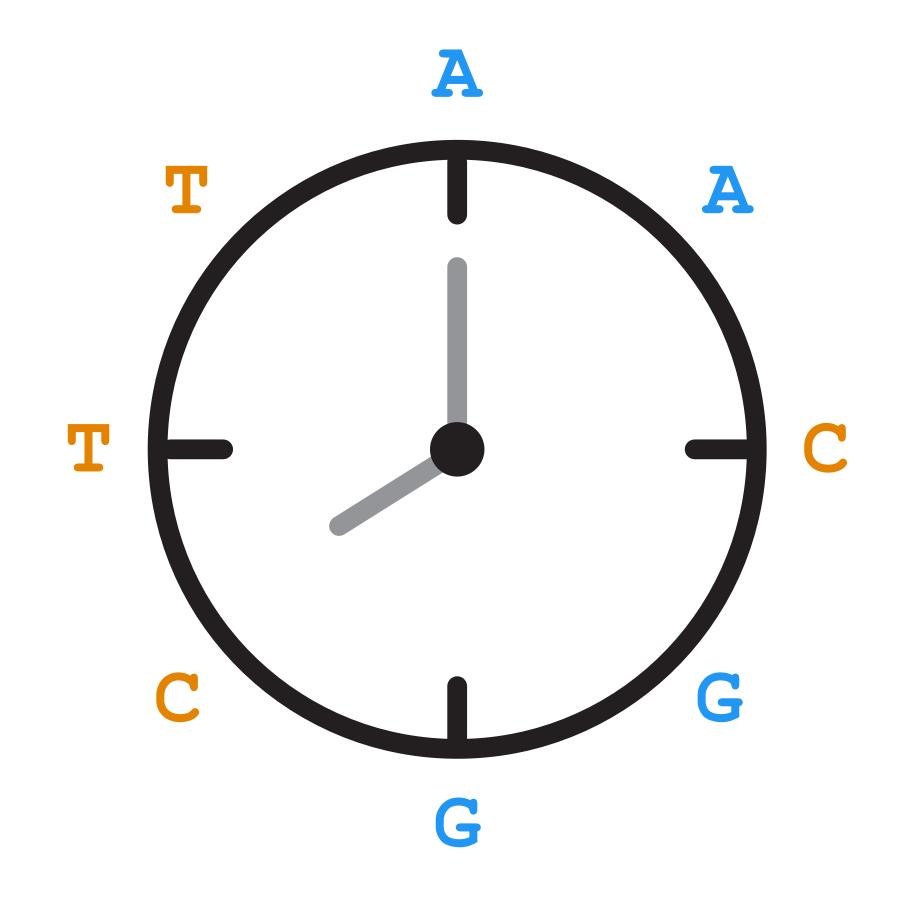
Phylogenetics Introduction to BEAST2 RL-V3 MPP

Rachel Warnock 17.06.25



Today's objectives

- Intro to BEAST2
- Node dating using BEAST2

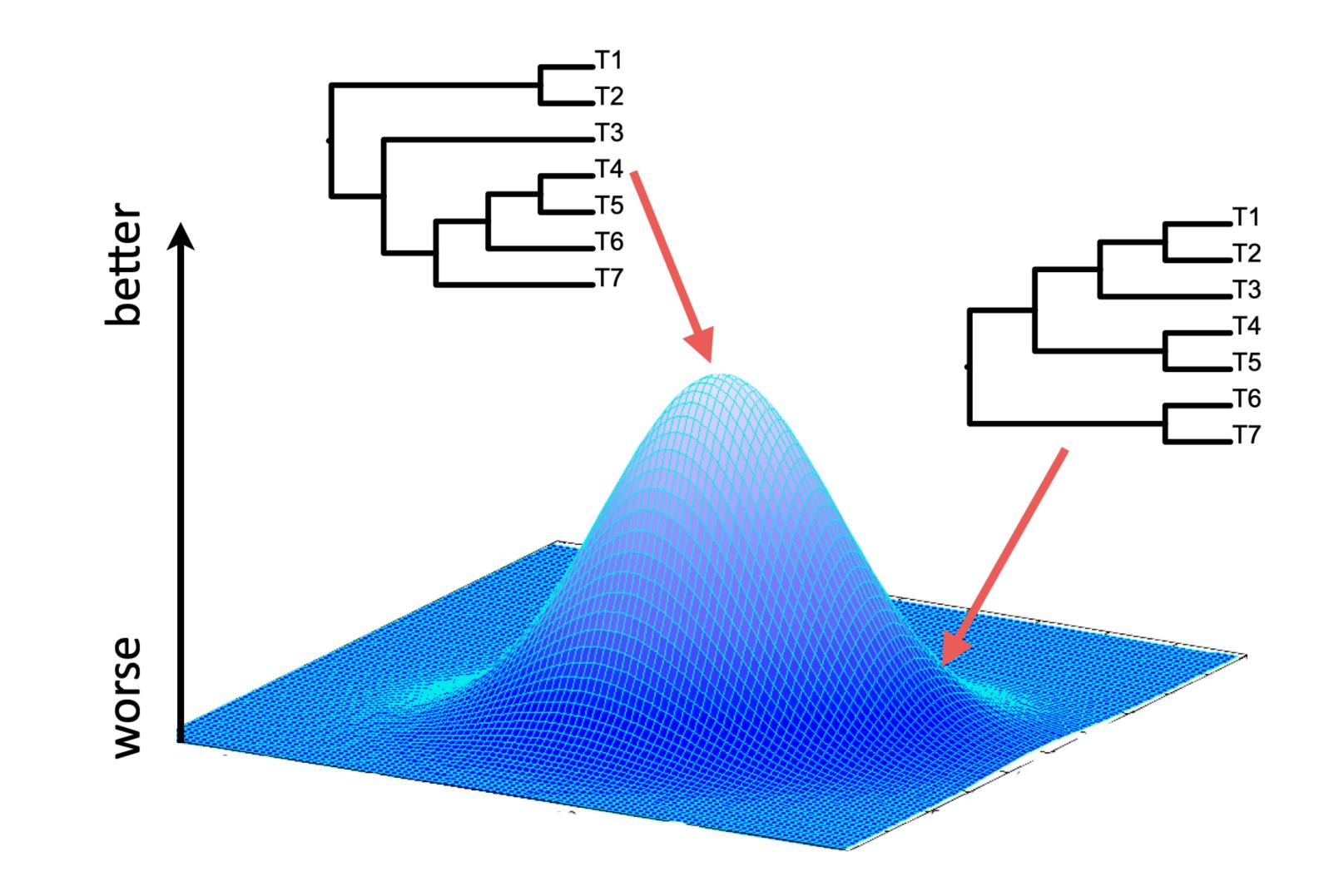




Recap



How do we find the 'best' tree?







It depends how you measure 'best'

Method	Criterion (tree s			
Maximum parsimony	Minimum numb			
Maximum likelihood	Likelihood score and model para			
Bayesian inference	Posterior proba model parameter			

Both maximum likelihood and Bayesian inference are model-based approaches

Note these are not the only approaches to tree-building but they are the most widely used

score)

ber of changes

re (probability), optimised over branch lengths

ameters

ability, integrating over branch lengths and ters



Bayesian divergence time estimation



We use a Bayesian framework priors likelihood P(data | model) P(model)



P(model | data) =



P(data)

marginal probability of the data



Bayesian divergence time estimation

The data

and / or

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

phylogenetics sample characters ages

Understanding the tripartite approach to Bayesian divergence time estimation Warnock, Wright. (2020) 8





Bayesian divergence time estimation

The data

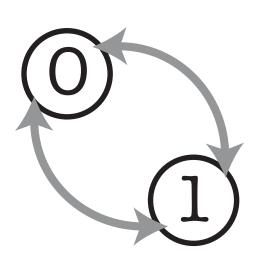
and / or

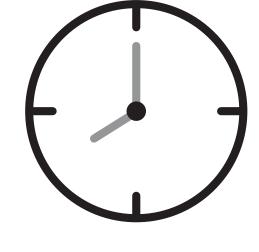
0101... ATTG... 1101... TTGC... 0100... ATTC...

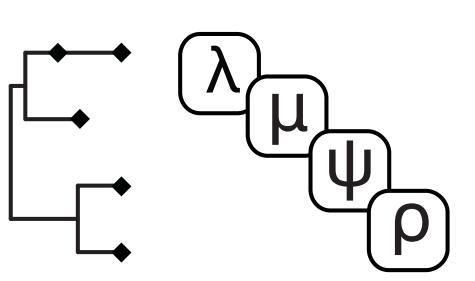
phylogenetics sample characters ages

substitution model

3 model components







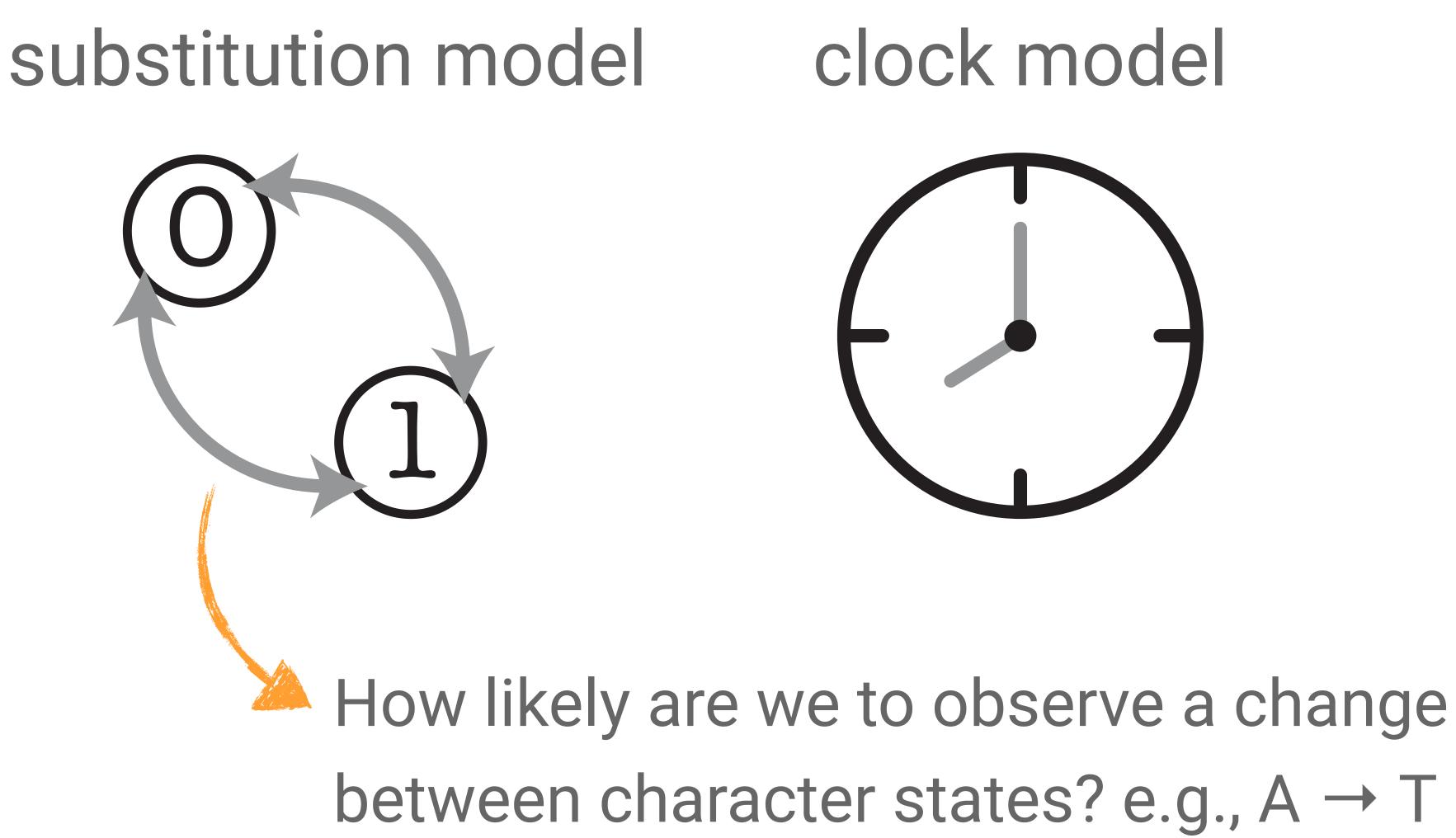
clock model

tree and tree model

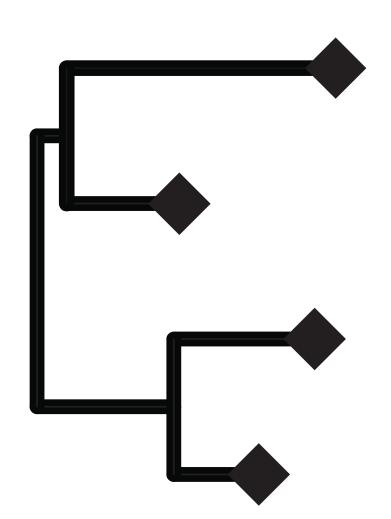
Understanding the tripartite approach to Bayesian divergence time estimation Warnock, Wright. (2020) 9





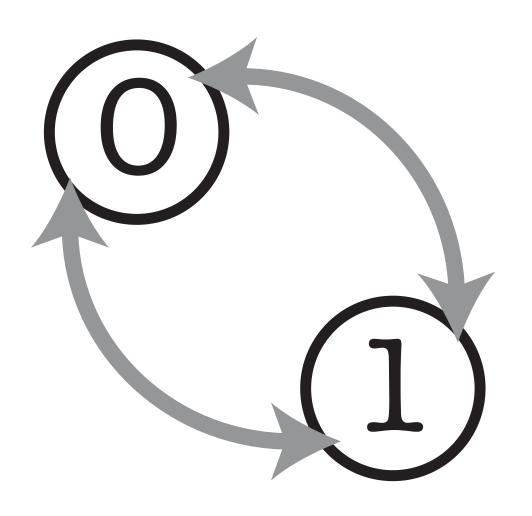


tree model





substitution model

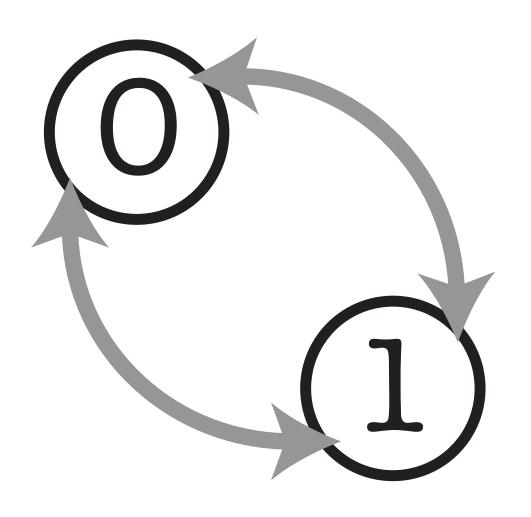


How have rates of evolution varied (or not) across the tree?

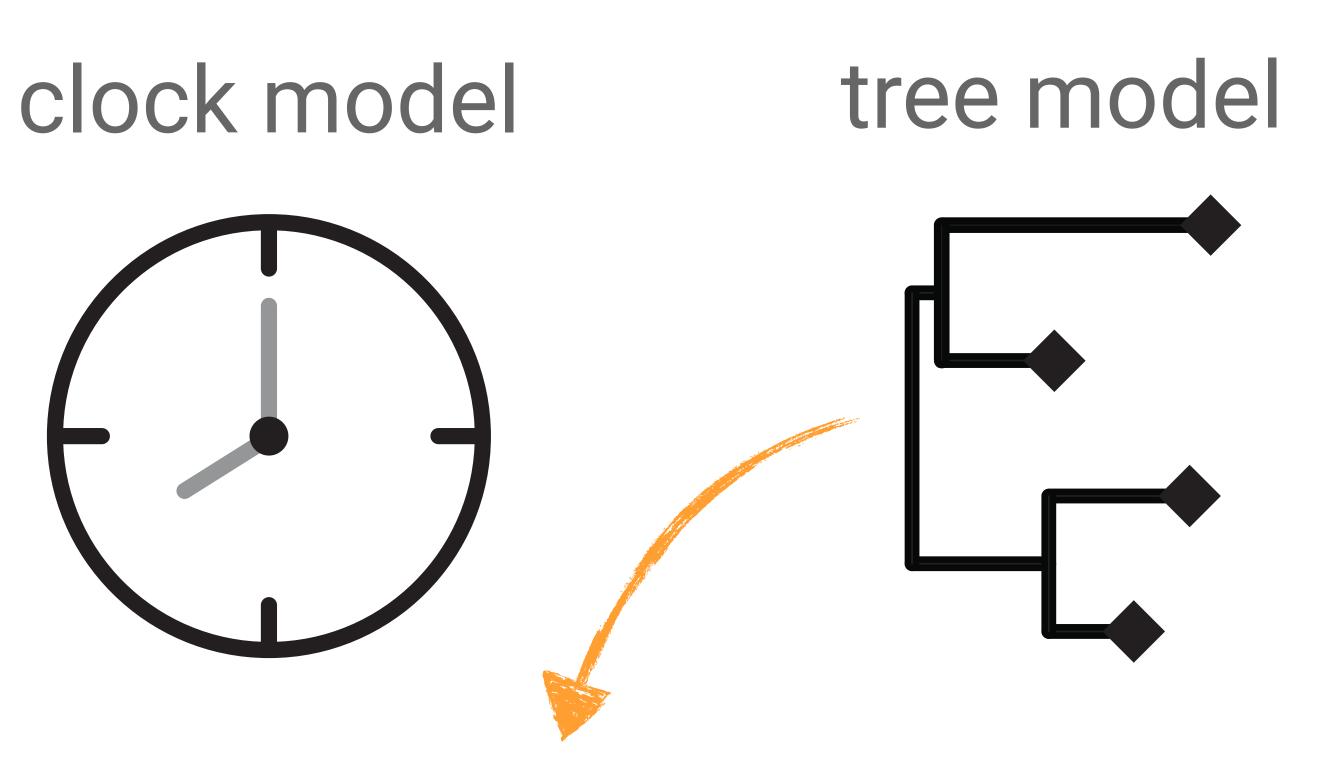
tree model clock model

11

substitution model



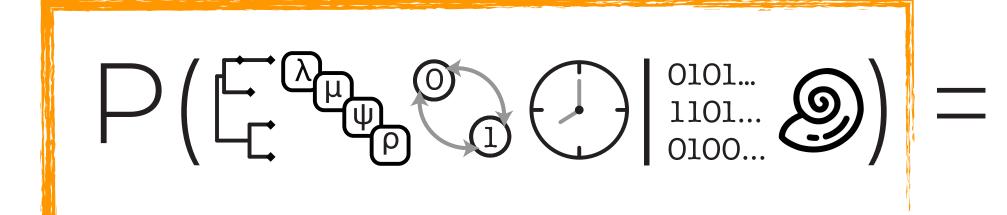
How have species originated, gone extinct and been sampled through time?



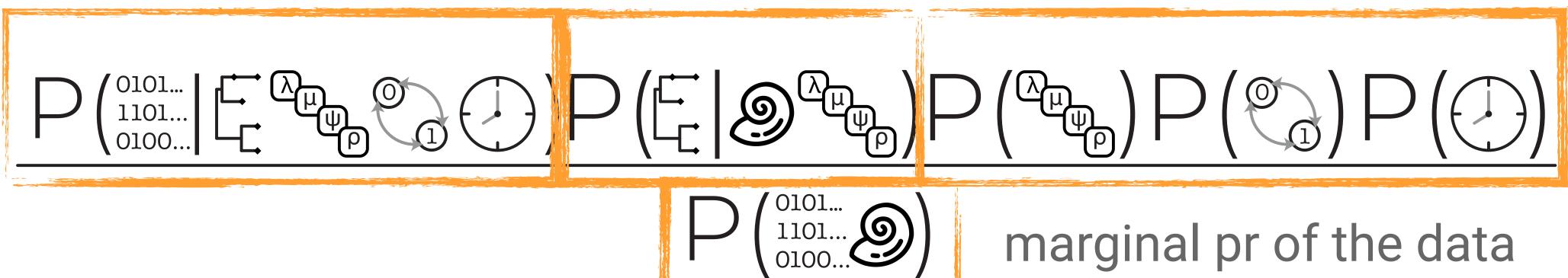


Bayesian divergence time estimation

posterior



likelihood



probability of the time tree

priors



RevBayes

Designed with extendability and flexibility in mind

Rev language, similar to R, and uses a graphical modelling framework

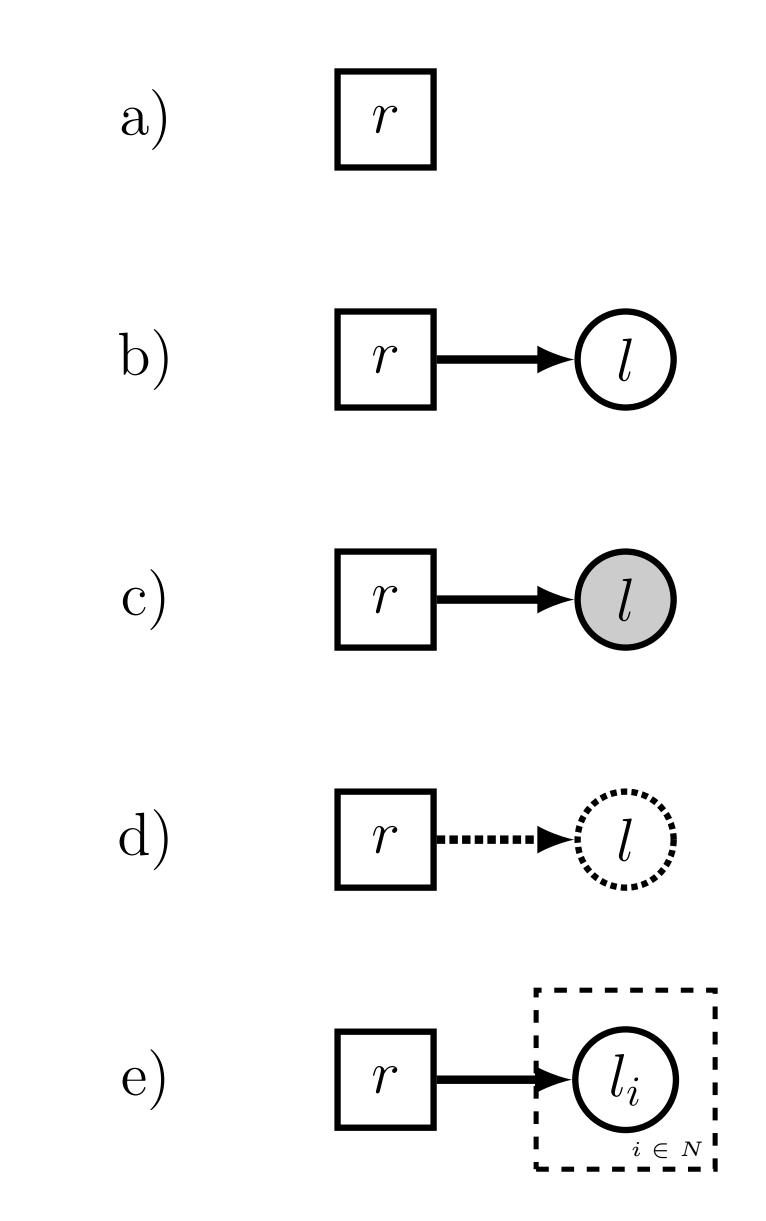
Developed and supported by a large international team of developers

revbayes.github.io





14



```
# constant node
r <- 10</pre>
```

```
# stochastic node 1 \sim dnExp(r)
```

```
# stochastic node (observed)
1.clamp(0.1)
```

```
# deterministic node
l := exp(r)
```

Intro to BEAST2



BEAST2

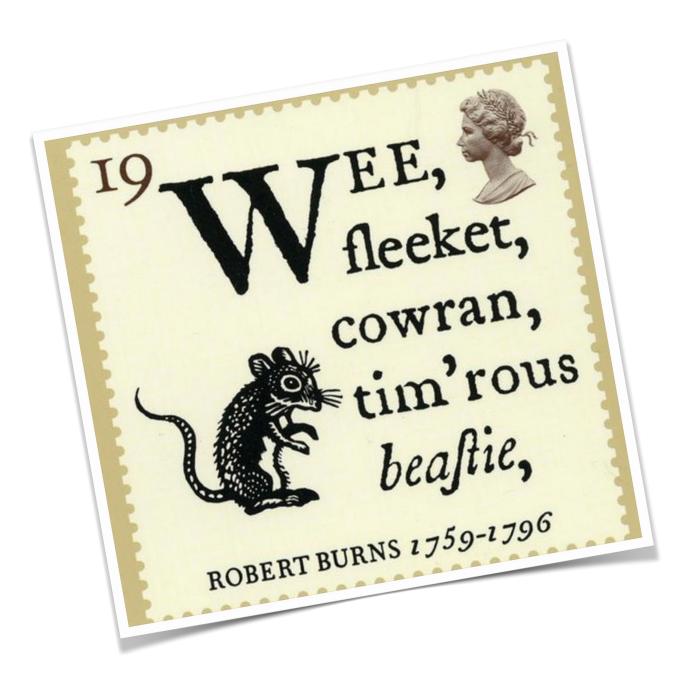
Also designed with extendability and flexibility in mind

Also developed and supported by a large international team of developers

Has a suite of apps that can used to generate input files and analysis the output

www.beast2.org

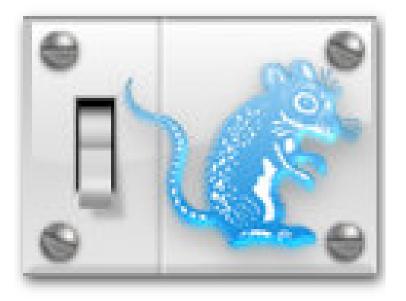




<u>Scots poem</u> - also the <u>BEAST2</u> logo!



BEAST2 toolkit and work flow



Step 1. generate the xml file in **BEAUti**

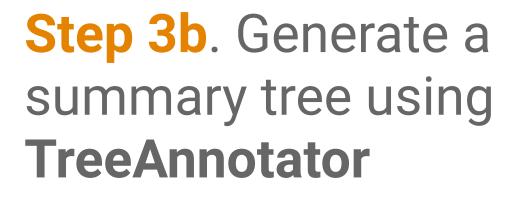


Step 2. run your analysis in **BEAST**



Step 3a. Examine you log files using Tracer





Step... any other downstream analysis



Step 4. Examine your summary tree in **FigTree**







BEAST2 input: the XML file

	••	•	\leftarrow \rightarrow \bigcirc Search
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117 117 118 118 119			

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popSize">1.0</parameter>

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L.InitializedTraitSet" traitname="type" value="EU856841_HongKong

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Caveat: if you want to use an option not available in BEAUti you have to learn how to edit the XML

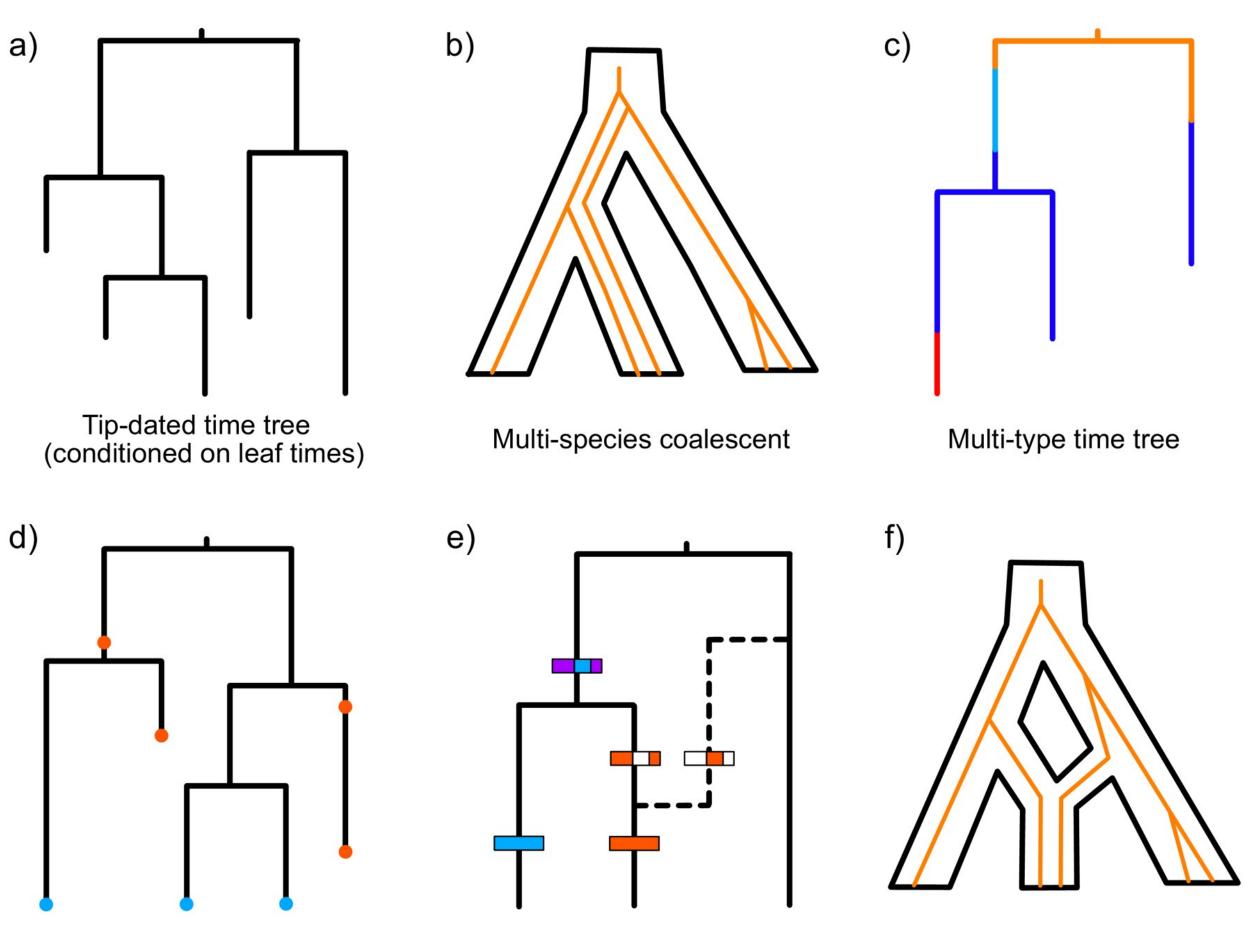


19



A wide range of models and tree structures

Note all tree models in BEAST2 incorporate a temporal component



Sampled ancestor time tree

Ancestral gene conversion graph

Species network with embedded gene tree

Bouckaert et al. (2019) PLOS Comp Bio 20





$\bullet \bullet \bullet \bullet$ $\blacksquare \lor \checkmark$

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Taming the BEAST news workshop

≪> All 음 Beginner

Introduction to BEAST2

This is a simple introductory tutorial to help you get started with using BEAST2 and its accomplices.

Jūlija Pečerska , Veronika Bošková and Louis du Plessis Updated 23 May 2025 by jugne

Skyline plots

Inference of past population dynamics using Bayesian Coalescent Skyline and Birth-Death Skyline plots.

Nicola F. Müller and Louis du Plessis Updated 11 Jun 2024 by tgvaughan

Troubleshooting convergence

issues

Post-processing and improving performance

David A. Rasmussen Updated 14 Apr 2025 by bjoelle

If you found Taming the BEAST helpful in designing your research

Joëlle Barido-Sottani, Veronika Bošková, Louis du Plessis, Denise Kühnert, Carsten Magnus, Venelin Mitov, Nicola F. Müller, Jūlija Pečerska, David A. Rasmussen, Chi Zhang, Alexei J. Drummond, Tracy A. Heath, Oliver G. Pybus, Timothy G. Vaughan, Tanja Stadler (2018). Taming the BEAST – A community teaching material resource for BEAST 2. Systematic Biology, 67(1), 170–-174. doi: 10.1093/sysbio/syx060

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Time-stamped

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Language Phylogenies Using Babel to analyse linguistic data Simon J. Greenhill and Konstantin Hoffmann Updated 29 Jul 2019 by KonstantinHoffmann	Prior selection Prior selection and clock calibration using Influenza A data. Veronika Bošková , Venelin Mitov and Louis du Plessis Updated 23 May 2025 by jugne			
Time-stamped data Remco Bouckaert , Walter Xie , Fábio K. Mendes and and Alexei Drummond Updated 9 Jun 2024 by walterxie	<section-header><section-header><section-header></section-header></section-header></section-header>			
g your research, please cite the following paper:				

https://taming-the-beast.org/

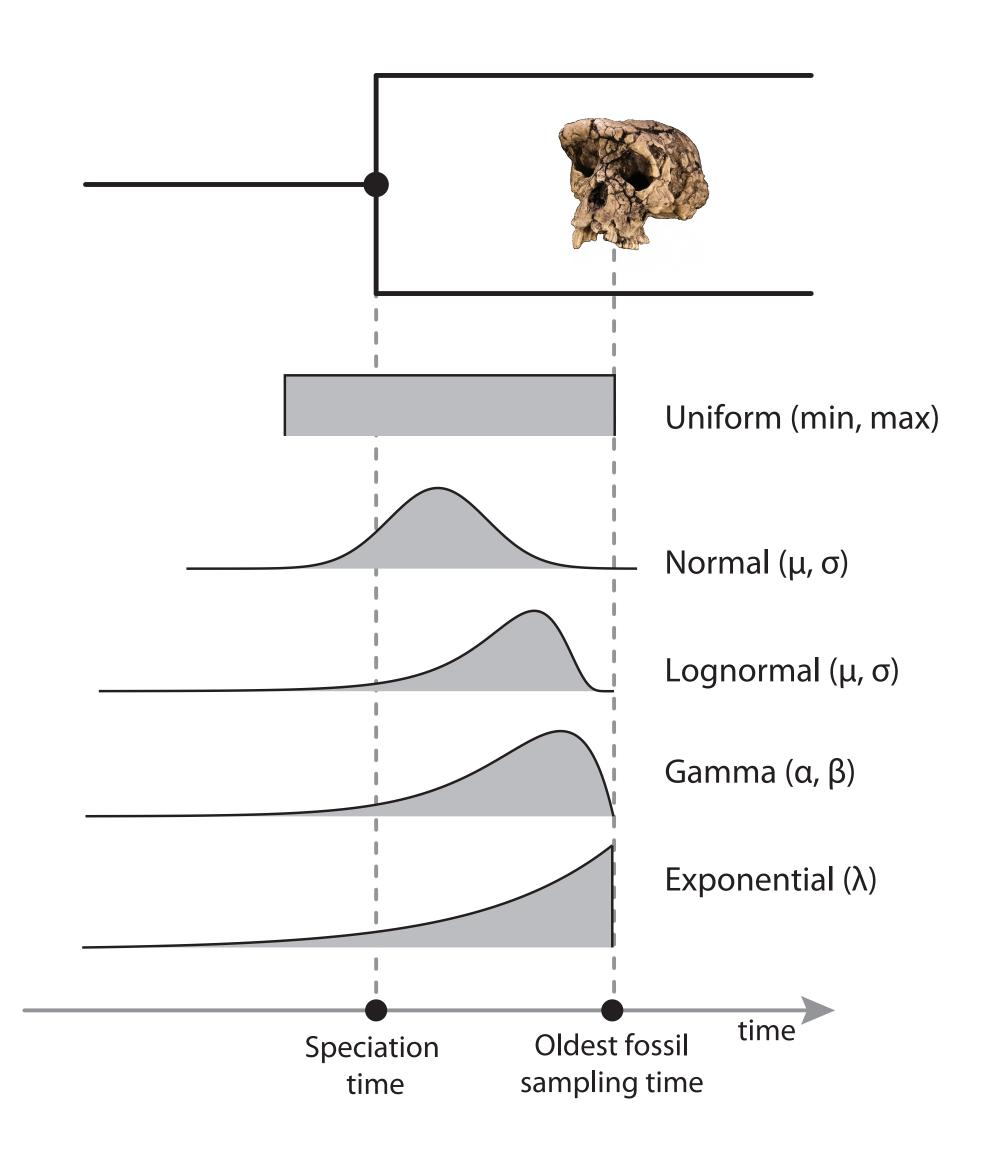


Recap: node dating





Node dating



We can use a calibration density to constrain internal node ages

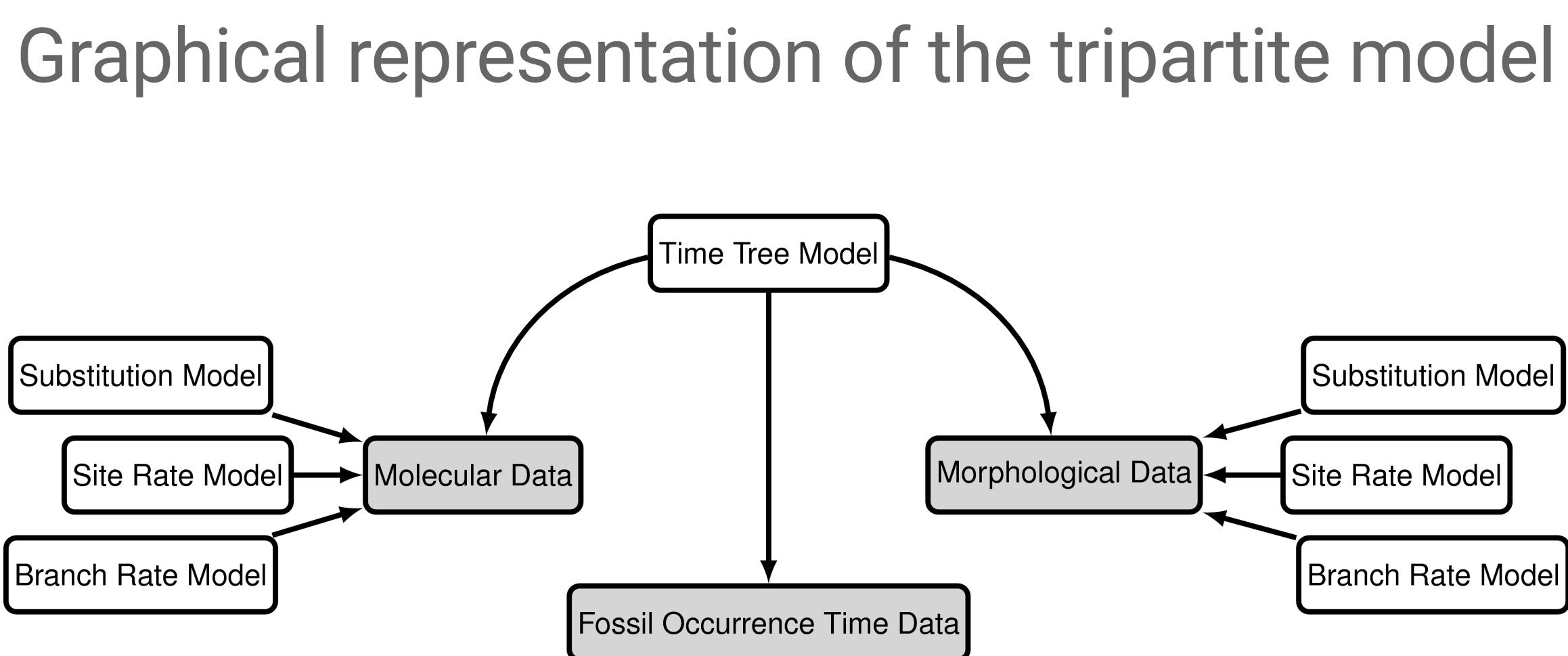
We typically use a birth-death process model to describe the tree generating process

Adapted from *Heath* (2012) Sys Bio





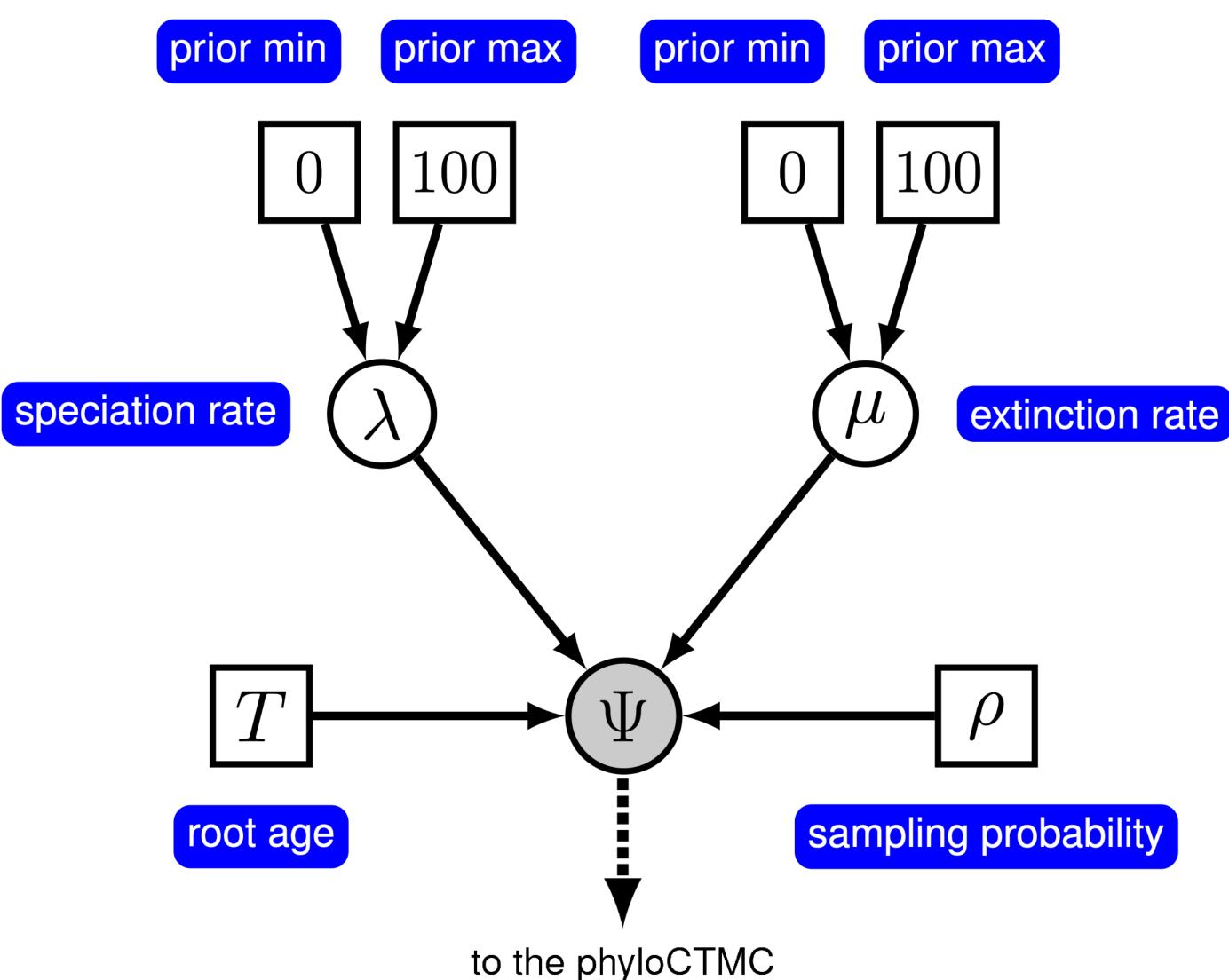






Graphical representation of the birthdeath process









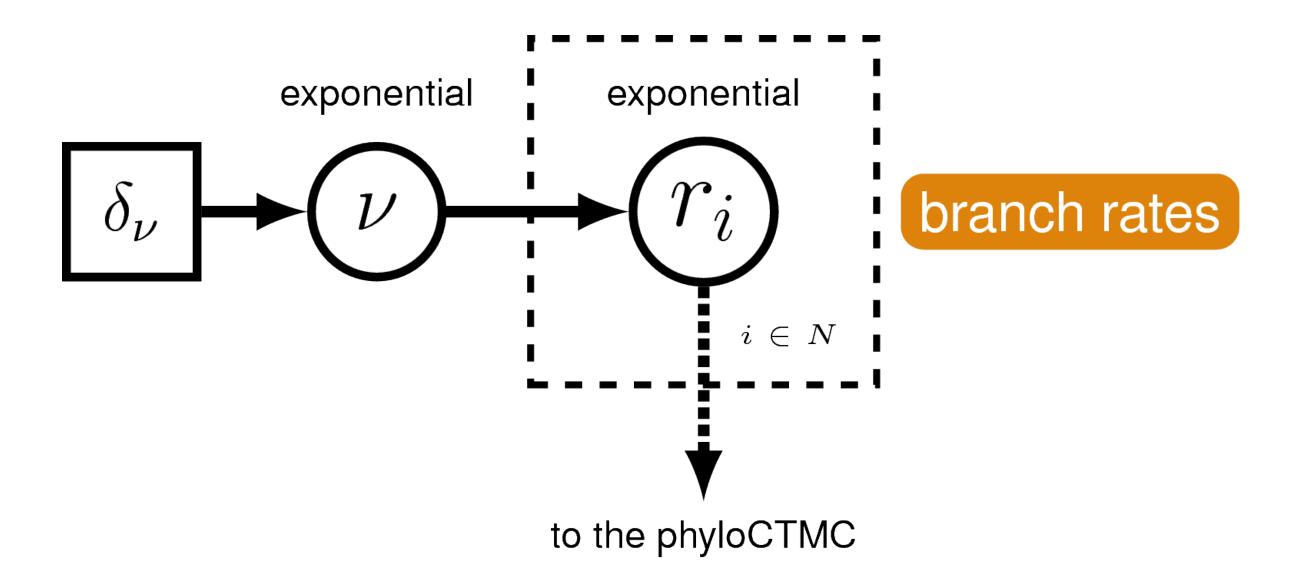
Graphical models: relaxed clock model



- b) Stochastic node
- c) Deterministic node
- **d**) (
- d) Clamped node (observed)



e) Plate











Scenario

Node dating with large datasets

If want (or have to) fix the tree topology

If fossil sampling is sparse or complex

If you have abundant fossil data, or are in topological position of fossils

If you're interested in the phylodynamic

If you want to use a specific model

	Software
	MCMCTree
	MCMCTree
	MCMCTree
interested in the	BEAST2, RevBayes
parameters	BEAST2, RevBayes
	BEAST2, RevBayes, MCMCTree





Recap



Pr(data | model) Pr(model)

Pr(model | data) =



Likelihood

Pr(model | data) =

The probability of the data given the model assumptions and parameter values

Pr(data | model) Pr(model)



Pr(data | model) Pr(model)

Pr(model | data) =

This represents our prior knowledge of the model parameters

Priors



Pr(data | model) Pr(model)

Pr(model | data) =



Pr(data)

Marginal probability

The probability of the data, given all possible parameter values. Can be thought of as a normalising constant



Reflects our combined knowledge based on the likelihood and the priors

posterior

Pr(data | model) Pr(model)

Pr(model | data) =



Bayesian tree inference

posterior

P([0101... 1101... 0100...

