference



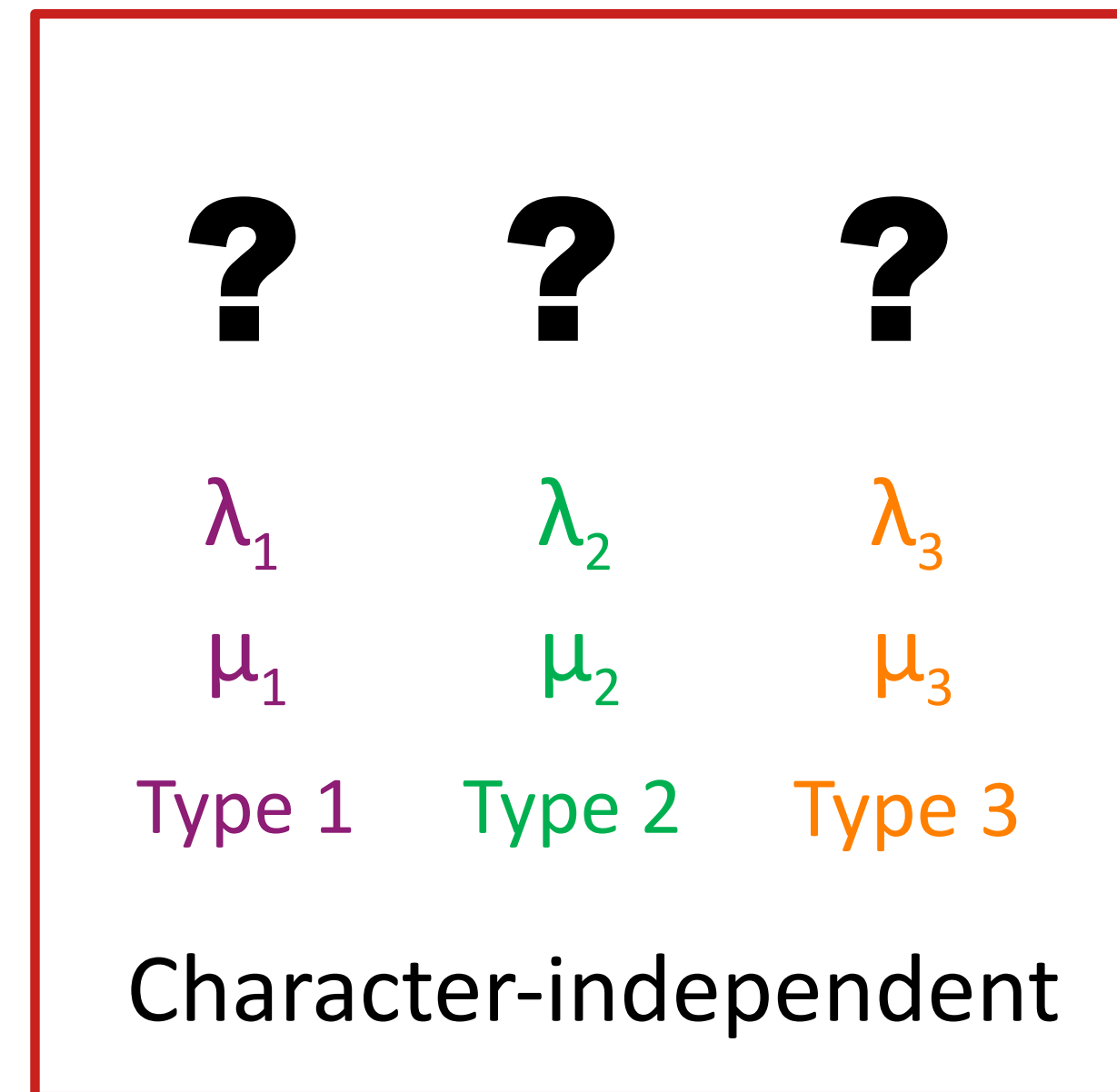
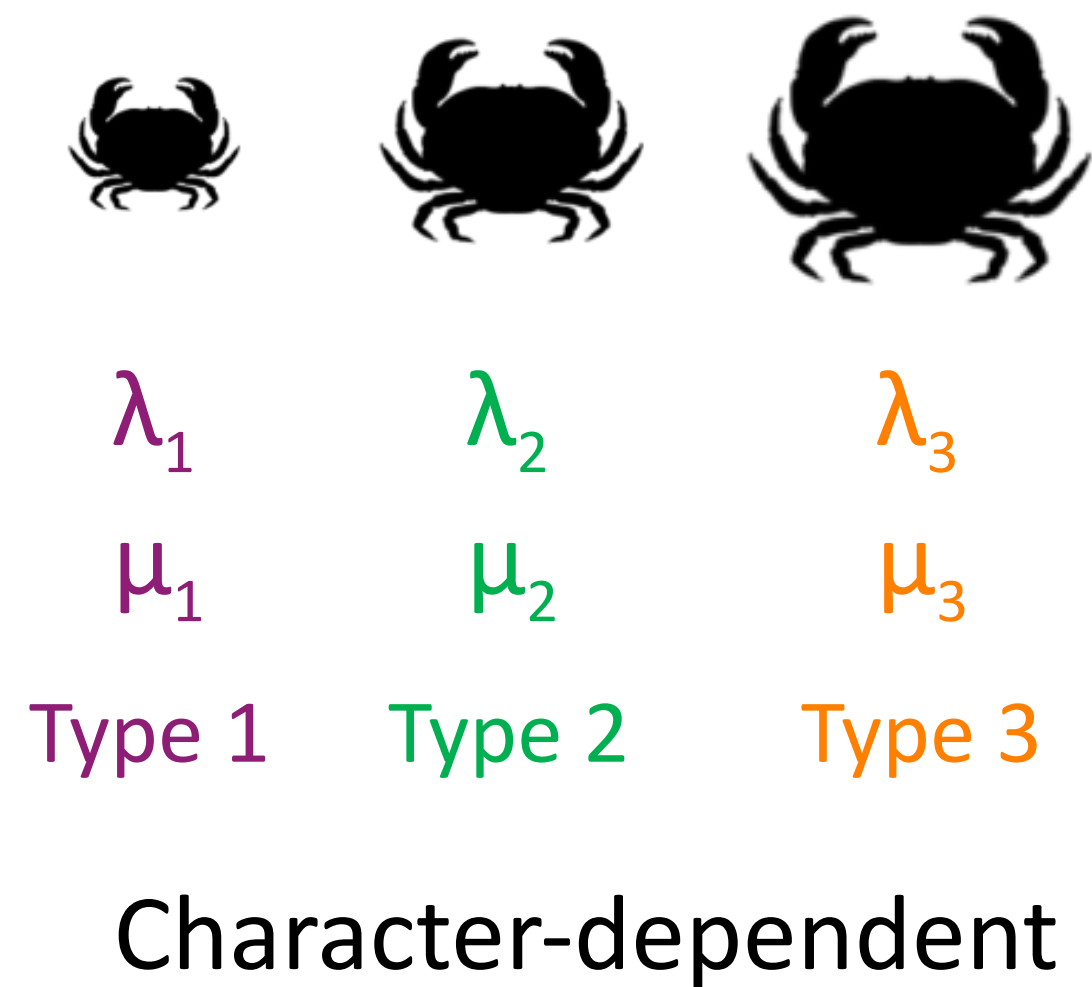
BDMM extensions

Integration with the skyline model: piecewise-constant rates per type

More next week



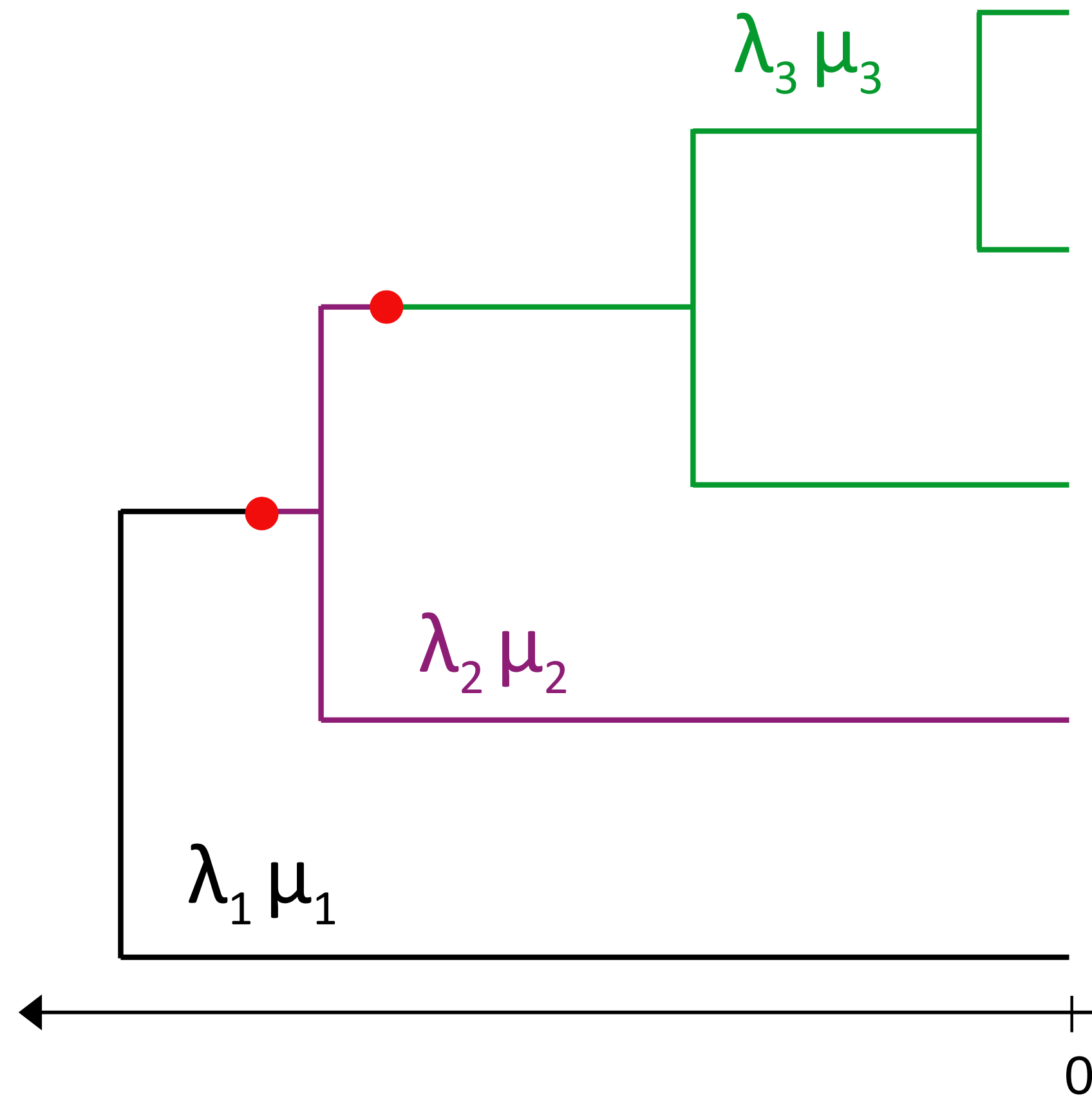
Character-dependent or independent?



In a character-independent model:

The **number of types** and the **type at the tips** is unknown

BAMM/MSBD model



Character-independent version of SSE

New estimated parameters:

N total number of types

Types of edges and tips

Rabosky *et al.* *Nat. Comm.* 2013
Barido-Sottani *et al.* *Sys. Bio.* 2020

Exercise

- input: time-calibrated phylogeny of 284 species of hummingbirds
- no phylogenetic character data
- the tree is fixed in this analysis

