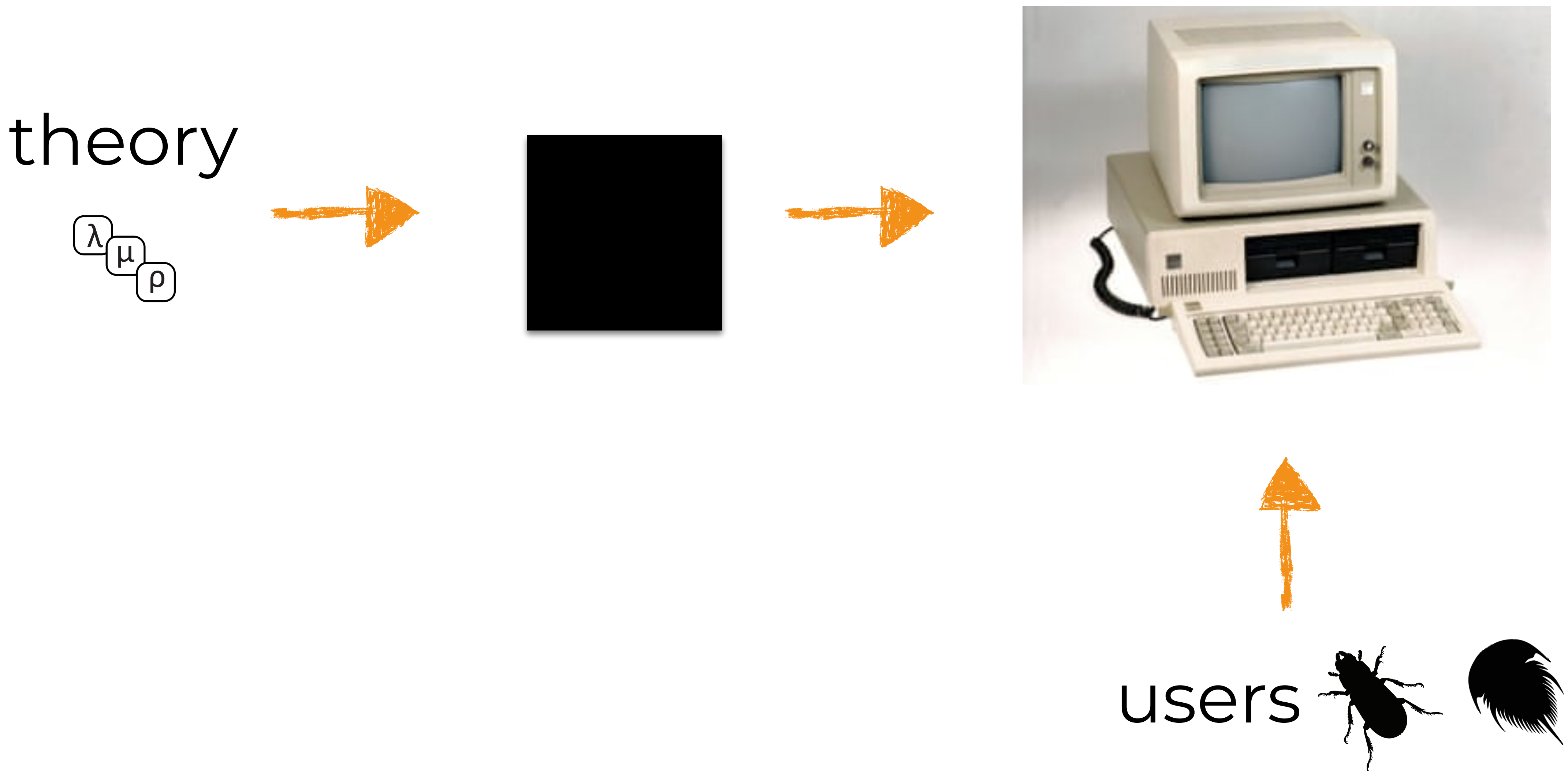
An introduction to graphical models and Bayesian phylogenetics using RevBayes

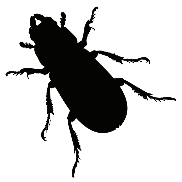
Phylogenetic inference — the old way



Phylogenetic inference — a better way?

theory

λ μ ρ

users  

Aims for RevBayes

General and flexible model specification

- Availability of (common) models
- Extendability

Easy to learn

- Well structured model specification
- Explicit models
- Documentation, examples and tutorials

Computational efficiency

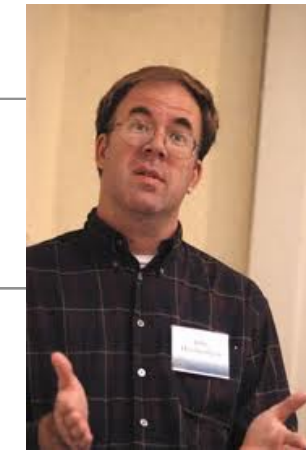
- Fast likelihood calculators
- Efficient (MCMC) algorithms

Höhna et al. 2016. Sys Bio

The RevBayes team

+ many others

Sebastian Höhna



John Huelsenbeck

Fredrik Ronquist

Tracy Heath

Michael Landis

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April Wright

Jeremy Brown

Bastien Boussau

Brian Moore

Mike May

Will Freyman

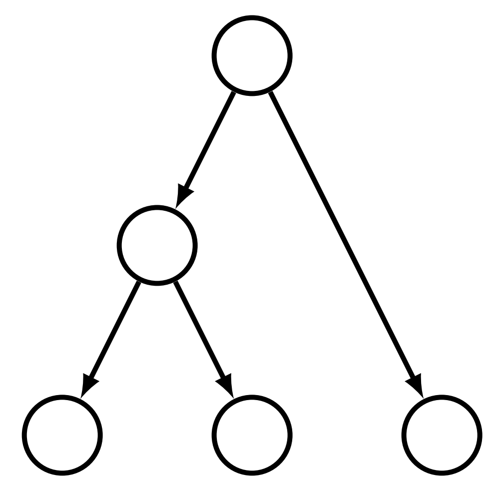
Wade Dismukes

Nicolas Lartillot

Graphical models

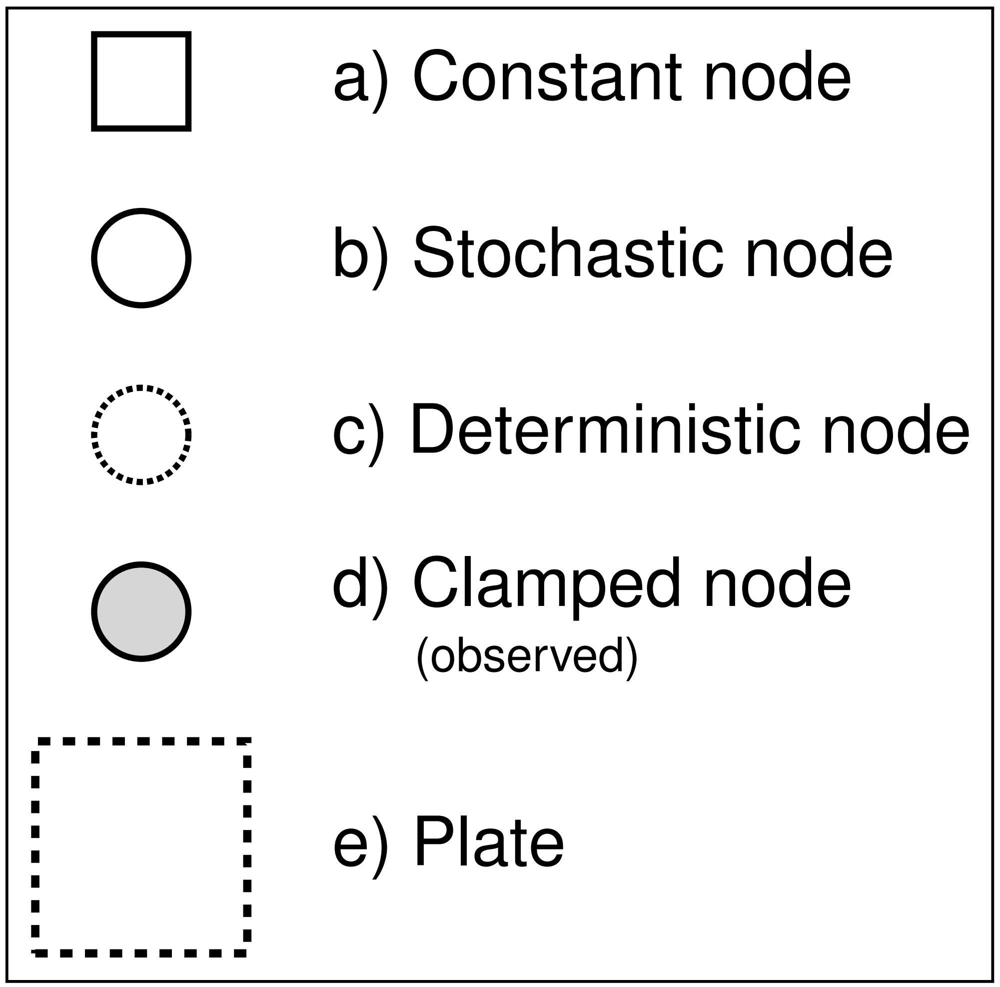
Graphical models provide tools for visually and computationally representing complex, parameter-rich probabilistic models

We can depict the conditional dependence structure of various parameters and other random variables



Höhna et al. 2014. Sys Bio

Graphical models — types of variables (nodes)



a) fixed-value variables

b) random variables that depend on other variables

c) variables determined by a specific function applied to another variable (transformations)

d) observed stochastic variables (data)

e) replication over a set of variables

Höhna et al. 2014. Sys Bio

Specifying graphical models using the Rev syntax

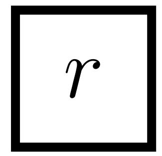
Table 1: `Rev` assignment operators, clamp function, and plate/loop syntax.

Operator	**Variable**
`<-`	constant variable
`~`	stochastic variable
`:=`	deterministic variable
`node.clamp(data)`	clamped variable
`=`	inference (*i.e.*, non-model) variable
`for(i in 1:N){...}`	plate

a) $\boxed{r}$

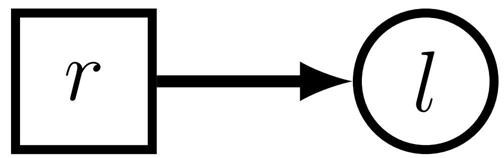
```
# constant node
r <- 10
```

a)

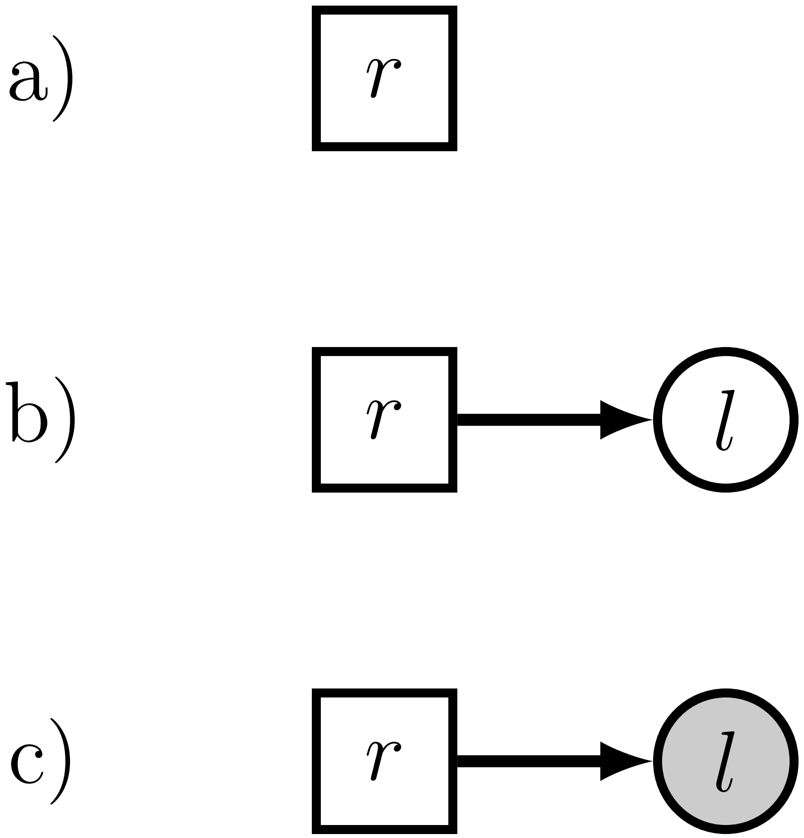



```
# constant node
r <- 10
```

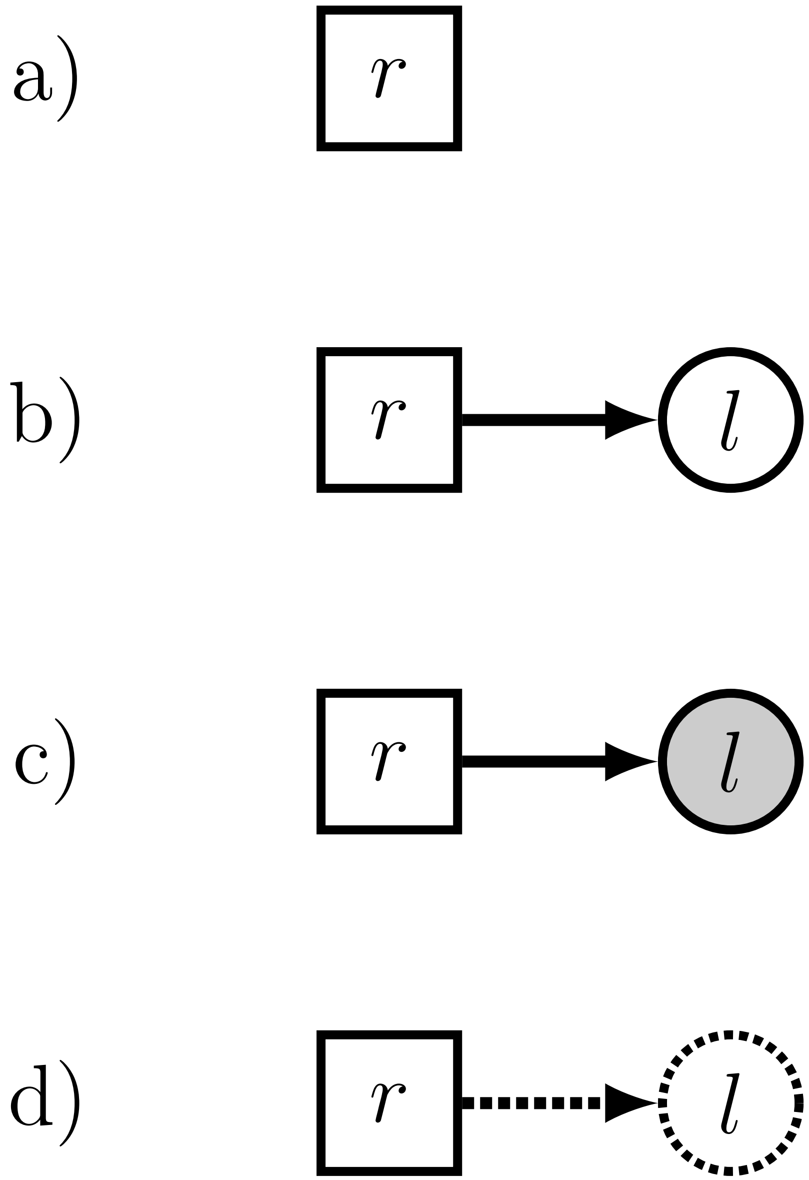
b)



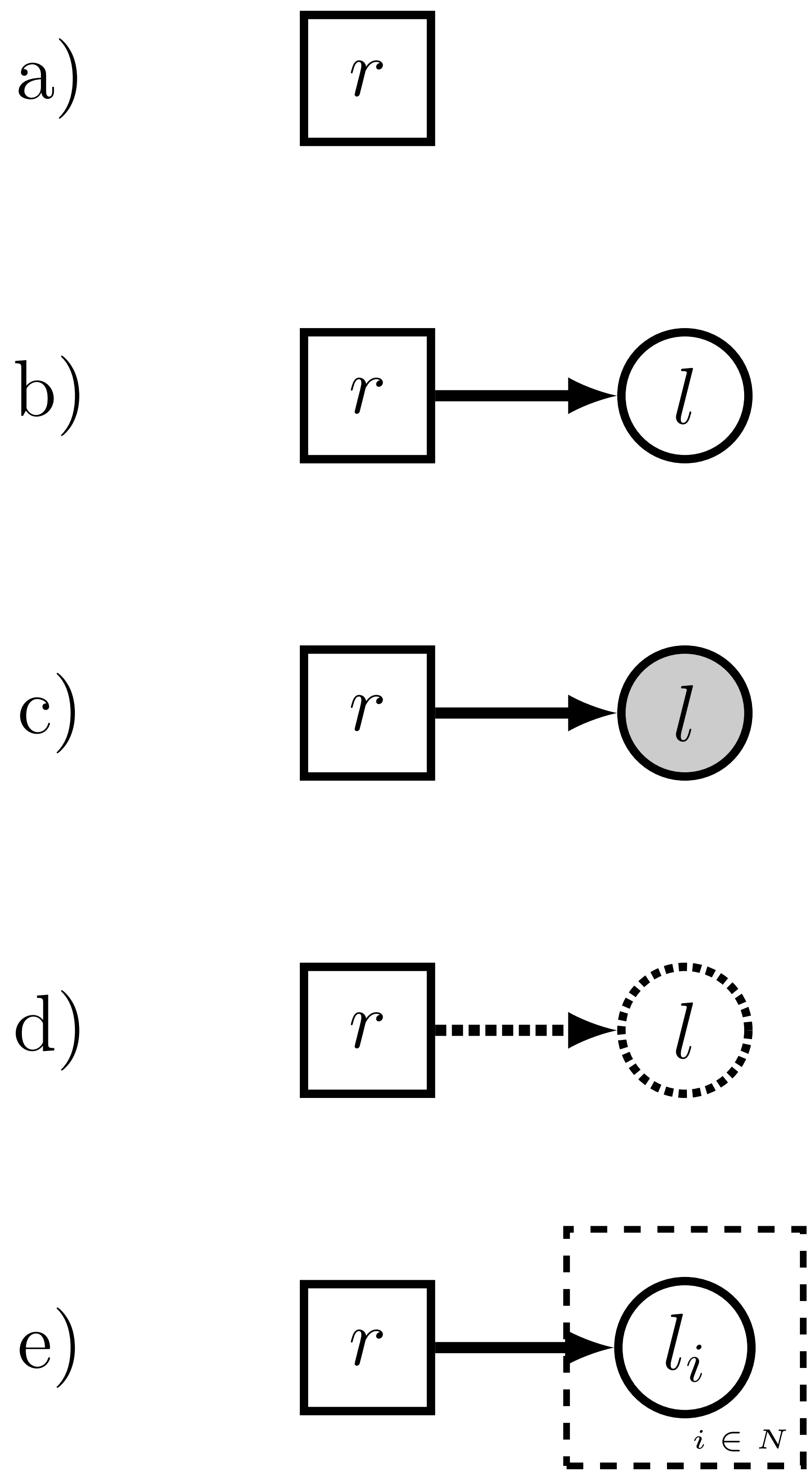

```
# stochastic node
l ~ dnExp(r)
```




```
# constant node
r <- 10


# stochastic node
l ~ dnExp(r)


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

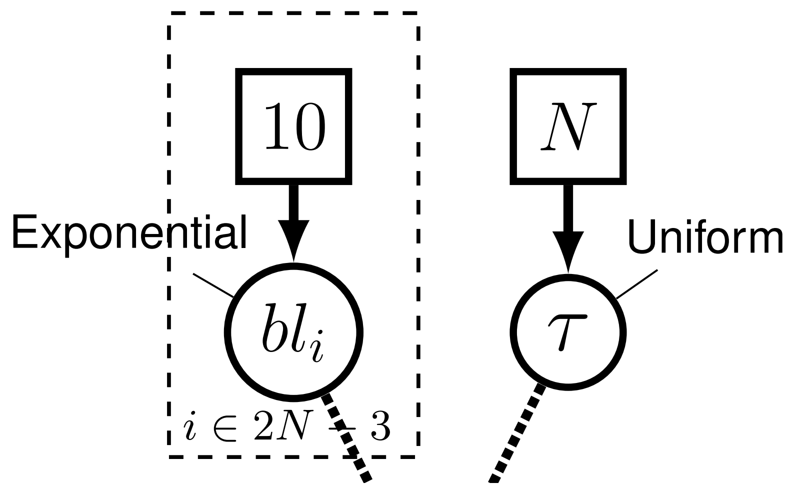



```
# constant node
r <- 10

# stochastic node
l ~ dnExp(r)

# stochastic node (observed)
l.clamp(0.1)

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



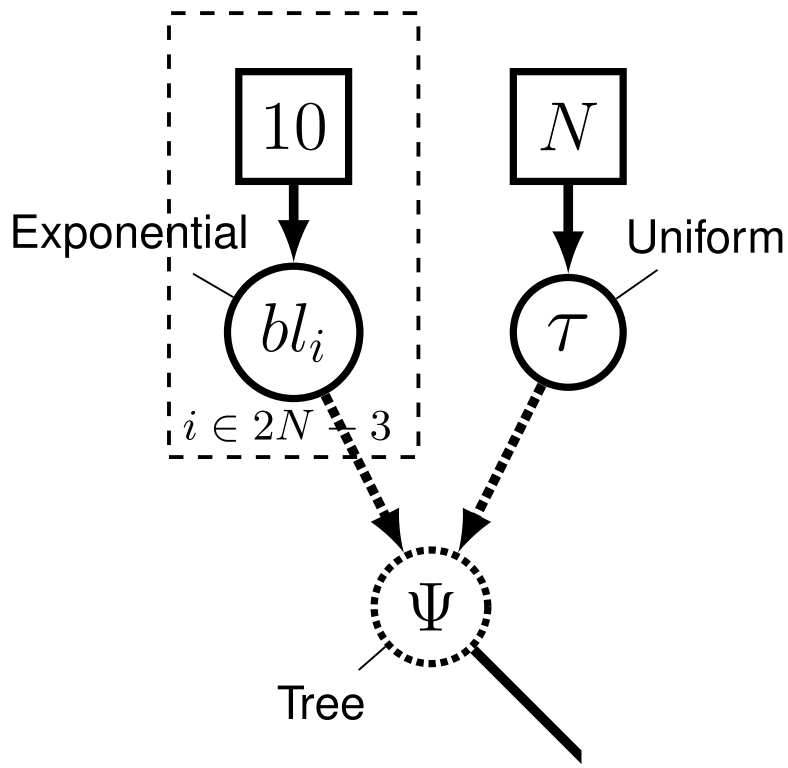

```
# constant node
r <- 10

# stochastic node
l ~ dnExp(r)

# stochastic node (observed)
l.clamp(0.1)

# deterministic node
l := exp(r)

# stochastic nodes (iid)
for (i in 1:N) {
    l[i] ~ dnExp(r)
}
```

Tree inference using morphology in RevBayes



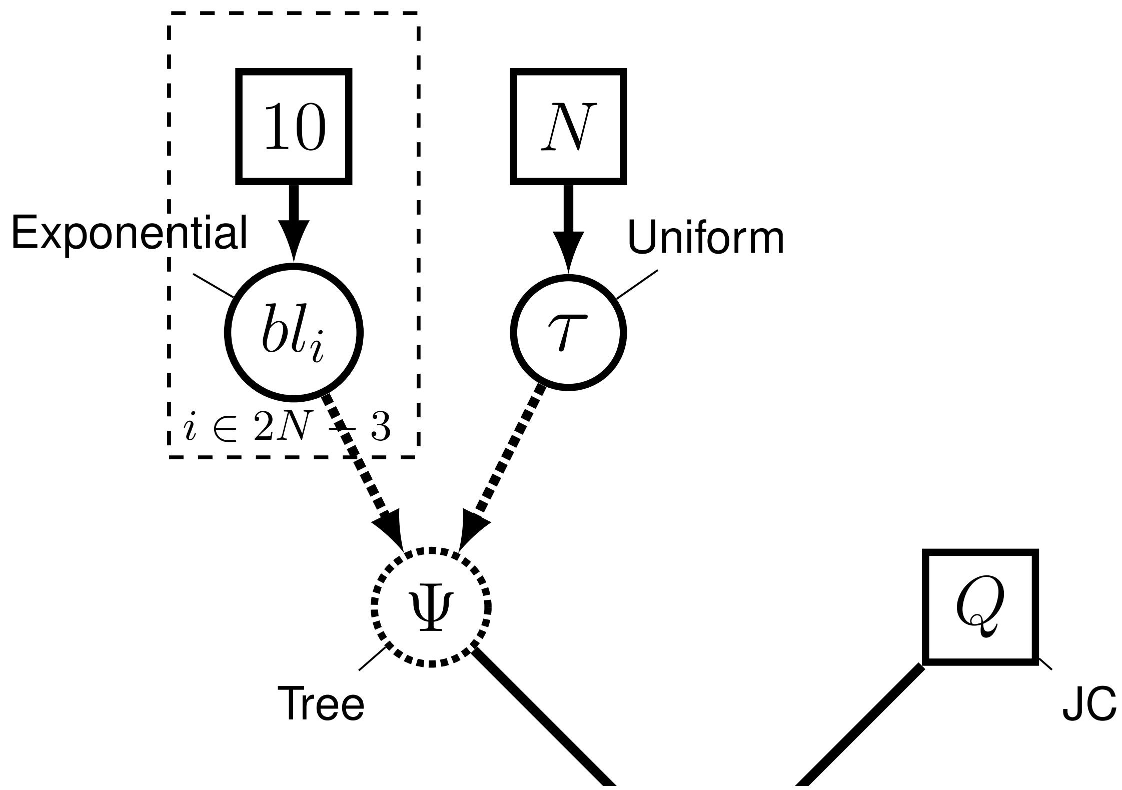
- The tree prior

Tree inference using morphology in RevBayes



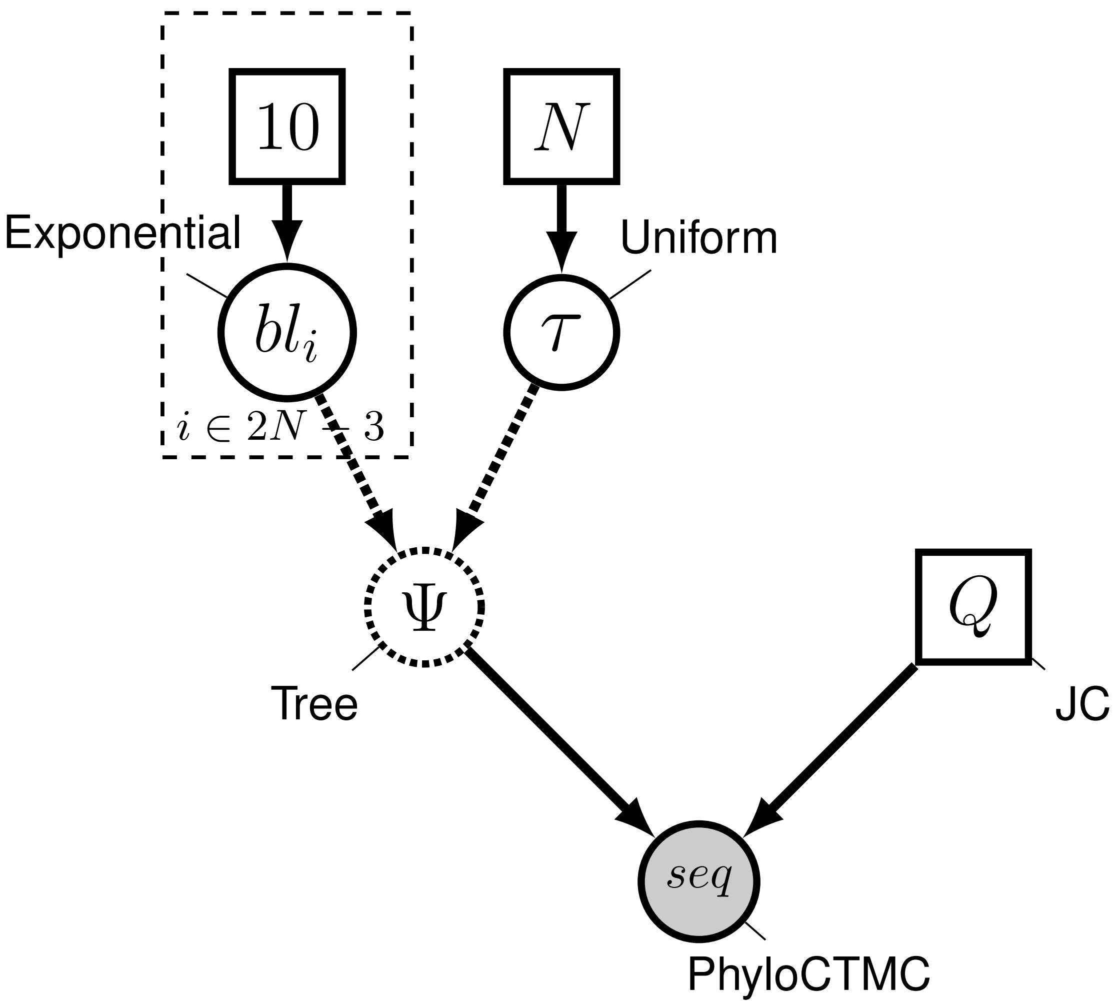
- The tree is a stochastic variable (node)

Tree inference using morphology in RevBayes



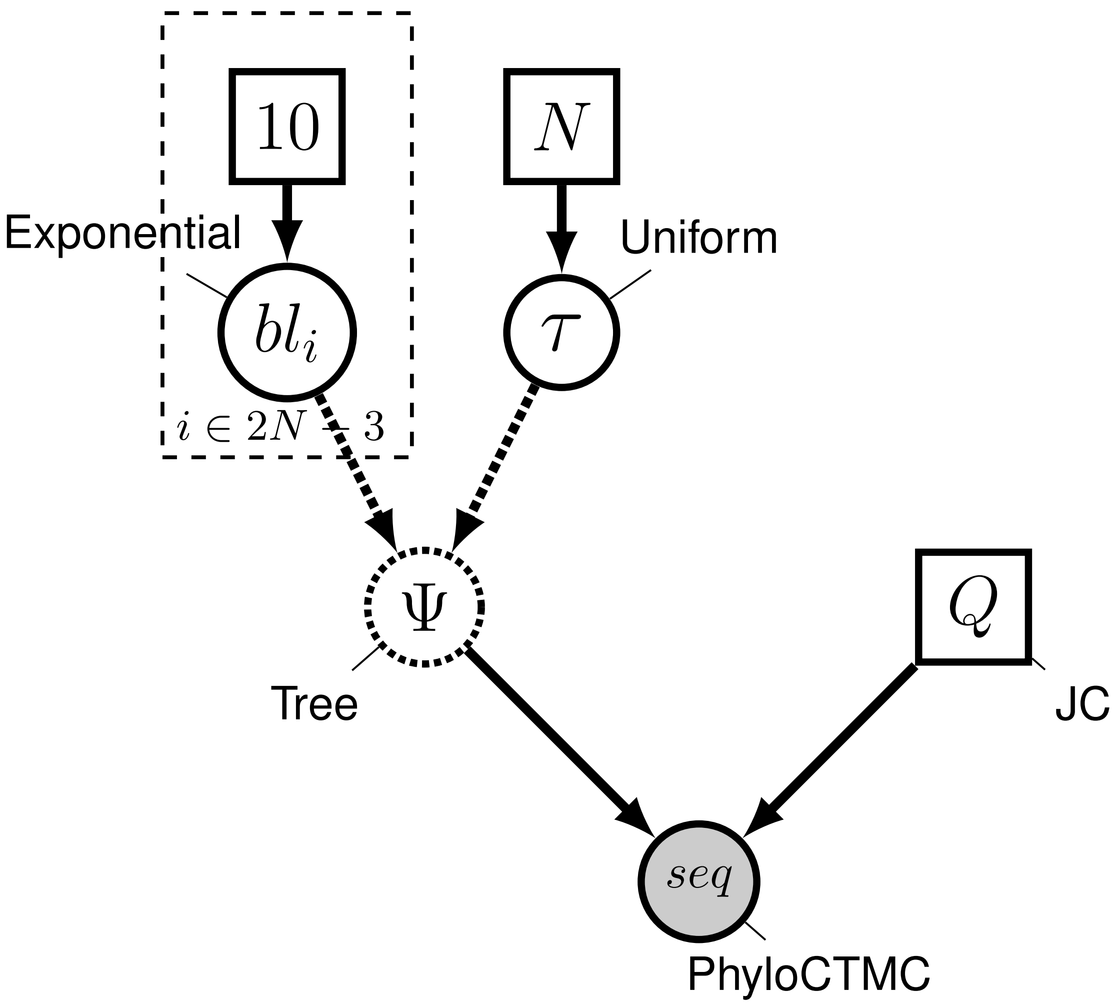
- Model of morphological evolution

Tree inference using morphology in RevBayes



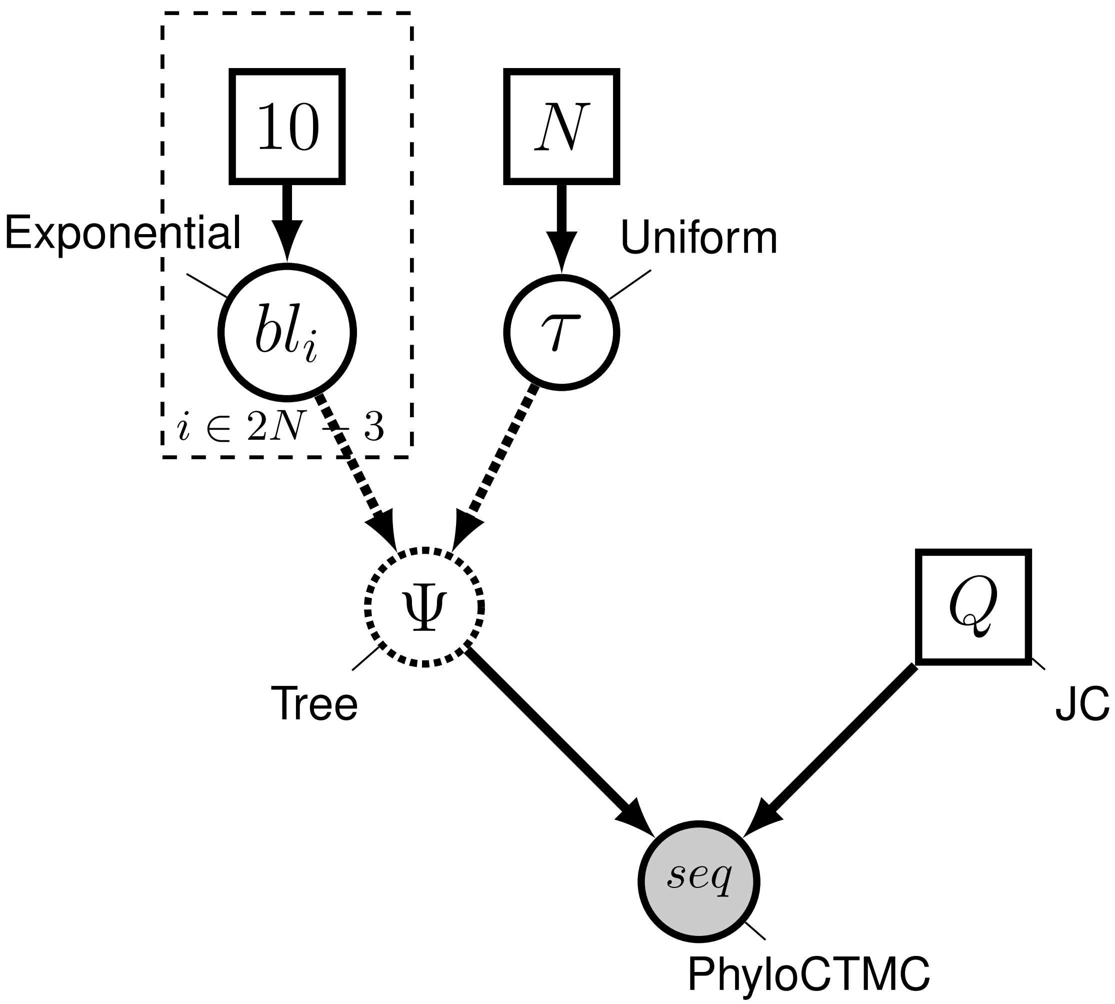
- The data is an observed stochastic variable

Tree inference using morphology in RevBayes




```
for (I in 1:n_branches) {
        bl[I] ~ dnExponential(10.0)
}
topology ~ dnUniformTopology(taxa)
psi := treeAssembly(topology, bl)


Q_morpho <- fnJC(2)


phyMorpho ~ dnPhyloCTMC( tree=psi,
siteRates=rates_morpho, Q=Q_morpho,
type="Standard", coding="variable" )

phyMorpho.clamp( data )
```

Tree inference using morphology in RevBayes

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Correcting for ascertainment bias