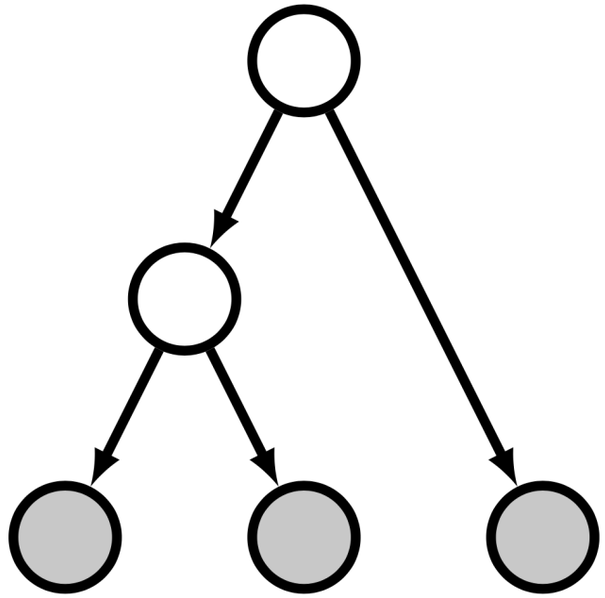
Intro. to Graphical Models

and

RevBayes

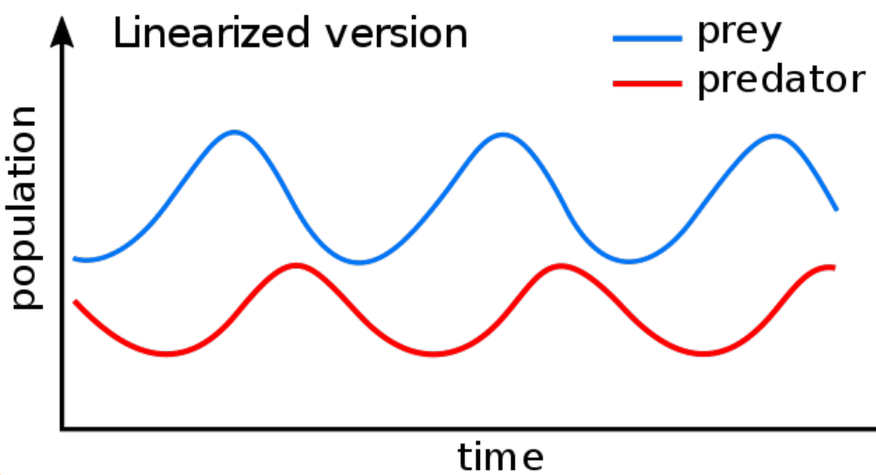


Jeremy M. Brown
Louisiana State University

What is a **model**?

Math

$$\frac{dx}{dt} = \alpha x - \beta xy,$$
$$\frac{dy}{dt} = \delta xy - \gamma y,$$



Biology

(something observed)

Equations and plot: https://en.wikipedia.org/wiki/Lotka–Volterra_equations

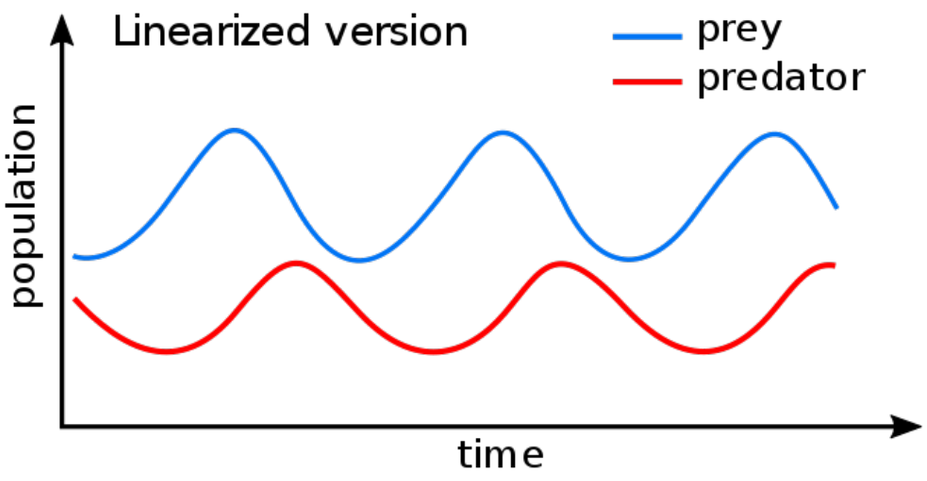
Lynx photo: Wikipedia (NPS Photo/Jacob W. Frank)

Snowshoe Hare photo: Wikipedia (D. Gordon E. Robertson)

What is a **model**?

Mathematical models try to explain important features of (biological) systems using (relatively simple) mathematical principles.

$$\frac{dx}{dt} = \alpha x - \beta xy,$$
$$\frac{dy}{dt} = \delta xy - \gamma y,$$



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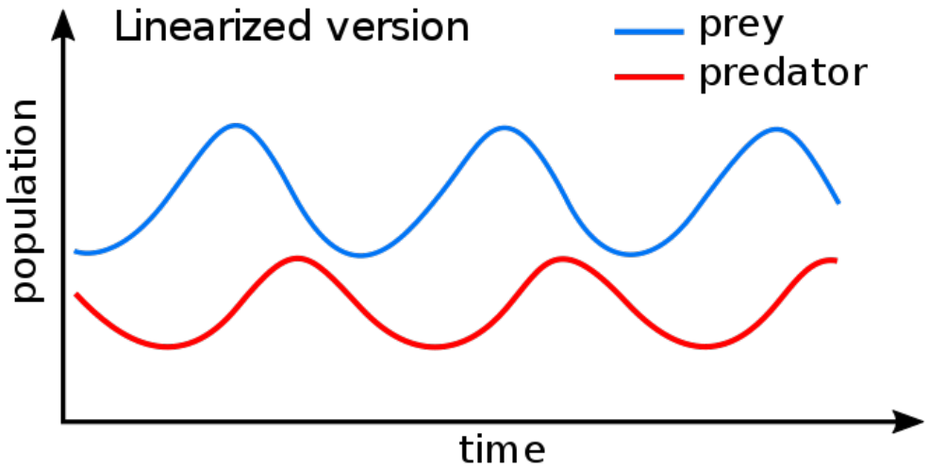
Deterministic and **Stochastic** Models

$$\frac{dx}{dt} = \alpha x - \beta xy,$$
$$\frac{dy}{dt} = \delta xy - \gamma y,$$



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Deterministic and **Stochastic** Models

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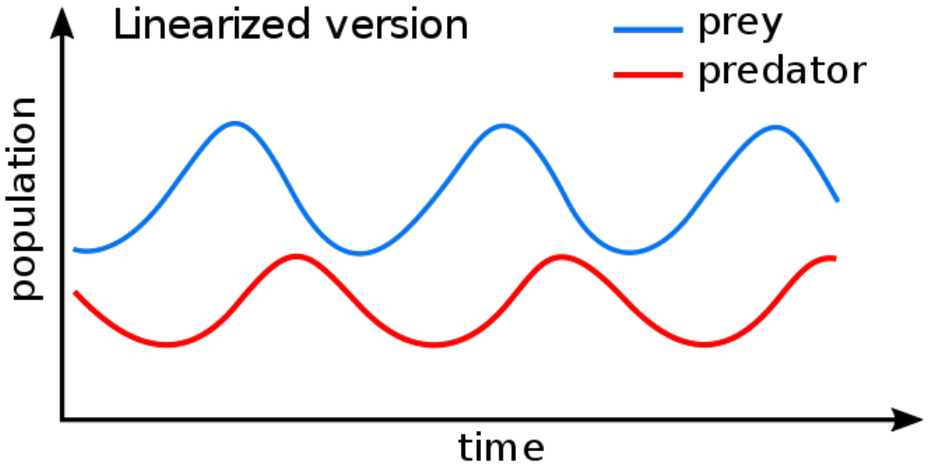

NO randomness

(no stochasticity)

(no probability statements)

Deterministic and **Stochastic** Models

$$\frac{dx}{dt} = \alpha x - \beta xy,$$
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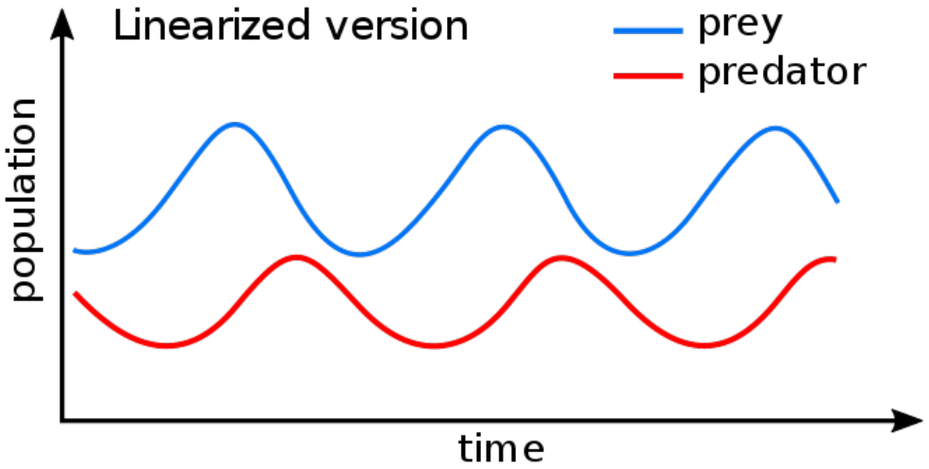

NO randomness

(no stochasticity)

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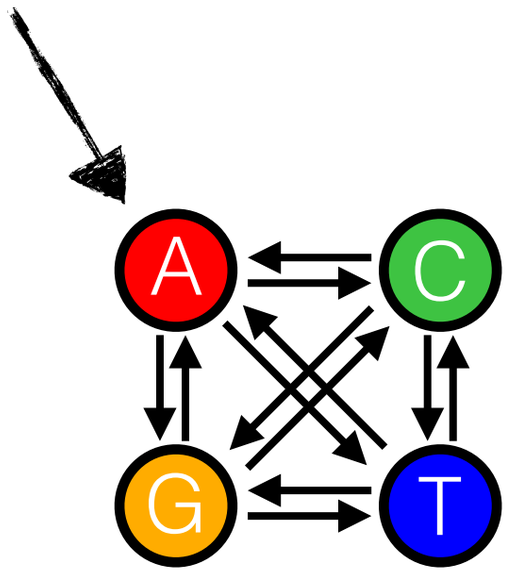
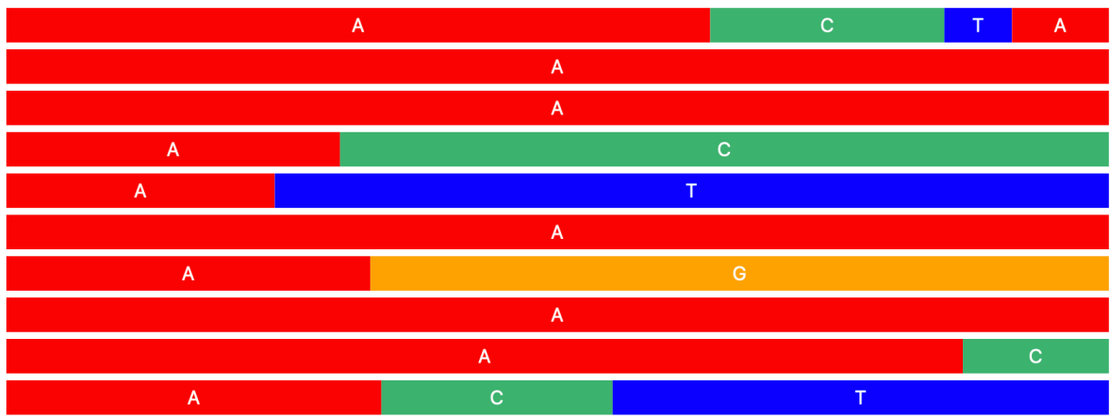




Randomness!

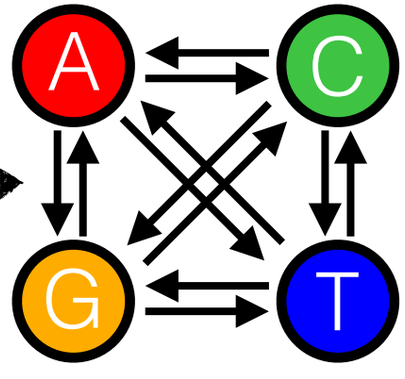
(stochasticity)

(probability statements)

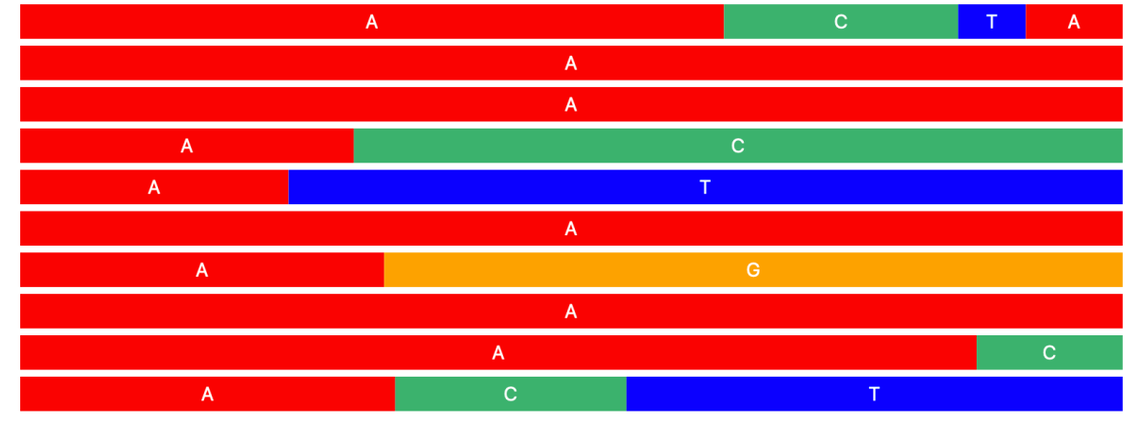
(variation in possible outcomes)

Stochastic Models

Probability Statements



Variable Outcomes



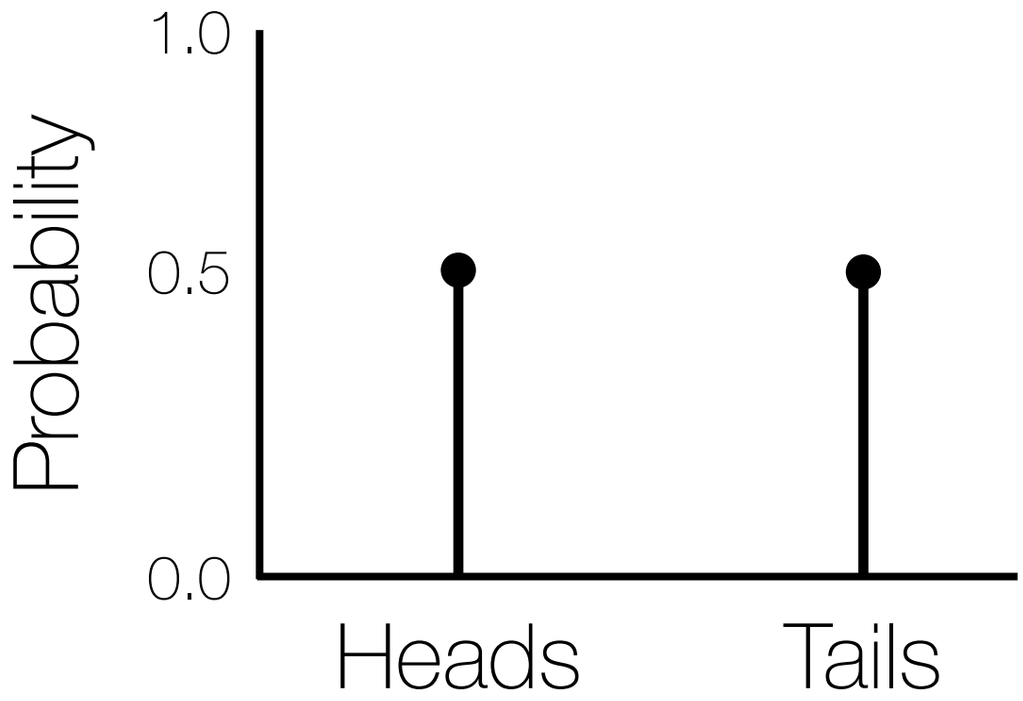
Randomness!

(stochasticity)

(probability statements)

(variation in possible outcomes)

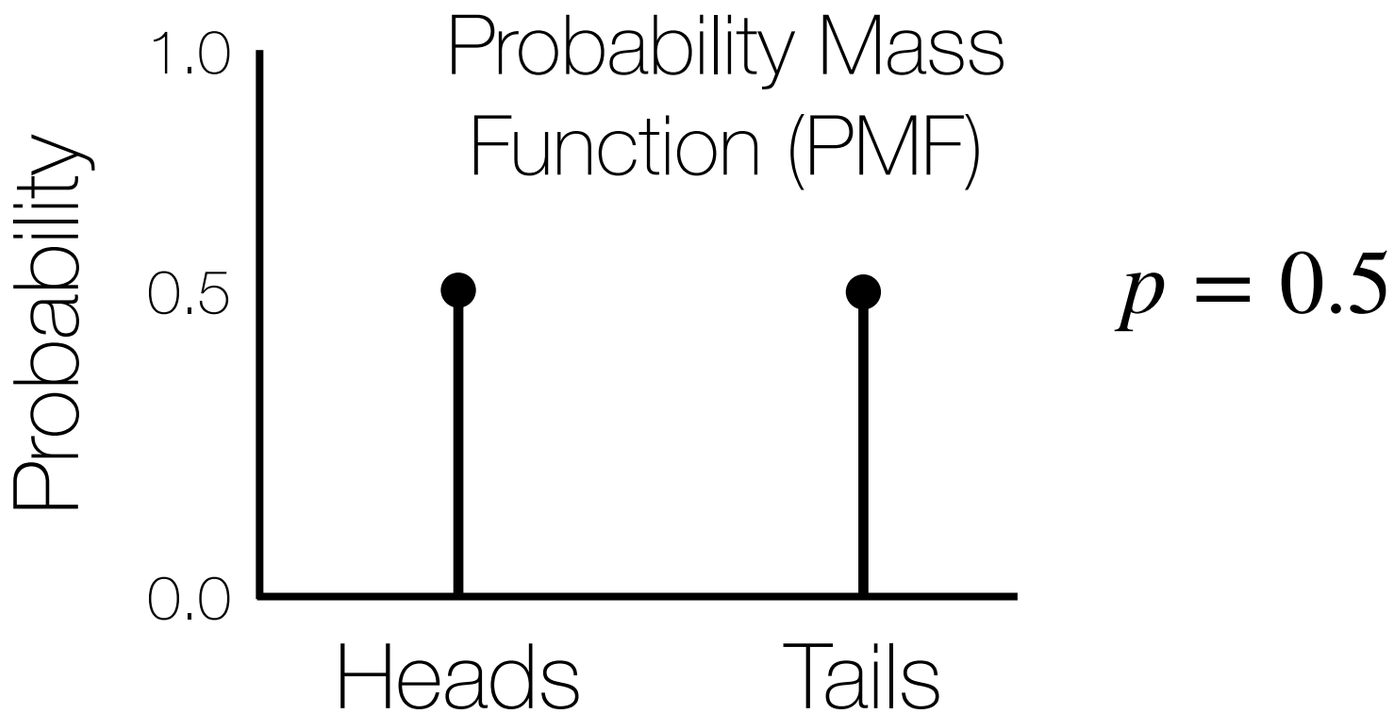
A simple **stochastic model**



Bernoulli

Describes the outcome of a single coin flip
(or other binary 0/1 trial)

A simple **stochastic model**



Bernoulli

One type of *discrete* distribution

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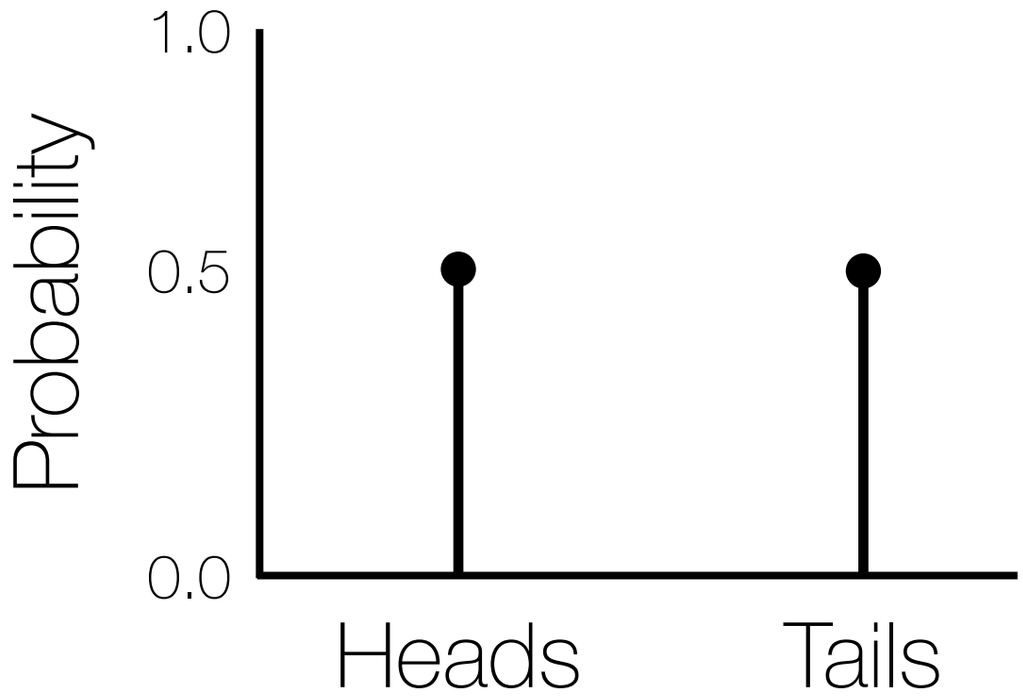
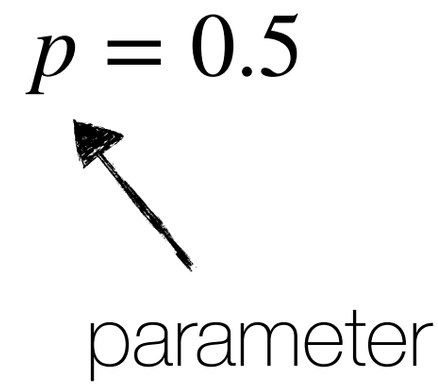
A simple **stochastic model**





$$P(\text{Heads}) = p$$

$$P(\text{Tails}) = 1\text{-}p$$

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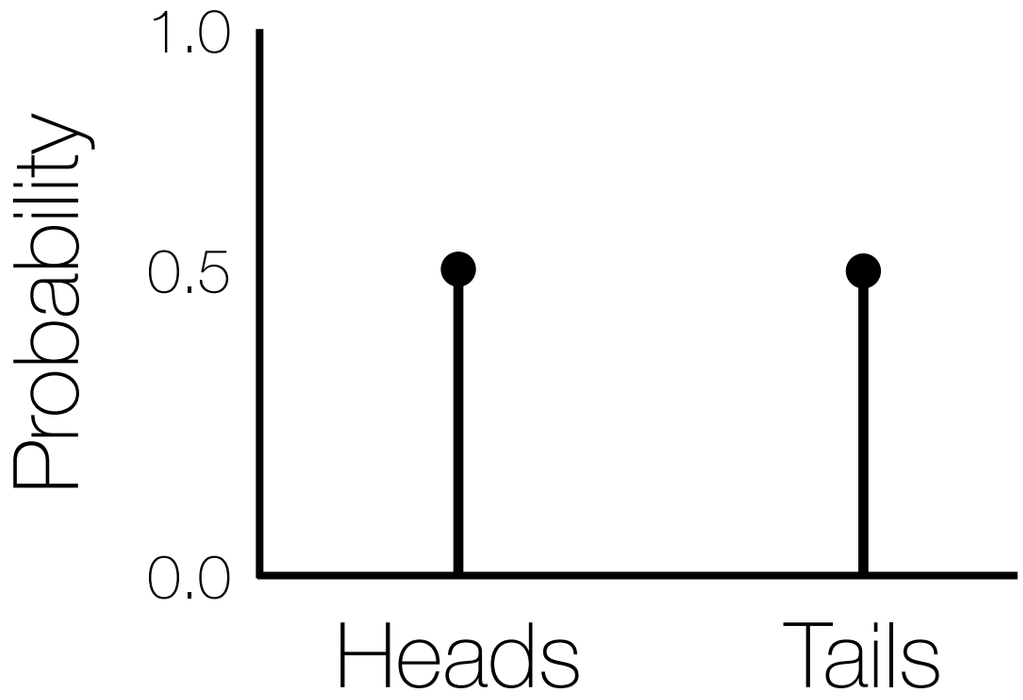
Let's build this model!



$p = 0.5$

RevBayes

```
moleuser@amphioxis-49-of-66:~$ rb

RevBayes version (1.1.1)
Build from tags/1.1.1 (rapture-588-gae00cc) on Sat Mar 19 00:48:15 UTC 2022

Visit the website www.RevBayes.com for more information about RevBayes.

RevBayes is free software released under the GPL license, version 3. Type 'license()' for details.

To quit RevBayes type 'quit()' or 'q()'.


> _
```

https://revbayes.github.io

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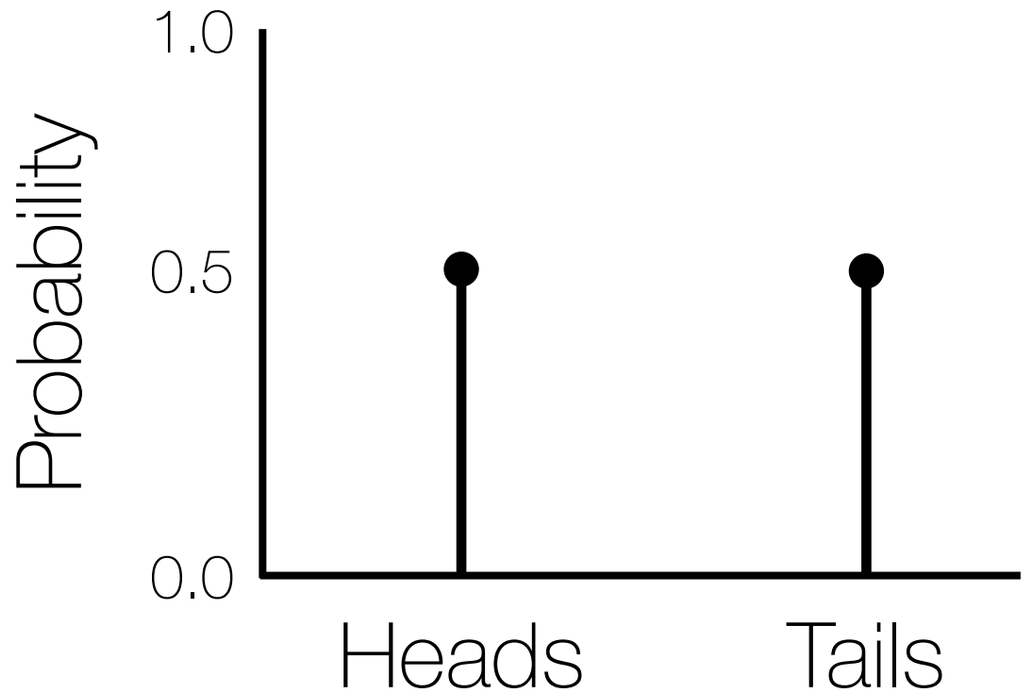
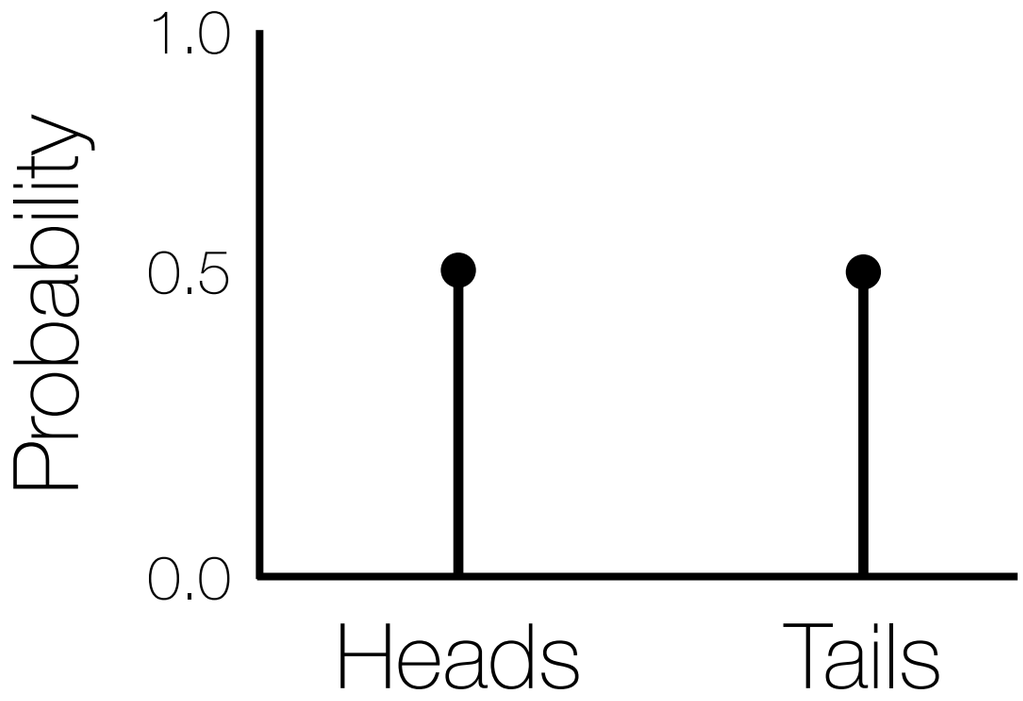
Let's build this stochastic model!



$p = 0.5$

$$z \sim \text{dnBernoulli}(0.5)$$
$$z$$

Let's build this stochastic model!



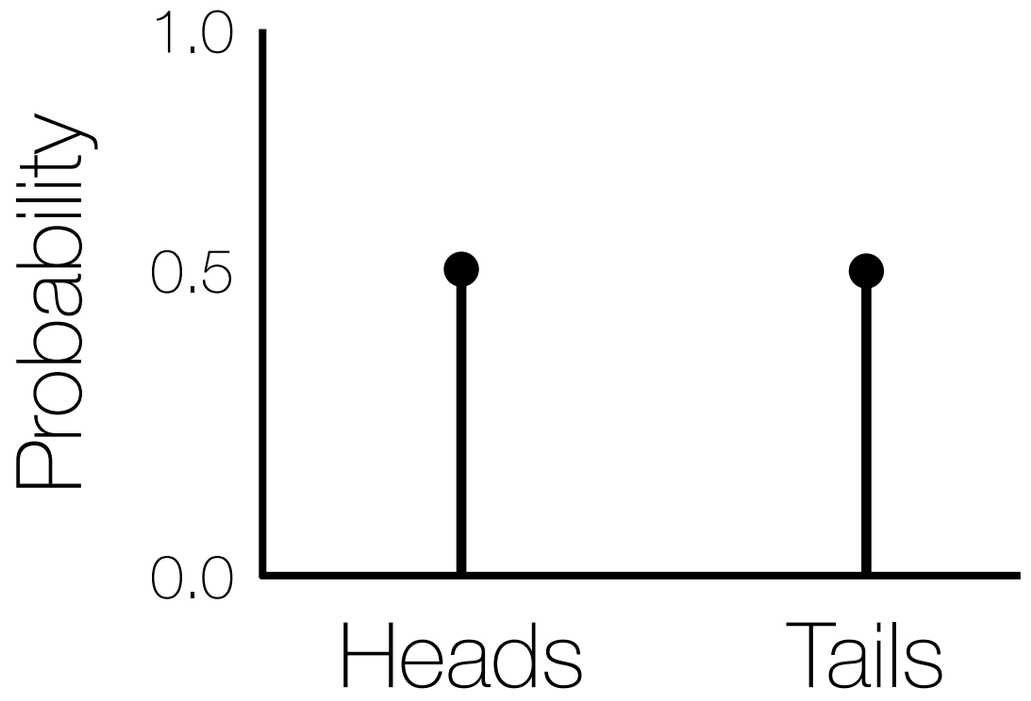
$p = 0.5$

Random Variable → z ~ dnBernoulli(0.5)

z

"distributed as"

Rev language intended to feel a lot like R, but you can't create random variables in R.



$p = 0.5$

```
> z  ~  dnBernoulli(0.5)
[> z
   0
> z  ~  dnBernoulli(0.5)
[> z
   0
> z  ~  dnBernoulli(0.5)
[> z
   1
> z  ~  dnBernoulli(0.5)
[> z
   1
> z  ~  dnBernoulli(0.5)
[> z
   1
> z  ~  dnBernoulli(0.5)
[> z
   1
> z  ~  dnBernoulli(0.5)
[> z
   1
> z  ~  dnBernoulli(0.5)
[> z
   0
```

When you create a random variable in RevBayes, it automatically initializes that variable by drawing a value from the corresponding probability distribution.

The Role of Models

(1) Can we explain the **important features** of the real world using relatively **simple mathematical principles** (prediction)?

(2) Within this mathematical framework, can we **learn about the processes** that generated our data (inference)?

The most useful models can answer 'yes' to both.

```
z ~ dnBernoulli(0.5)
z
```

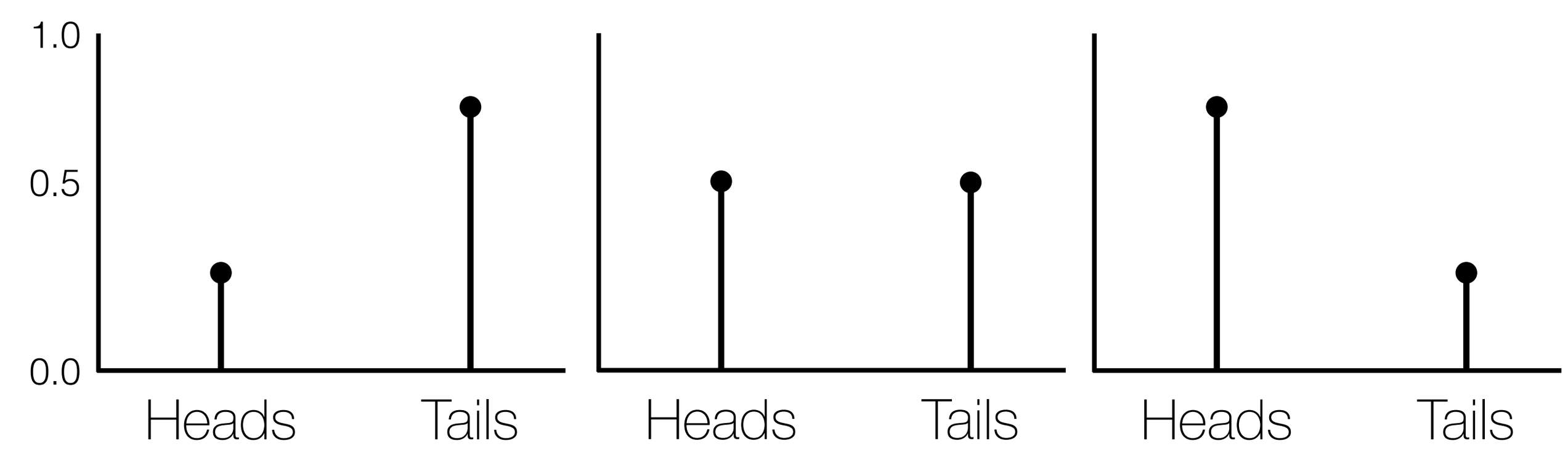
(1) ✓

(2) X

p=0.5
No data

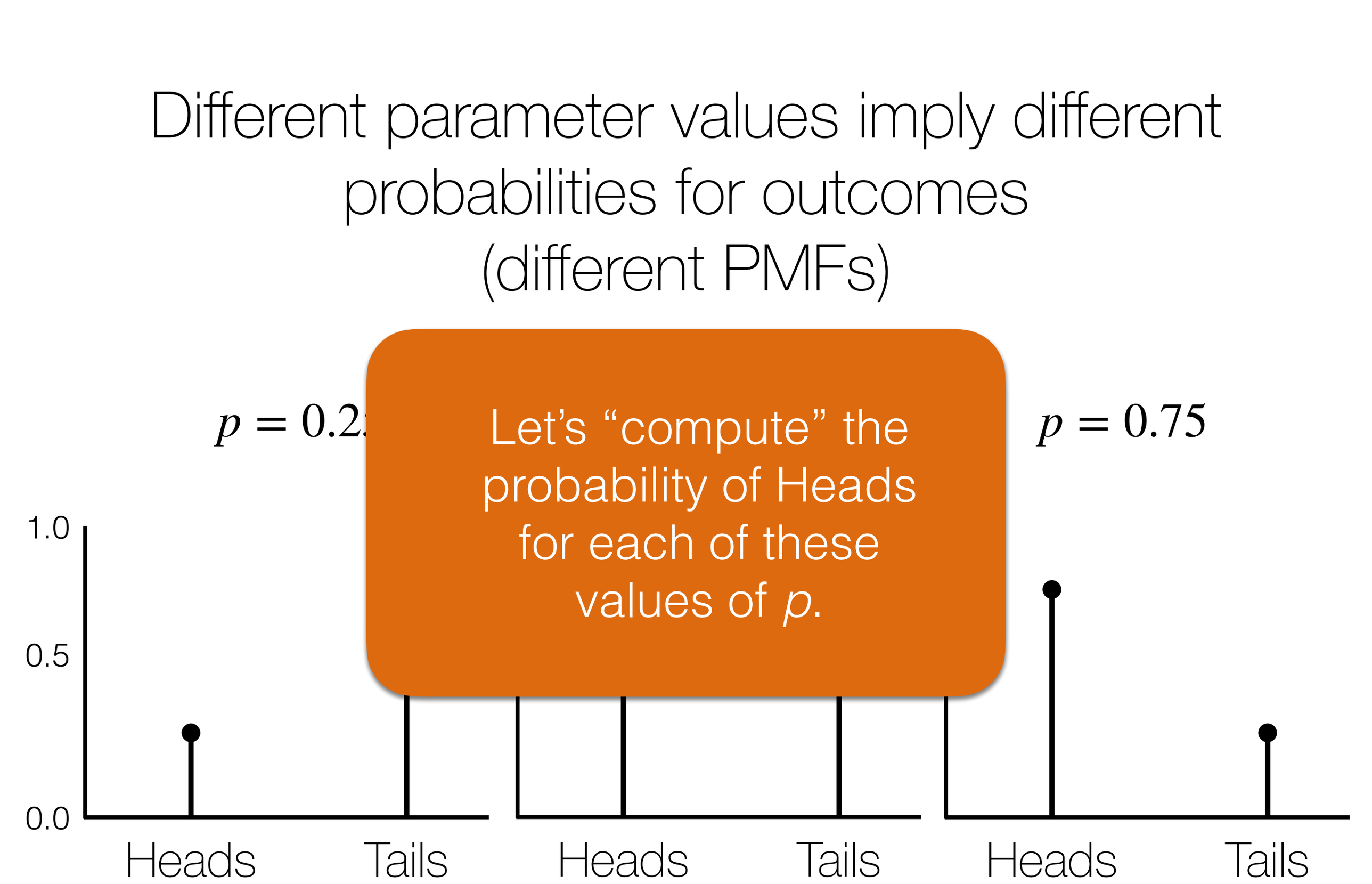
Different parameter values imply different probabilities for outcomes (different PMFs)

$p = 0.25$ $p = 0.5$ $p = 0.75$



Different parameter values imply different probabilities for outcomes (different PMFs)

Let's "compute" the probability of Heads for each of these values of *p*.



Computing Likelihoods

```
p <- 0.5
z ~ dnBernoulli(p)
z.clamp(1)
z.probability()
```

Here is where we attach our data (i.e., Heads) to our model. This is known as “clamping”.

Here we compute:

$$P(Heads \mid p = 0.5)$$

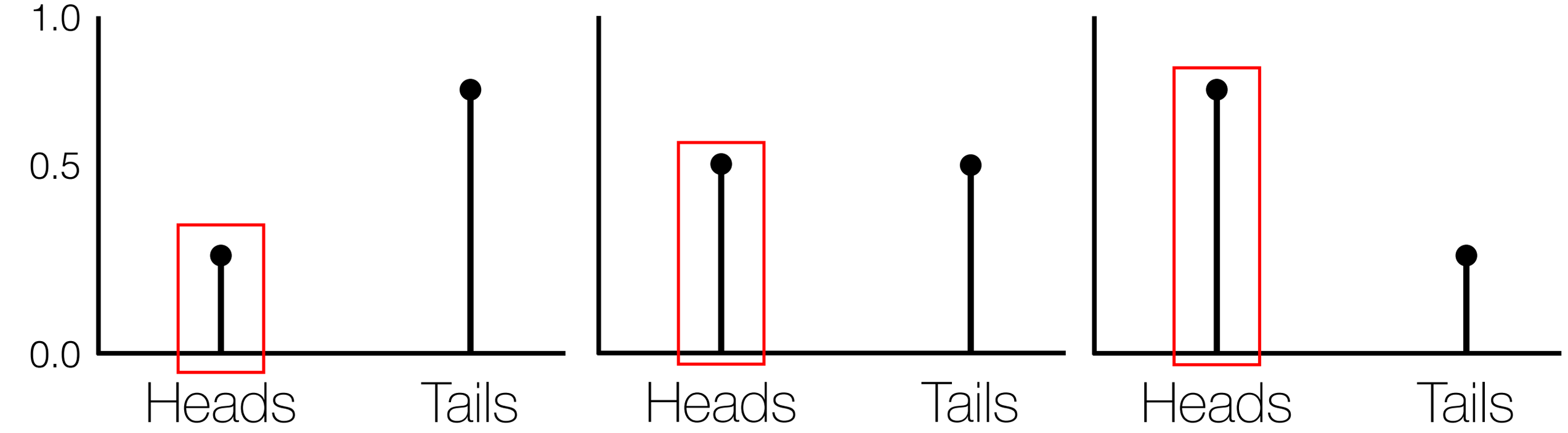
$$L(p = 0.5; Heads)$$

```
> p <- 0.25
> z ~ dnBernoulli(p)
> z.clamp(1)
> z.probability()
  0.25
```

```
> p <- 0.5
> z ~ dnBernoulli(p)
> z.clamp(1)
> z.probability()
  0.5
```

```
> p <- 0.75
> z ~ dnBernoulli(p)
> z.clamp(1)
> z.probability()
  0.75
```

$p = 0.25$ $p = 0.5$ $p = 0.75$



```
> p <- 0.25
> z ~ dnBernoulli(p)
> z.clamp(1)
> z.probab
  0.25
```

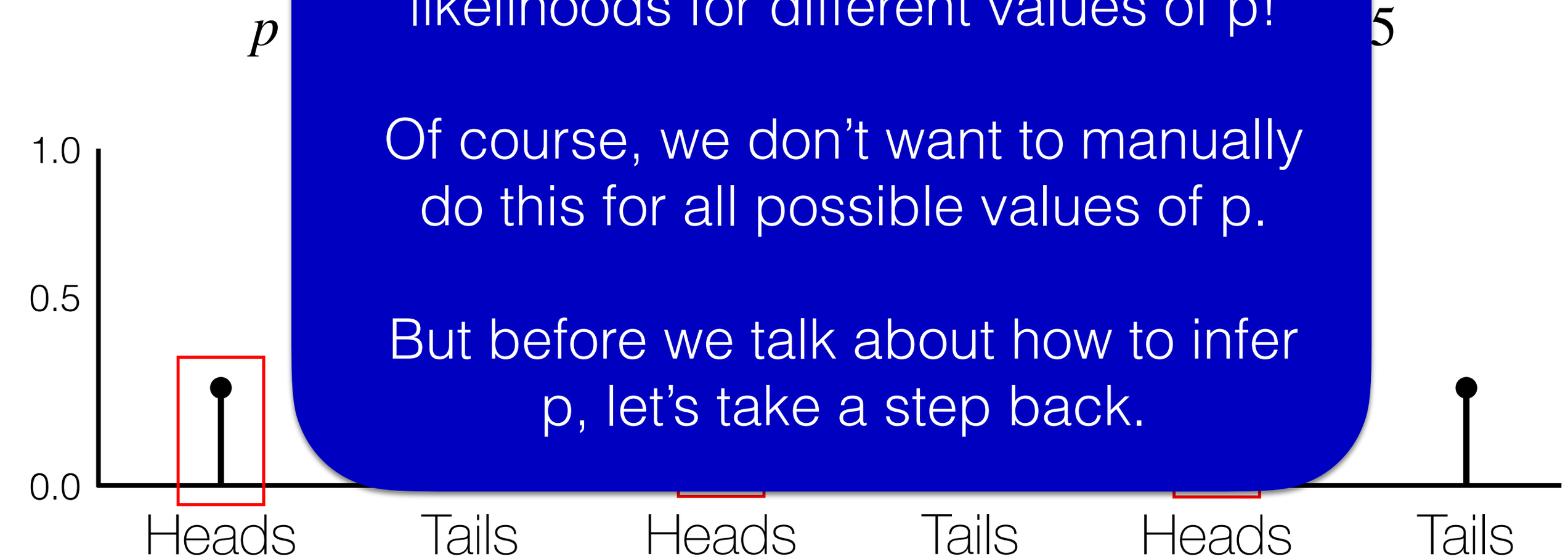
```
> p <- 0.5
> z ~ dnBernoulli(p)
> z.clamp(1)
```

```
> p <- 0.75
> z ~ dnBernoulli(p)
> z.clamp(1)
> ility()
```

Being able to attach data to the model allows us to compare the likelihoods for different values of p!

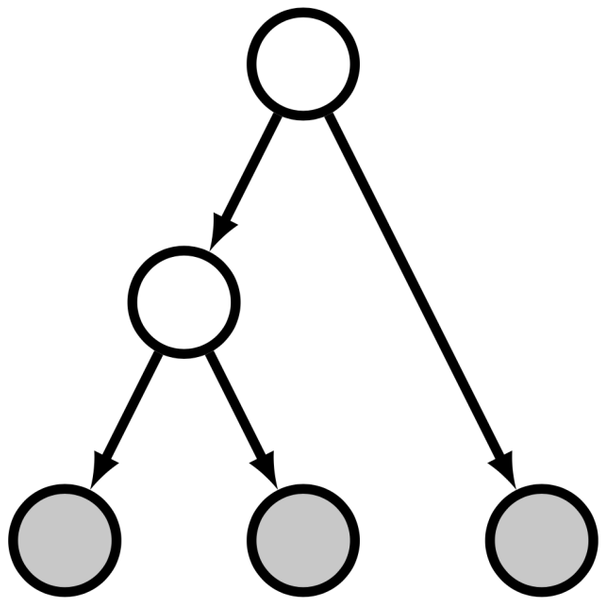
Of course, we don't want to manually do this for all possible values of p.

But before we talk about how to infer p, let's take a step back.



Graphical Models

Graphical models provide a means of depicting the dependencies among parameters in probabilistic models.

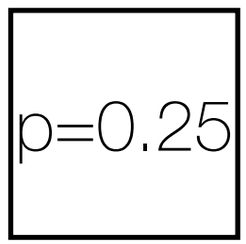


The “graphical” part of the name graphical models has to do with their basis on graphs, and not anything to do with drawing.

But it is convenient that graphical models can also be drawn, to clearly depict the structure of the model.

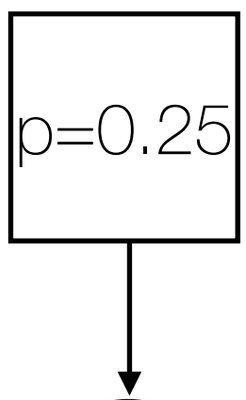
Building a Graphical Model

p is fixed at 0.25



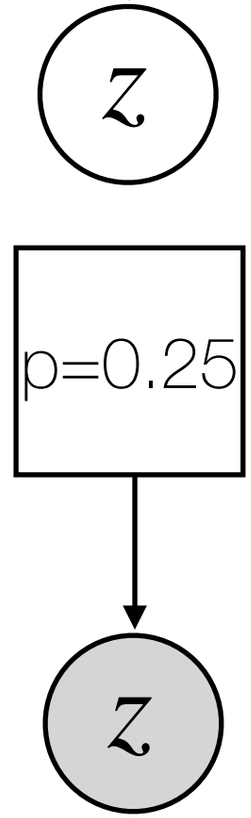

```
> p <- 0.25
```

z depends on *p*
z is a Bernoulli r.v.

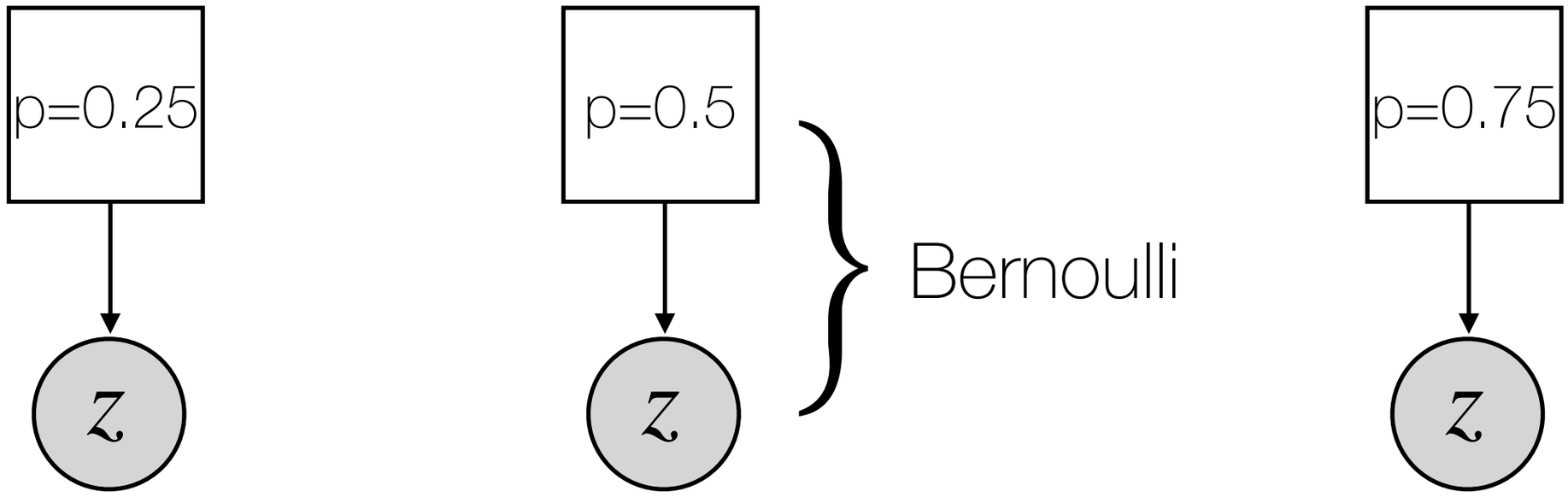



```
> z ~ dnBernoulli(p)
```

We “observed” a value of 1 for *z*.




```
> z.clamp(1)
```




```
> p <- 0.25
> z ~ dnBernoulli(p)
> z.clamp(1)
> z.probability()
  0.25
```

```
> p <- 0.5
> z ~ dnBernoulli(p)
> z.clamp(1)
> z.probability()
  0.5
```

```
> p <- 0.75
> z ~ dnBernoulli(p)
> z.clamp(1)
> z.probability()
  0.75
```

What are the possible building blocks for graphical models?

Jeremy M. Brown

RevBayes Syntax

sqrt(16) abs(-11)	**functions and arguments**	choose(6,3) ls() max([2.1,5.5,7.8])

test <- v(5,9,12) test test[2]	**vectors**	test[1] <- 5 test[2] <- 9 test[3] <- 12 test

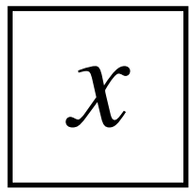
for (i in 1:5){
print(i)
}
	for loops	for (i in 1:3){
		print(test[i])
		}

https://revbayes.github.io/tutorials/intro/rev.html

https://revbayes.github.io/documentation/

Graphical Model Syntax

Symbol



Type

Constant Node

Description

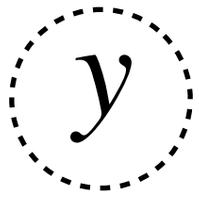
Constant nodes are like standard variables in a programming language. They are assigned fixed values.

Rev Example

```
x <- 2.3
```

Graphical Model Syntax

Symbol



Type

Deterministic Node

Description

Deterministic nodes depend on the values of other nodes, but in a deterministic (fixed) way. They have no probability distribution intrinsically associated with them.

Rev Example

```
y := 2 * x
```

Graphical Model Syntax

Symbol

Type

Stochastic Node

Description

Stochastic nodes represent random variables and take on values according to some probability distribution. These distributions may have parameters defined in other nodes in the model graph. The type of distribution associated with a node is often not written explicitly when a model is drawn, but it must be specified.

Rev Example

```
z ~ dnBernoulli(0.5)
```

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Graphical Model Syntax

Symbol

Type

Clamped Stochastic Node

Description

Data can be viewed as the observed outcome of a stochastic node. Clamping involves assigning a set of observations to an associated stochastic node. Clamping data allows the values of other parameters in the model to be inferred.

Rev Example

```
z ~ dnBernoulli(0.5)
z.clamp(1)
```

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Graphical Model Syntax

Symbol

Type

Conditional Dependency

Description

Arrows indicate conditional dependencies and are directional. The node (variable) that the arrow points to depends on the value of the node at the other end of the arrow. For instance, if *p* points to *Z*, then we say that *Z* is dependent on *p*.

Rev Example

```
p <- 0.5
z ~ dnBernoulli(p)
s := z*3
```

Graphical Model Syntax

Symbol

Type

Plate

Description

Plates simply represent repetition and make it easier to depict graphical models with a repetitive structure. For instance, the example above shows *N* instances of the clamped variable, *z*, with each instance indexed by *i*. Plates can be used with any type of node, but are commonly used with clamped nodes representing data.

Rev Example

```
N <- 10
for (i in 1:N){
     z[i]  ~  dnBernoulli(0.5)
     z[i].clamp(1)
     }
```

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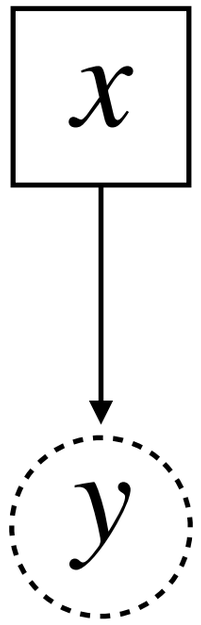
Super Simple Models



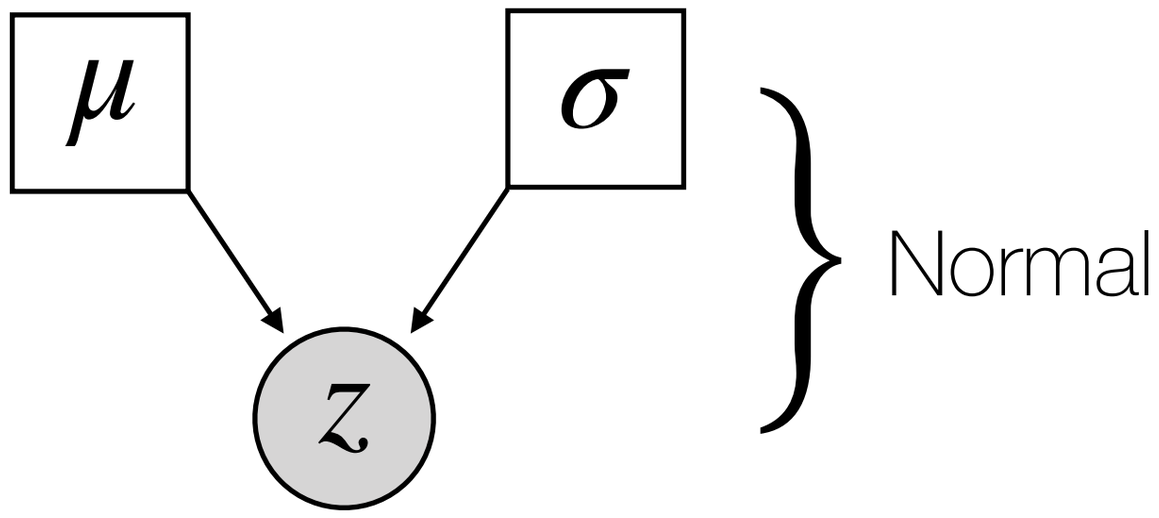

```
x <- 2
y := x / 4
```

What's the structure of this model?

What would happen if *x* was set to 16?

Try changing *x* without changing *y*, but then look at value of *y*.

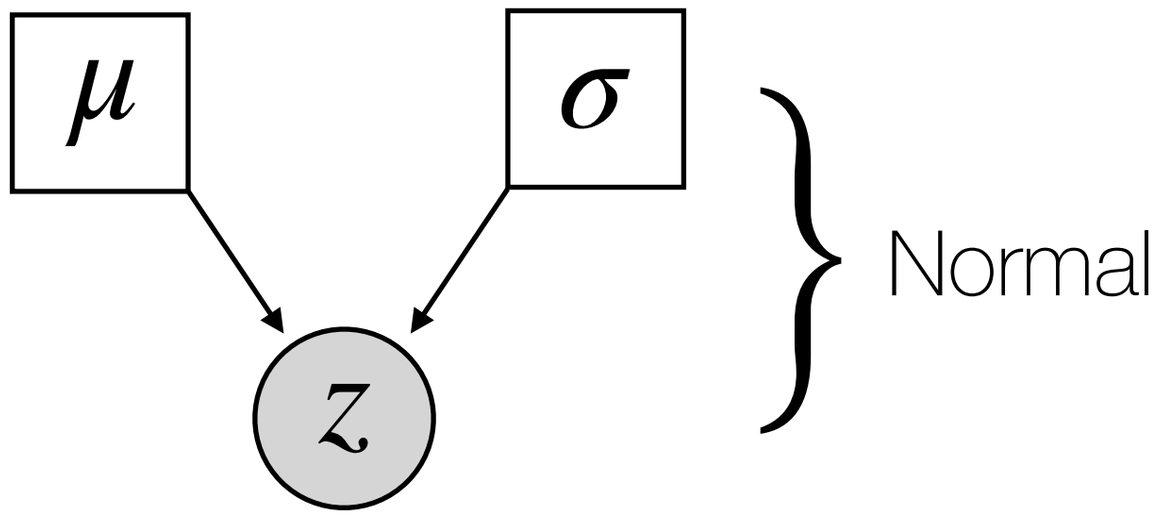
Super Simple Models




```
m <- 10
s <- 0.1
z ~ dnNormal(m,s)
z.clamp(10.01)
```

What's the structure of this model?
What can we infer about this model?

Super Simple Models



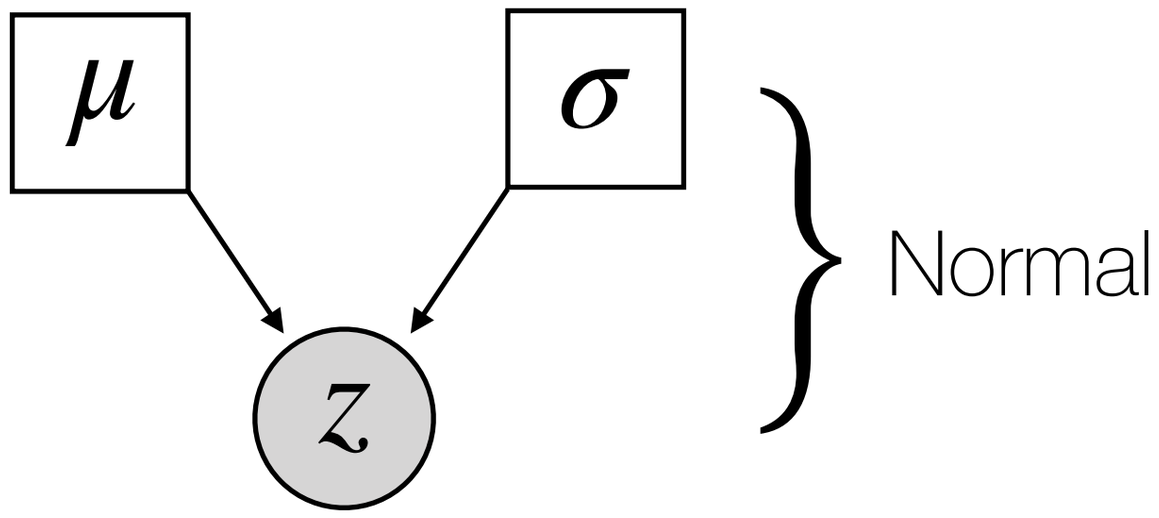

```
m <- 10
s <- 0.1
z ~ dnNormal(m,s)
z.clamp(10.01)
```

What's the structure of this model?

What can we infer about this model?

Nothing to infer! Only nodes are constant or clamped.

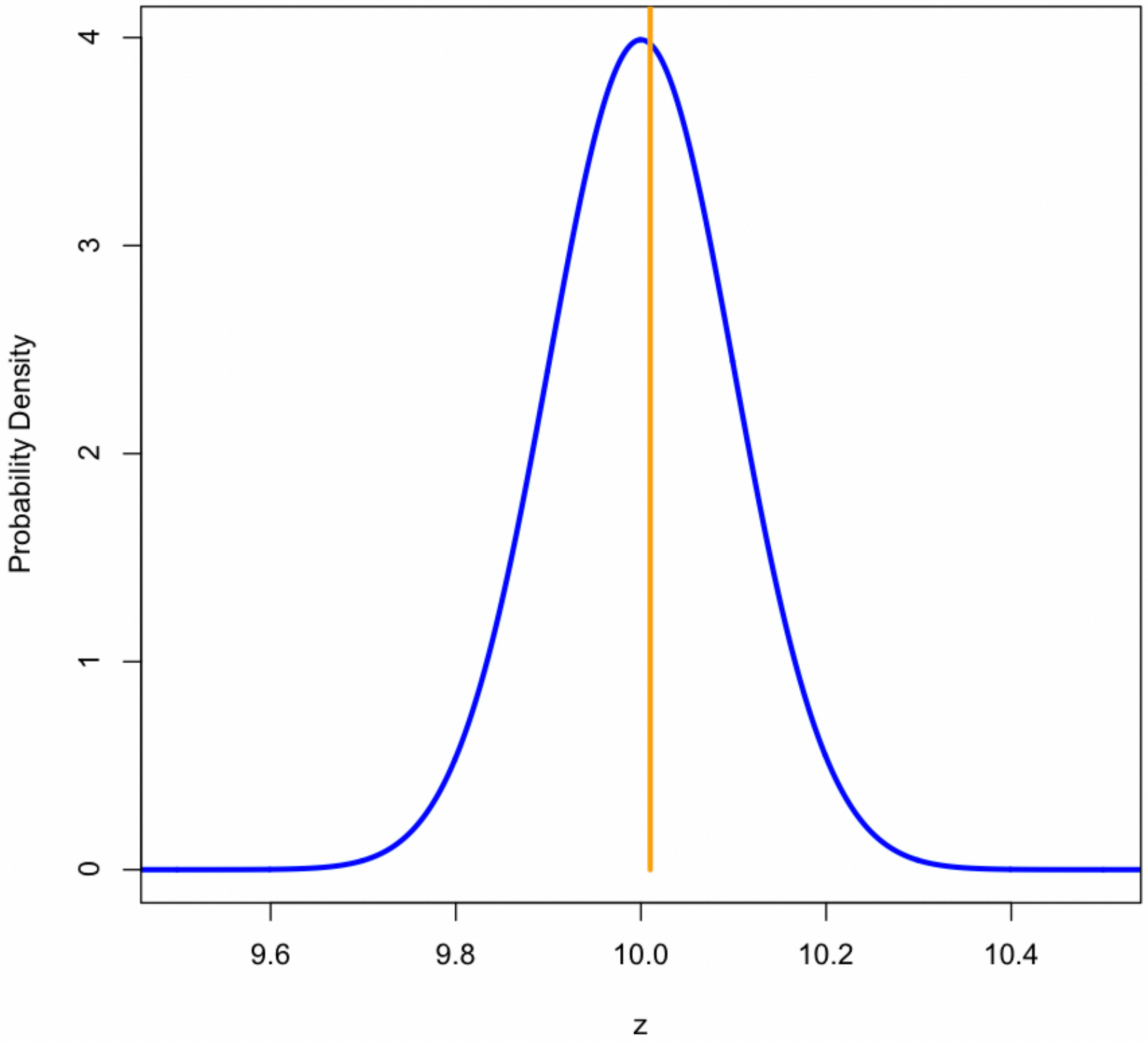
Super Simple Models



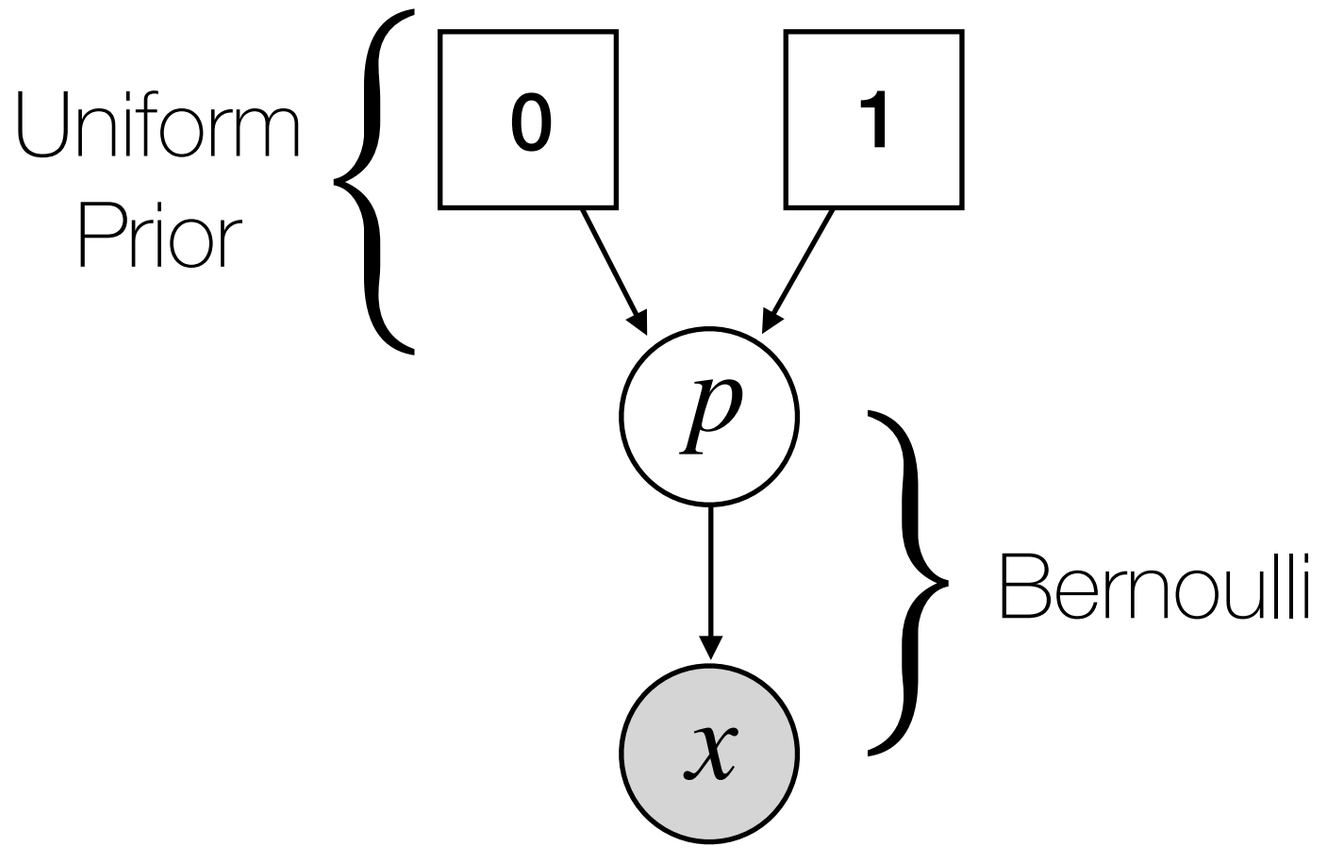

```
m <- 10
s <- 0.1
z ~ dnNormal(m,s)
z.clamp(10.01)
```

What's the probability of our "observed" value?

Probability Density Function (PDF)

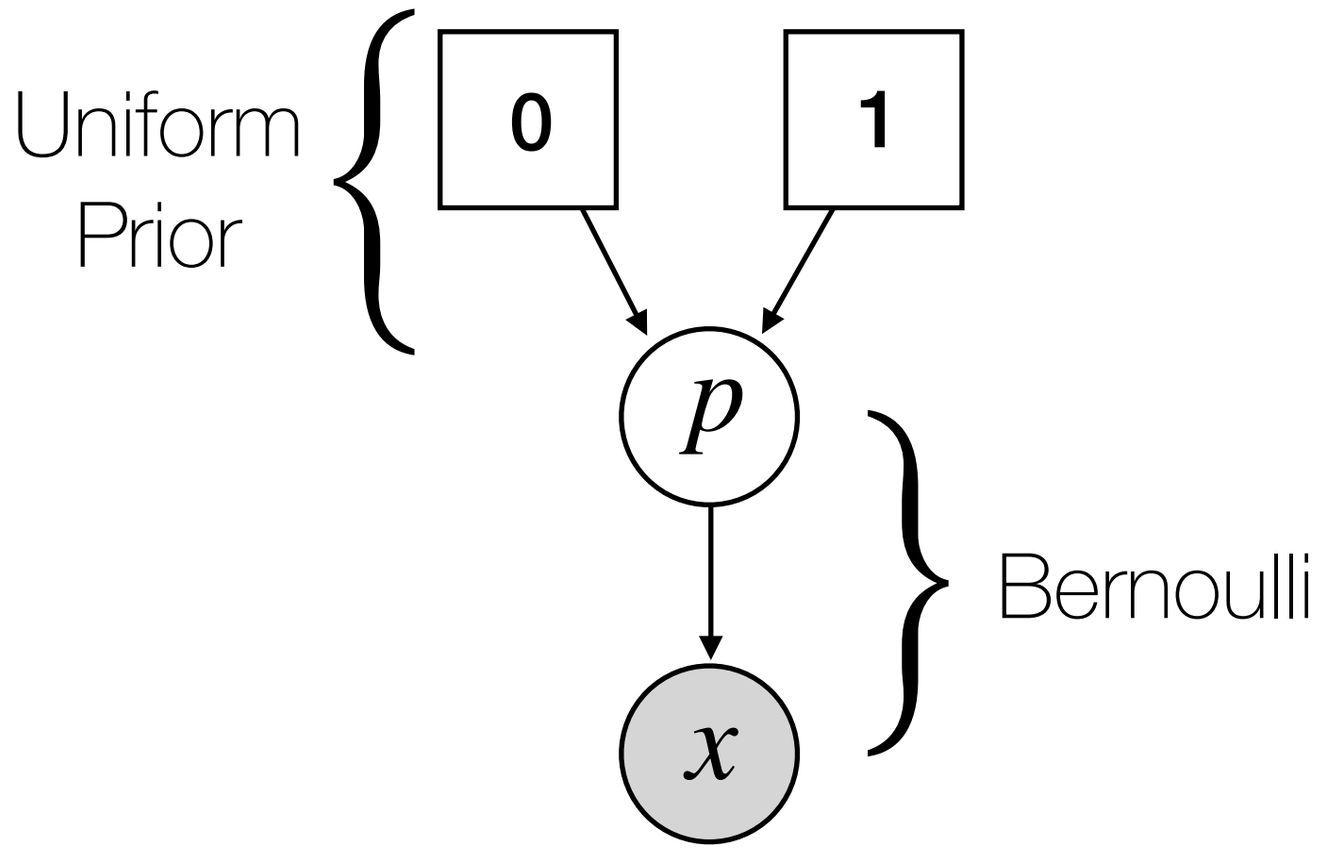


Single Bernoulli Trial



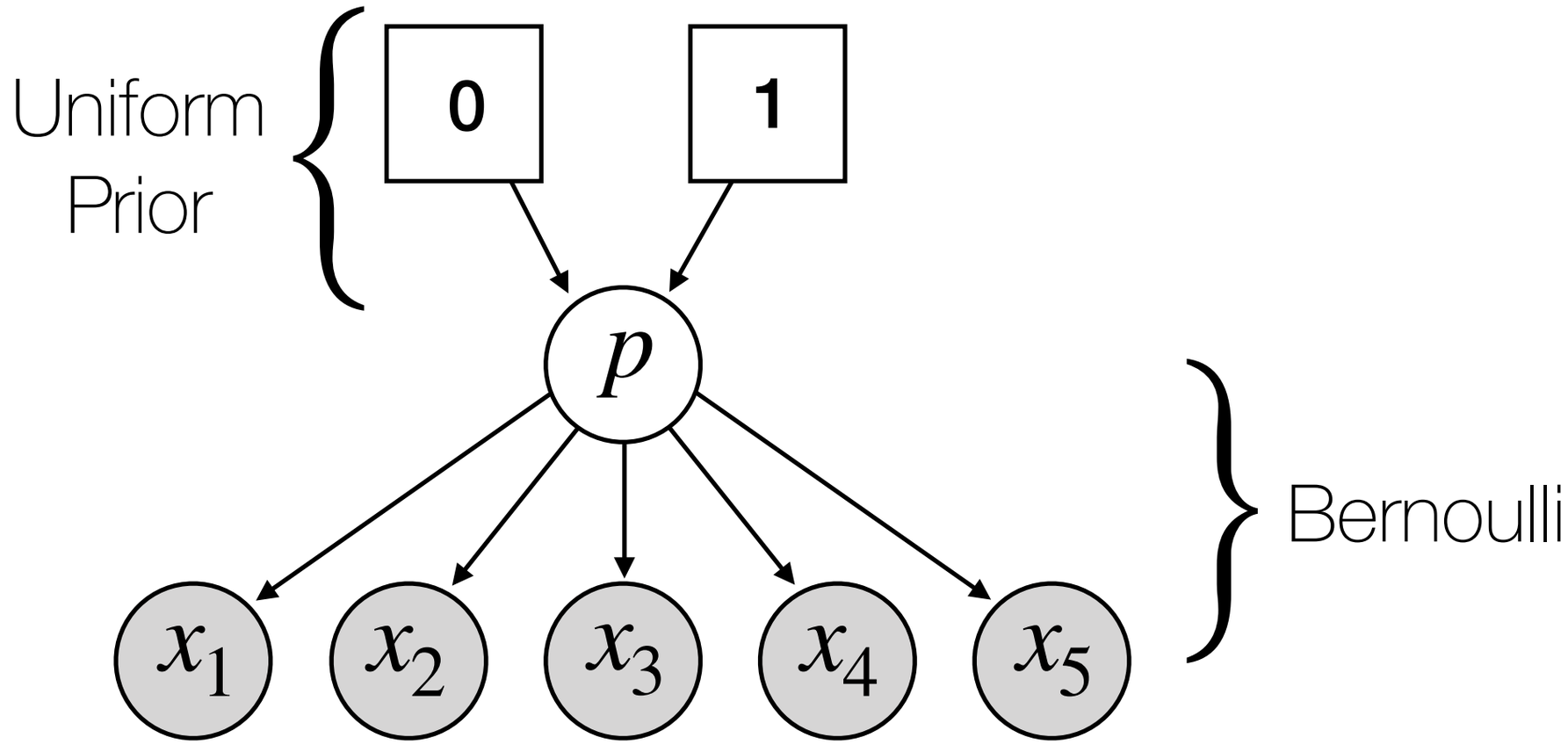
What's the structure of this model?
What can we infer about this model?
How much information will we have?

Single Bernoulli Trial



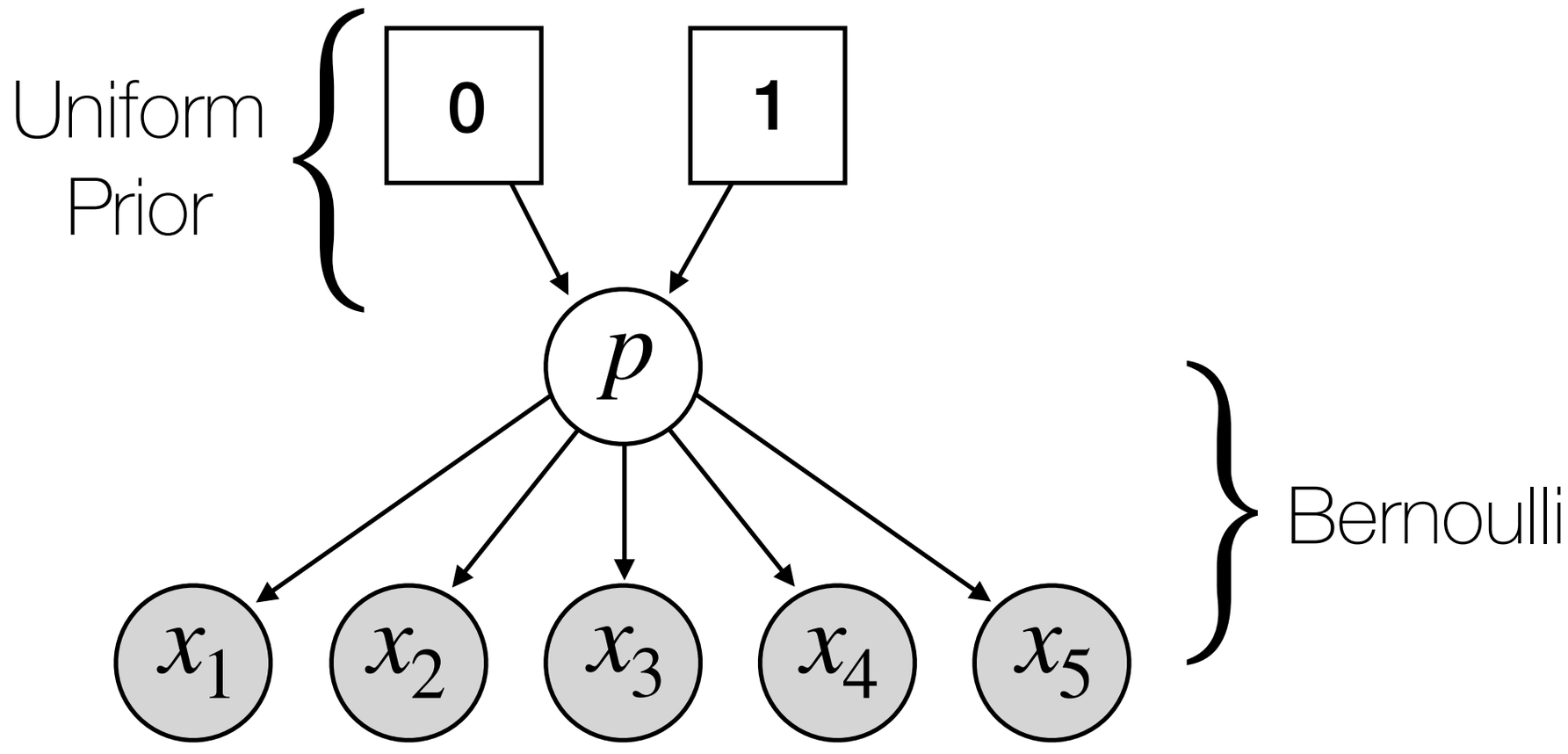

```
p ~ dnUnif(0,1)
x ~ dnBernoulli(p)
x.clamp(0)
```

Series of Bernoullis with Linked *p*



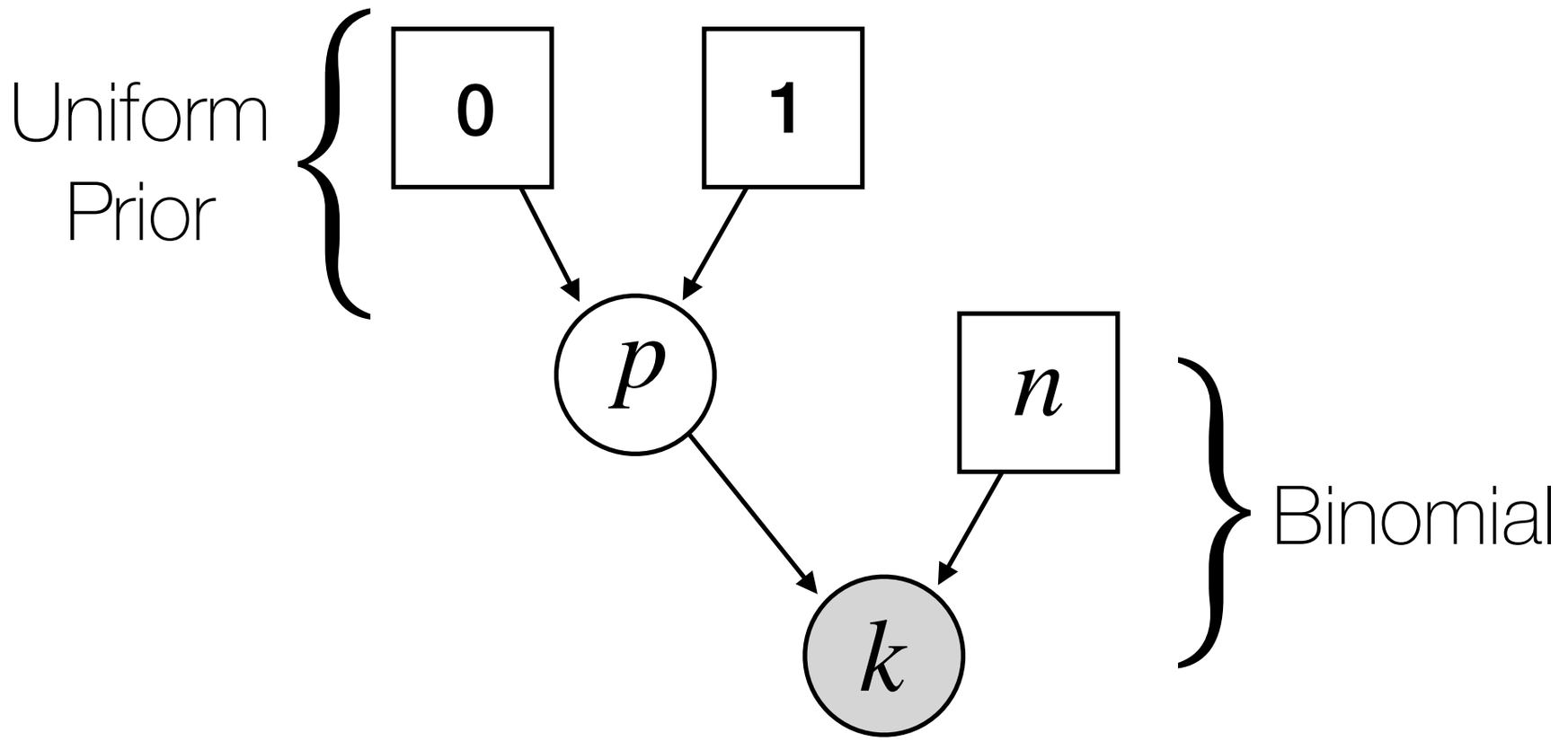
What can we infer about this model?
How much information will we have (relative to a single Bernoulli)?

Series of Bernoullis with Linked *p*



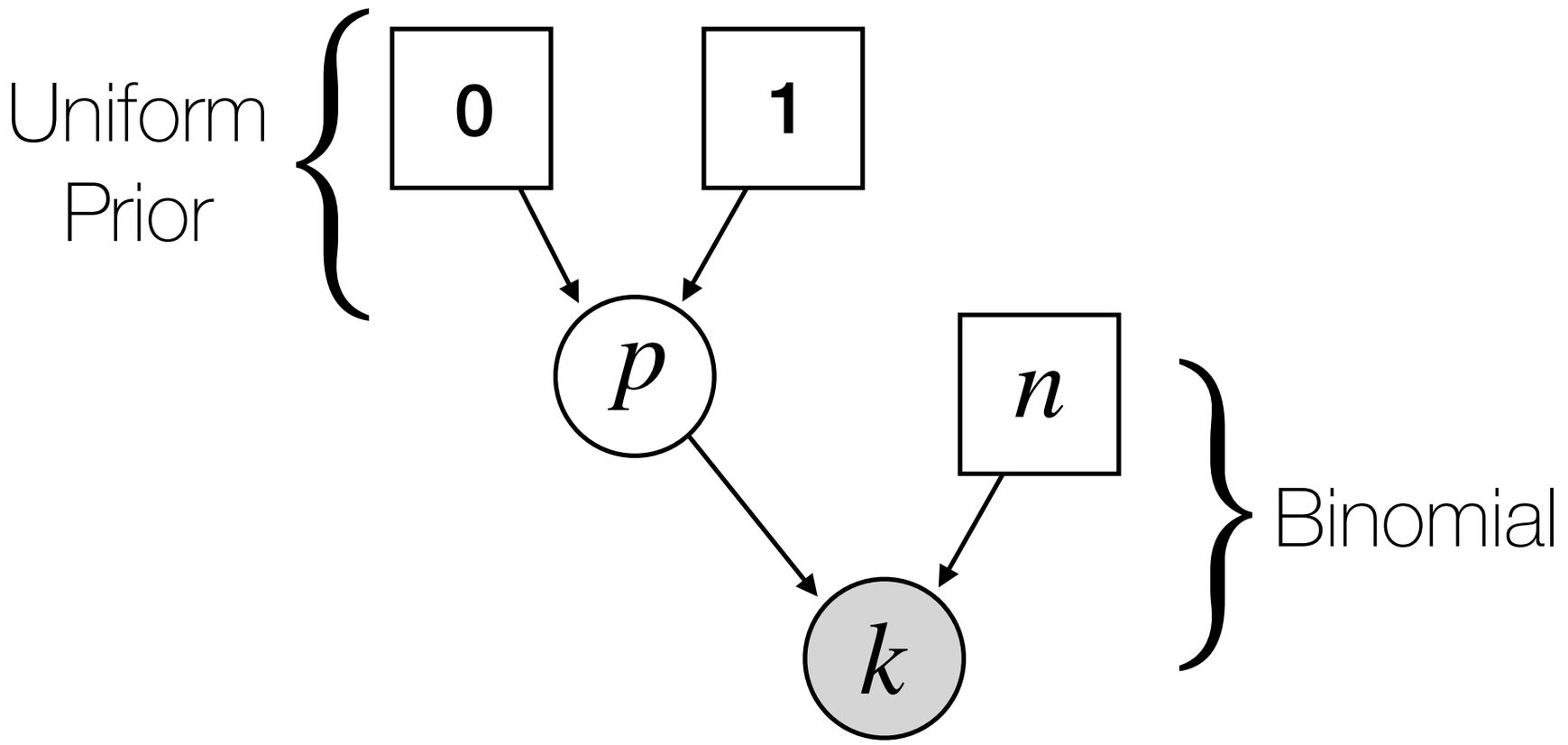

```
p ~ dnUnif(0,1)
for (i in 1:5){x[i] ~ dnBernoulli(p)}
x[1].clamp(0)
x[2].clamp(1)
x[3].clamp(1)
x[4].clamp(0)
x[5].clamp(1)
```

Single Binomial



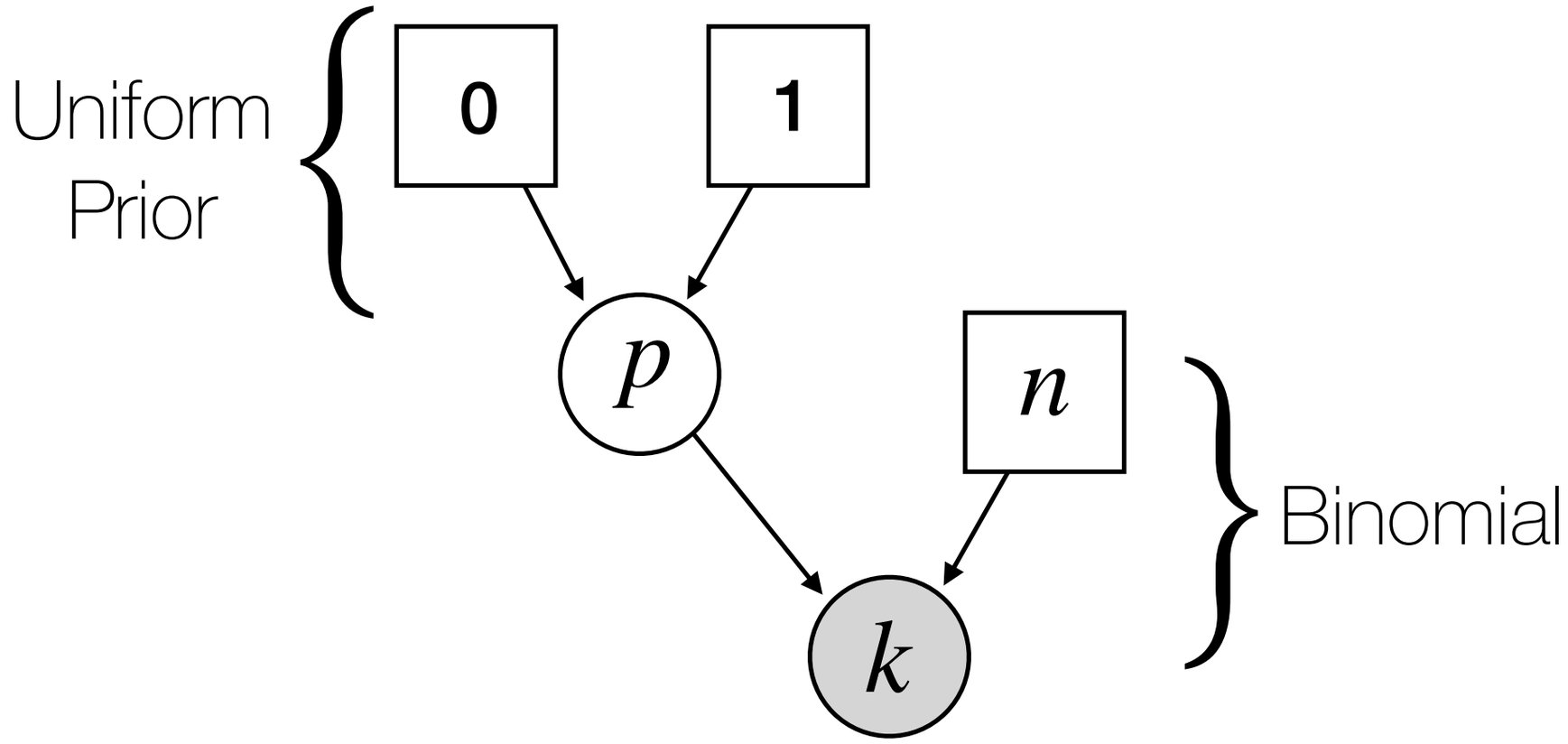
How does this model relate to the Bernoulli models?

Single Binomial




```
p ~ dnUnif(0,1)
n <- 5
k ~ dnBinomial(n,p)
k.clamp(3)
```

Setting up MCMC in RevBayes

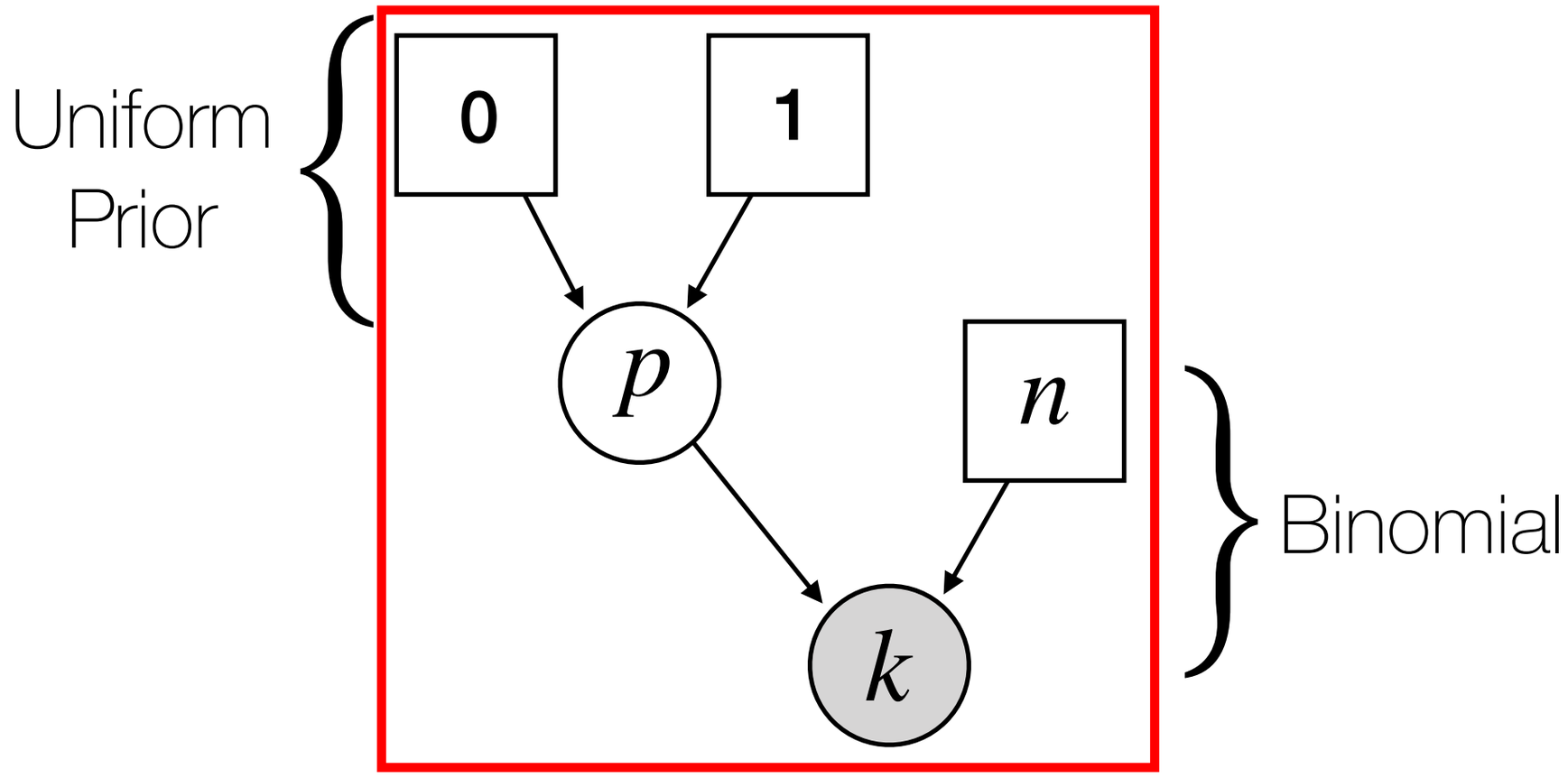


First, create a model object. You can pass any of the nodes to the constructor as a “handle”.

```
myModel = model(n)
```

NOTE: We use the = assignment operator for “workspace” variables.

Setting up MCMC in RevBayes



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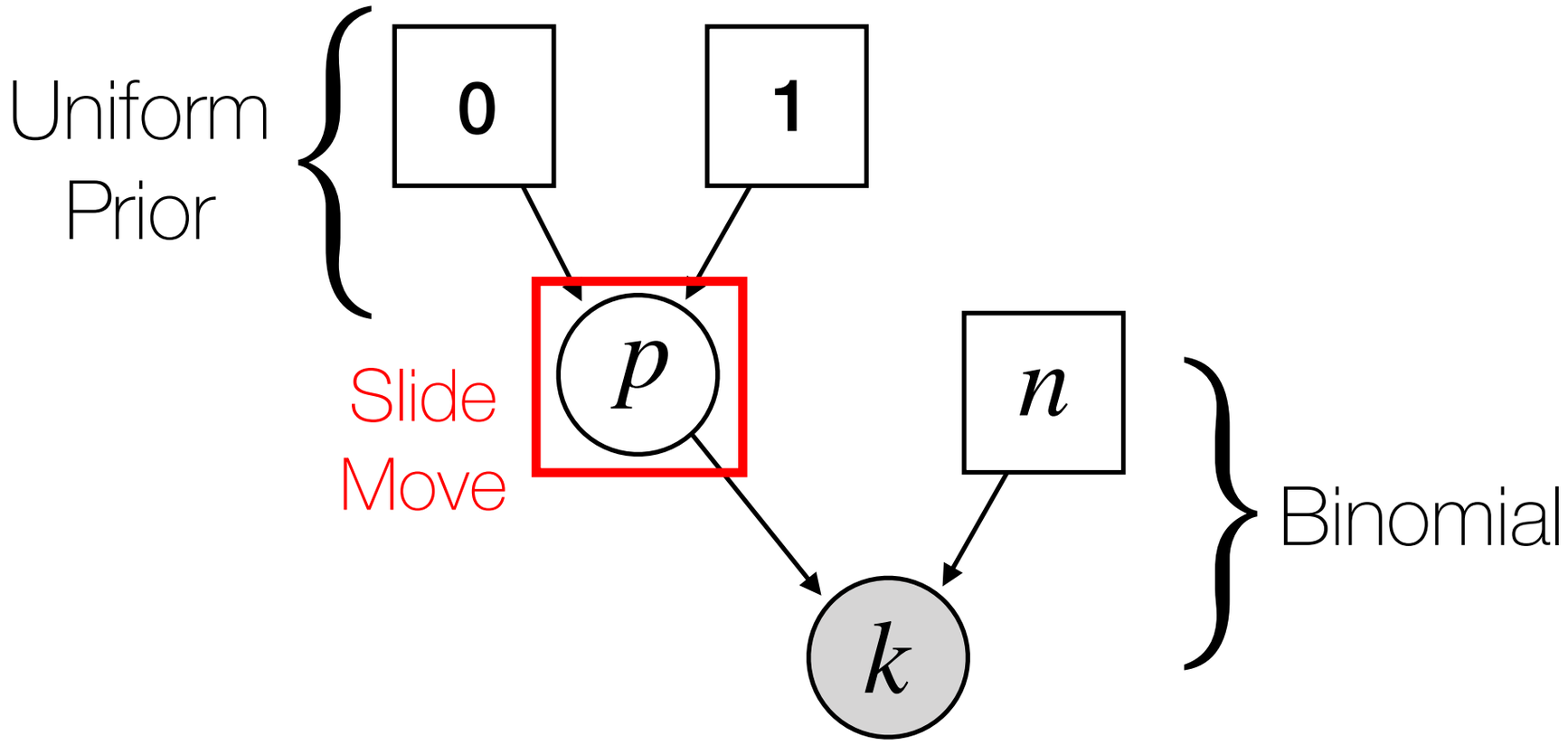


Next, we need to define a proposal distribution (move) for any parameters we are trying to infer.

```
moves = VectorMoves()
moves.append( mvSlide(p,delta=0.1,weight=1) )
```

Many different move types are available in RevBayes.

Setting up MCMC in RevBayes

As our MCMC runs, we need to keep track of our progress and sampled parameter values. To do that we use monitors.

```
monitors = VectorMonitors()
monitors.append( mnScreen(printgen=1000,p) )
monitors.append( mnModel(filename="myMCMC.log", printgen=10) )
```

```
   Running MCMC simulation
   This simulation runs 1 independent replicate.
   The simulator uses 1 different moves in a random move schedule with 1 moves per iteration

Iter        |      Posterior   |     Likelihood   |          Prior   |              p   |    elapsed   |        ETA   |
-------------------------------------------------------------------------------------------------------------------
0           |       -10.2115   |       -10.2115   |              0   |     0.08309243   |   00:00:00   |   --:--:--   |
1000        |        -4.8278   |        -4.8278   |              0   |      0.5133643   |   00:00:00   |   --:--:--   |
2000        |       -4.97547   |       -4.97547   |              0   |       0.453571   |   00:00:00   |   00:00:00   |
3000        |       -4.78164   |       -4.78164   |              0   |      0.5619349   |   00:00:00   |   00:00:00   |
4000        |       -5.18177   |       -5.18177   |              0   |      0.7290954   |   00:00:00   |   00:00:00   |
5000        |       -5.98066   |       -5.98066   |              0   |      0.2898232   |   00:00:00   |   00:00:00   |
6000        |       -4.78464   |       -4.78464   |              0   |      0.5540578   |   00:00:00   |   00:00:00   |
7000        |       -4.78044   |       -4.78044   |              0   |      0.5690397   |   00:00:00   |   00:00:00   |
8000        |       -4.79273   |       -4.79273   |              0   |       0.541859   |   00:00:00   |   00:00:00   |
9000        |       -4.96352   |       -4.96352   |              0   |      0.4572184   |   00:00:00   |   00:00:00   |
10000       |       -4.80438   |       -4.80438   |              0   |      0.6120314   |   00:00:00   |   00:00:00   |
```

Setting up MCMC in RevBayes

Next we create an MCMC object.

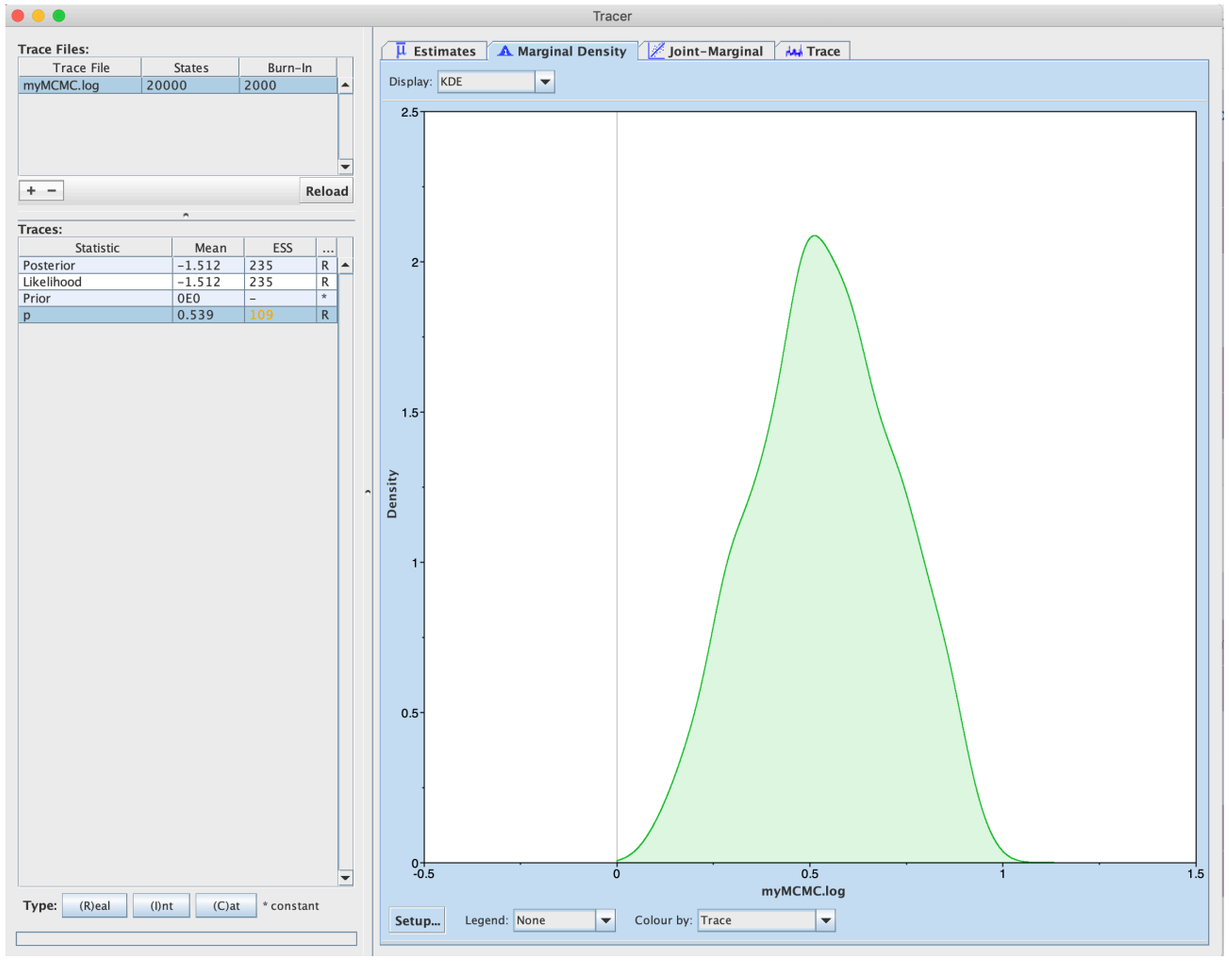
```
myMCMC = mcmc(myModel,moves,monitors)
```

Now, we start the MCMC!

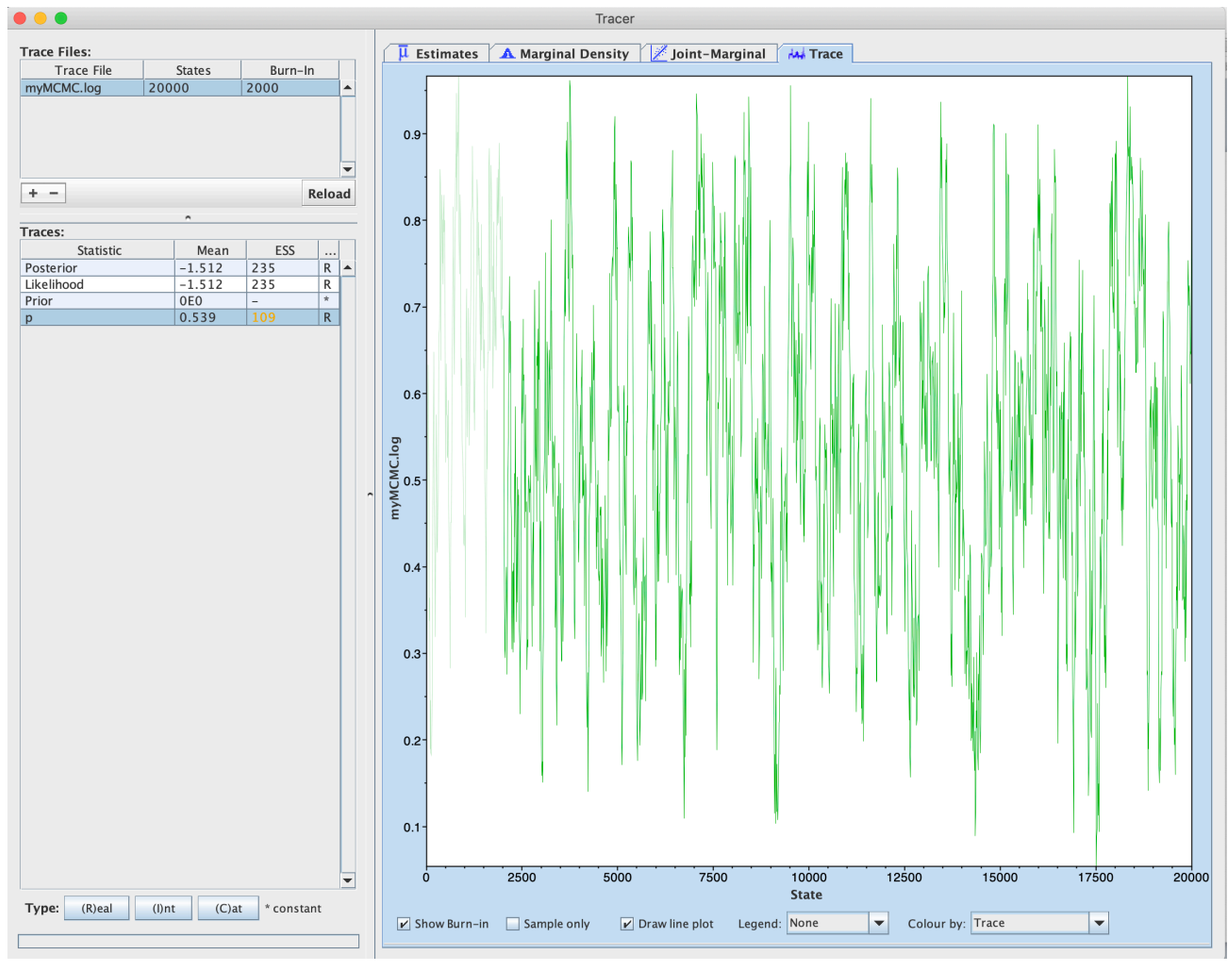
```
myMCMC.run(20000)
```

Wait - what does this 20,000 mean?

Tracer



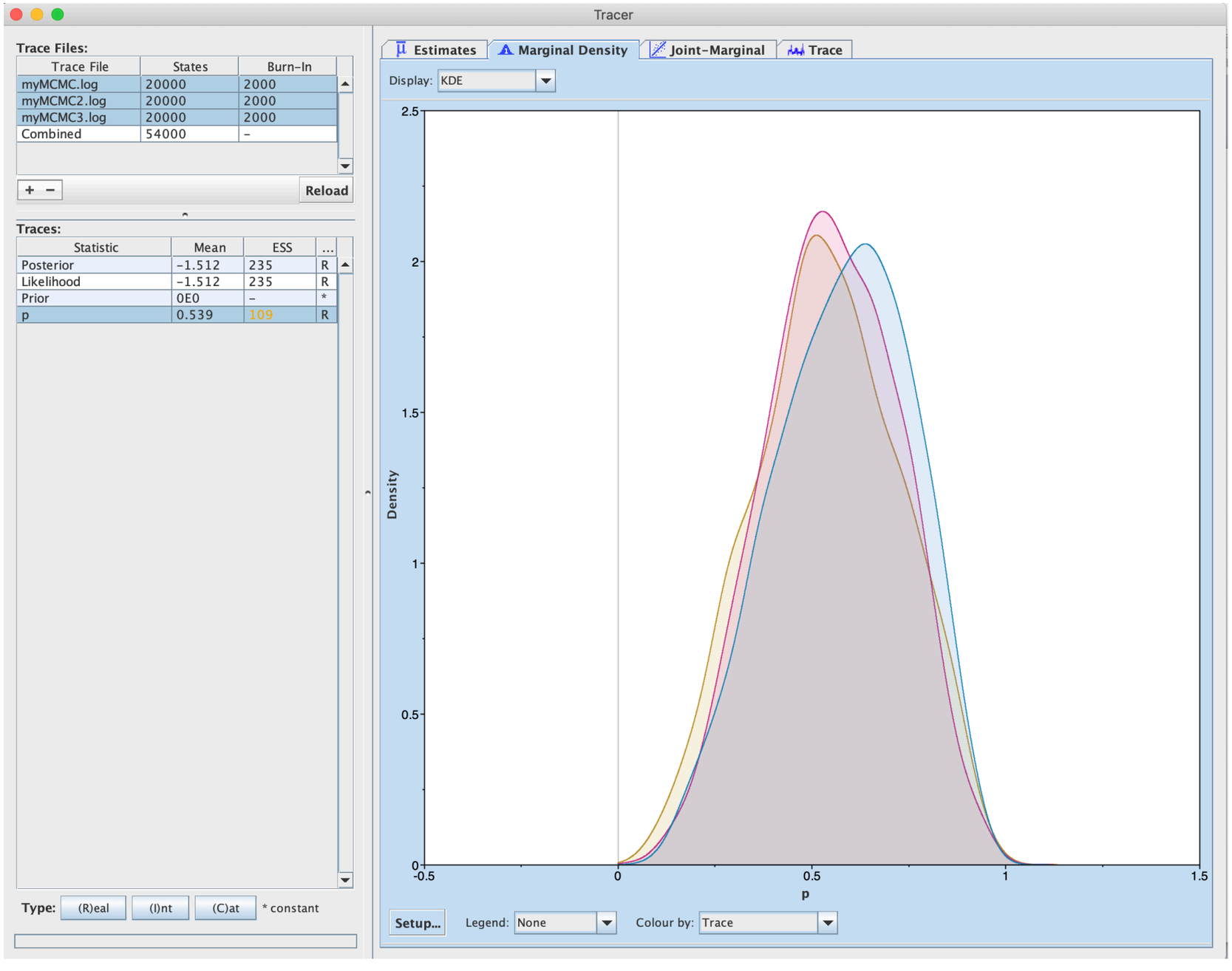
Marginal Distribution

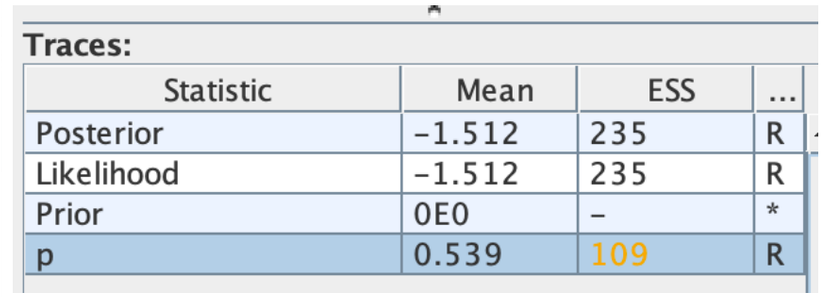


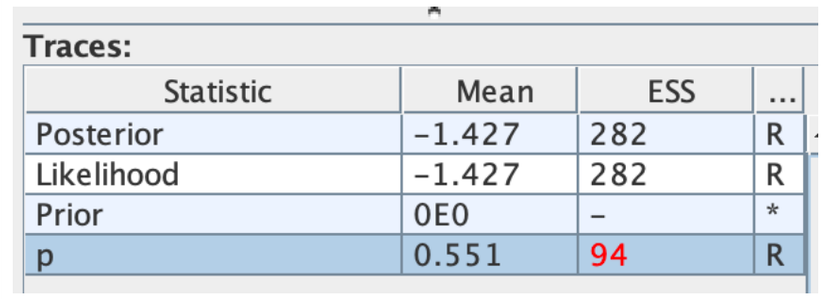
Trace Plot

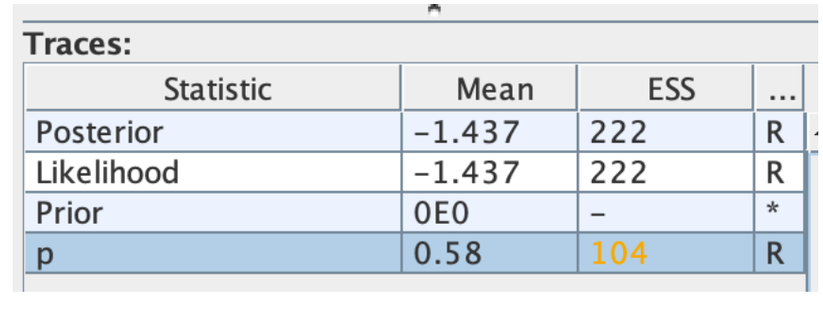
Jeremy M. Brown

Assessing Convergence

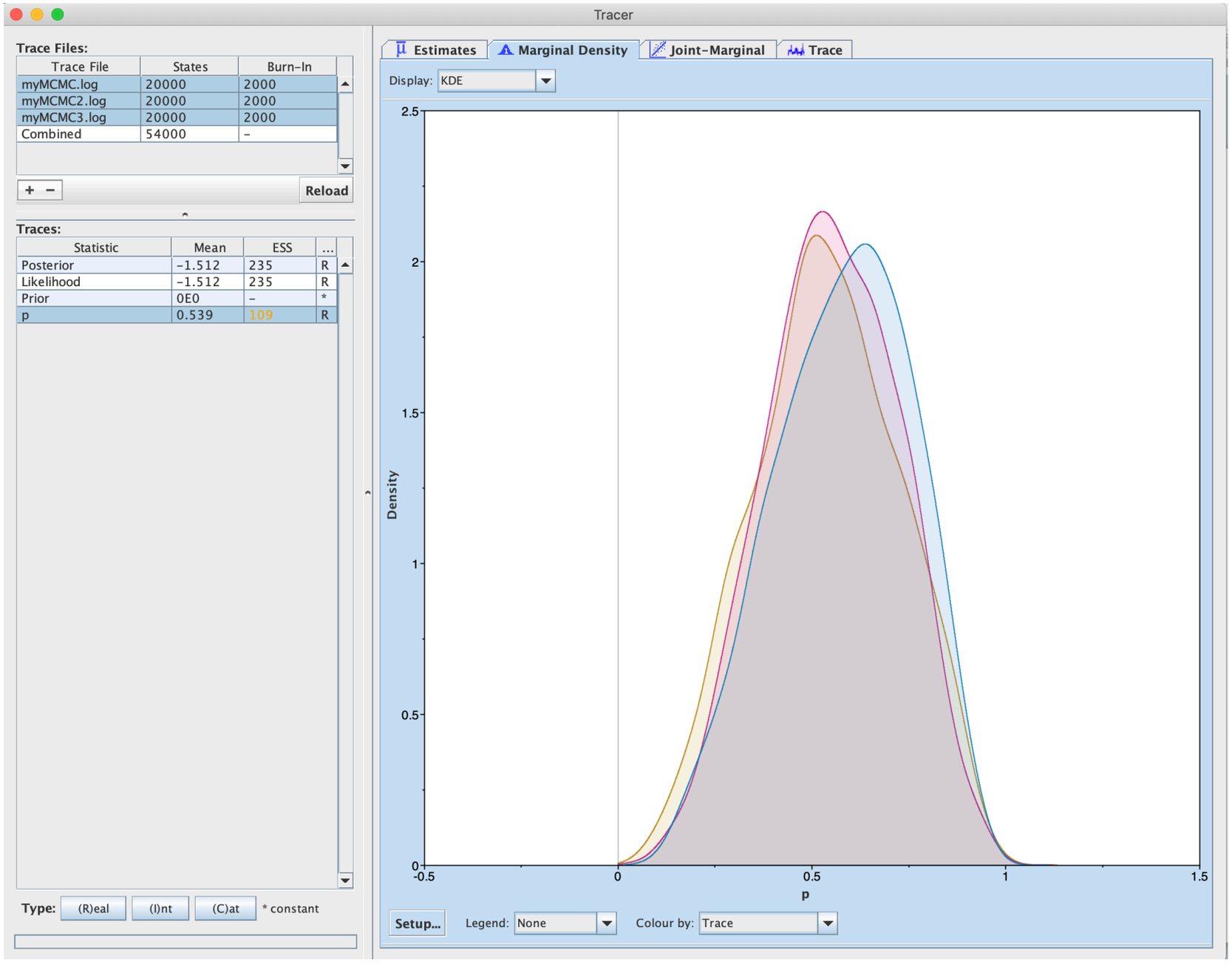


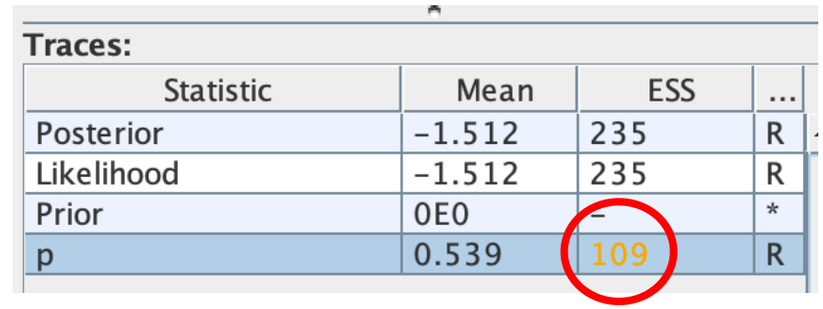


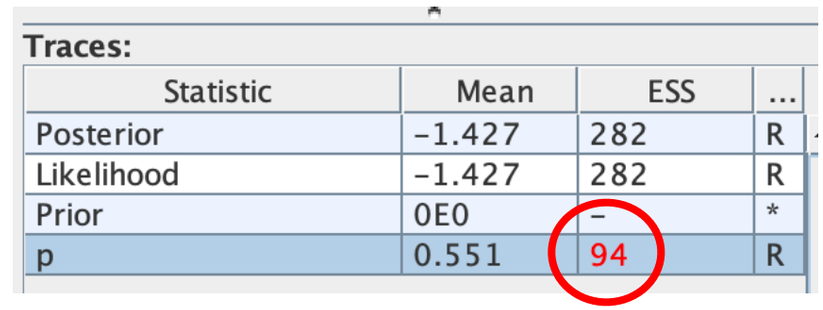


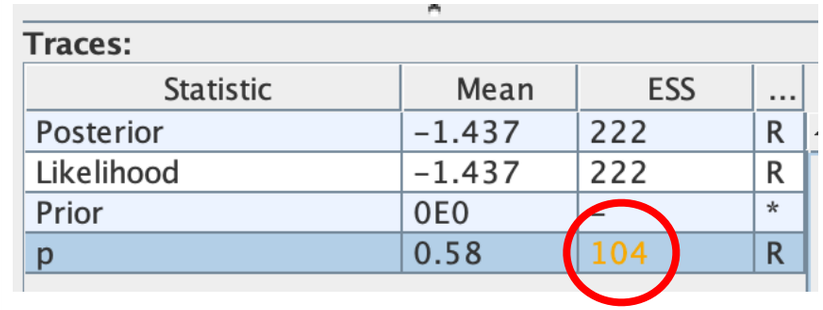


Assessing Convergence









How many samples did we draw during our MCMC analyses?

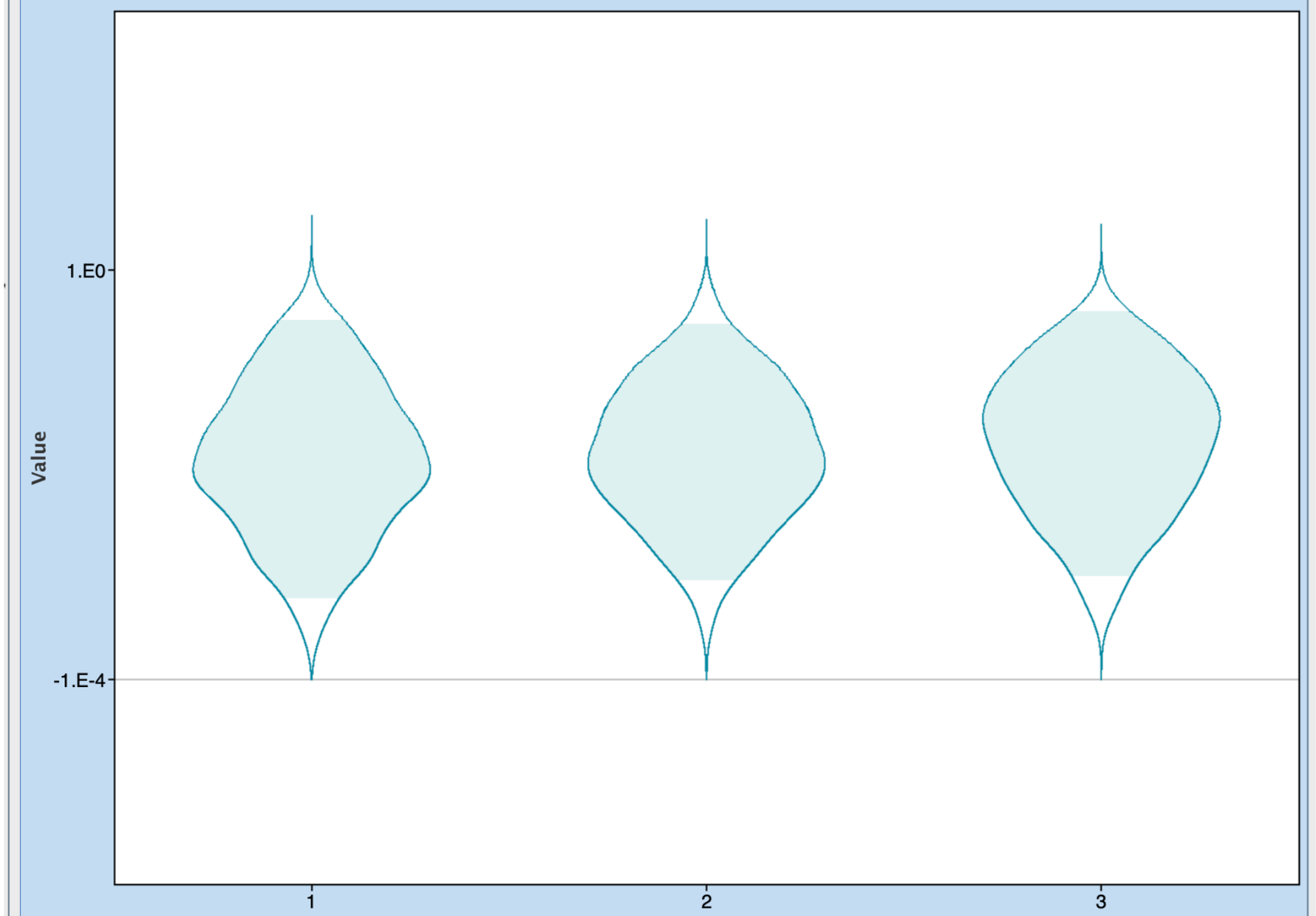
Jeremy M. Brown

95% Highest Posterior Density (HPD) Intervals

Jeremy M. Brown

Estimates | Marginal Density | Joint-Marginal | Trace

Summary Statistic	myMCMC.logp	myMCMC2.logp	myMCMC3.logp
mean	0.5389	0.5515	0.5805
stderr of mean	0.0175	0.0173	0.0171
stdev	0.1828	0.1681	0.1745
variance	0.0334	0.0283	0.0305
median	0.5357	0.5512	0.5908
value range	[0.0543, 0.9669]	[0.0437, 0.9709]	[0.0958, 0.9501]
geometric mean	0.5024	0.5219	0.5495
95% HPD interval	[0.1984, 0.878]	[0.2426, 0.8685]	[0.2526, 0.8996]
auto-correlation time (ACT)	164.7238	190.594	173.4795
effective sample size (ESS)	109.3	94.5	103.8
number of samples	1801	1801	1801



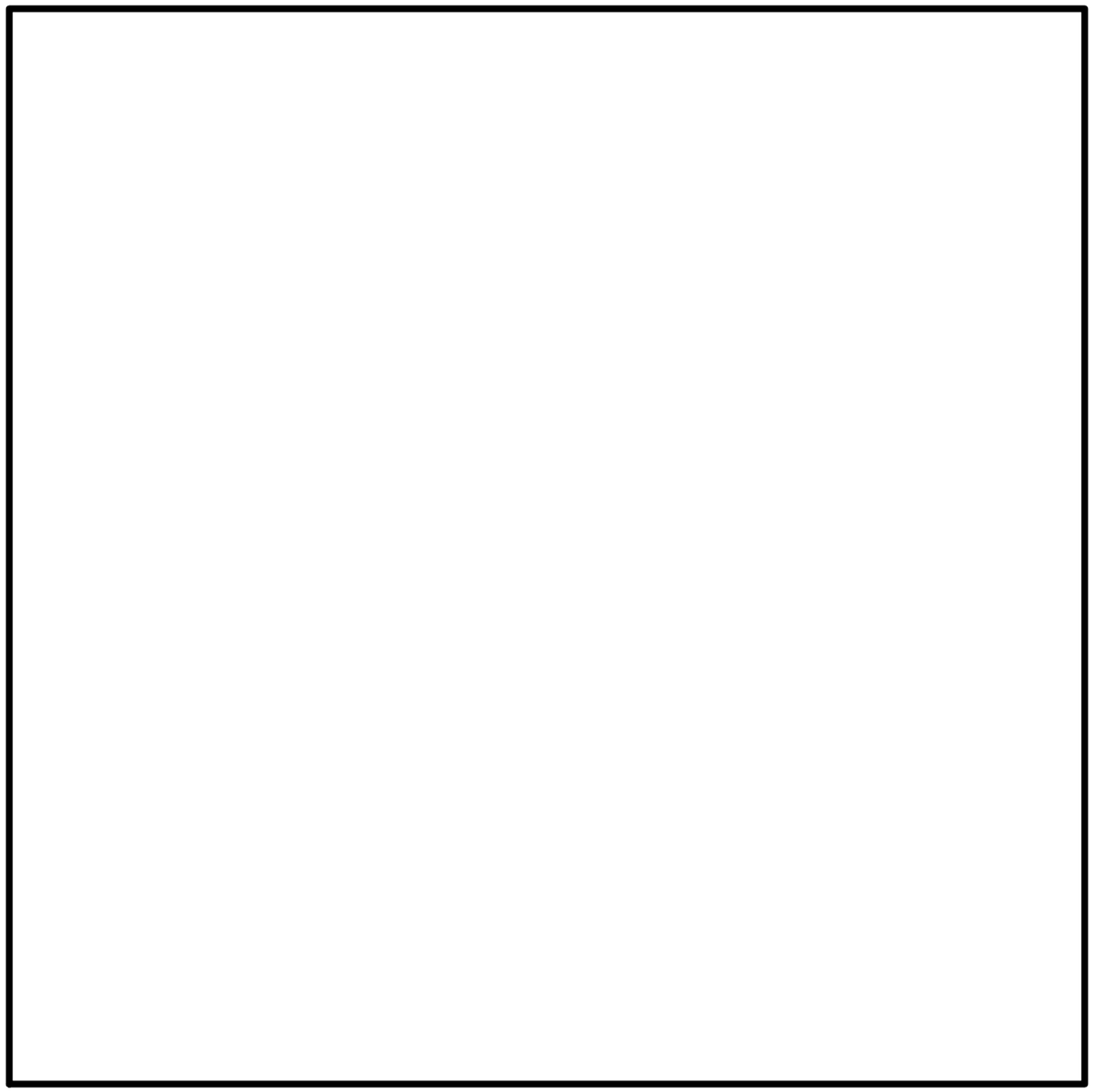
Setup... Show: violin

Phylogenetic Graphical Models

Jeremy M. Brown

Model Space (conceptual)

All Possible Ways Genes Could Evolve



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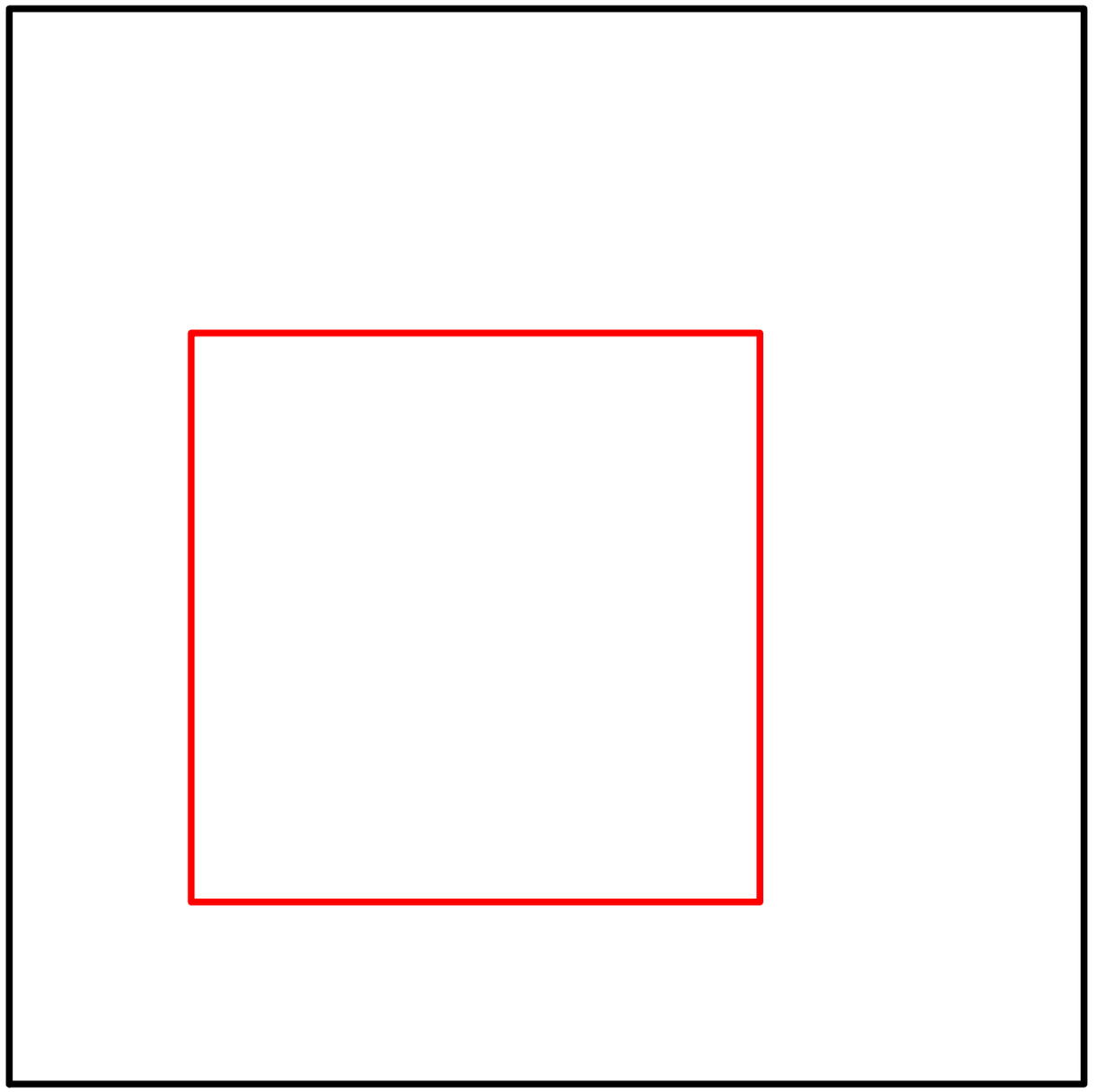
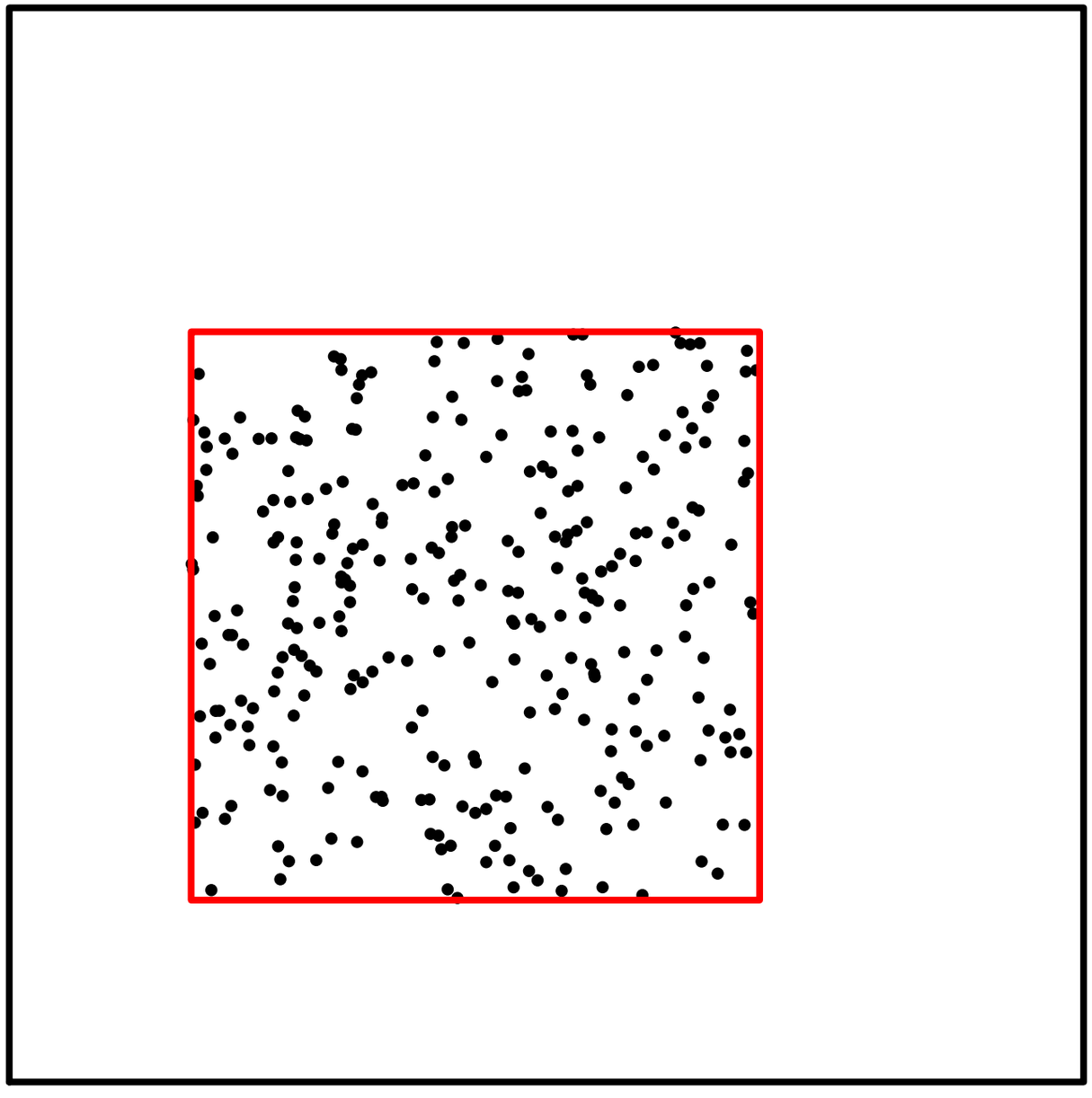


The Types of Evolution That Are Built Into Many Programs

Our Hope

All Possible Ways Genes Could Evolve

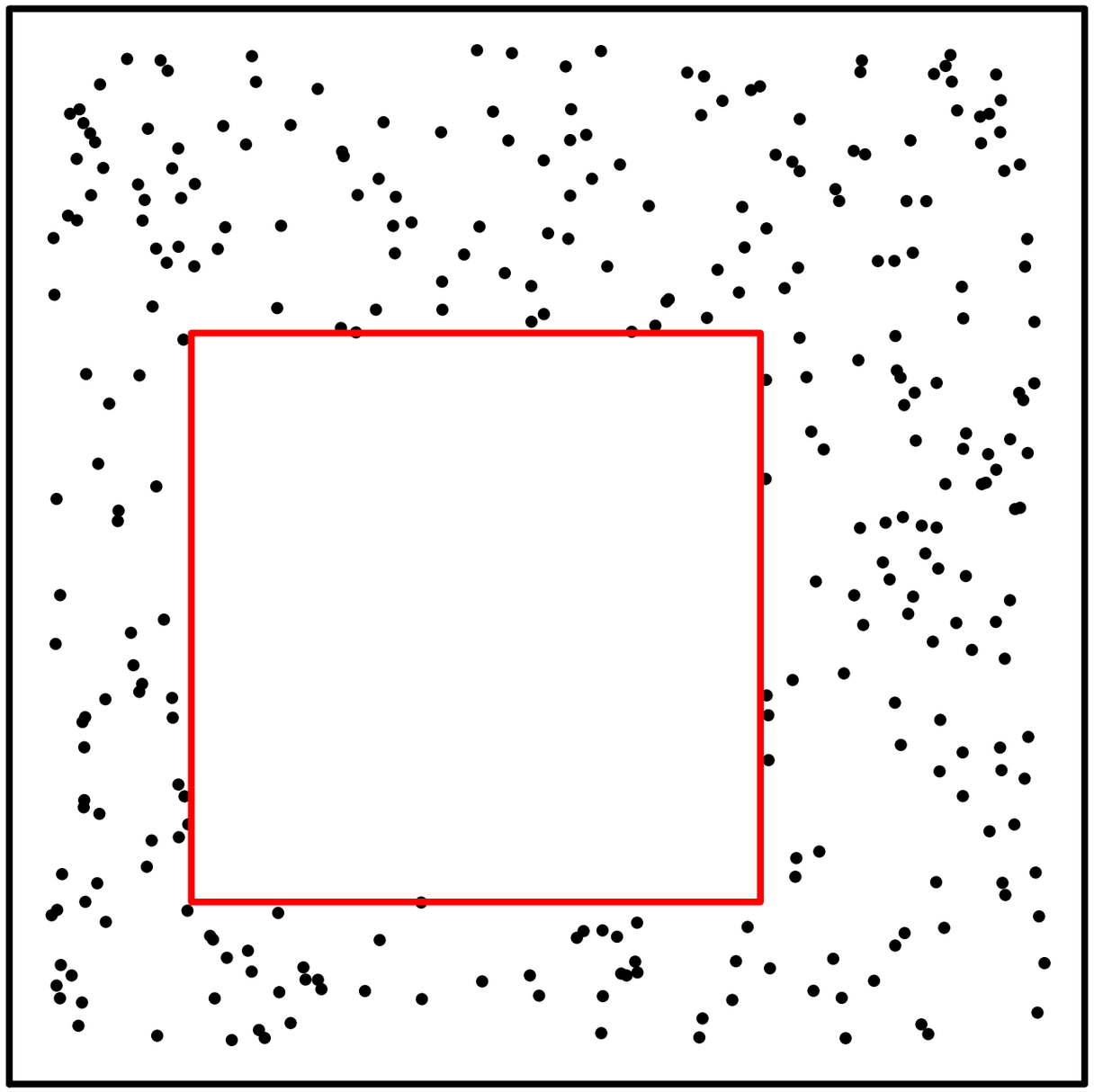


The Types of Evolution That Are Built Into Many Programs

Jeremy M. Brown

Our Fears

All Possible Ways Genes Could Evolve

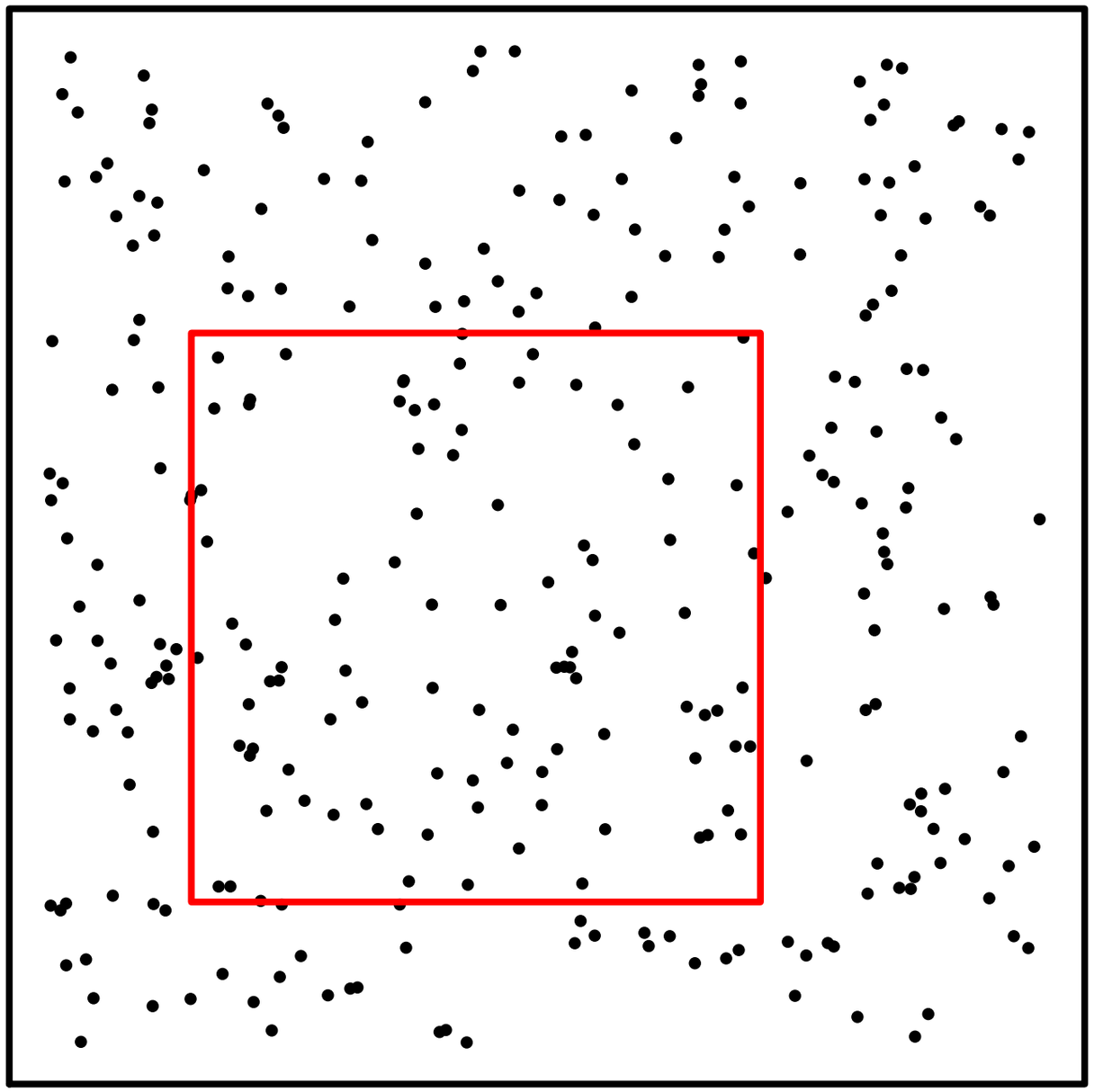


The Types of Evolution That Are Built Into Many Programs

Jeremy M. Brown

The Probable Truth

All Possible Ways Genes Could Evolve



The Types of Evolution That Are Built Into Many Programs

Jeremy M. Brown

The Probable Truth

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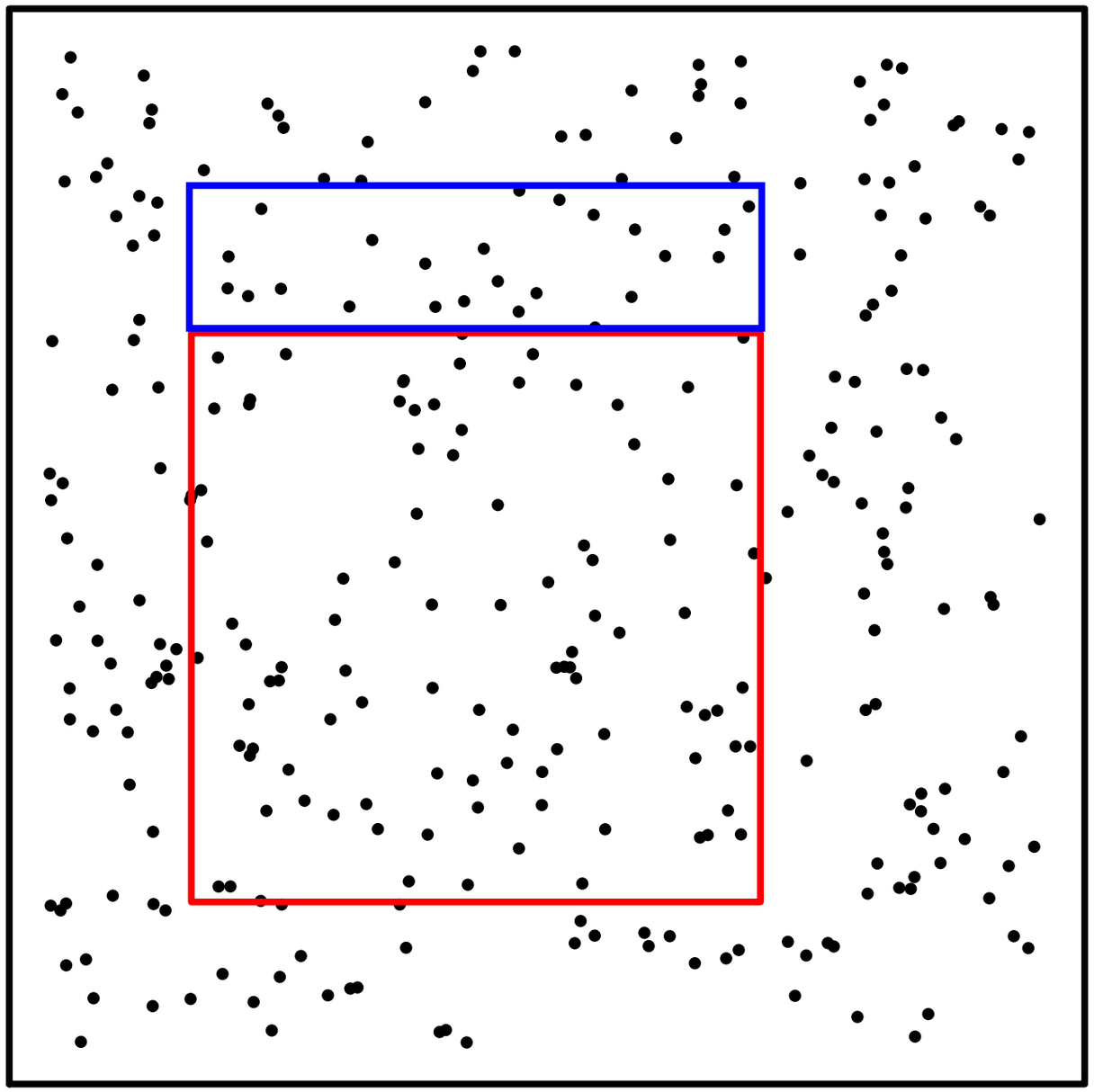
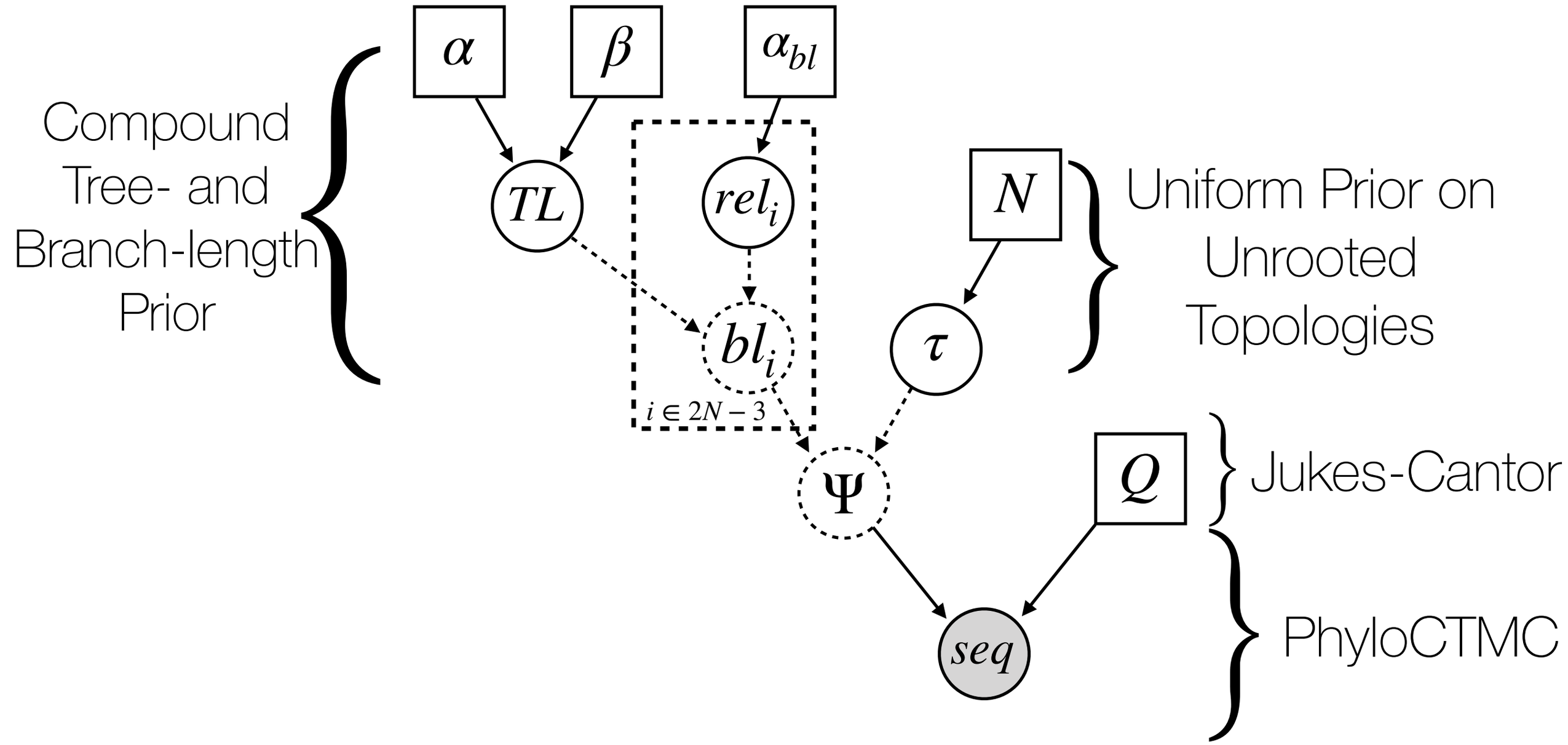


The Types of Evolution That Are Built Into Many Programs

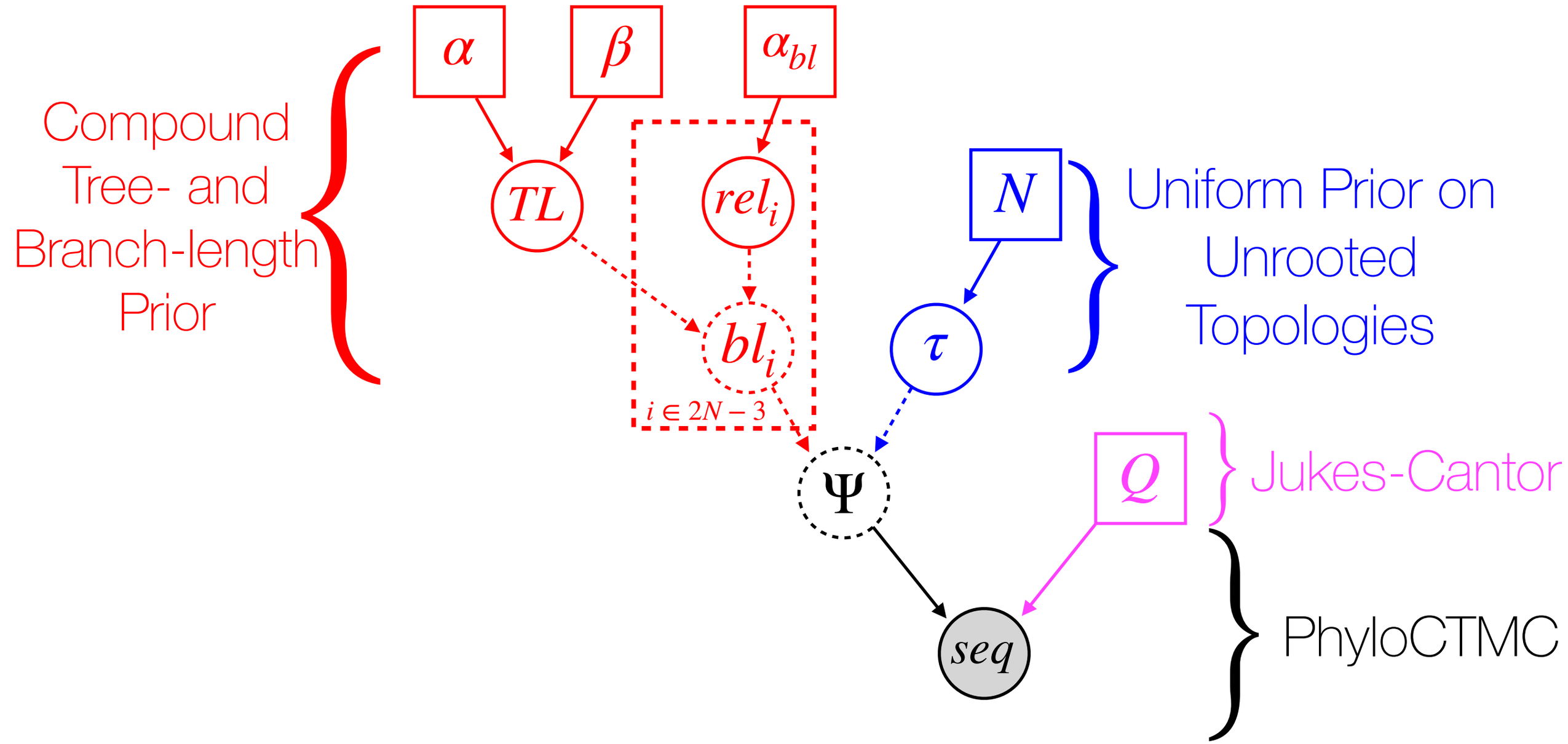
Types of Evolution that You'd Like to Try!

Jeremy M. Brown

Jukes-Cantor



Jukes-Cantor



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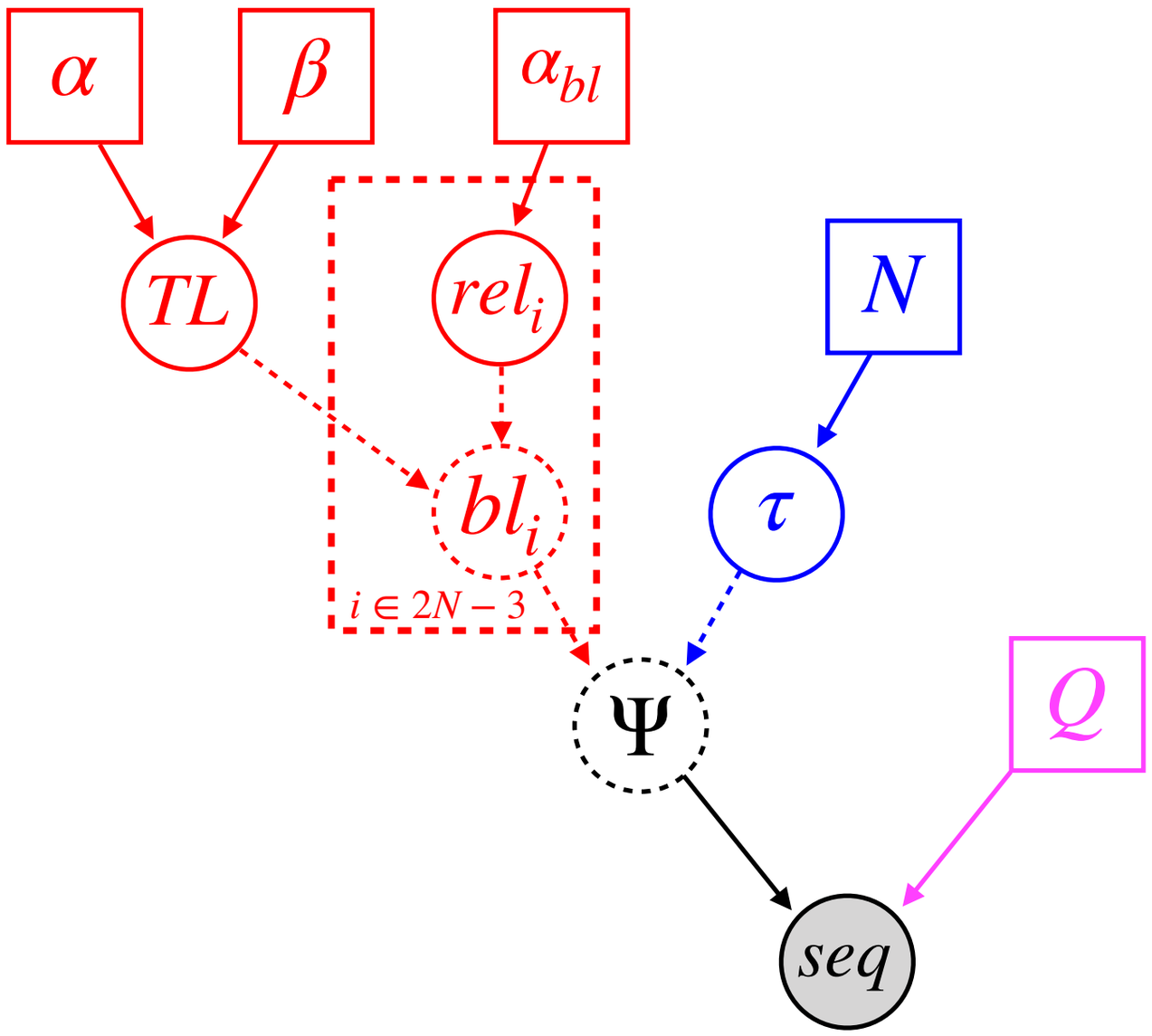


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n_branches <- 2 * n_taxa - 3

topology ~ dnUniformTopology(taxa)

alpha <- 2
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TL ~ dnGamma(alpha,beta)

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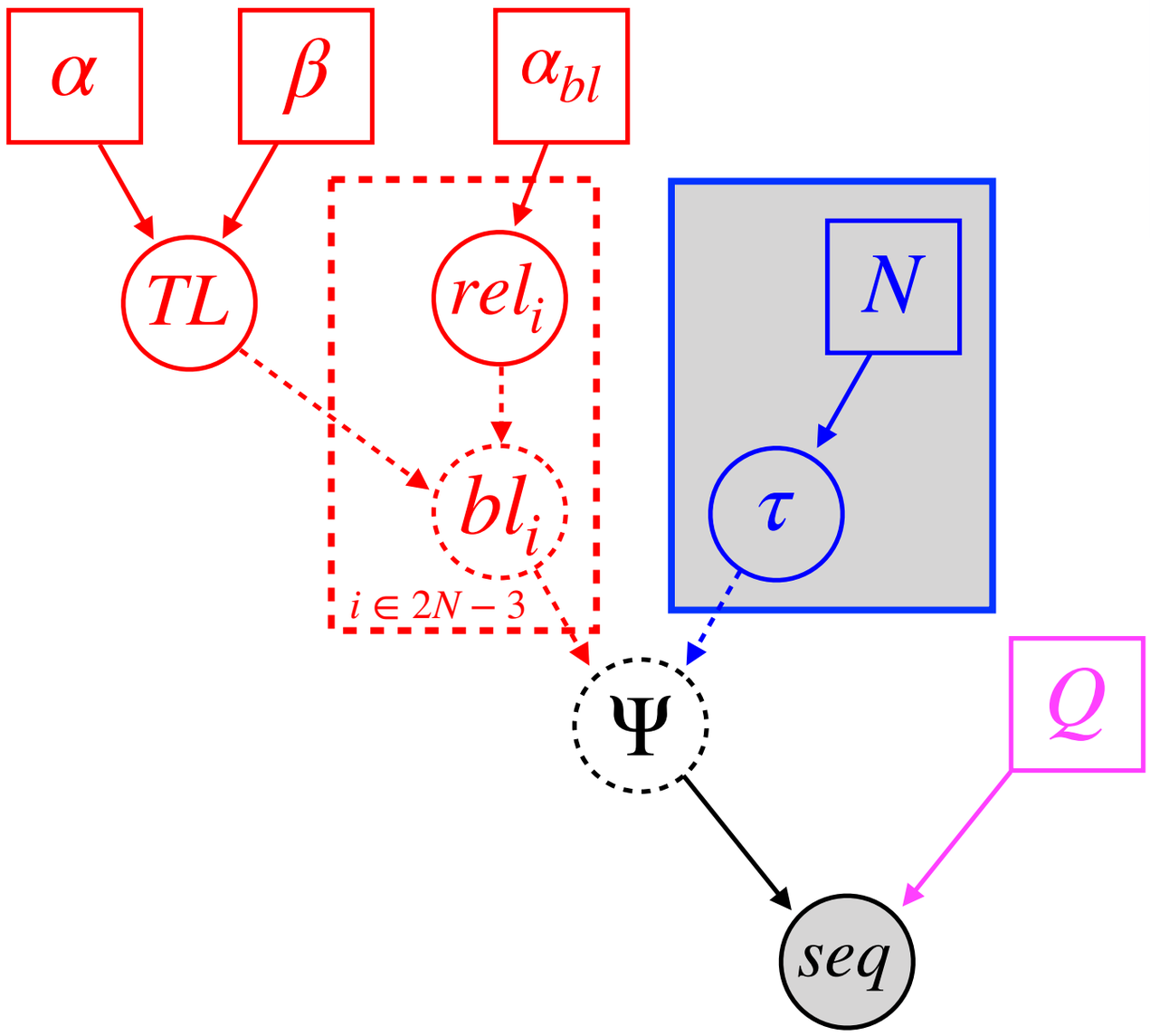
Jukes-Cantor

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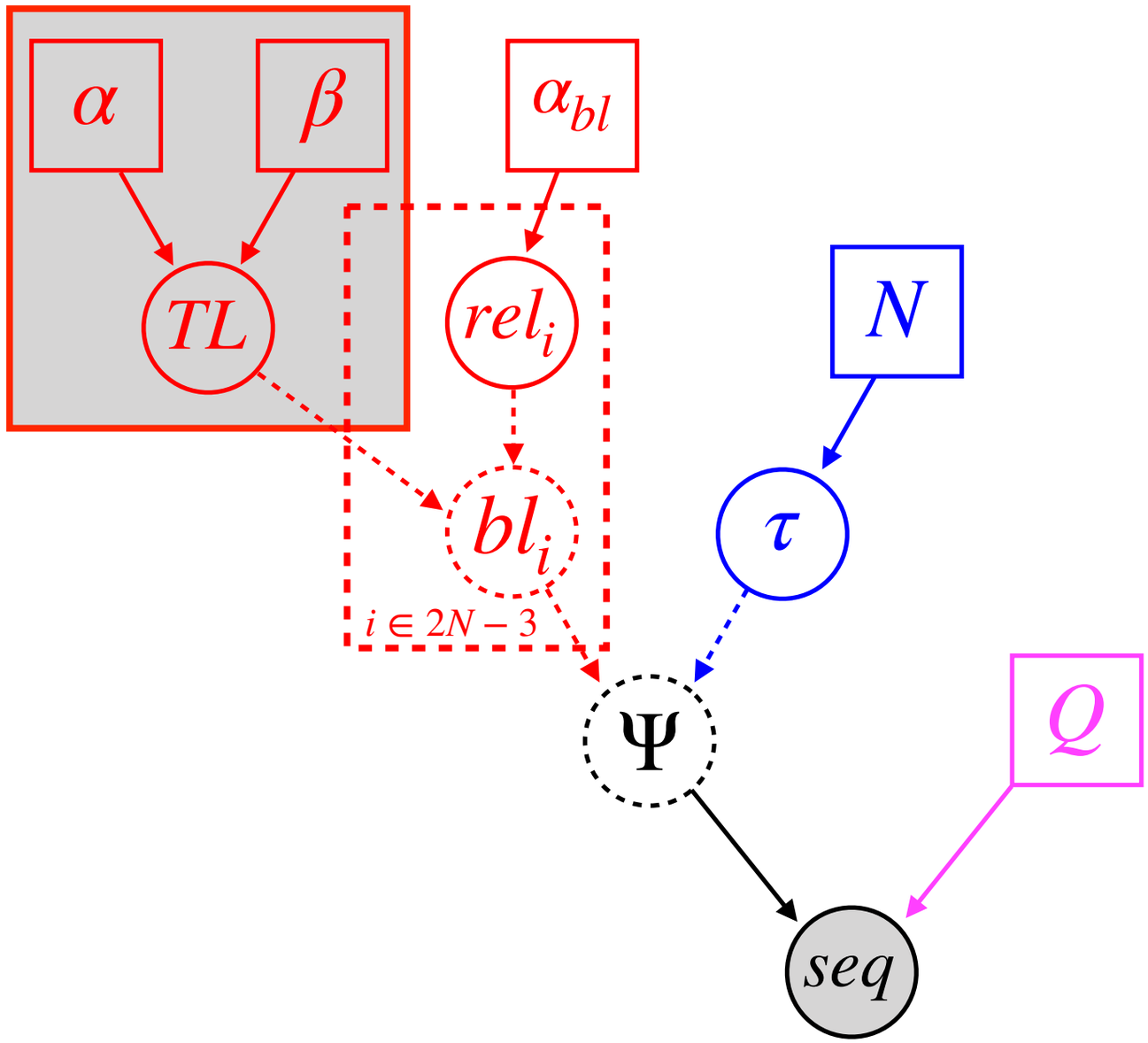
Jukes-Cantor

(Compound Dirichlet tree- and branch-length prior)



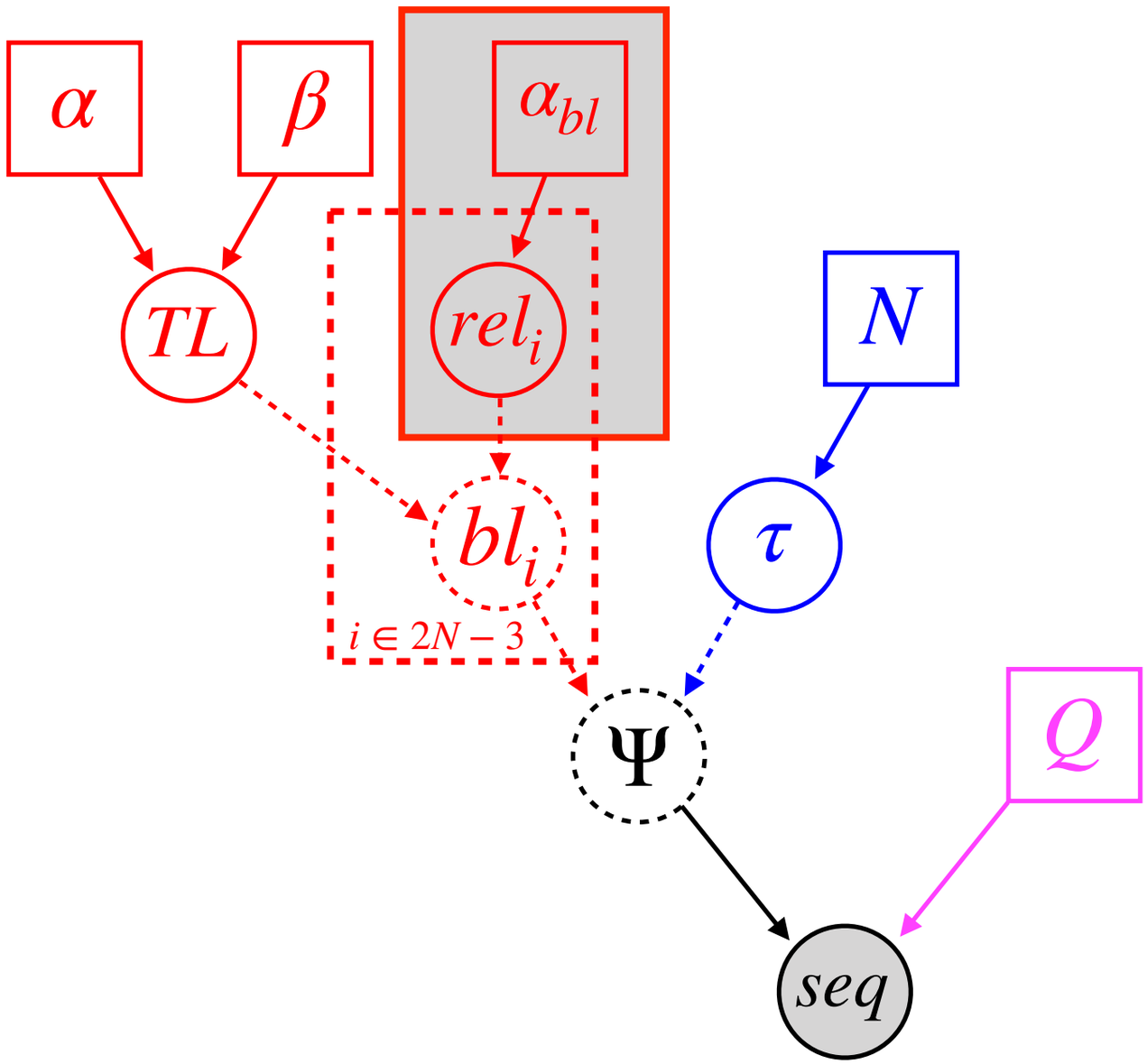
Tree Length

$Gamma(\alpha, \beta)$

Jeremy M. Brown

Jukes-Cantor

(Compound Dirichlet tree- and branch-length prior)



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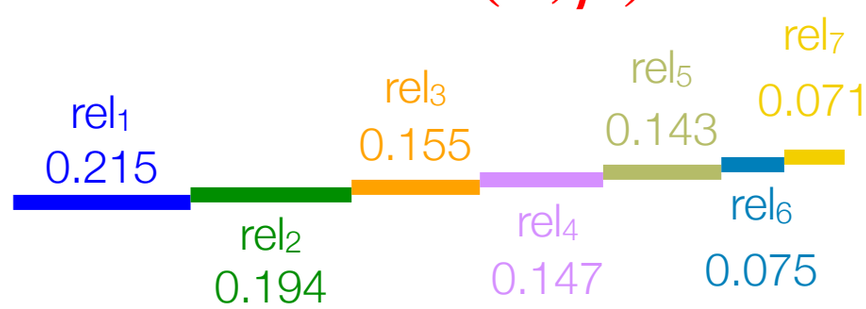


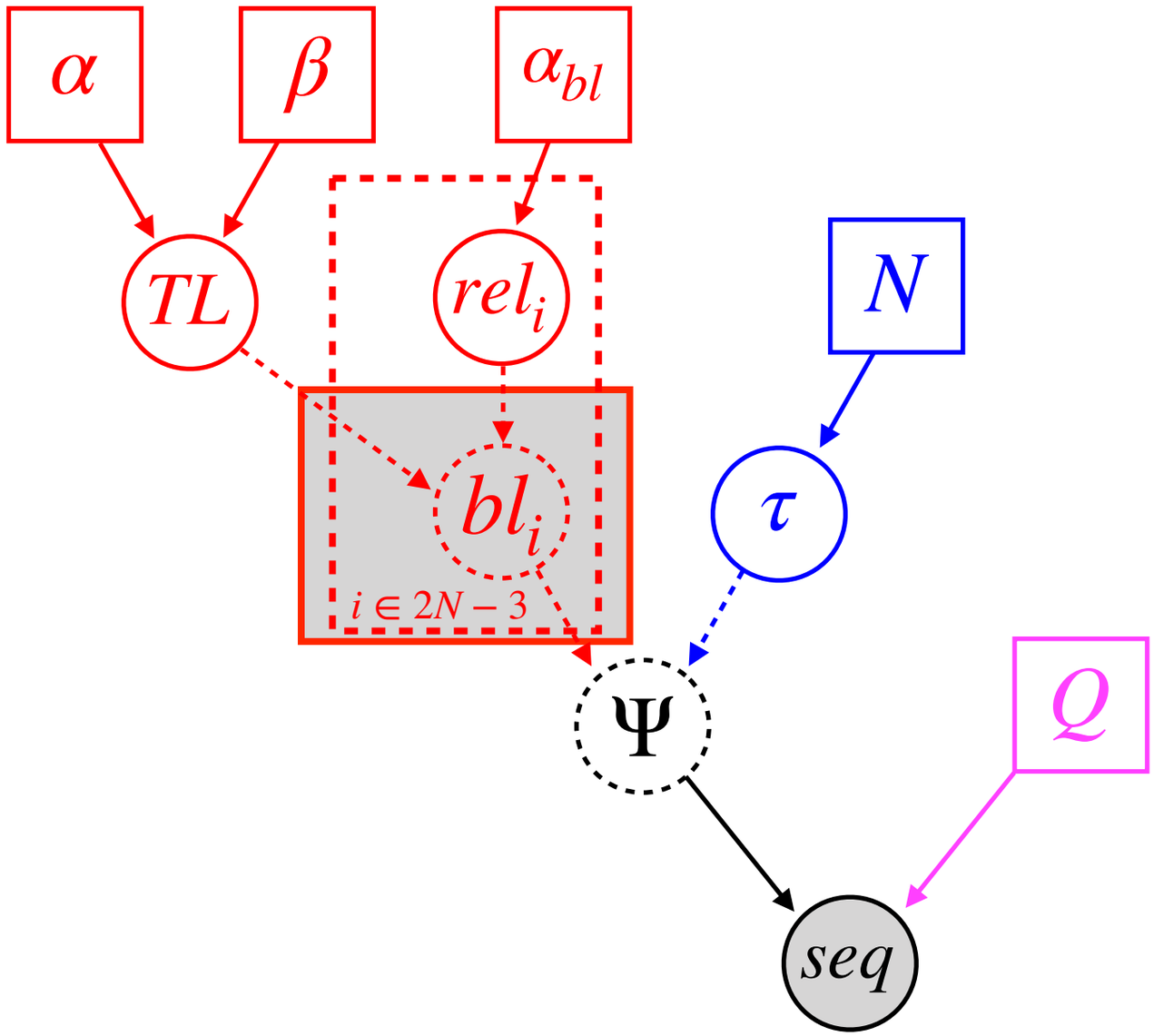
Relative Branch Lengths

$Dir(\alpha_{bl})$

Jeremy M. Brown

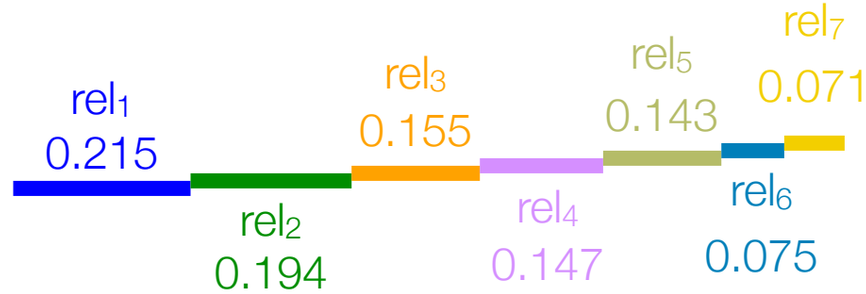
Jukes-Cantor

(Compound Dirichlet tree- and branch-length prior)



Tree Length

$Gamma(\alpha, \beta)$



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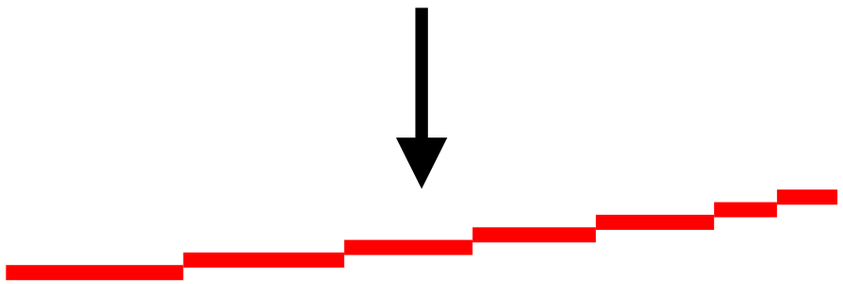

Branch Lengths

Jeremy M. Brown

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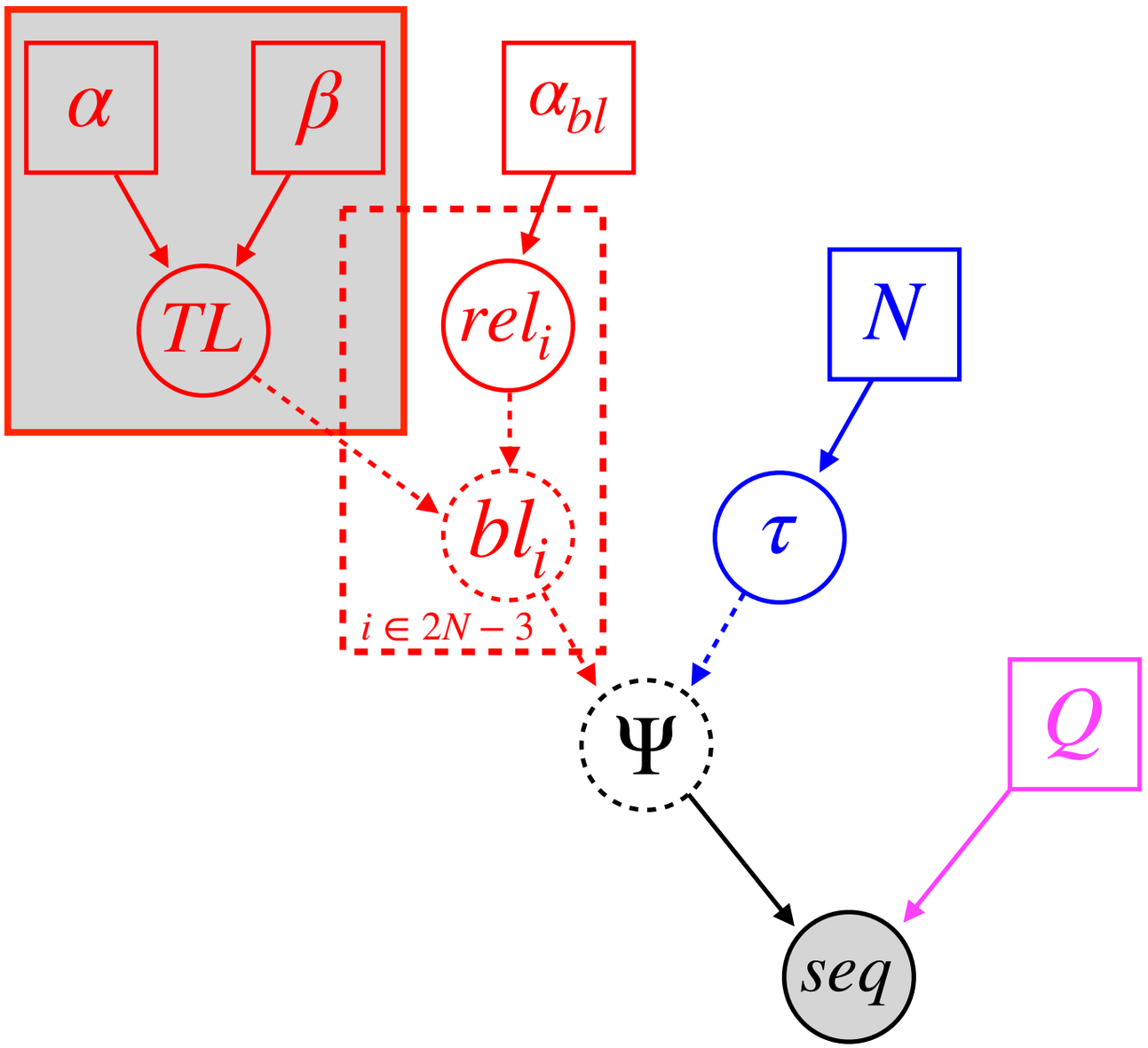


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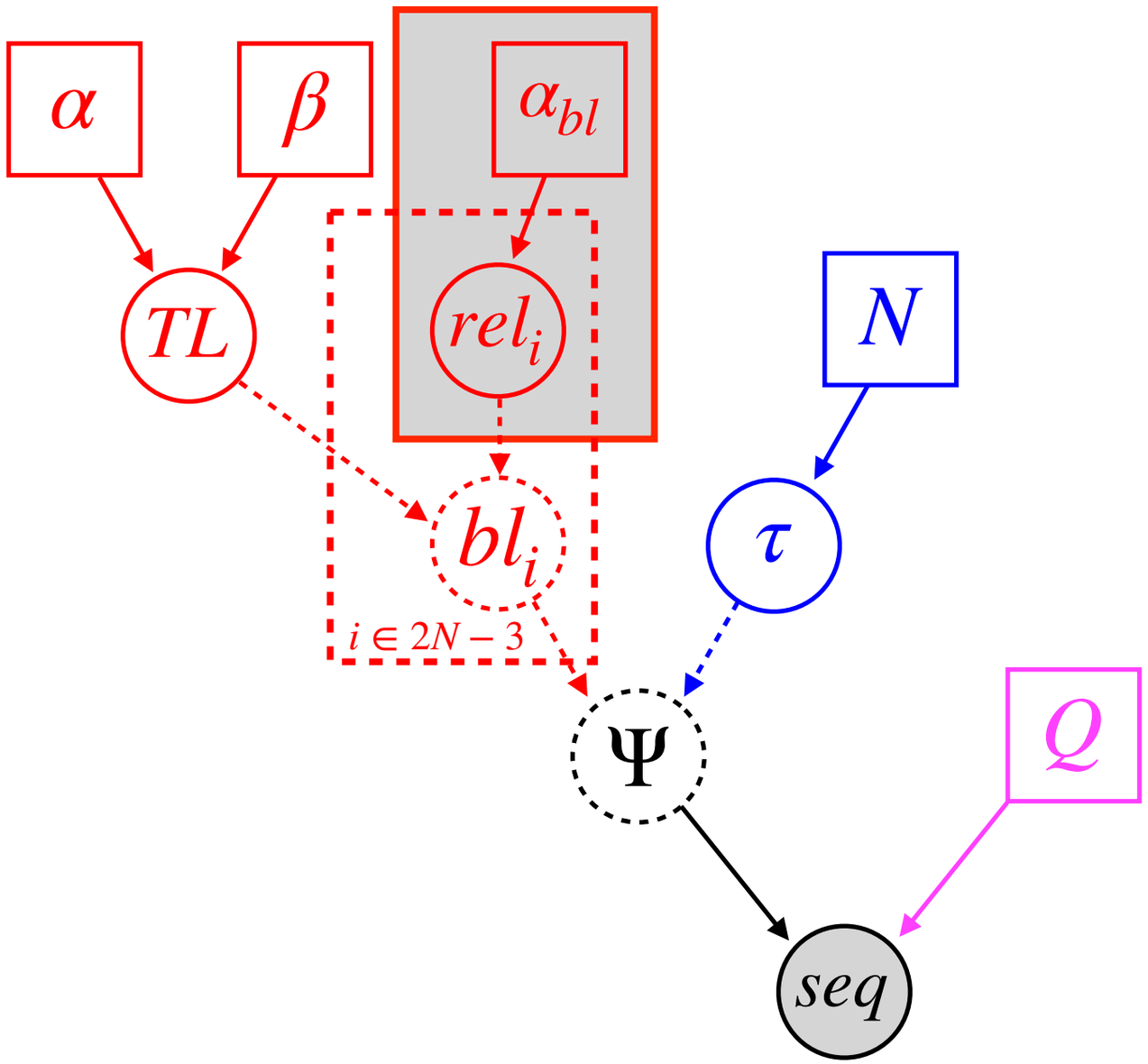
Jukes-Cantor

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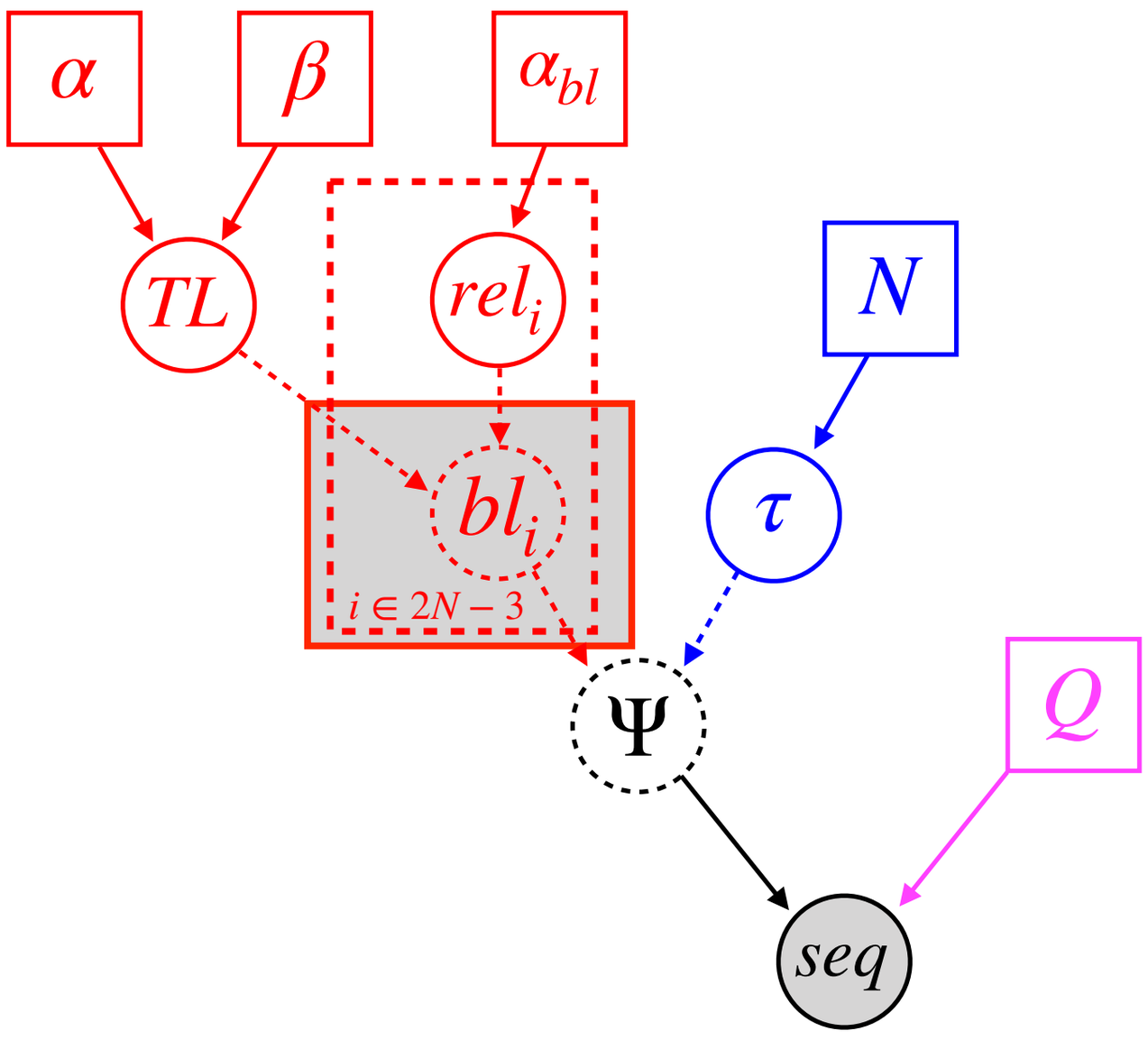


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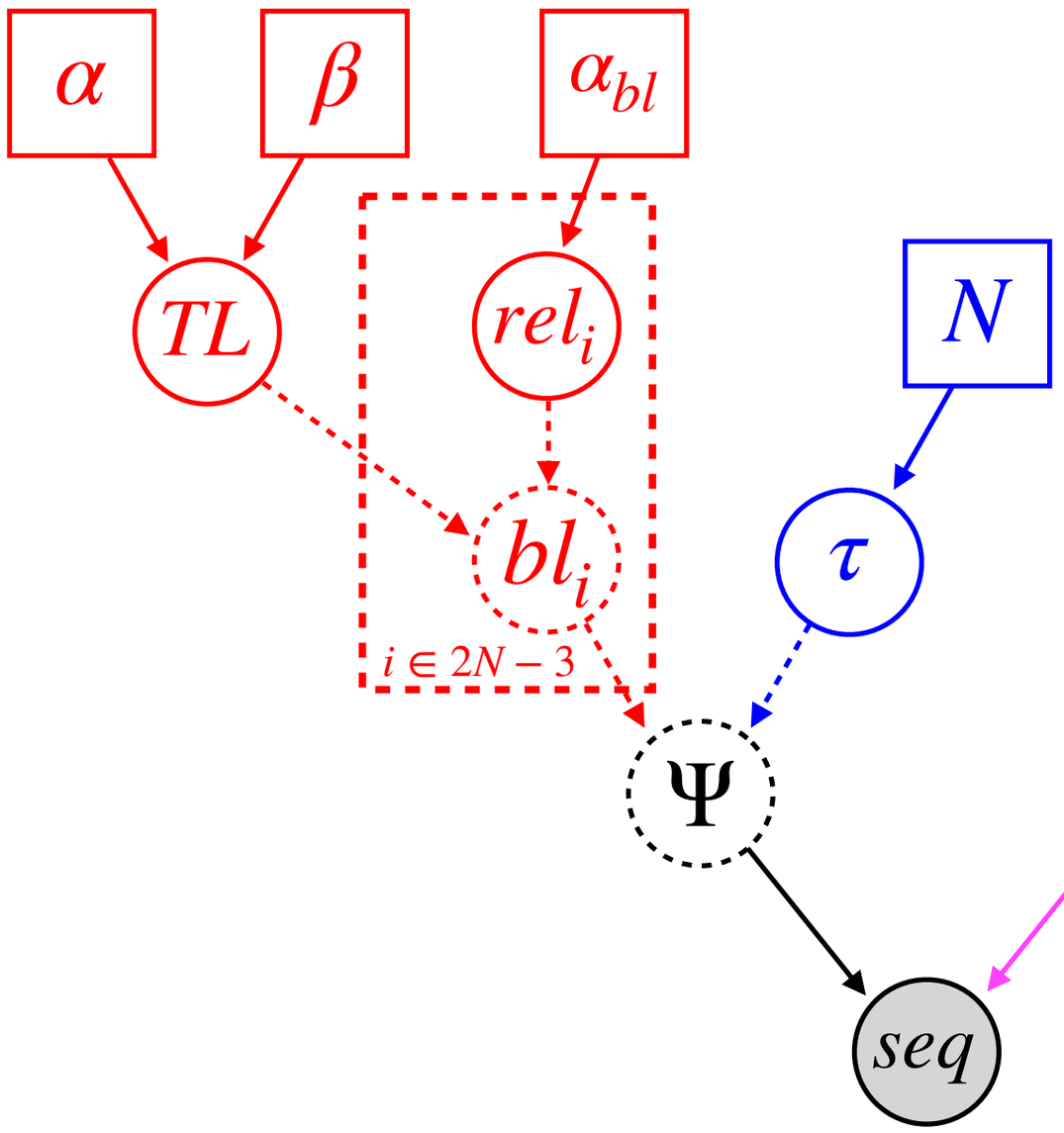
Jukes-Cantor

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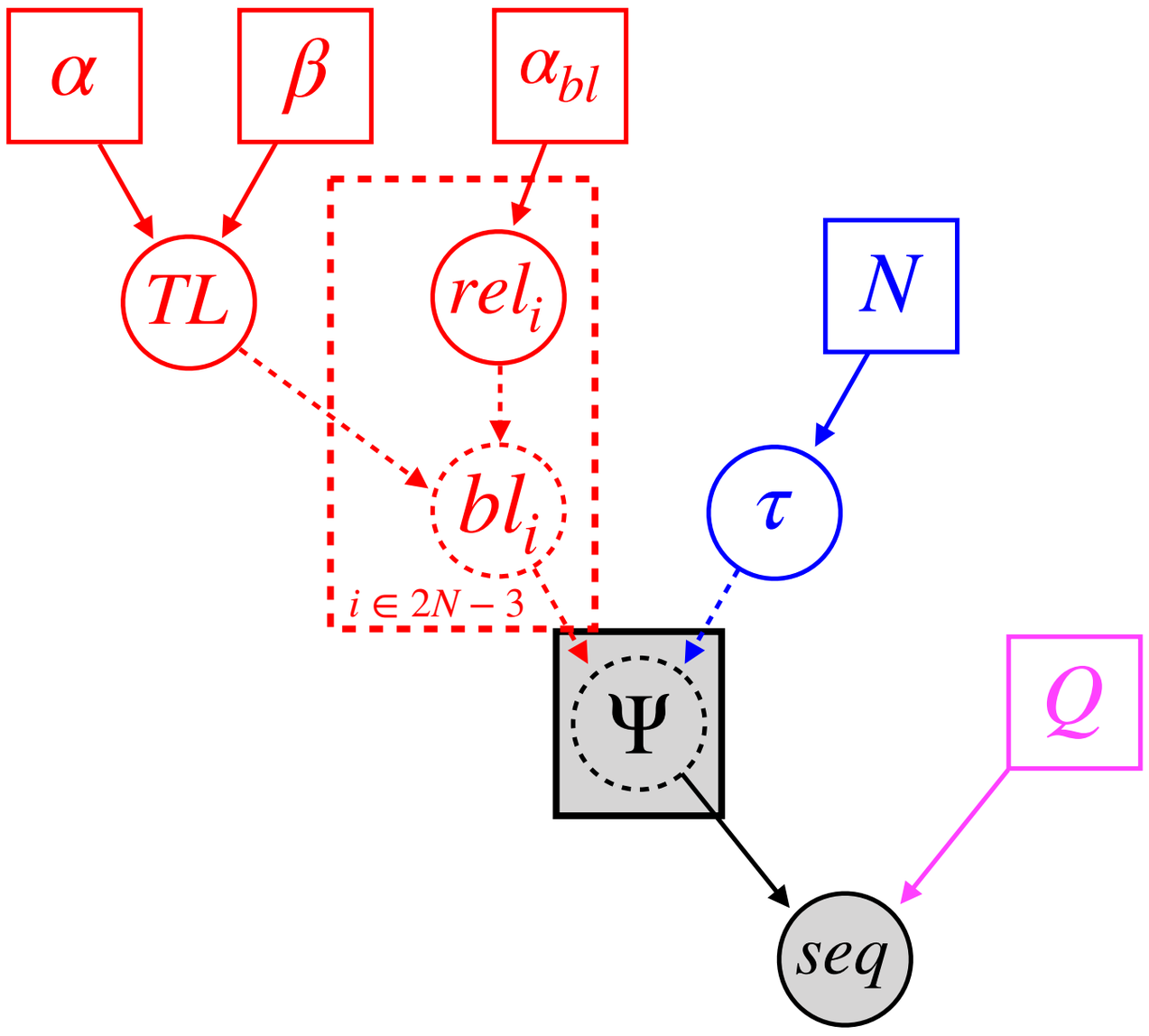
psi := treeAssembly(topology, br_lens)

seq ~ dnPhyloCTMC(tree=psi,Q=Q,type="DNA")

seq.clamp(data)
```

Jeremy M. Brown

Jukes-Cantor




```
data = readDiscreteCharacterData("myData.nex")
taxa <- data.taxa()
n_taxa <- data.ntaxa()
n_branches <- 2 * n_taxa - 3

topology ~ dnUniformTopology(taxa)

alpha <- 2
beta <- 4

TL ~ dnGamma(alpha,beta)

alpha_bl <- 1.0

rel_branch_lengths ~ dnDirichlet(rep(alpha_bl,n_branches))

br_lens := rel_branch_lengths * TL

Q <- fnJC(4)

psi := treeAssembly(topology, br_lens)

seq ~ dnPhyloCTMC(tree=psi,Q=Q,type="DNA")

seq.clamp(data)
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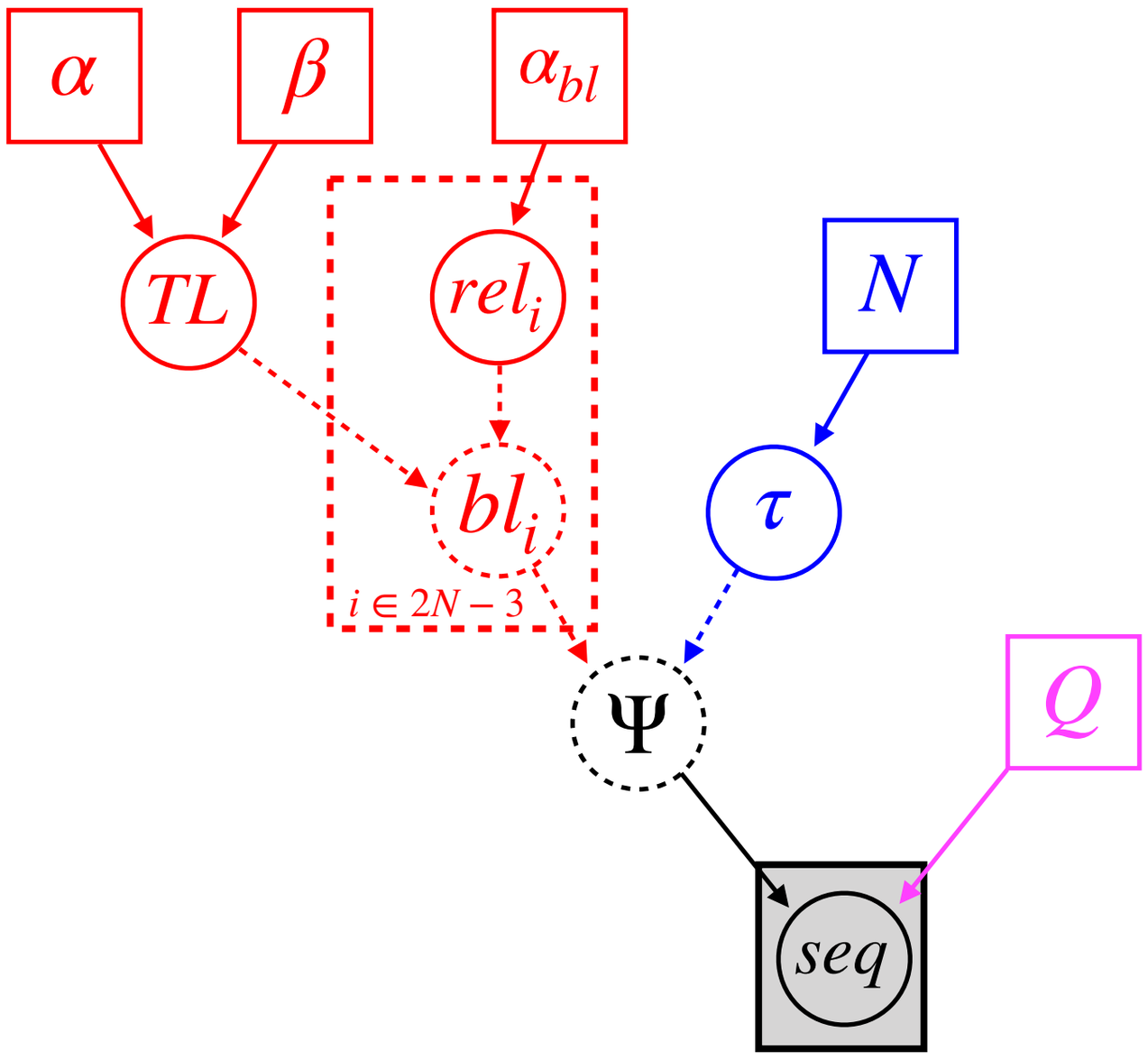
Jeremy M. Brown

Jukes-Cantor

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alpha <- 2
beta <- 4

TL ~ dnGamma(alpha,beta)

alpha_bl <- 1.0

rel_branch_lengths ~ dnDirichlet(rep(alpha_bl,n_branches))

br_lens := rel_branch_lengths * TL

Q <- fnJC(4)

psi := treeAssembly(topology, br_lens)

seq ~ dnPhyloCTMC(tree=psi,Q=Q,type="DNA")

seq.clamp(data)
```

Jukes-Cantor

TL

rel_i

τ

Inferring these parameters under Jukes-Cantor.

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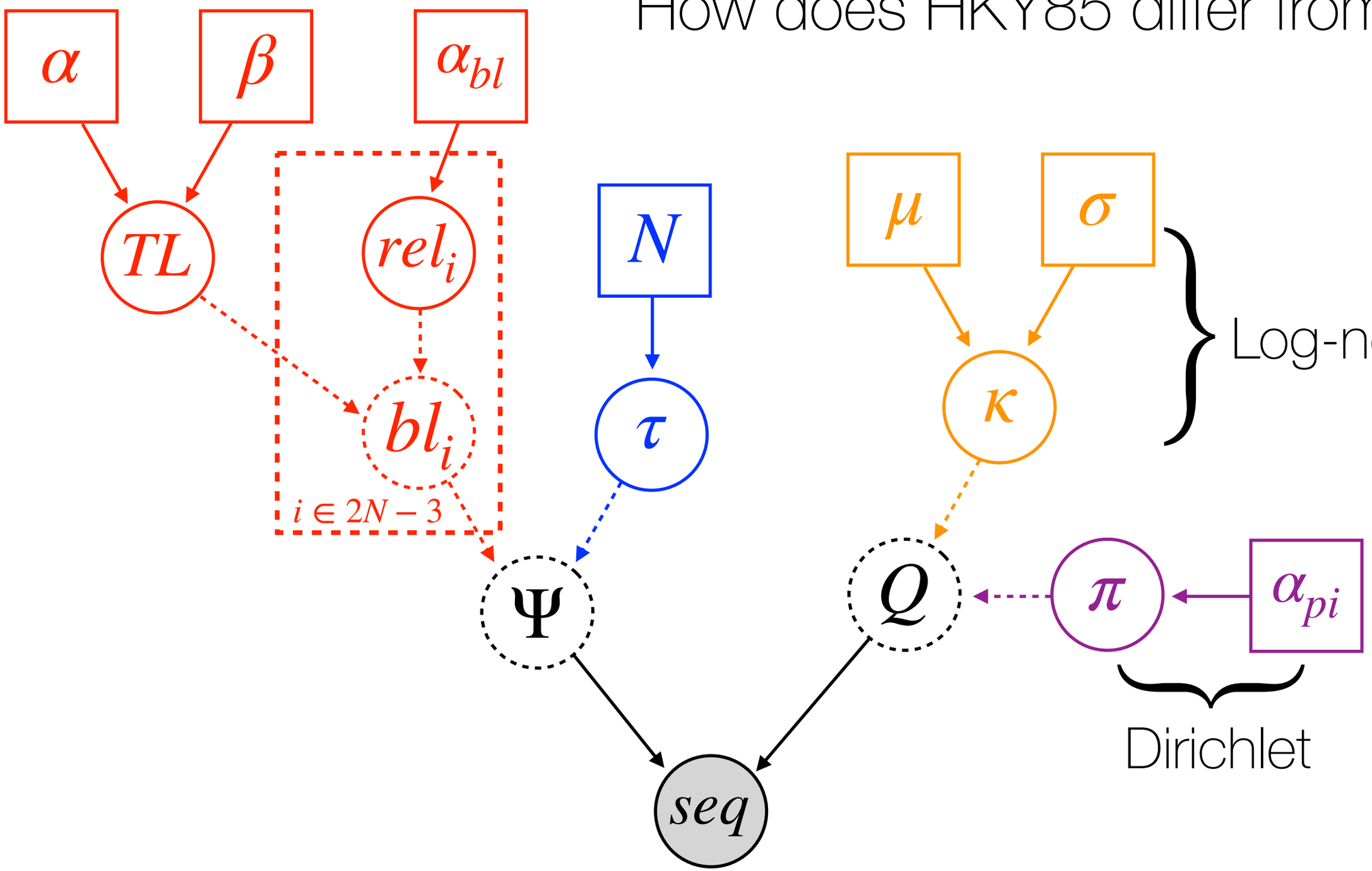
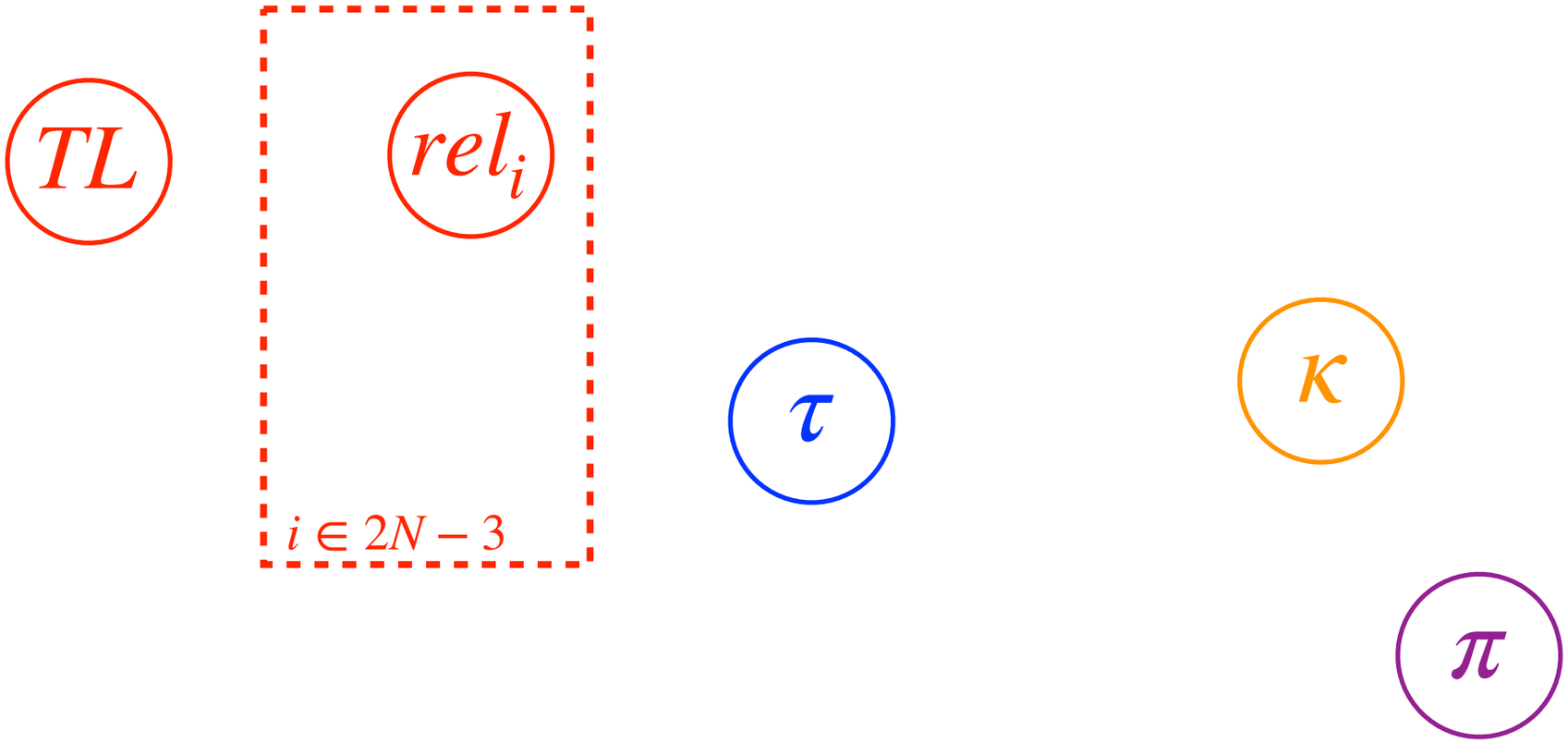
HKY85

How does HKY85 differ from JC?



HKY85

How does HKY85 differ from JC?



HKY85

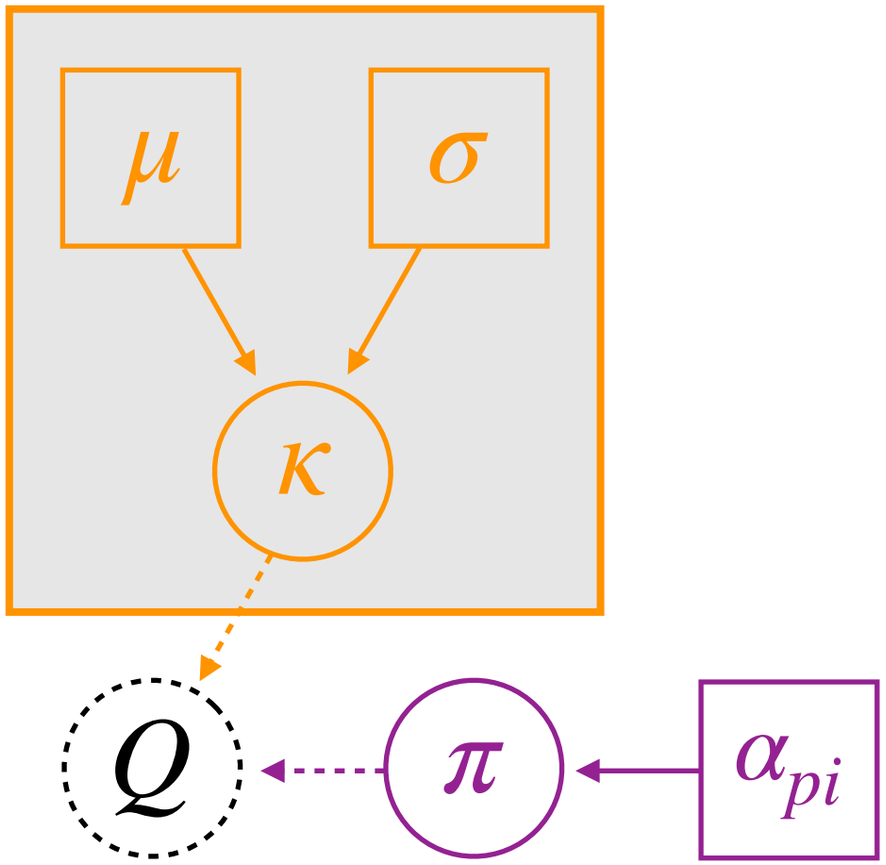
How does HKY85 differ from JC?

Transition-Transversion Rate Ratio

```
mu <- 0
sigma <- 1
kappa ~ dnLognormal(mu,sigma)
```

```
alpha_pi <- 1.0
pi ~ dnDirichlet( rep(alpha_pi,4) )

Q := fnHKY(kappa,pi)
```



HKY85

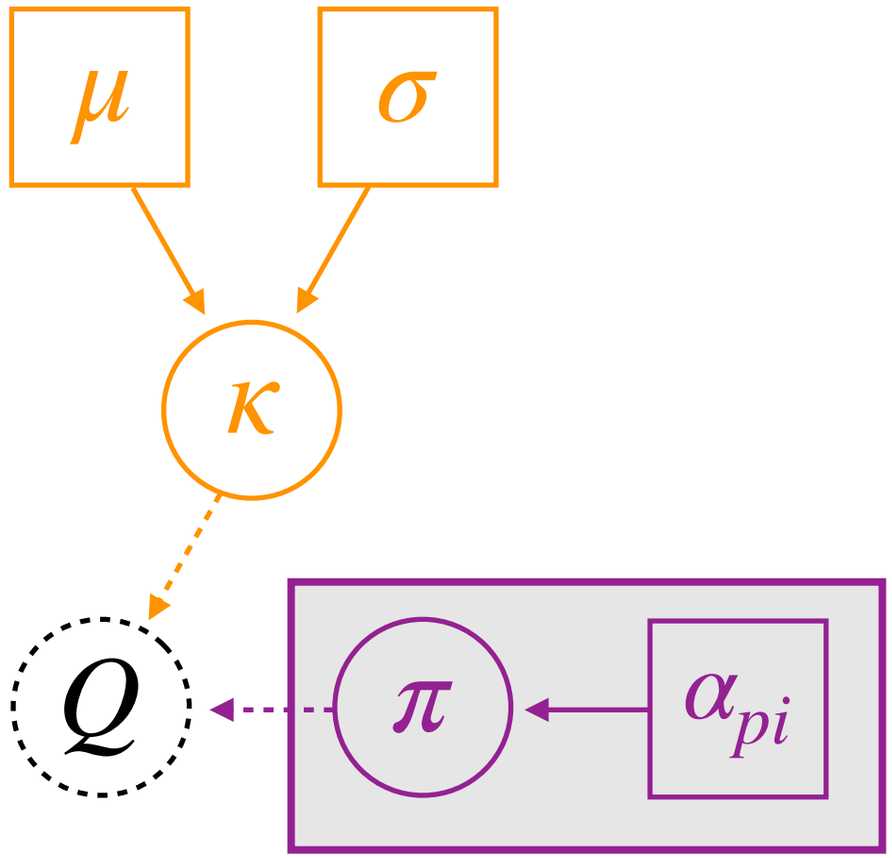
How does HKY85 differ from JC?

```
mu <- 0
sigma <- 1
kappa ~ dnLognormal(mu,sigma)
```

```
alpha_pi <- 1.0
pi ~ dnDirichlet( rep(alpha_pi,4) )
```

Variable Base Frequencies

Q := fnHKY(kappa,pi)



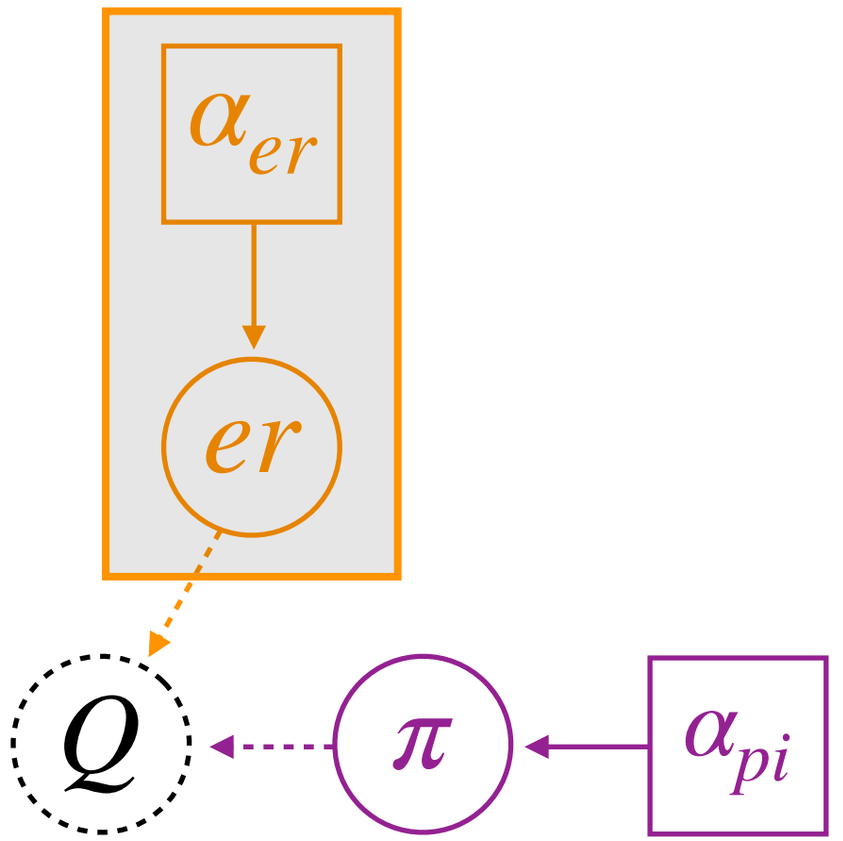
General Time Reversible (GTR)

Variable Exchangeabilities

```
alpha_er <- 1.0
er ~ dnDirichlet( rep(alpha_er,6) )
```

```
alpha_pi <- 1.0
pi ~ dnDirichlet( rep(alpha_pi,4) )

Q := fnGTR(er,pi)
```



Things to Remember

As we add more stochastic nodes, **remember to assign moves** to all of them!

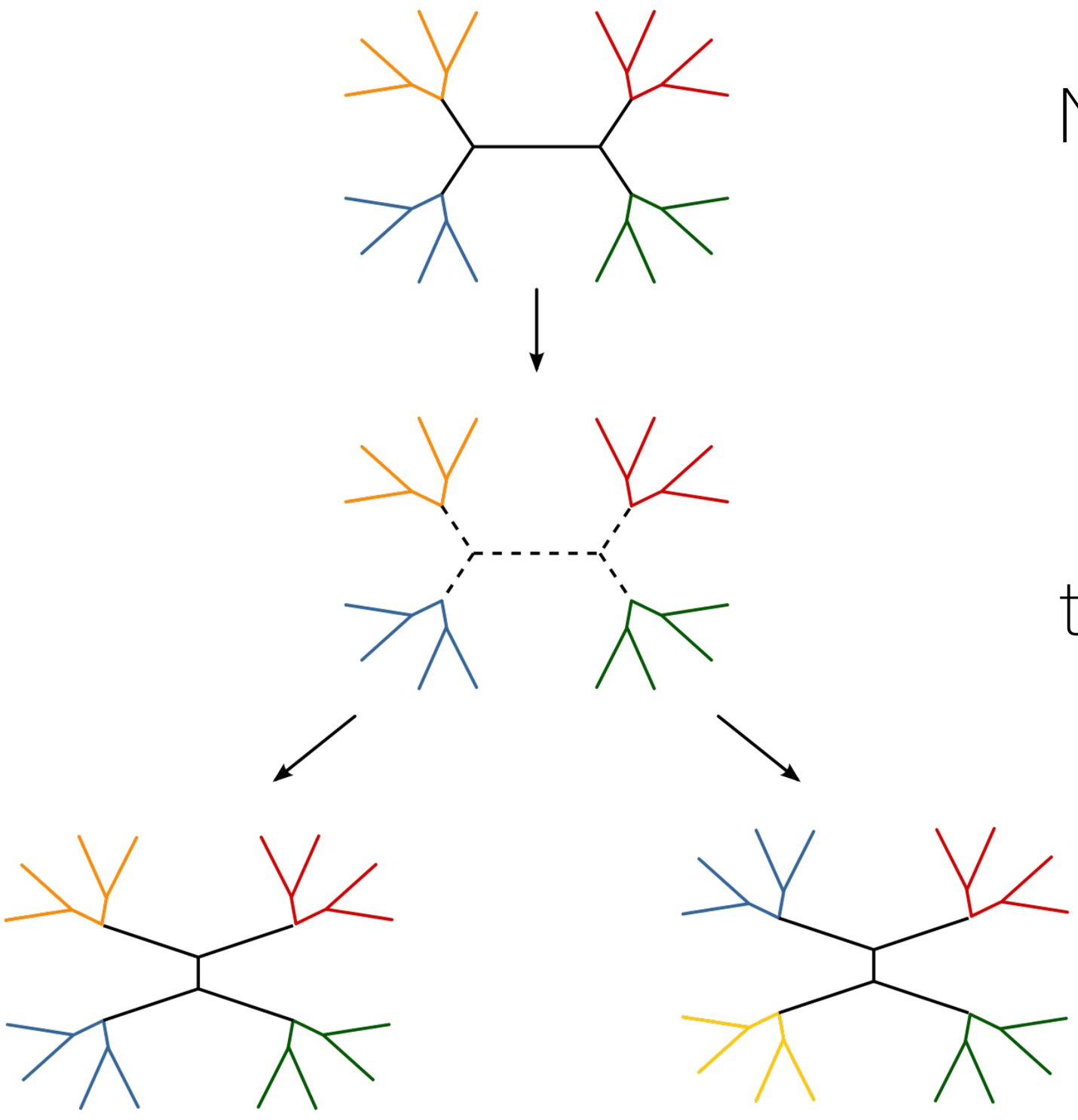
Vectors modeled with a Dirichlet should have a joint proposal mechanism, since they need to sum to 1. Here are a couple:

mvBetaSimplex

mvDirichletSimplex

You'll often want to run analyses on the same dataset with multiple models. Start by saving your simplest model into a text file (.rev). Then, copy and paste the code into a file for the next model and adjust as necessary. Keep going as you work your way to more complex models.

Topology Moves

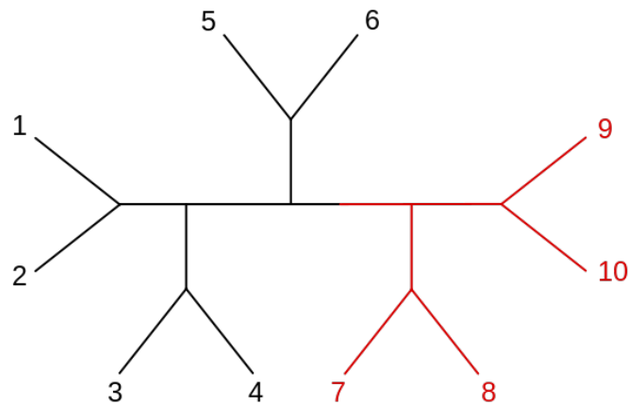


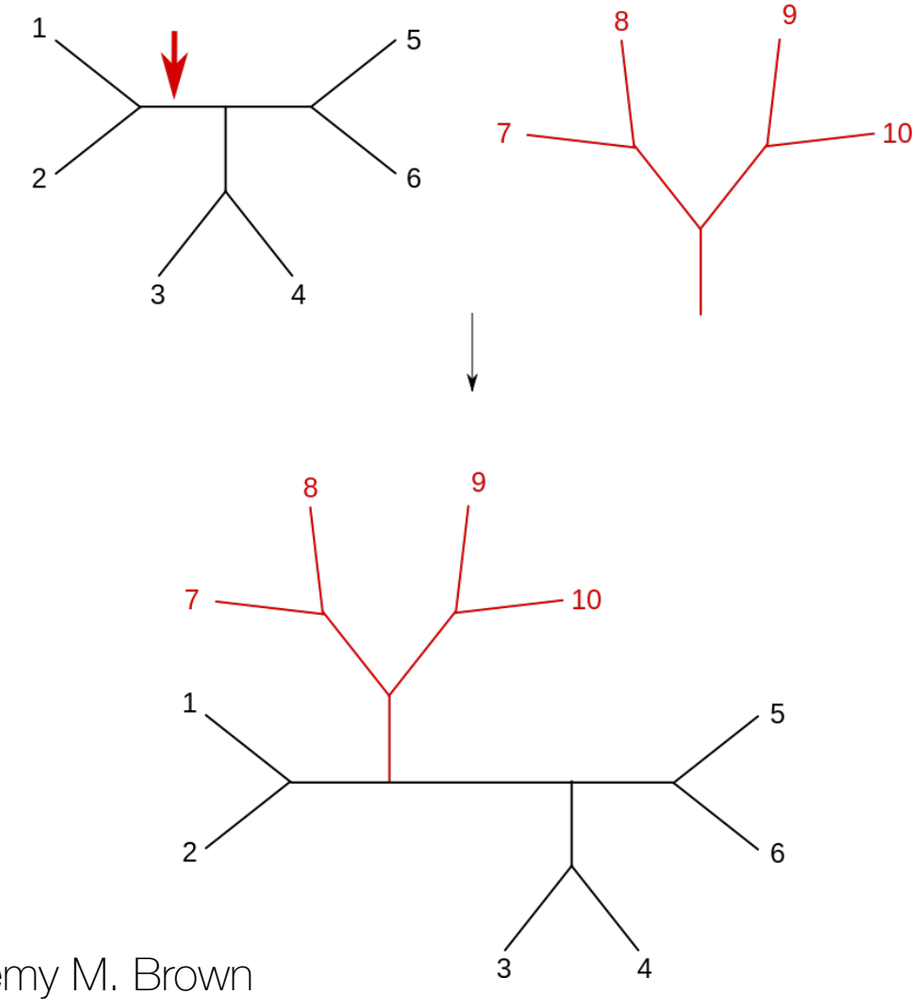
Nearest-Neighbor Interchange (NNI)

The most minor topological move.

https://en.wikipedia.org/wiki/Tree_rearrangement

Topology Moves





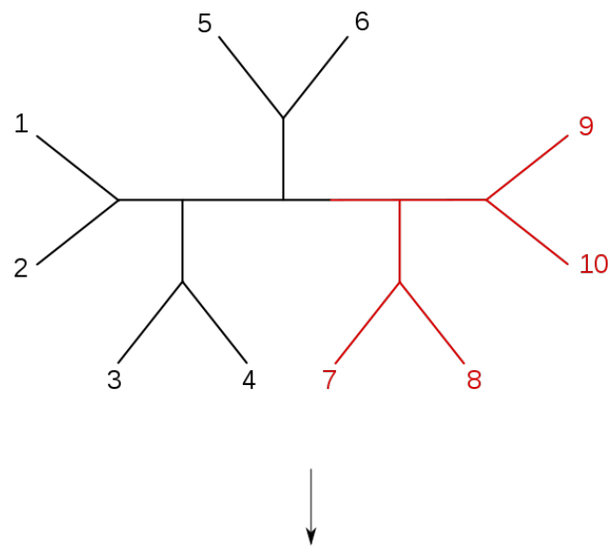
Subtree Prune and Regraft (SPR)

Intermediate topological move.

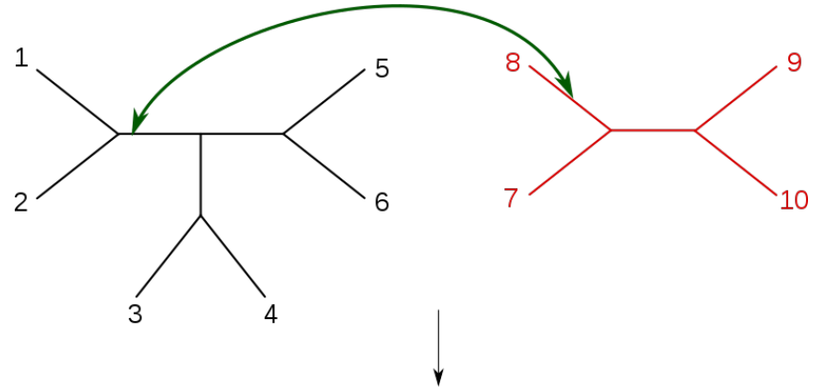
Often a good balance between exploring new tree space without disrupting things too much.

https://en.wikipedia.org/wiki/Tree_rearrangement

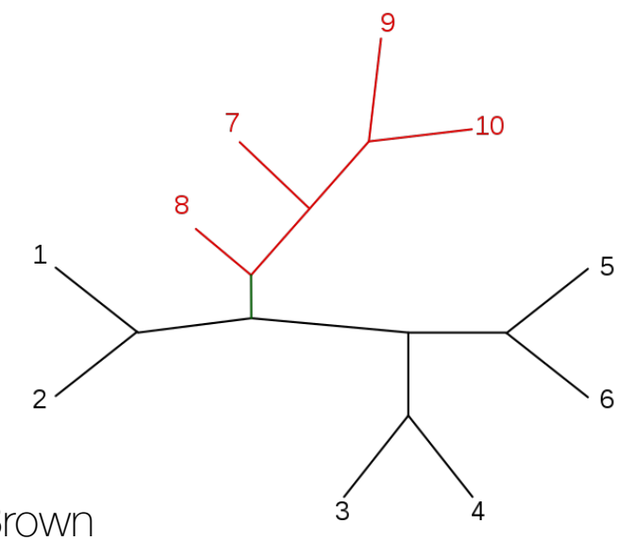
Topology Moves



Tree Bisection and Reconnection (TBR)



Disruptive topological move.



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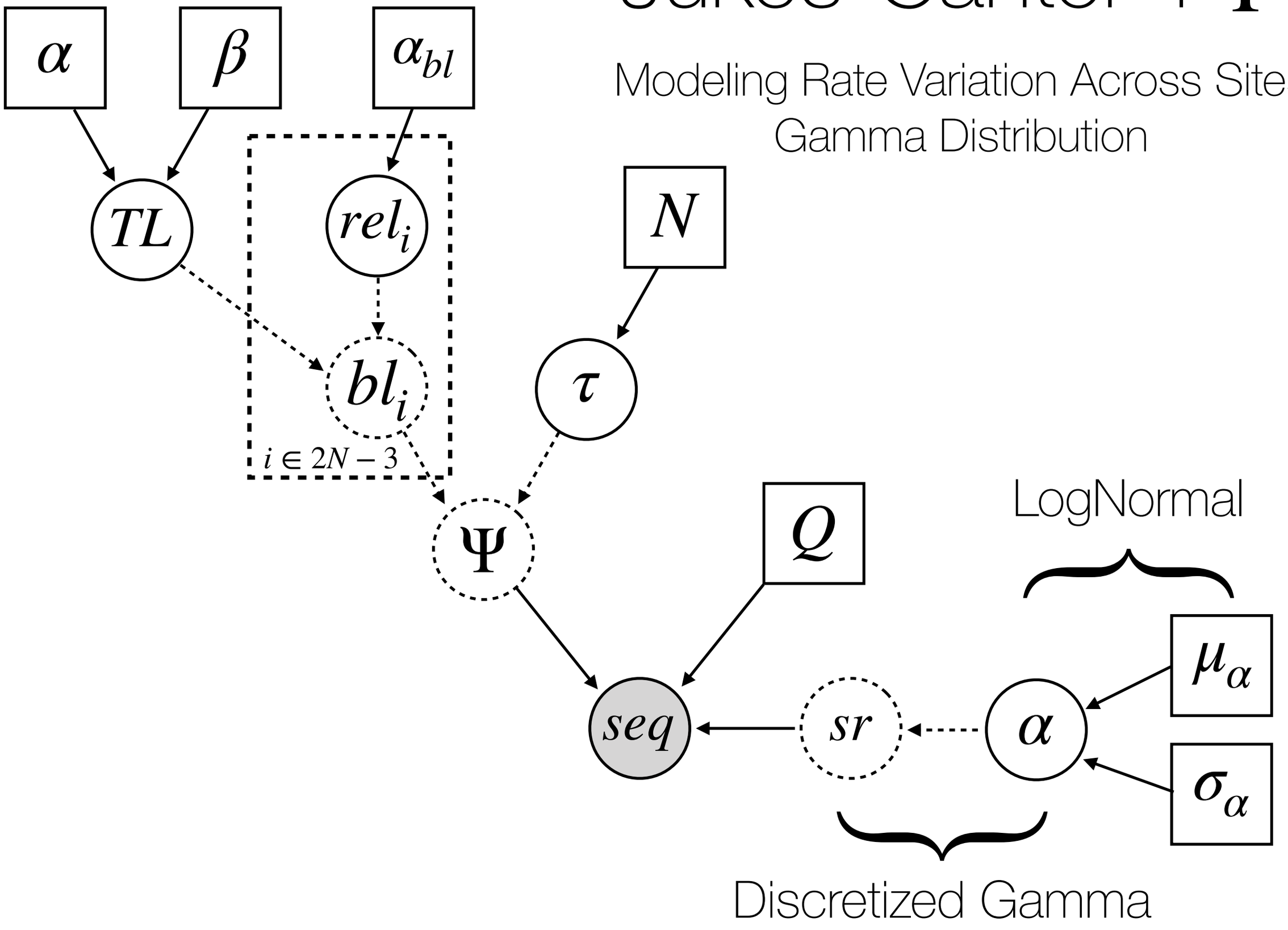
https://en.wikipedia.org/wiki/Tree_rearrangement

Jukes-Cantor + Γ

Modeling Rate Variation Across Sites
Gamma Distribution



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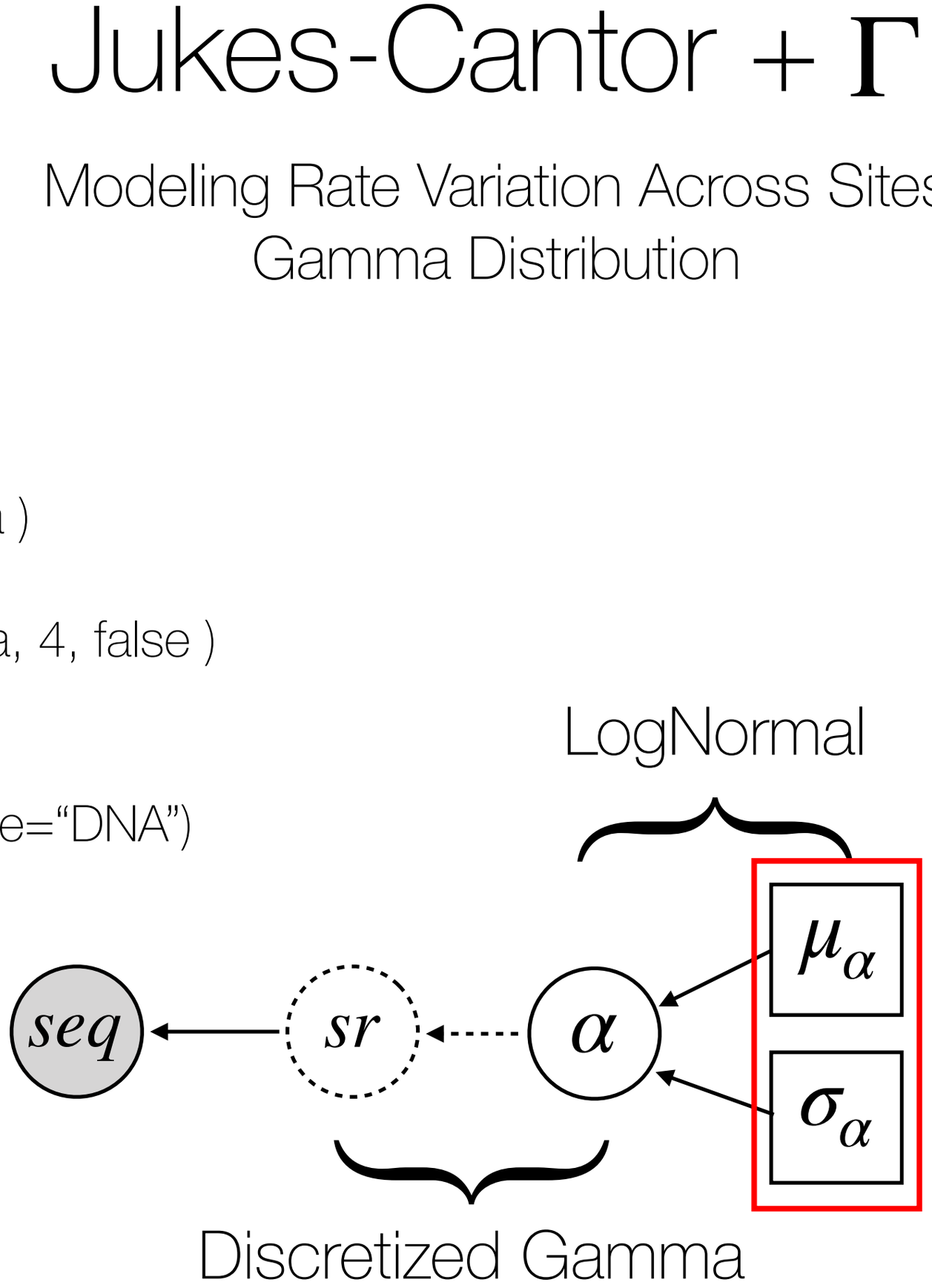
Modeling Rate Variation Across Sites
Gamma Distribution

```
mu_a <- ln(5.0)
sigma_a <- 0.587405

alpha ~ dnLognormal( mu_a, sigma_a )
sr := fnDiscretizeGamma( alpha, alpha, 4, false )

seq ~ dnPhyloCTMC(tree=psi,Q=Q,
                  siteRates=sr,type="DNA")
```



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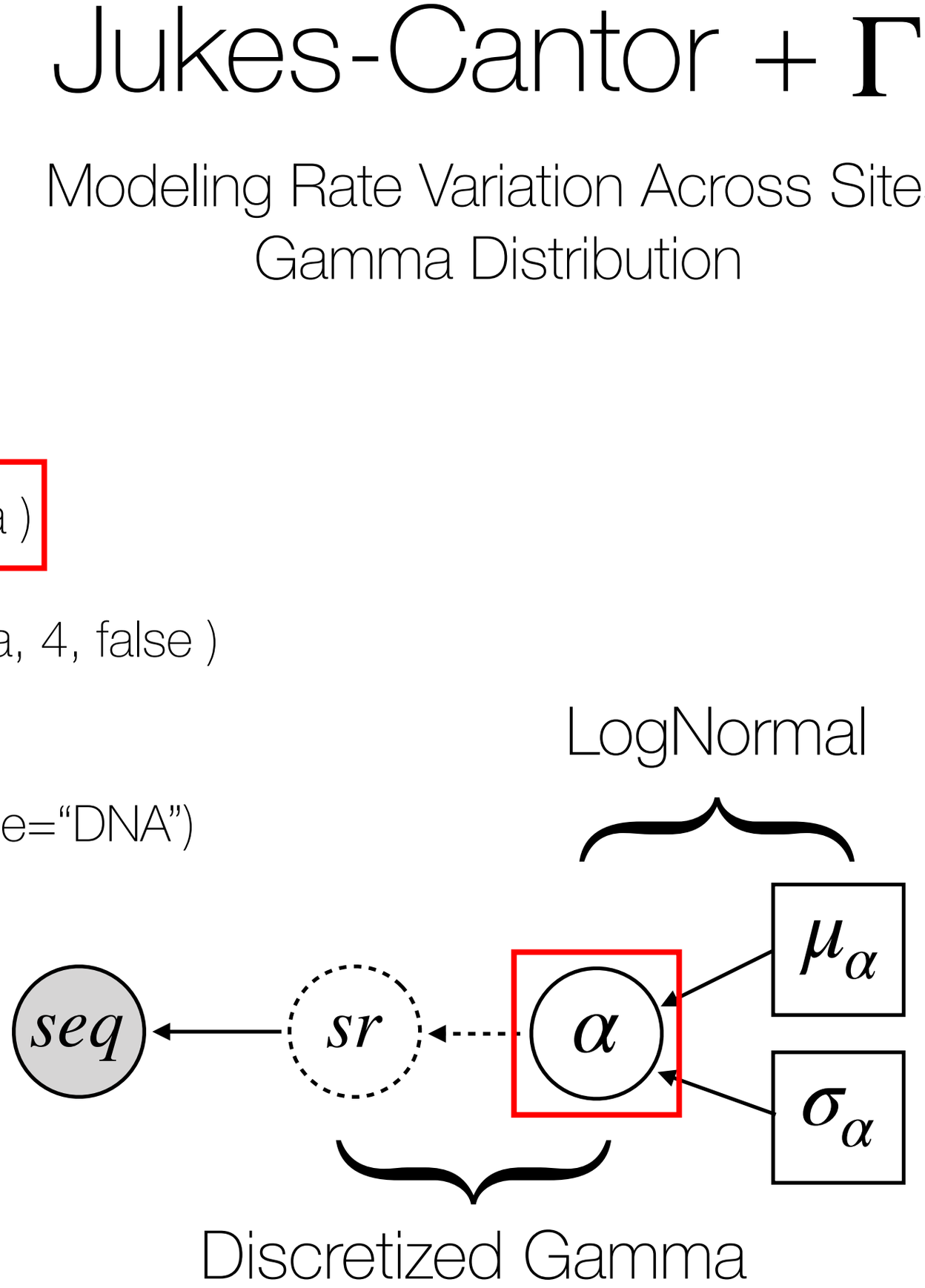

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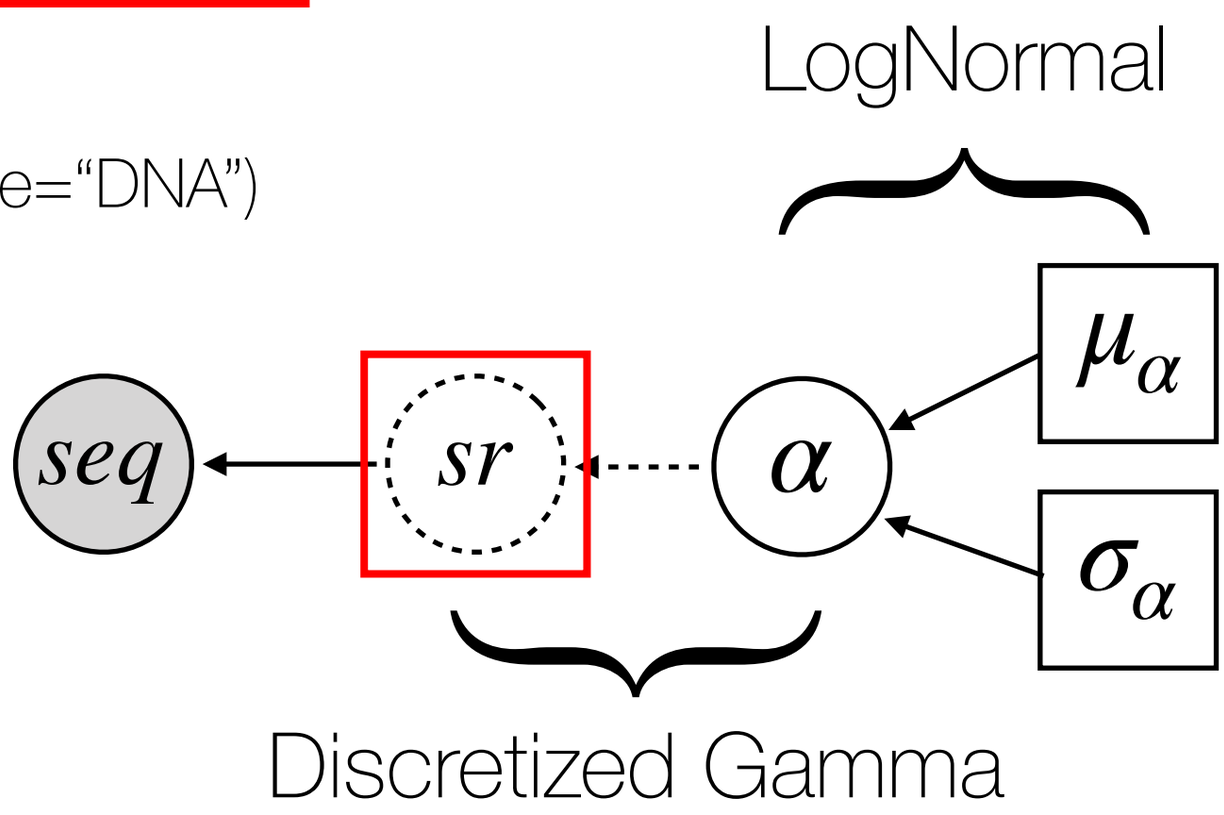

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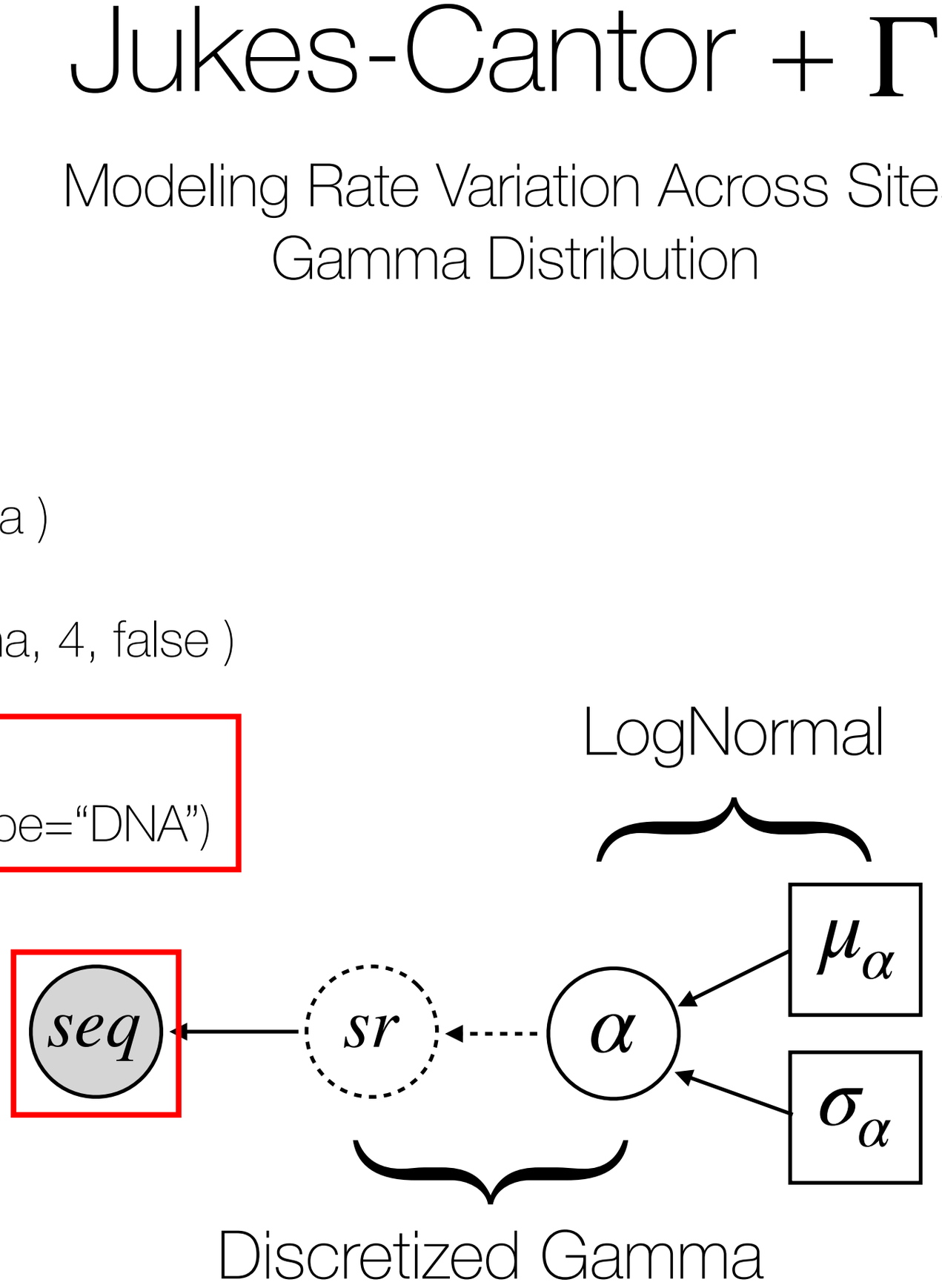

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Jukes-Cantor + Γ

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```
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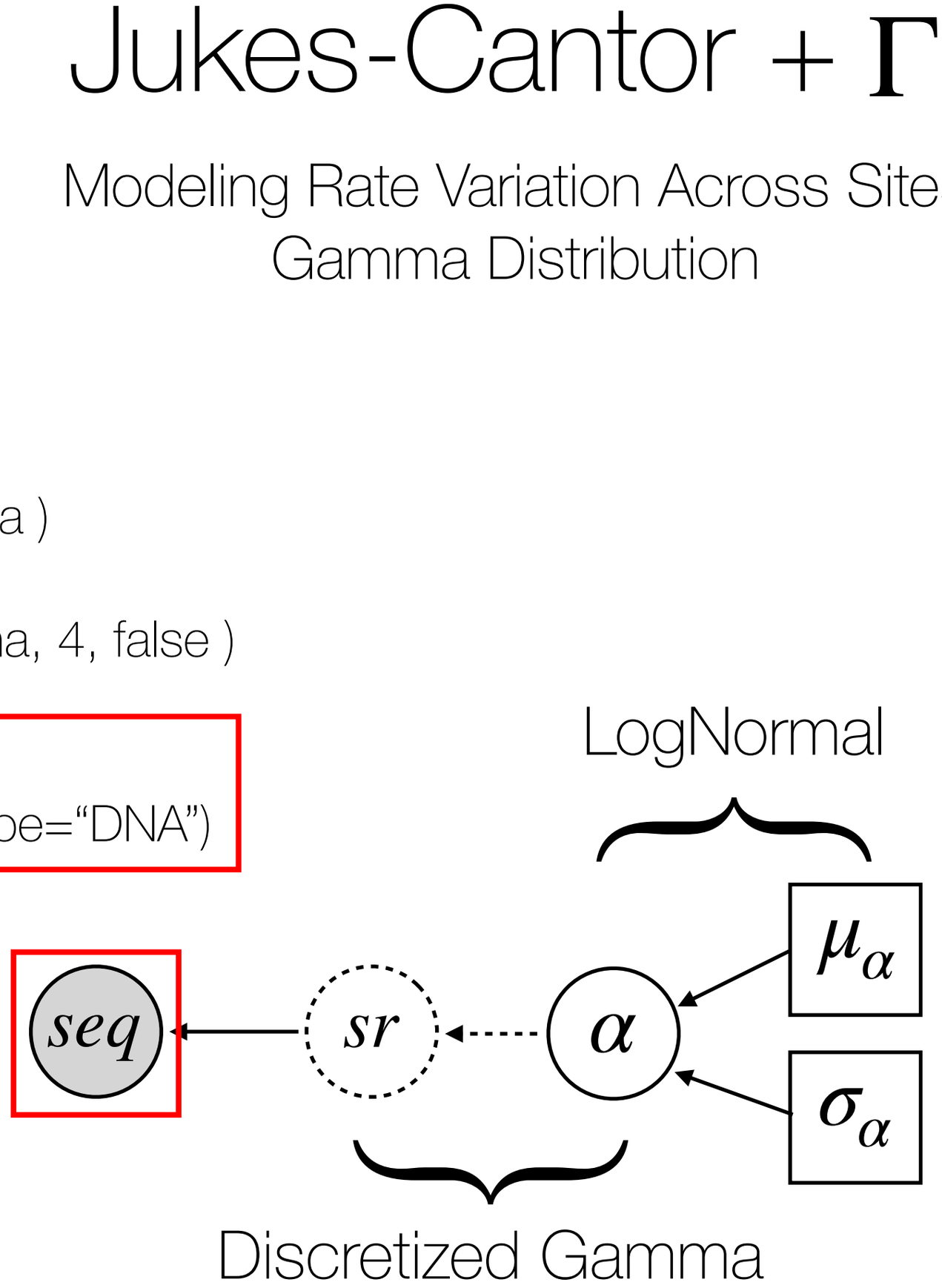
```

Can add + Γ to any "standard" model of sequence evolution.



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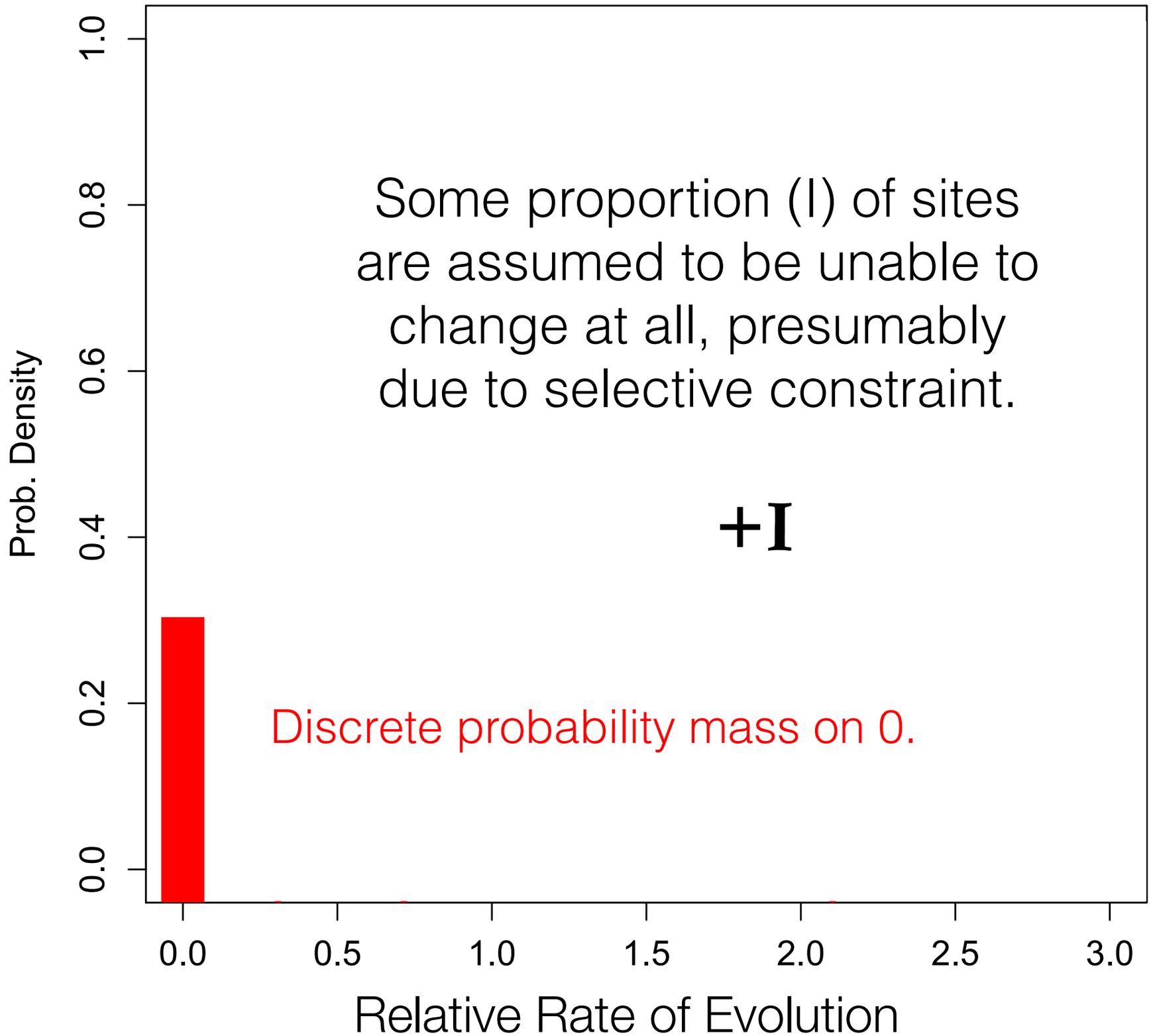
Modeling Rate Variation Across Sites

Proportion of Invariable Sites



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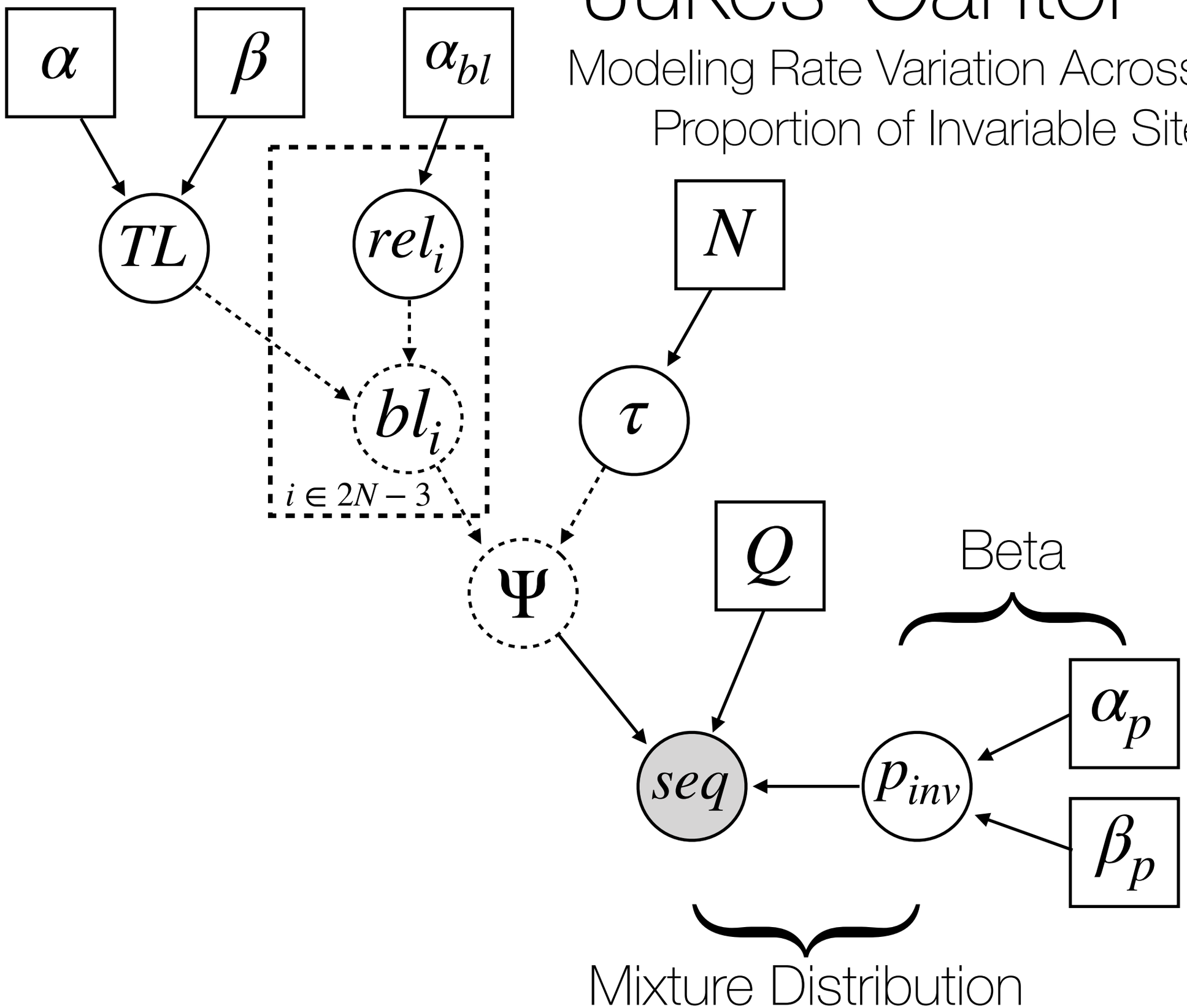
Modeling Rate Variation Across Sites
Proportion of Invariable Sites



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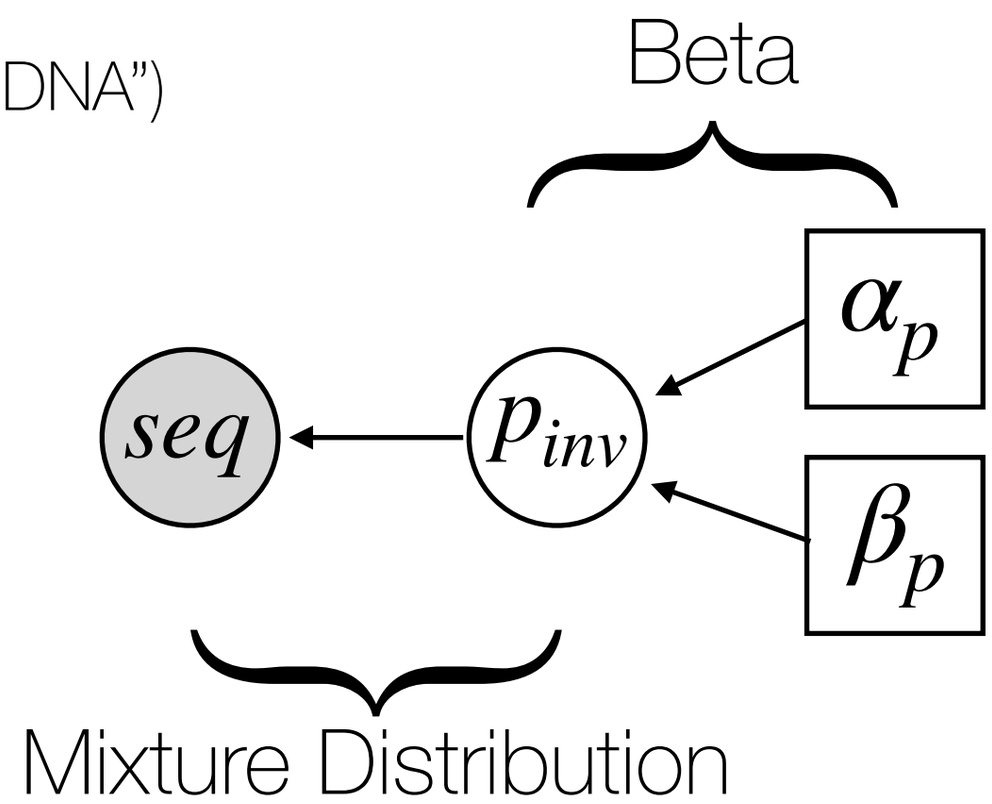
Modeling Rate Variation Across Sites
Proportion of Invariable Sites

```
alpha_p <- 1.0
beta_p <- 1.0

p_inv ~ dnBeta( alpha_p, beta_p )

seq ~ dnPhyloCTMC(tree=psi, Q=Q,
                  pInv=p_inv, type="DNA")
```



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Jukes-Cantor + I

Modeling Rate Variation Across Sites
Proportion of Invariable Sites

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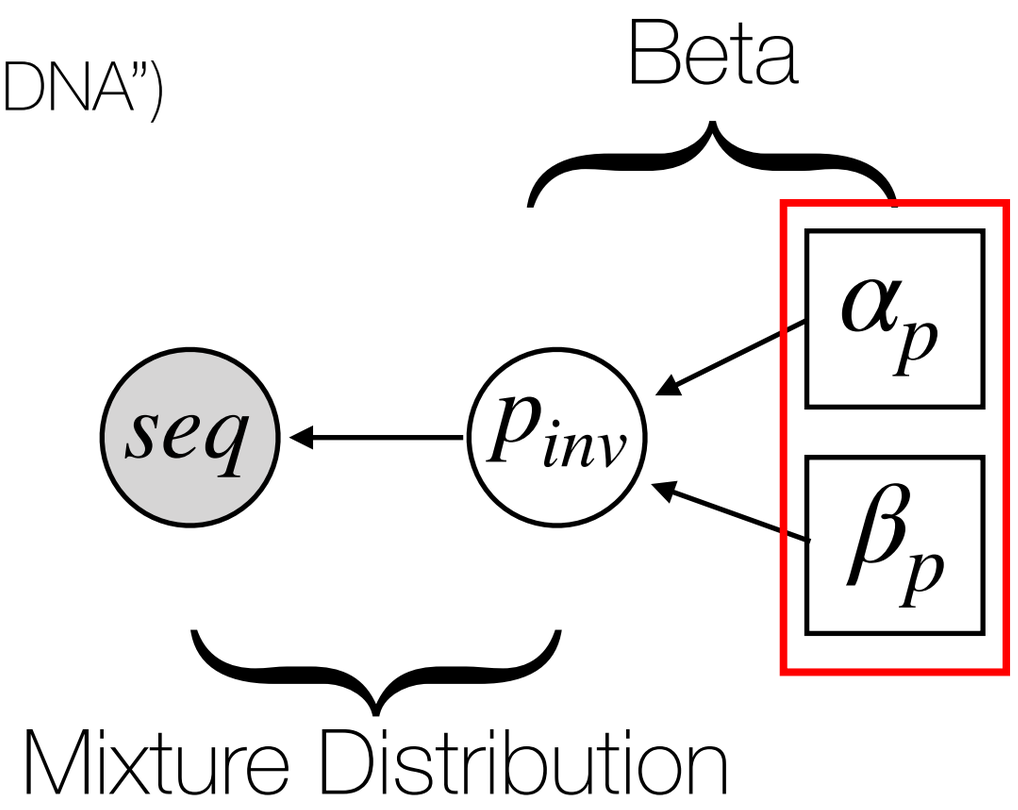

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Jukes-Cantor + I

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Proportion of Invariable Sites

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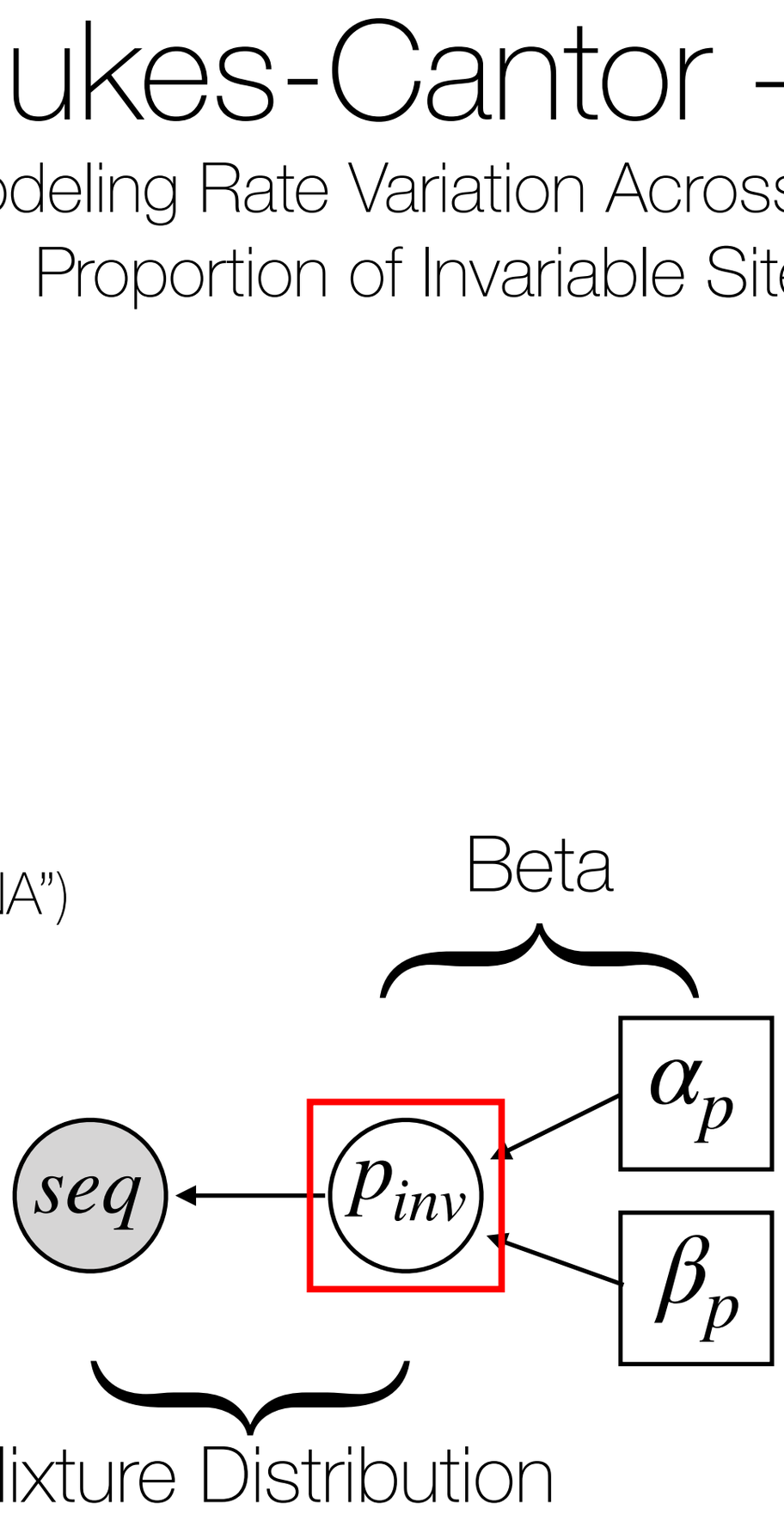

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Proportion of Invariable Sites

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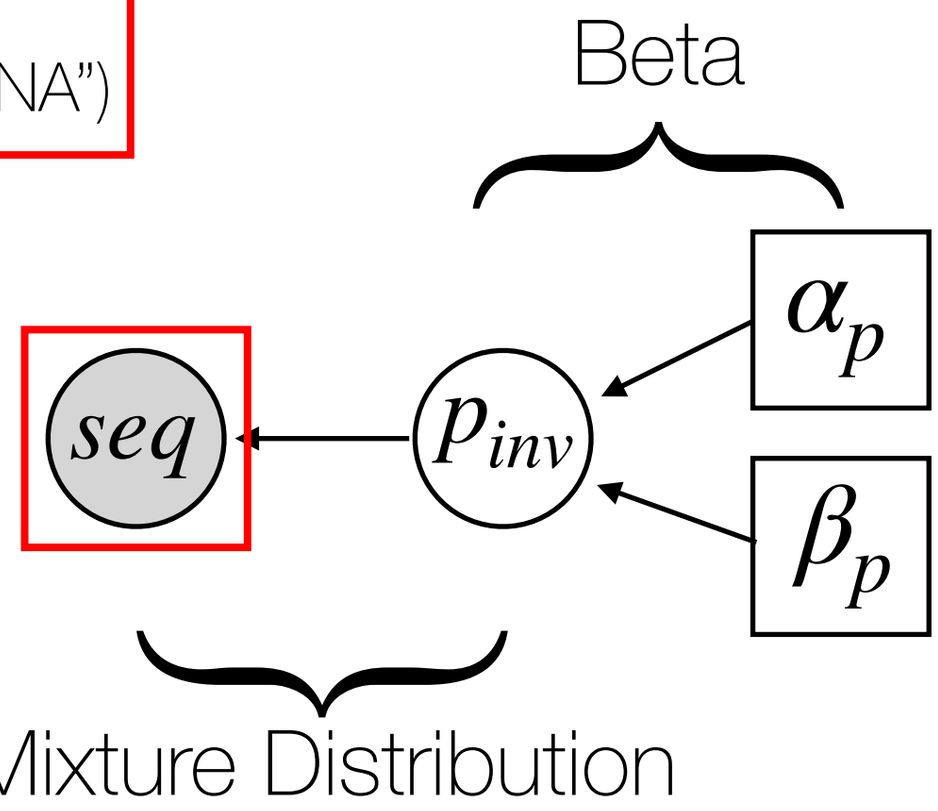

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Jukes-Cantor + I

Modeling Rate Variation Across Sites
Proportion of Invariable Sites

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beta_p <- 1.0

p_inv ~ dnBeta( alpha_p, beta_p )
```

```
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```
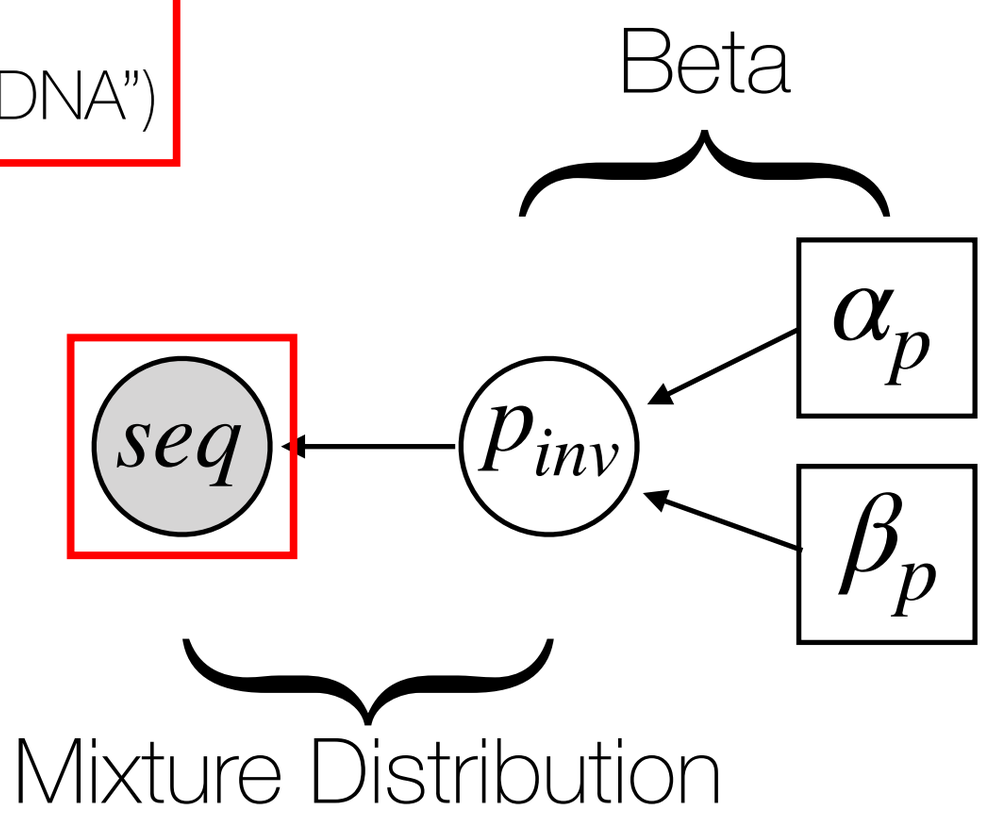

Can also add + I to any "standard" model of sequence evolution.



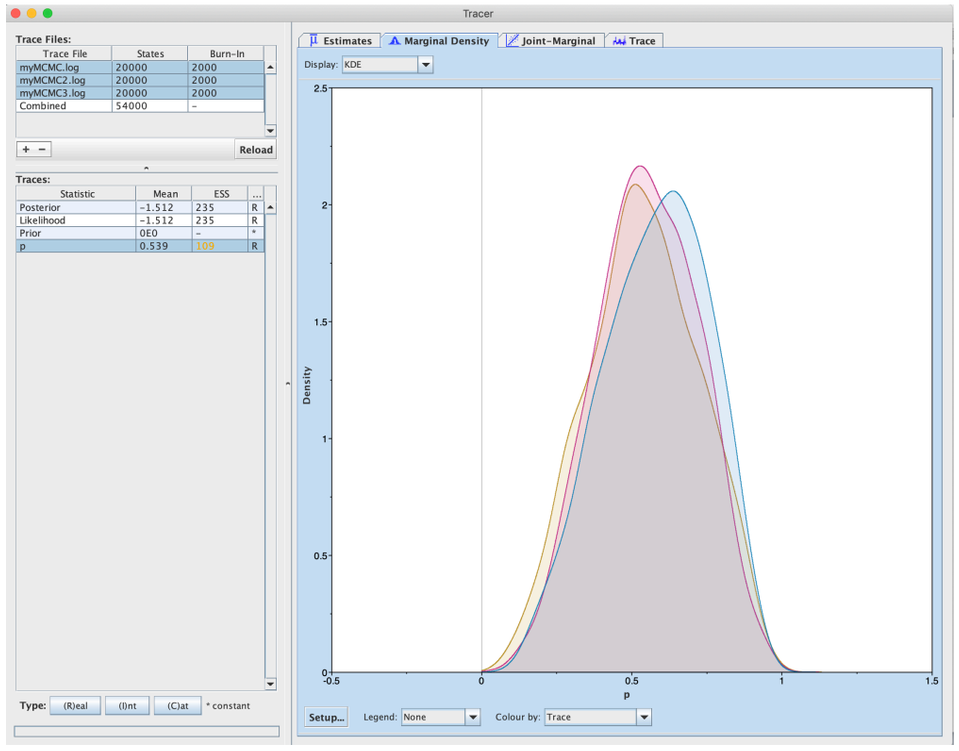
Summarizing Phylogenetic MCMC Output

For scalar (numerical) parameters, we often report:

Mean

Median

95% Highest Posterior Density Interval



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Summarizing Phylogenetic MCMC Output

For trees, we often report:

Maximum A Posteriori (MAP) Tree

("Best" Tree)

```
mapTree(run1Trees)
```

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Summarizing Phylogenetic MCMC Output

For trees, we often report:

Maximum A Posteriori (MAP) Tree

("Best" Tree)

Majority-Rule Consensus Tree

(Formed from all bipartitions with posterior > 0.5)

```
consensusTree(run1Trees,0.5)
```

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Summarizing Phylogenetic MCMC Output

For trees, we often report:

Maximum A Posteriori (MAP) Tree

("Best" Tree)

Majority-Rule Consensus Tree

(Formed from all bipartitions with posterior > 0.5)

Greedy Consensus Tree

(Formed by ranking bipartitions and adding them until tree is fully resolved)

```
consensusTree(run1Trees,0.0)
```

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Summarizing Phylogenetic MCMC Output

For trees, we often report:

Maximum A Posteriori (MAP) Tree

("Best" Tree)

Majority-Rule Consensus Tree

(Formed from all bipartitions with posterior > 0.5)

Greedy Consensus Tree

(Formed by ranking bipartitions and adding them until tree is fully resolved)

Maximum Clade Credibility Tree

(Sampled tree whose product of bipartition probabilities is greatest)

```
mccTree(run1Trees)
```

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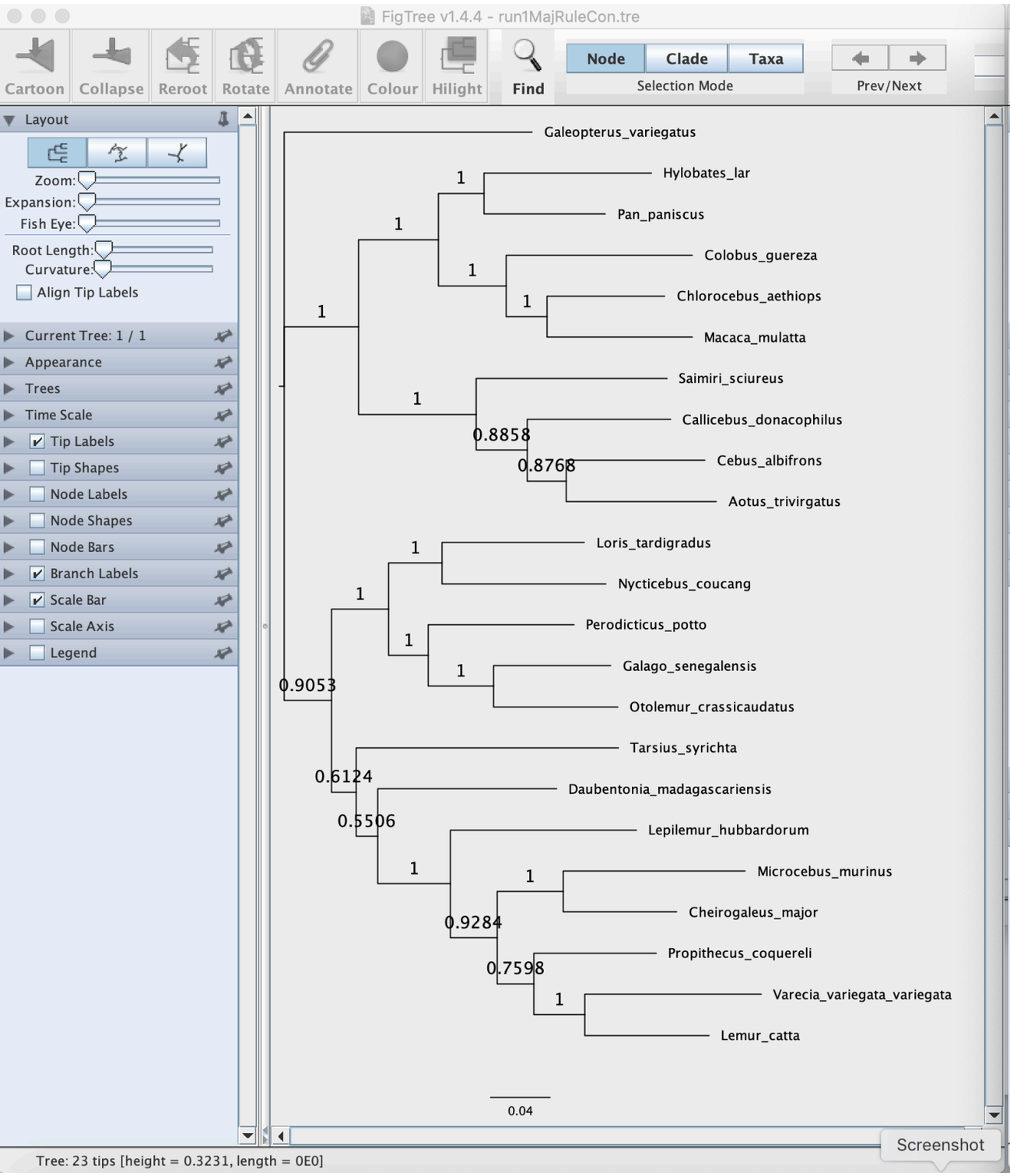
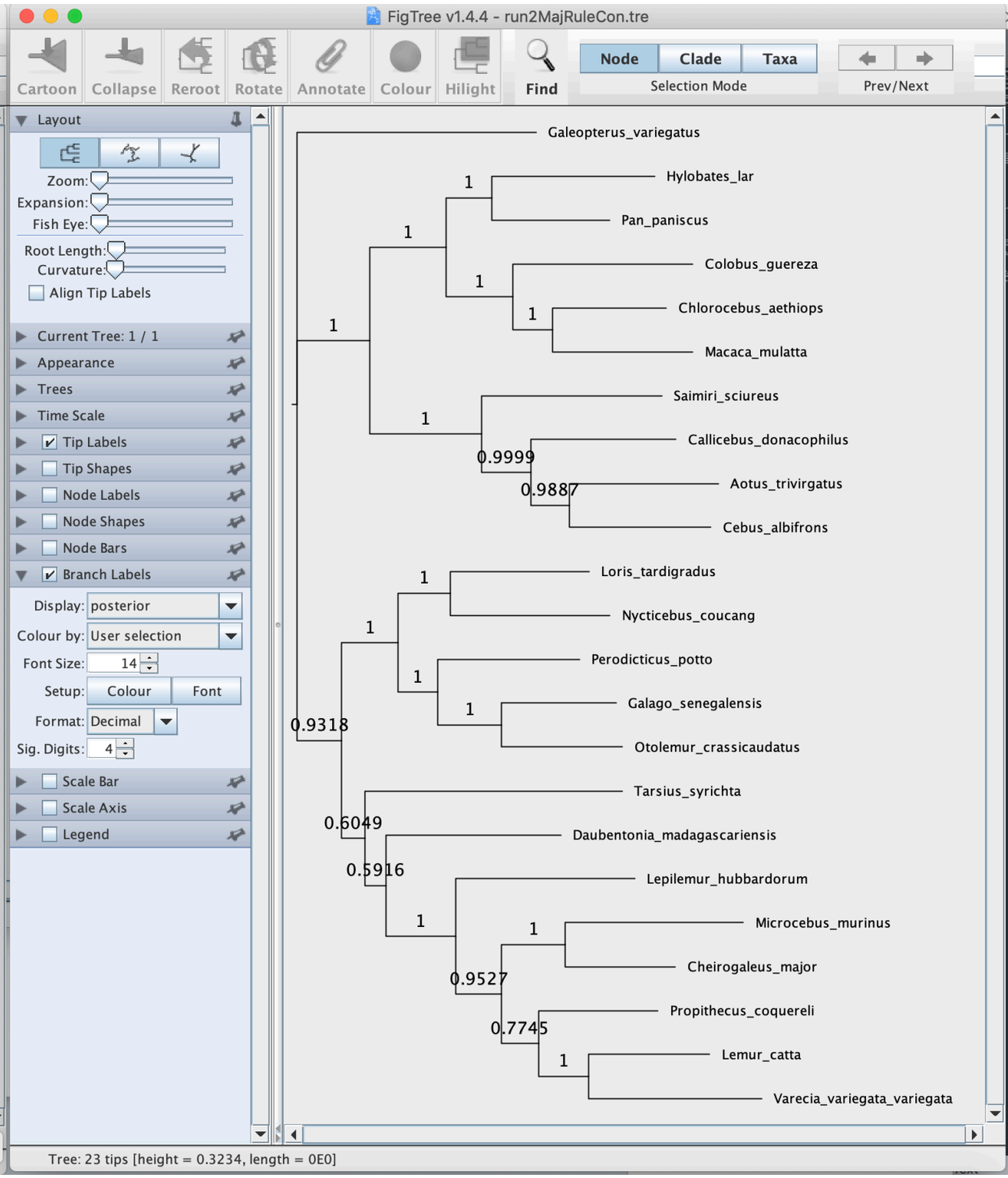
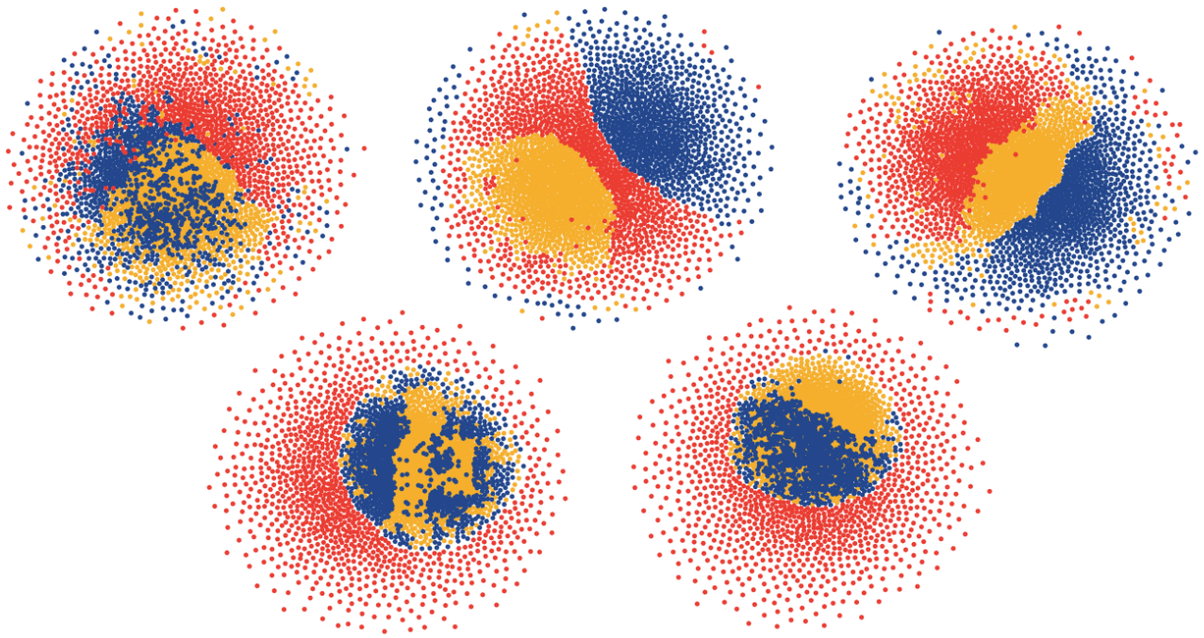
Assessing Topological Convergence





Assessing Topological Convergence



Visualizations of Tree Space

```
run1Trees = readTrees(“run1.trees”)
run2Trees = readTrees(“run2.trees”)
    maxdiff([run1Trees,run2Trees])
```

Finds the biggest difference in estimated marginal posterior probabilities for all bipartitions across different replicates.

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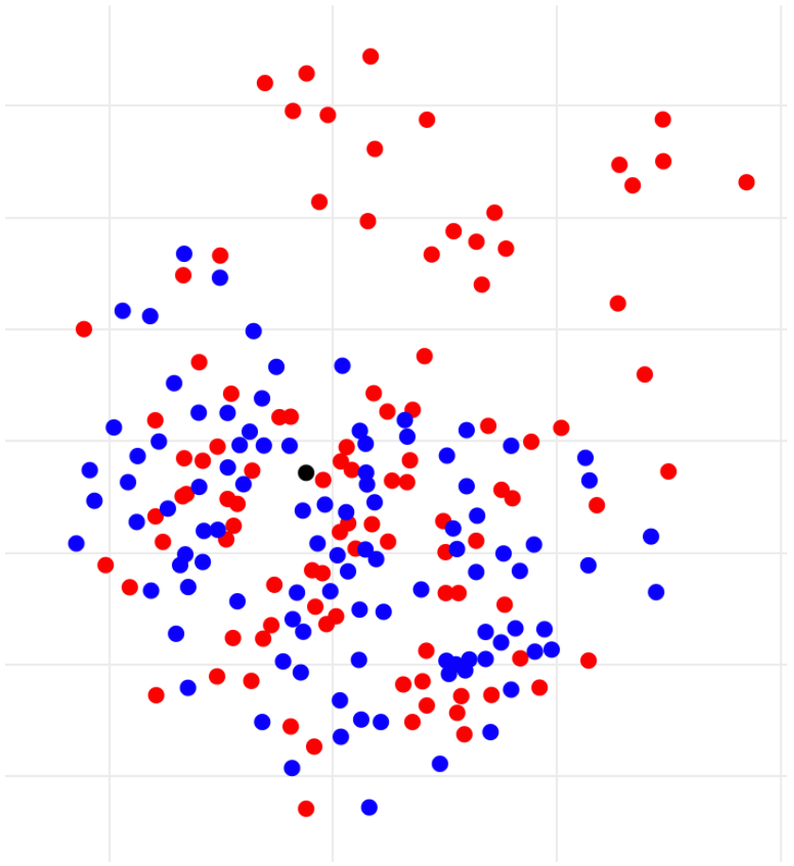
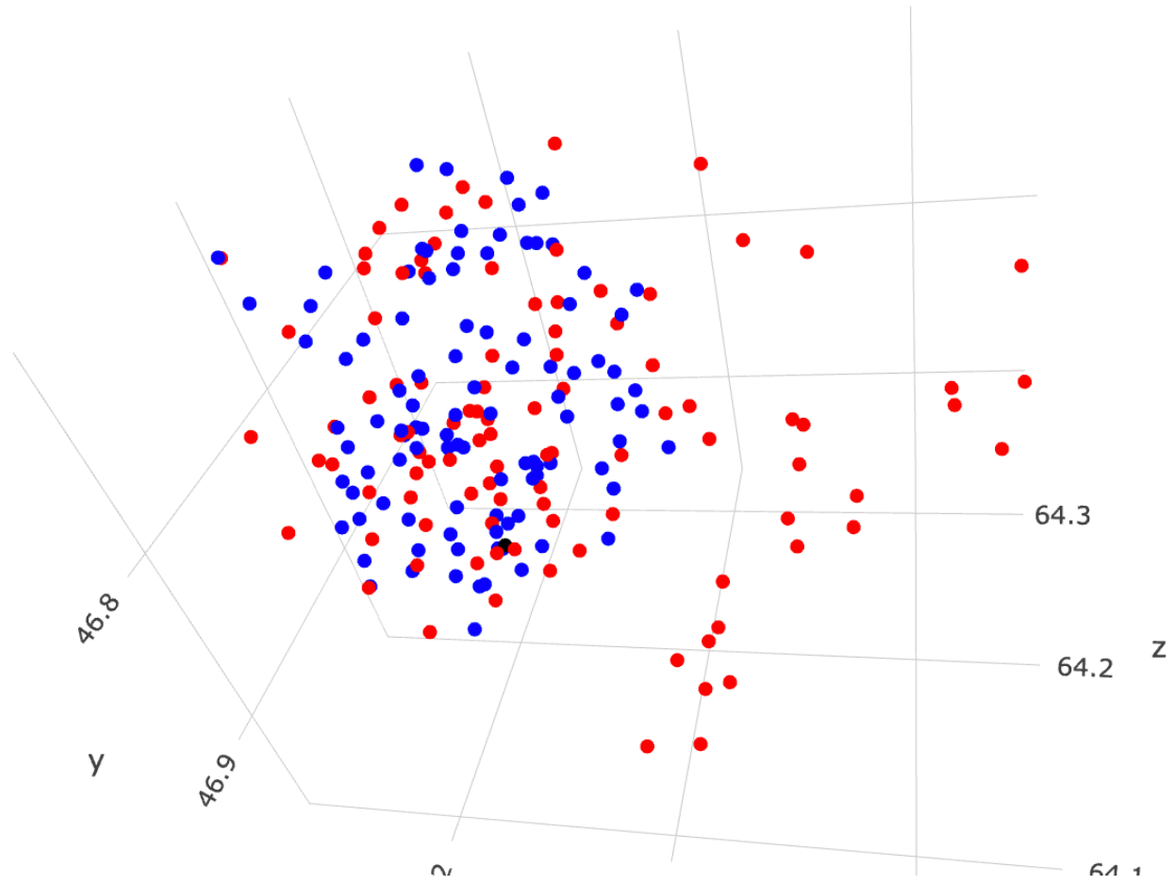
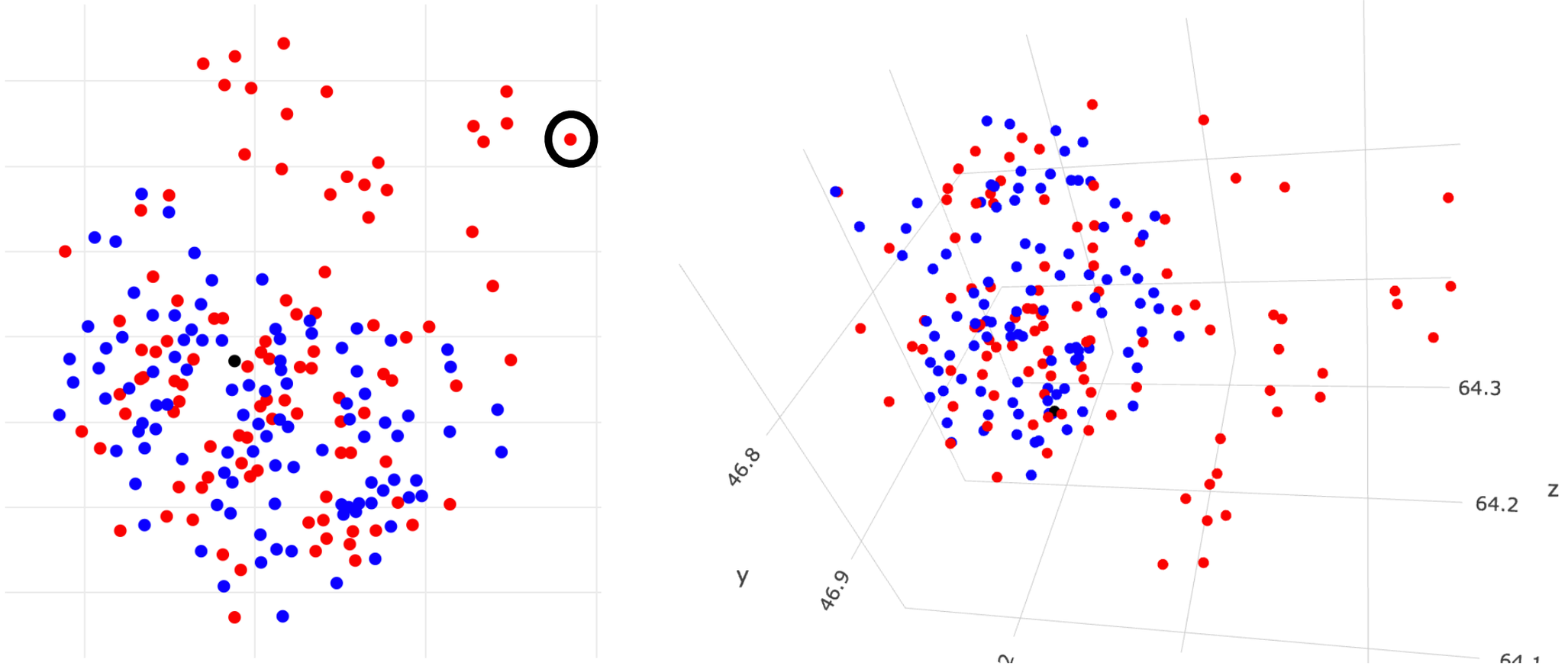
2D

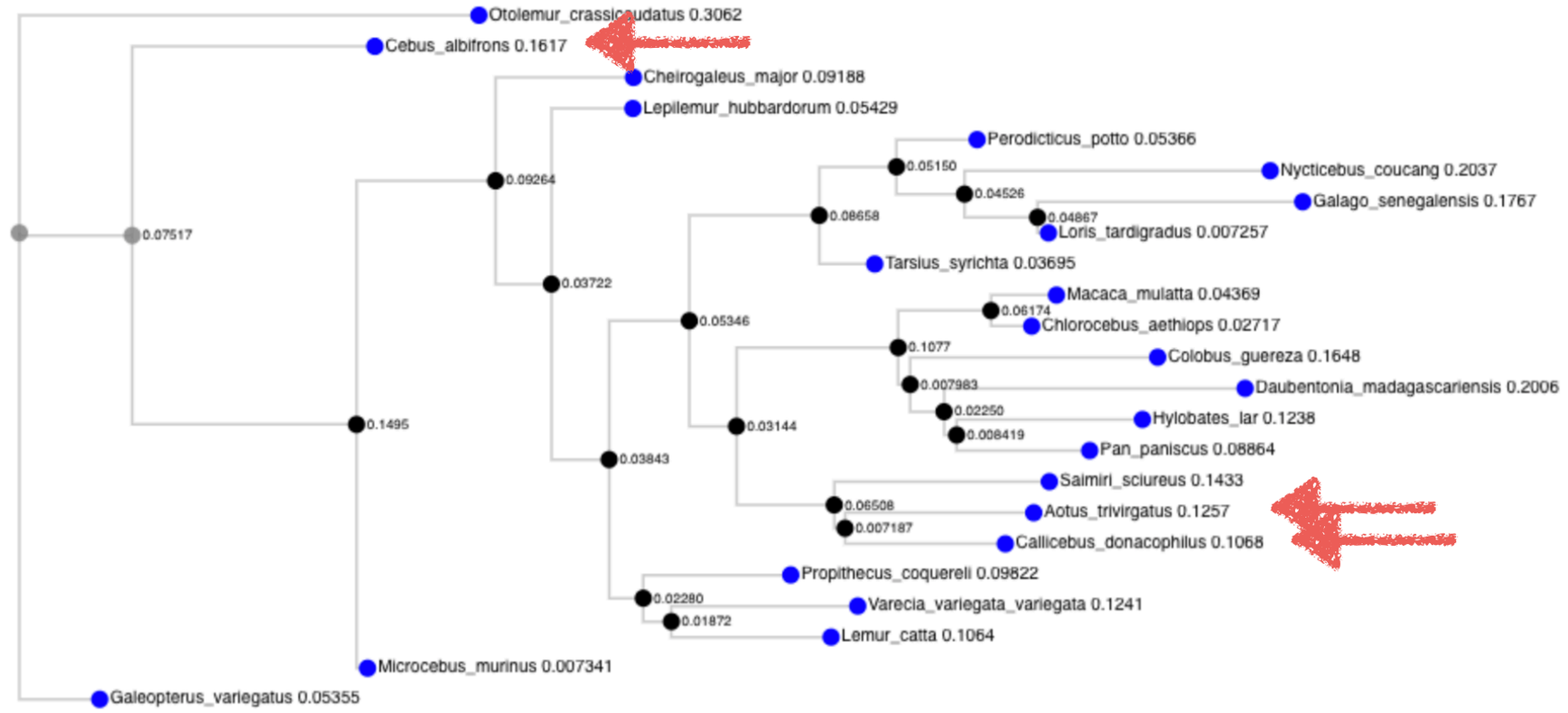


3D




64.3
64.2
z
46.8
y
46.9

Tree 10


Otolemur_crassicaudatus 0.3062
Cebus_albifrons 0.1617
Cheirogaleus_major 0.09188
Lepilemur_hubbardorum 0.05429
Perodicticus_potto 0.05366
Nycticebus_coucang 0.2037
Galago_senegalensis 0.1767
Loris_tardigradus 0.007257
Tarsius_syrichta 0.03695
Macaca_mulatta 0.04369
Chlorocebus_aethiops 0.02717
Colobus_guereza 0.1648
Daubentonia_madagascariensis 0.2006
Hylobates_lar 0.1238
Pan_paniscus 0.08864
Saimiri_sciureus 0.1433
Aotus_trivirgatus 0.1257
Callicebus_donacophilus 0.1068
Propithecus_coquereli 0.09822
Varecia_variegata_variegata 0.1241
Lemur_catta 0.1064
Microcebus_murinus 0.007341
Galeopterus_variegatus 0.05355
0.07517
0.09264
0.03722
0.1495
0.03843
0.05150
0.04526
0.04867
0.08658
0.06174
0.05346
0.1077
0.007983
0.02250
0.008419
0.03144
0.06508
0.007187
0.02280
0.01872

RevBayes Tutorial Setup

After logging on to your VM…

```
cd ~

cp -r moledata/revbayes/ ./

cd revbayes/genetree/

mv ./scripts/*.Rev .
```

RevBayes CTMC Tutorial

https://revbayes.github.io/tutorials/ctmc/

I strongly encourage you to try building at least one Rev script yourself for this tutorial, rather than simply running those that are already available.

Also note that in the scripts that are already written, the default number of replicate runs is 4. This is great for assessing convergence, but will cause analyses to run fairly slowly. You can reduce this to 2 to make sure that runs finish in a reasonable amount of time.

You'll also want to change the printgen option of mnModel and mnFile to 10 (rather than 1). Otherwise, output files get huge!

Jeremy M. Brown

RevBayes CTMC Tutorial

https://revbayes.github.io/tutorials/ctmc/

Look at Table 1 in the tutorial above.

Using the model descriptions in the table, use the same principles we've been practicing to set up each of these models in RevBayes.

Fill out Table 2 for as many models as you can.

```
rb mcmc_JC.Rev
```

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End

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