Homework Review

What was different about setting up Normal model compared to the Binomial?

Did you run into any difficulties?

How did the output look? Was convergence good?

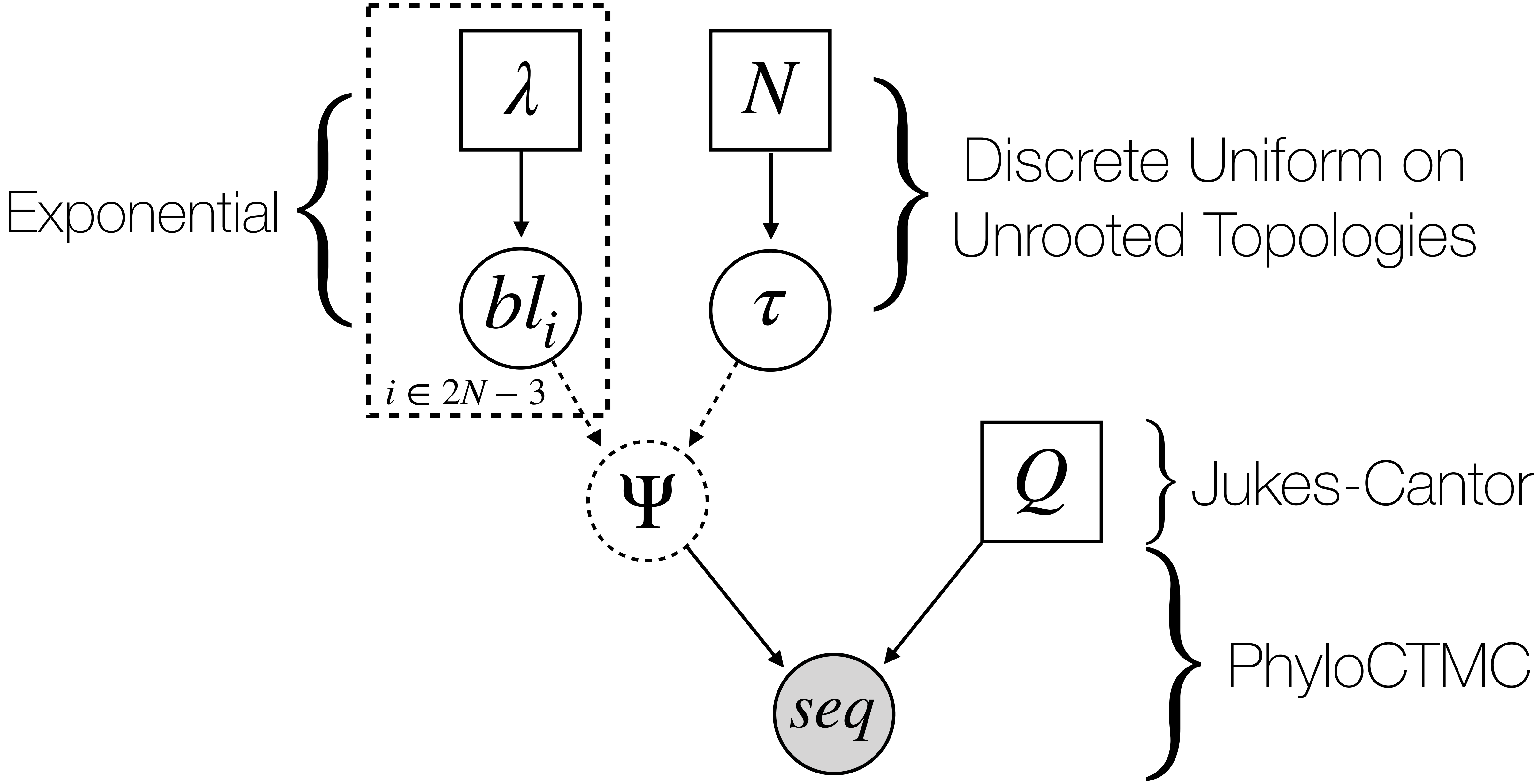
Did you run multiple replicates?

What effect, if any, did changing your prior have?

Phylogenetic Graphical Models

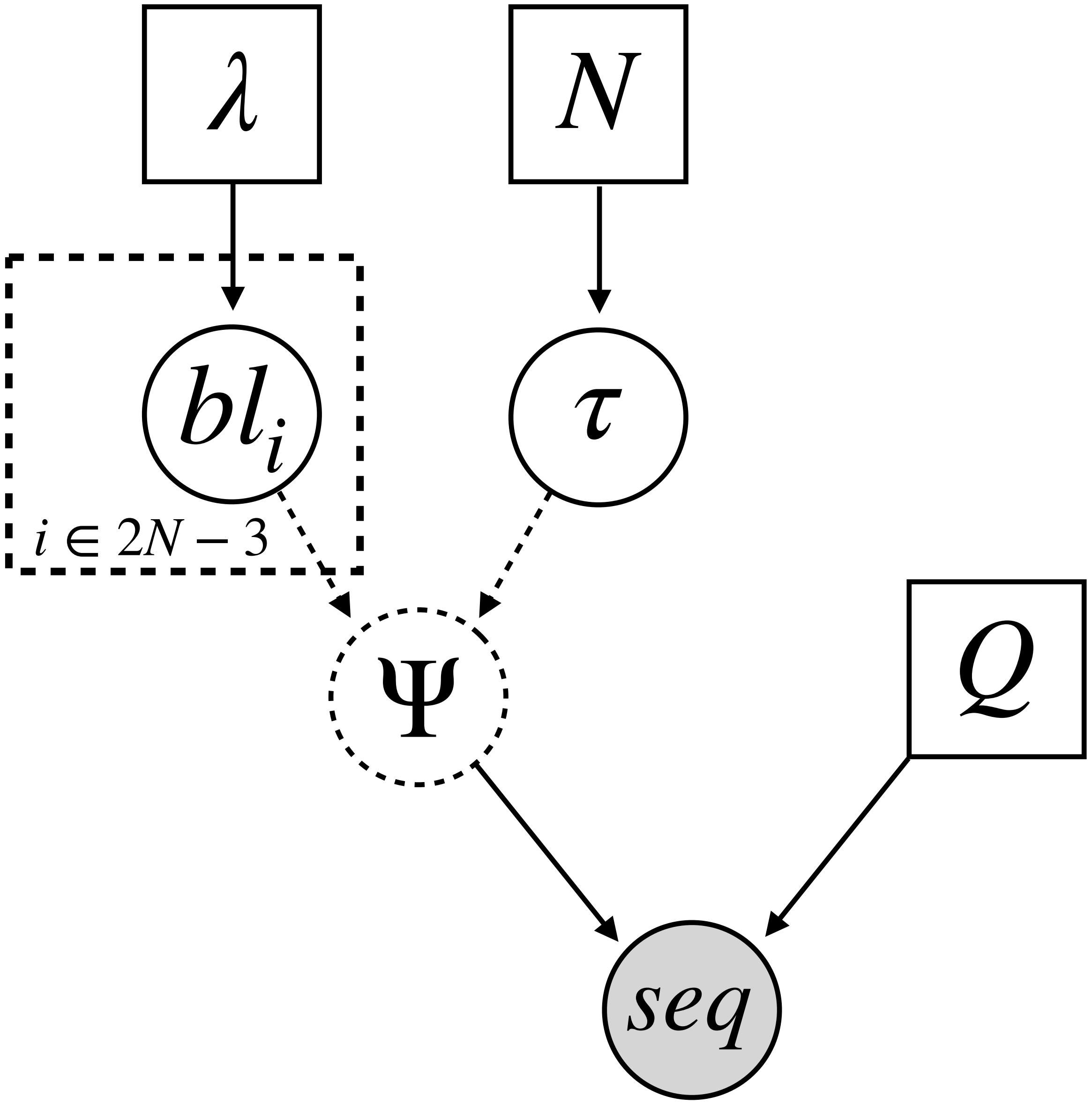
Jukes-Cantor

(Exponential branch-length prior)



Jukes-Cantor

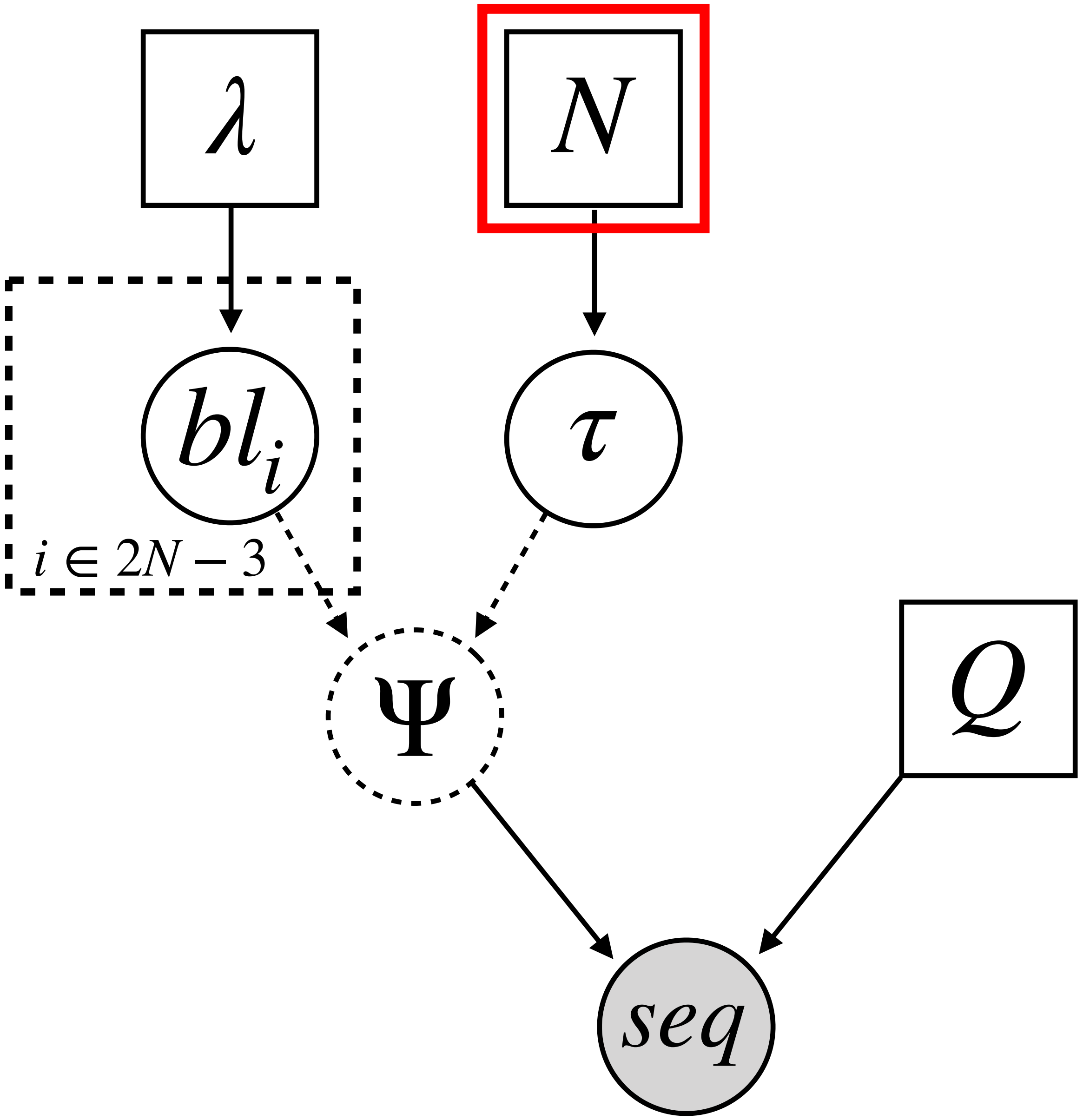
(Exponential branch-length prior)



```
data = readDiscreteCharacterData(“myData.nex”)
taxa <- data.taxa()

lambda <- 10

for (i in 1:n_branches){
    bl[i] ~ dnExponential(lambda)
}

topology ~ dnUniformTopology(taxa)

psi := treeAssembly(topology, br_lens)

Q <- fnJC(4)

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

seq.clamp(data)
```

Jukes-Cantor

(Exponential branch-length prior)



Reading in dataset and extracting list of taxa

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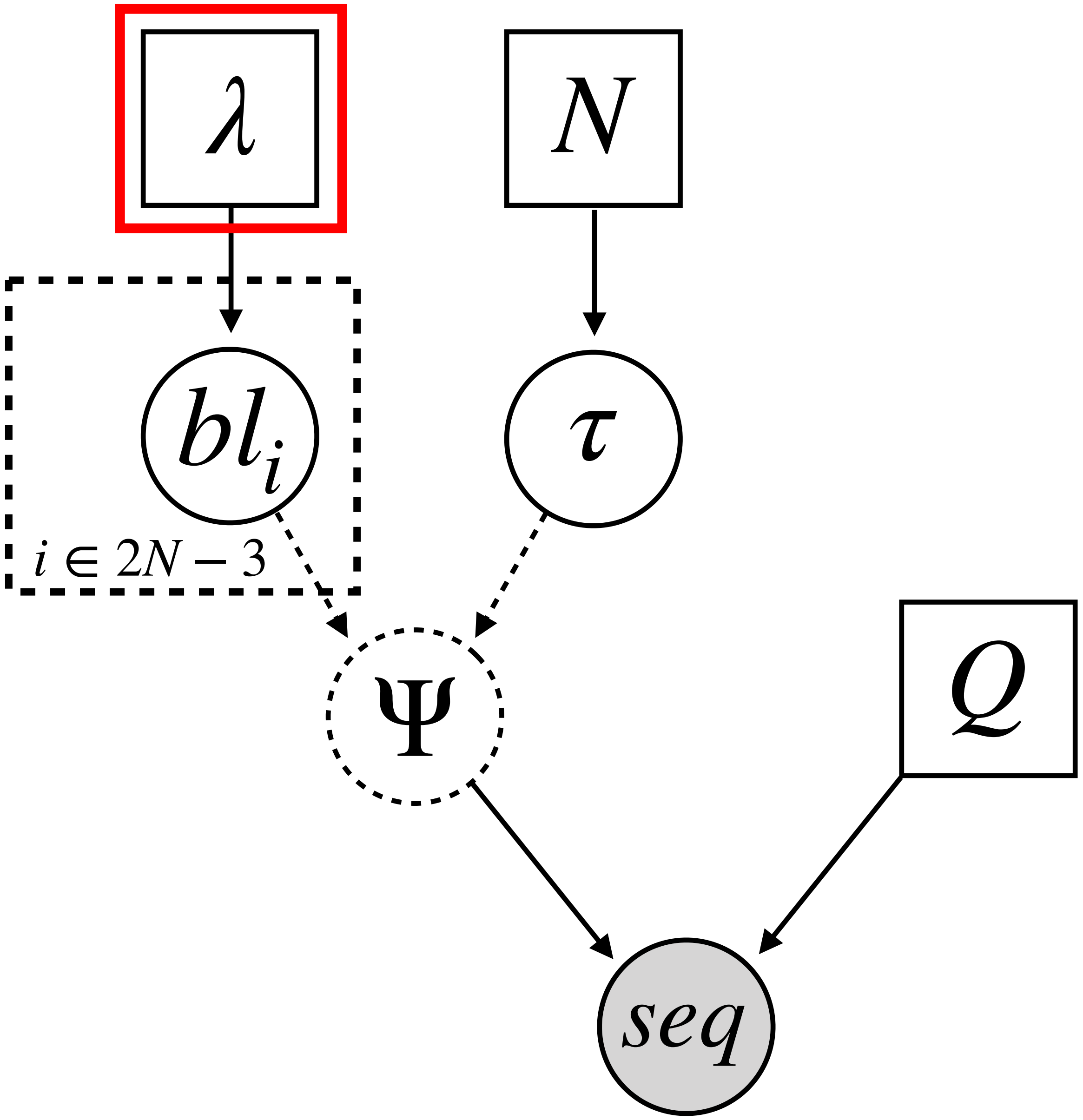

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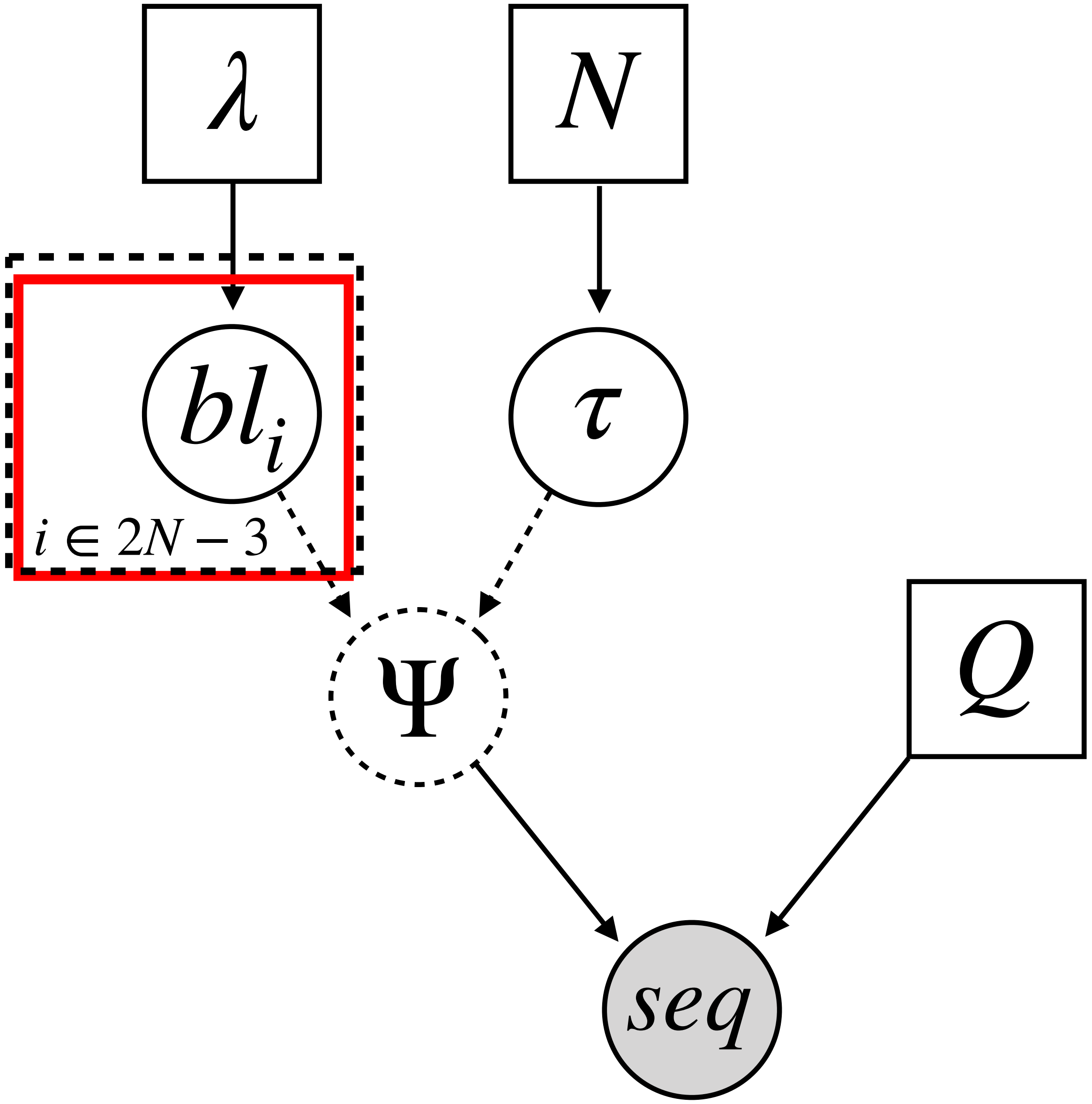

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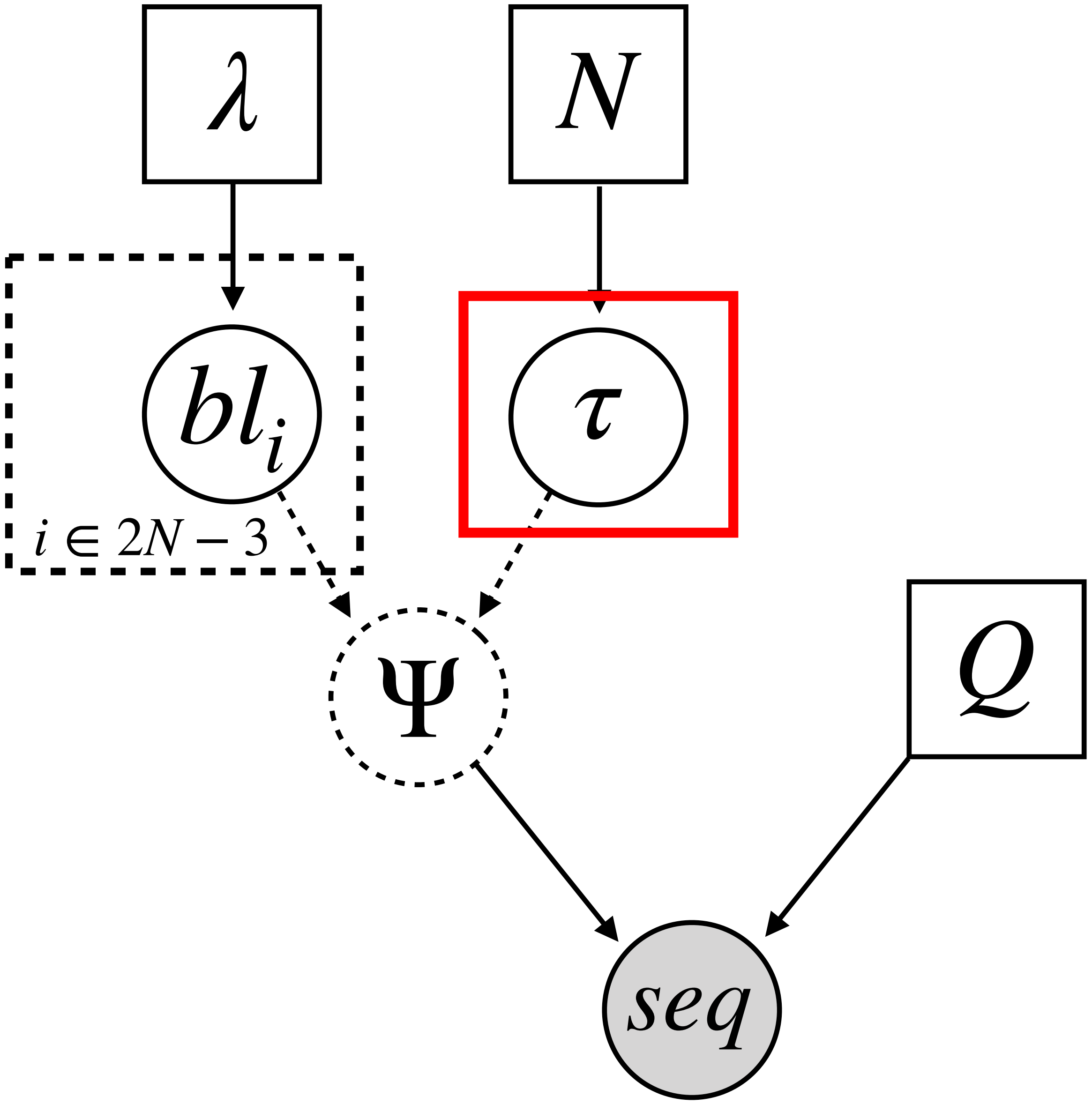
Jukes-Cantor

(Exponential branch-length prior)



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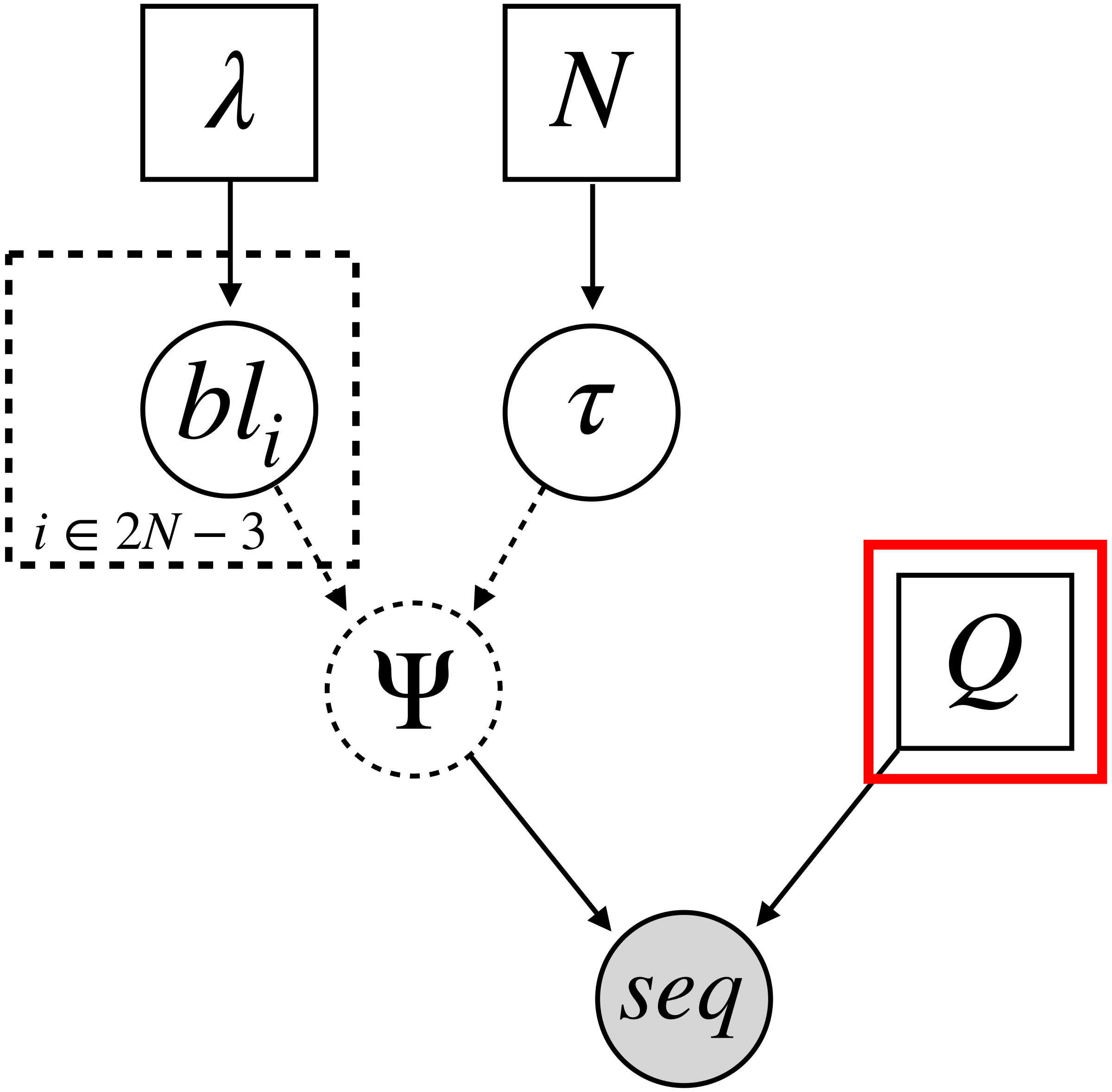
(Exponential branch-length prior)



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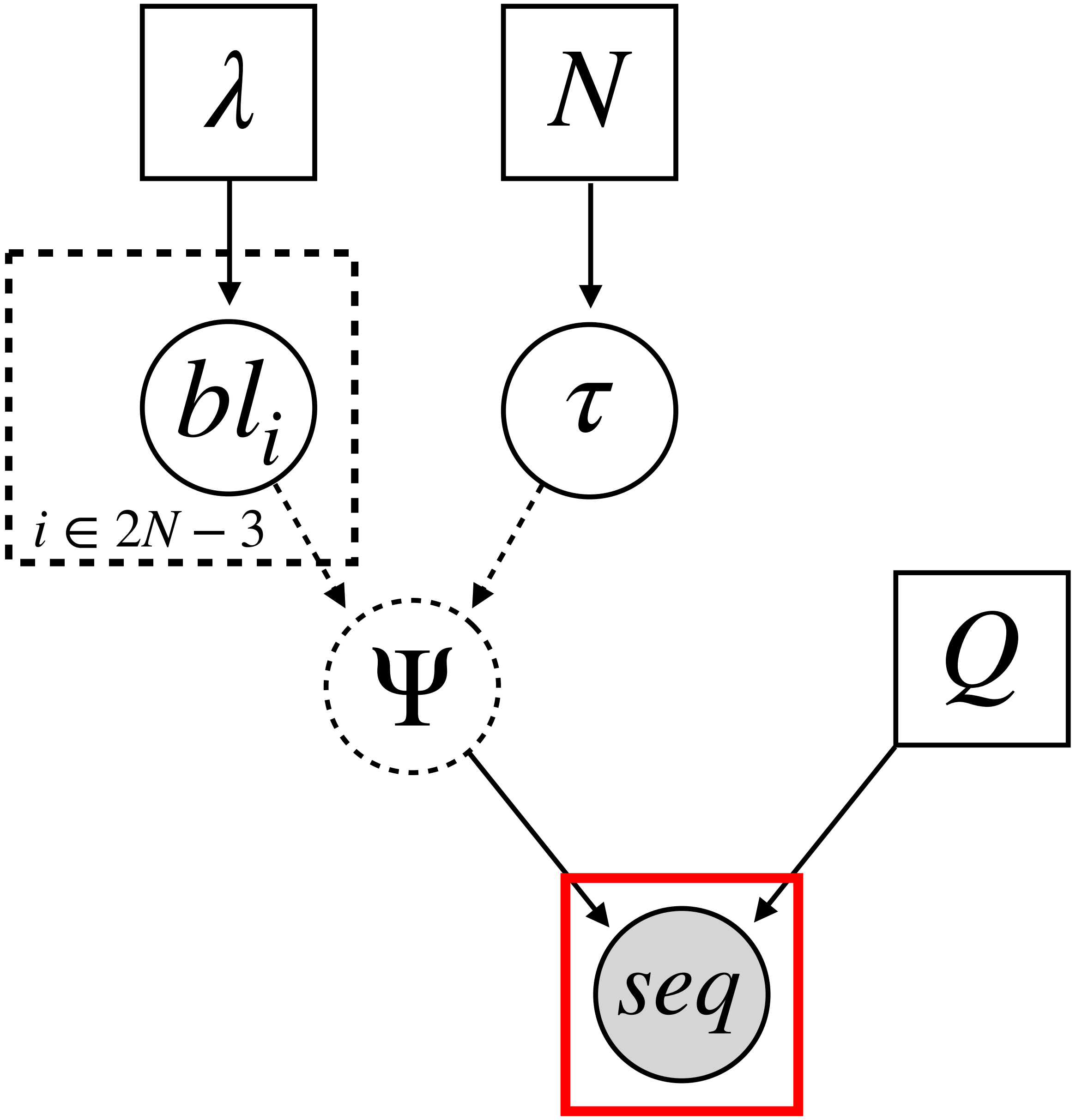

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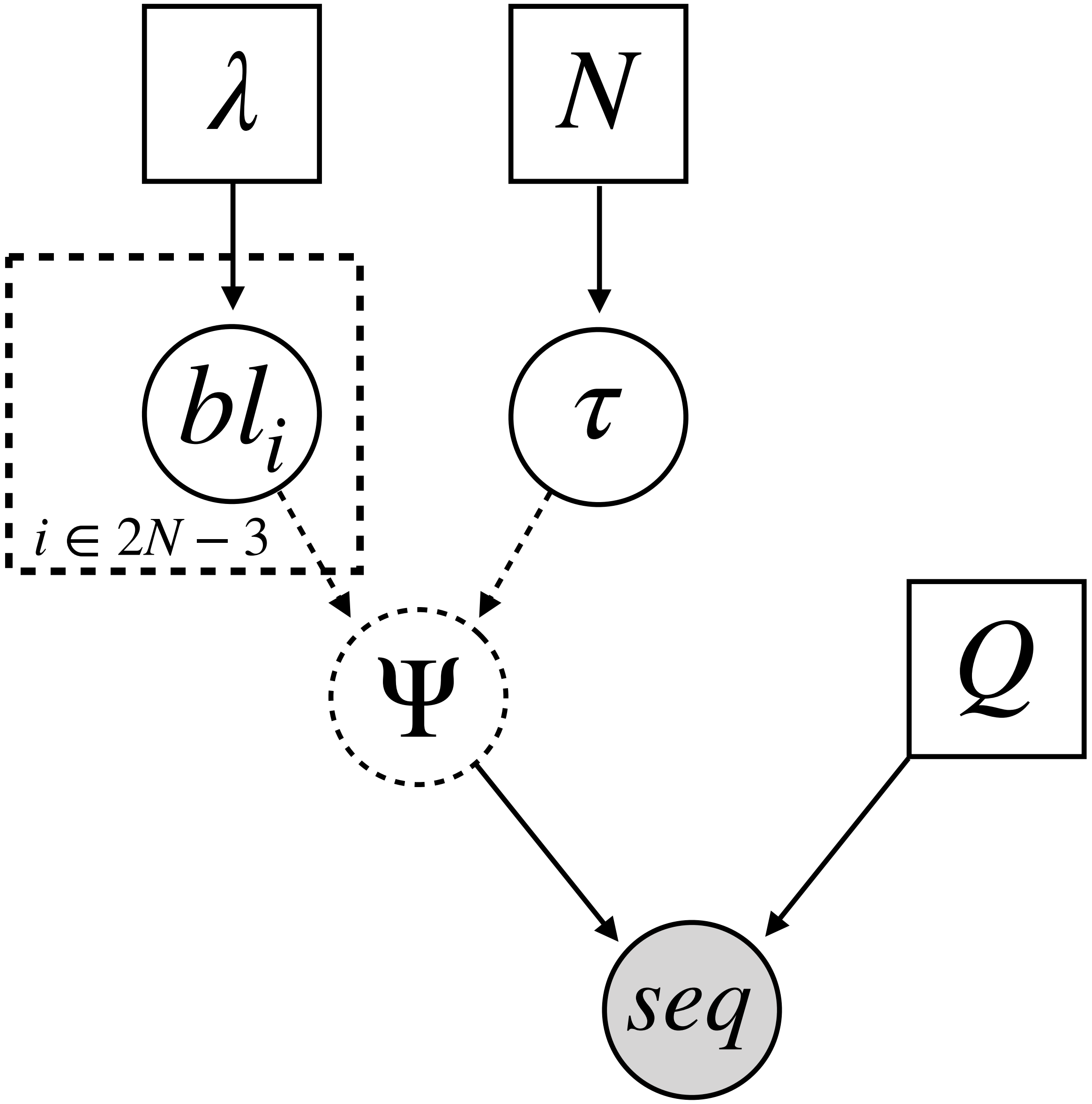
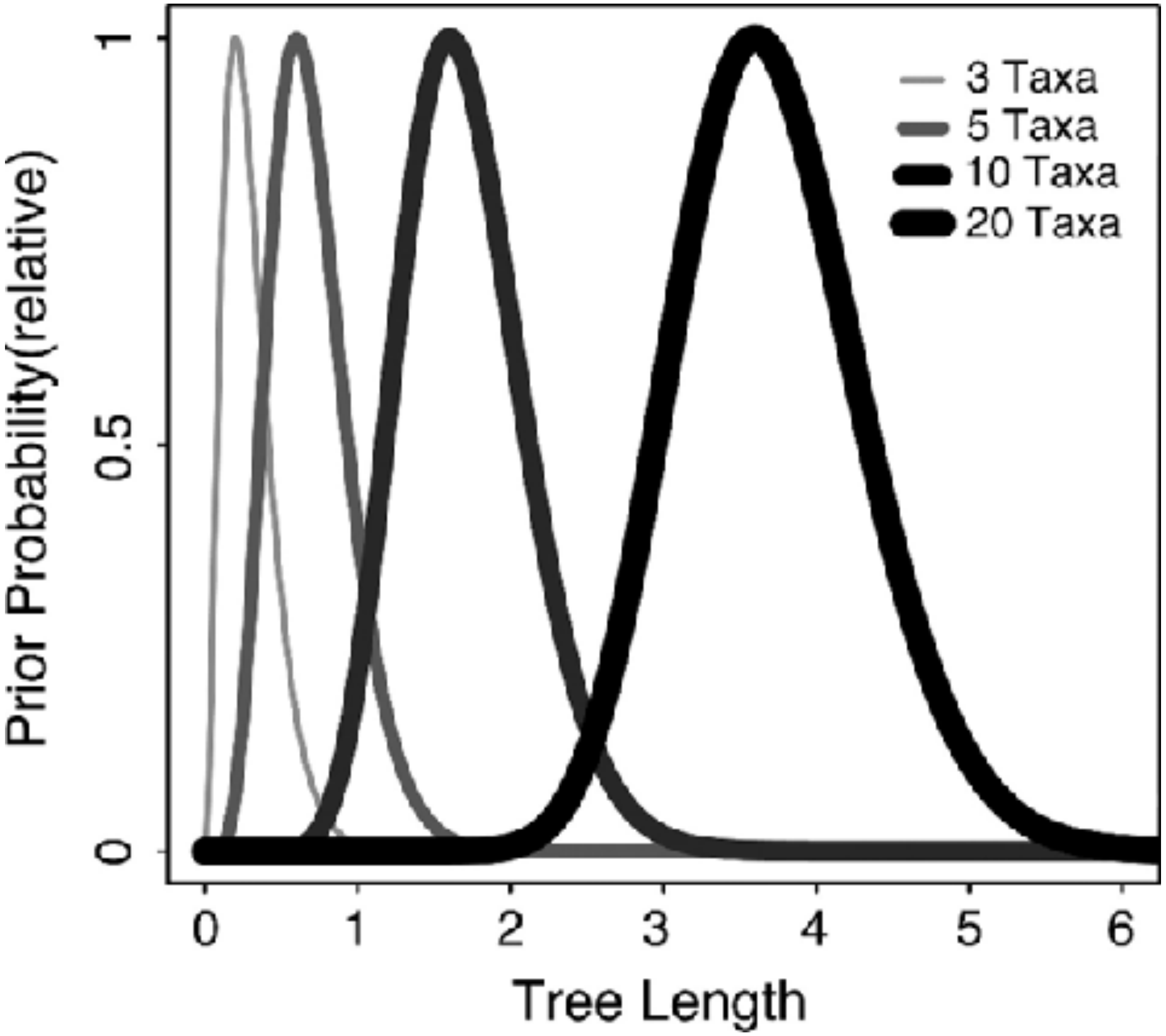
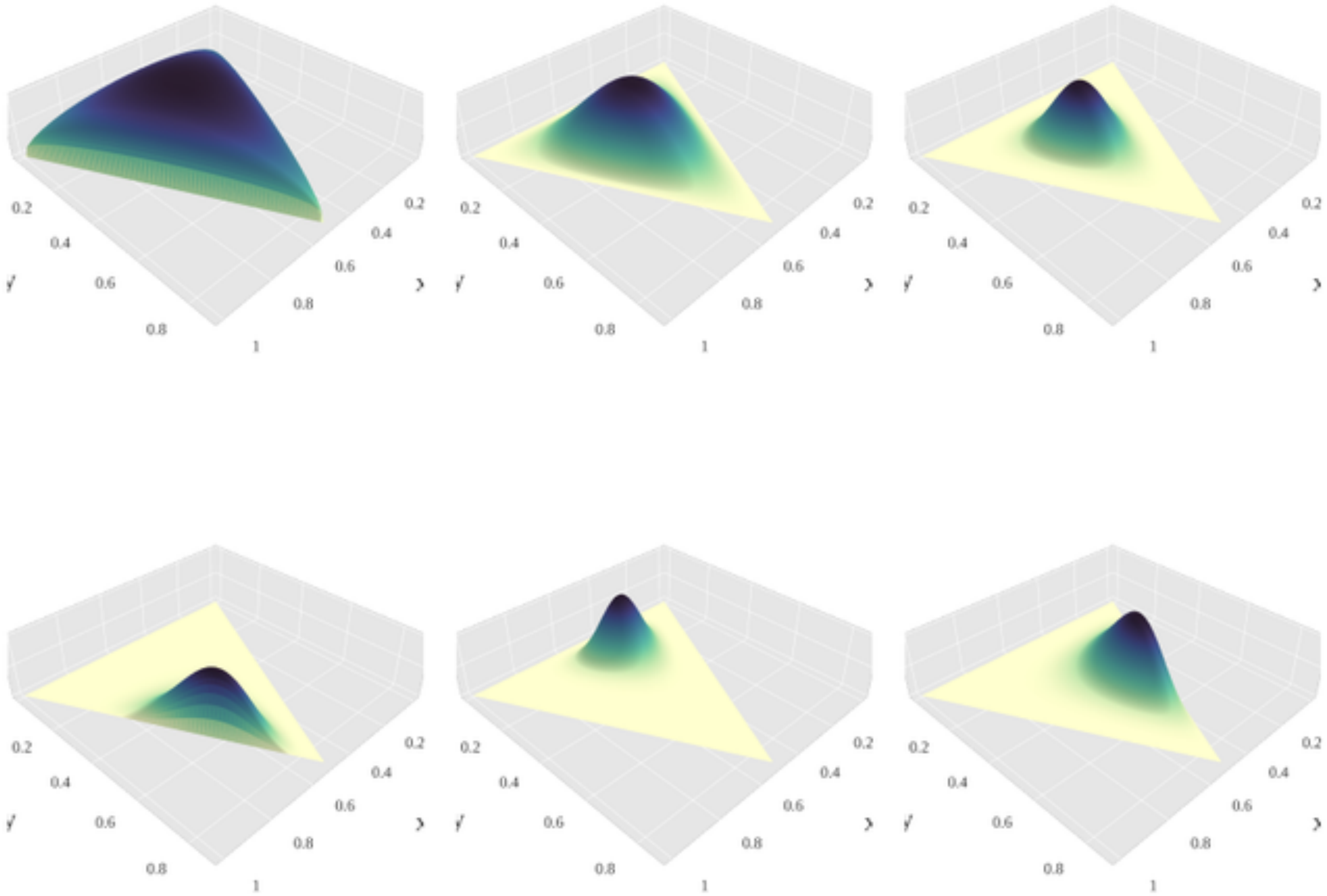
Jukes-Cantor

(Exponential branch-length prior)





Dirichlet Distribution

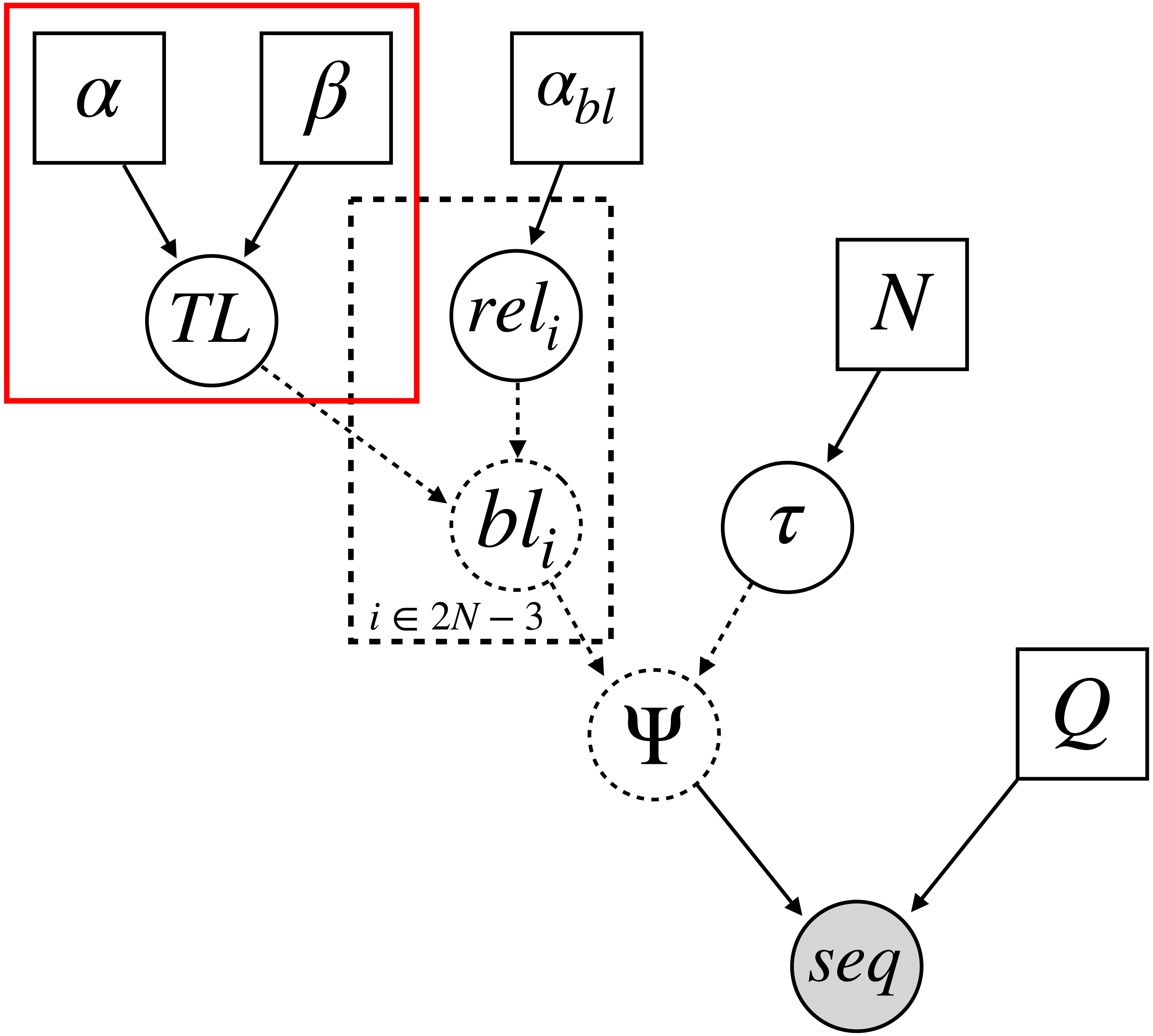


The Dirichlet distribution is a multivariate generalization of the Beta distribution. It describes the joint distribution of a set of parameters, each of which is bounded between 0 and 1, **and whose sum is 1**.

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

Jukes-Cantor

(Compound Dirichlet tree- and branch-length prior)

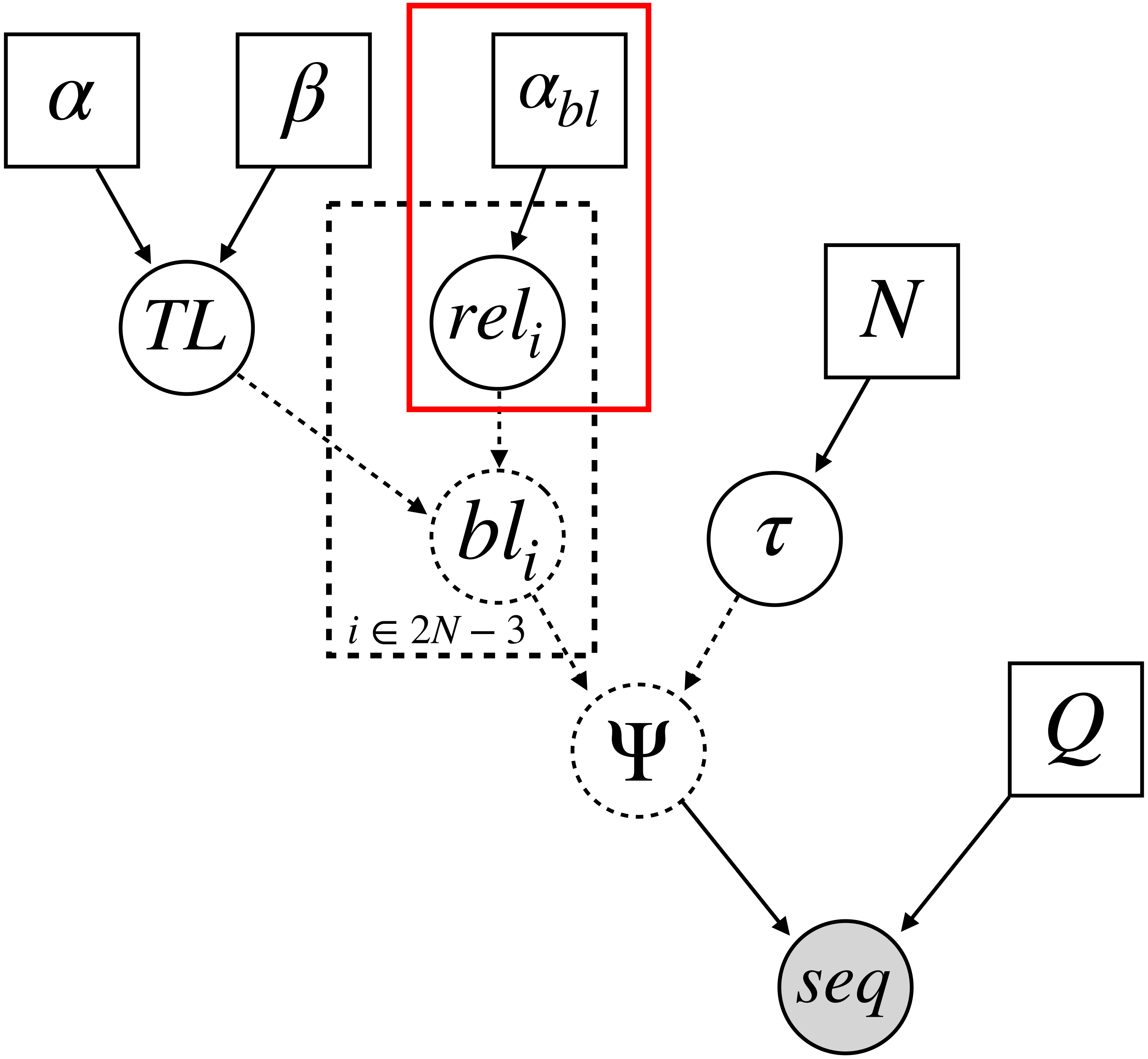


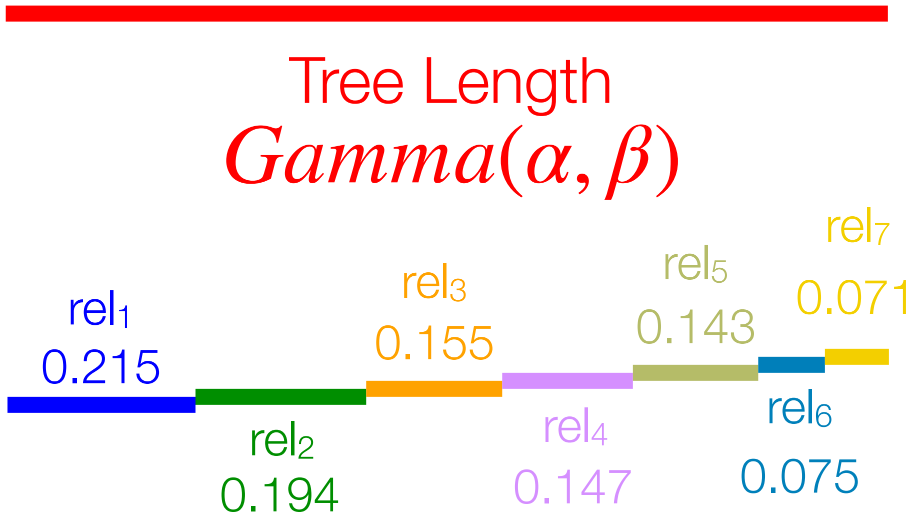
Tree Length

$Gamma(\alpha, \beta)$

Jukes-Cantor

(Compound Dirichlet tree- and branch-length prior)



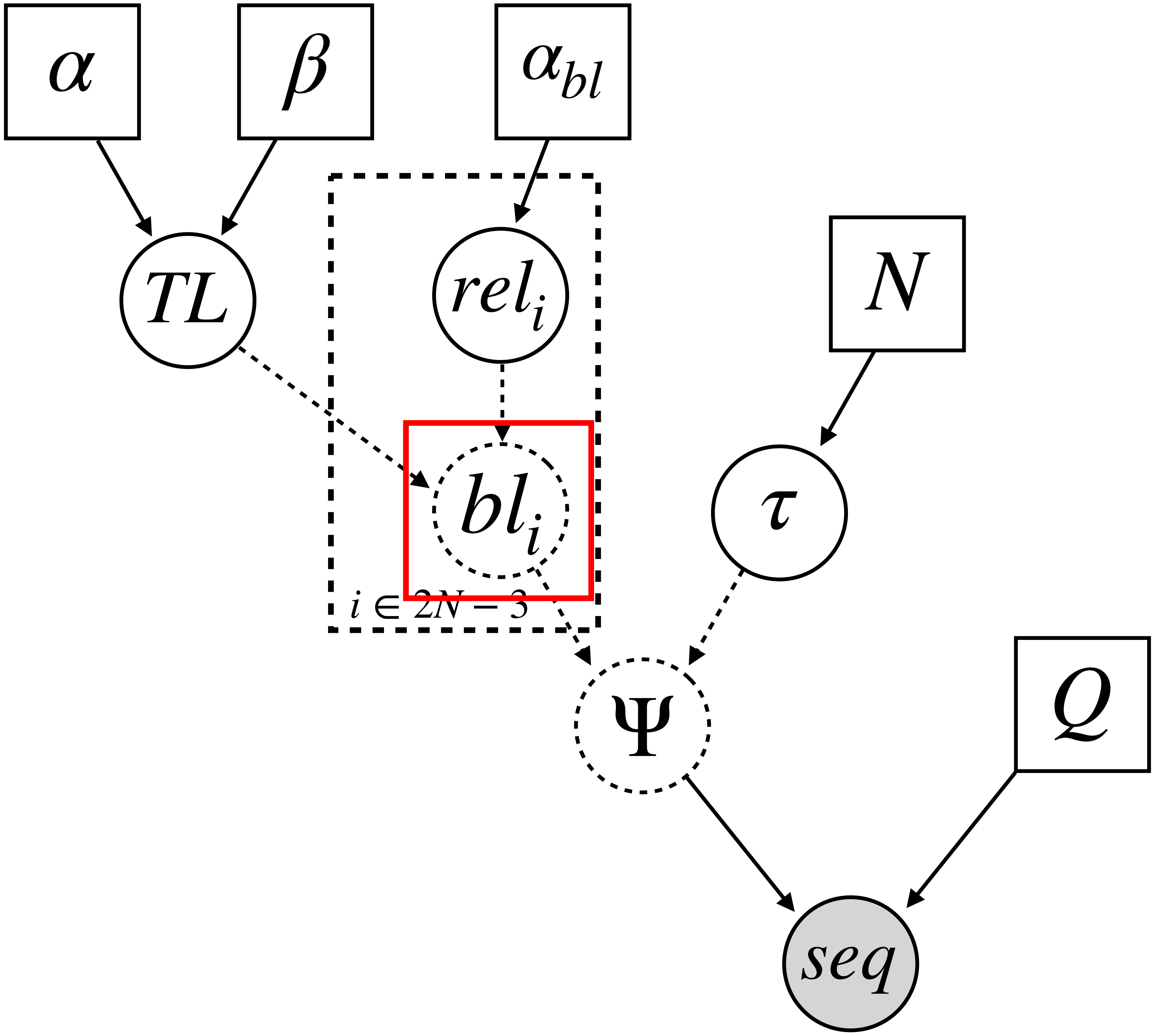


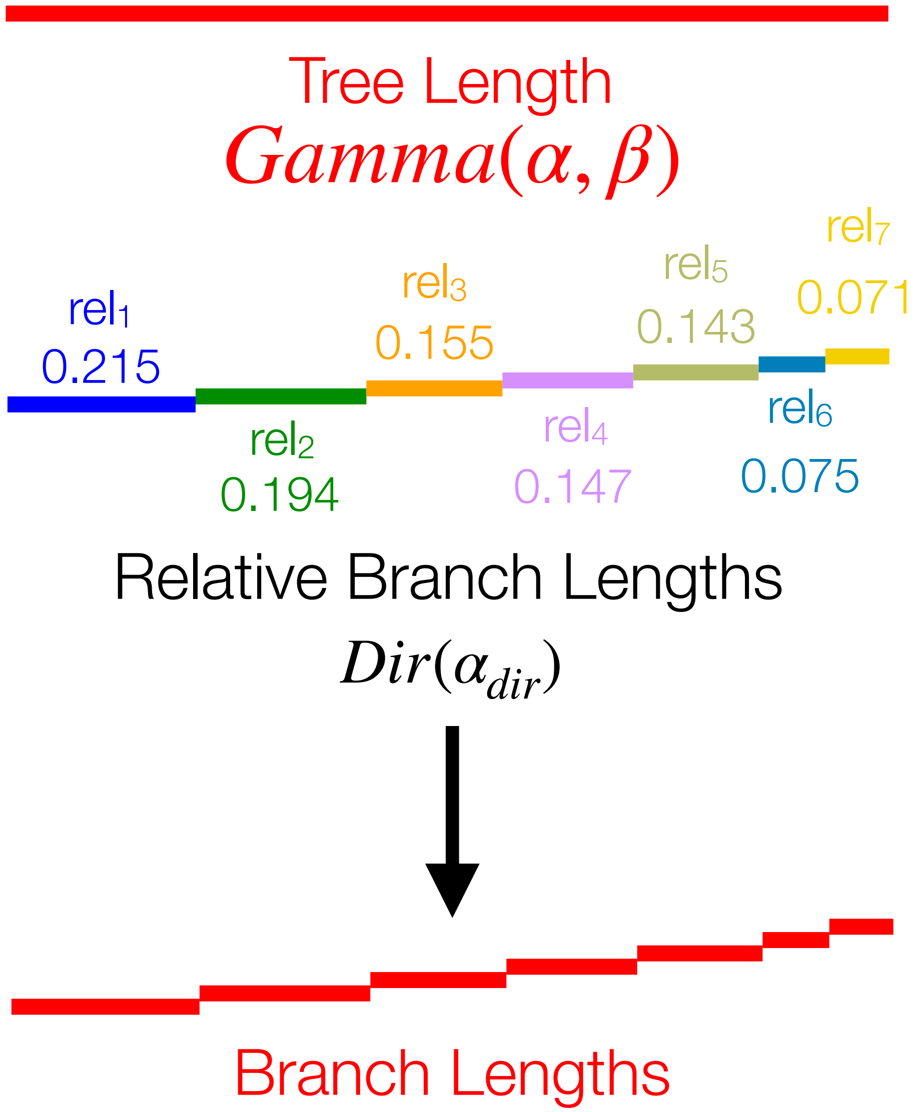
Tree Length
$Gamma(\alpha, \beta)$

Relative Branch Lengths
$Dir(\alpha_{dir})$

Jukes-Cantor

(Compound Dirichlet tree- and branch-length prior)





Tree Length

$Gamma(\alpha, \beta)$

Relative Branch Lengths

$Dir(\alpha_{dir})$

Branch Lengths

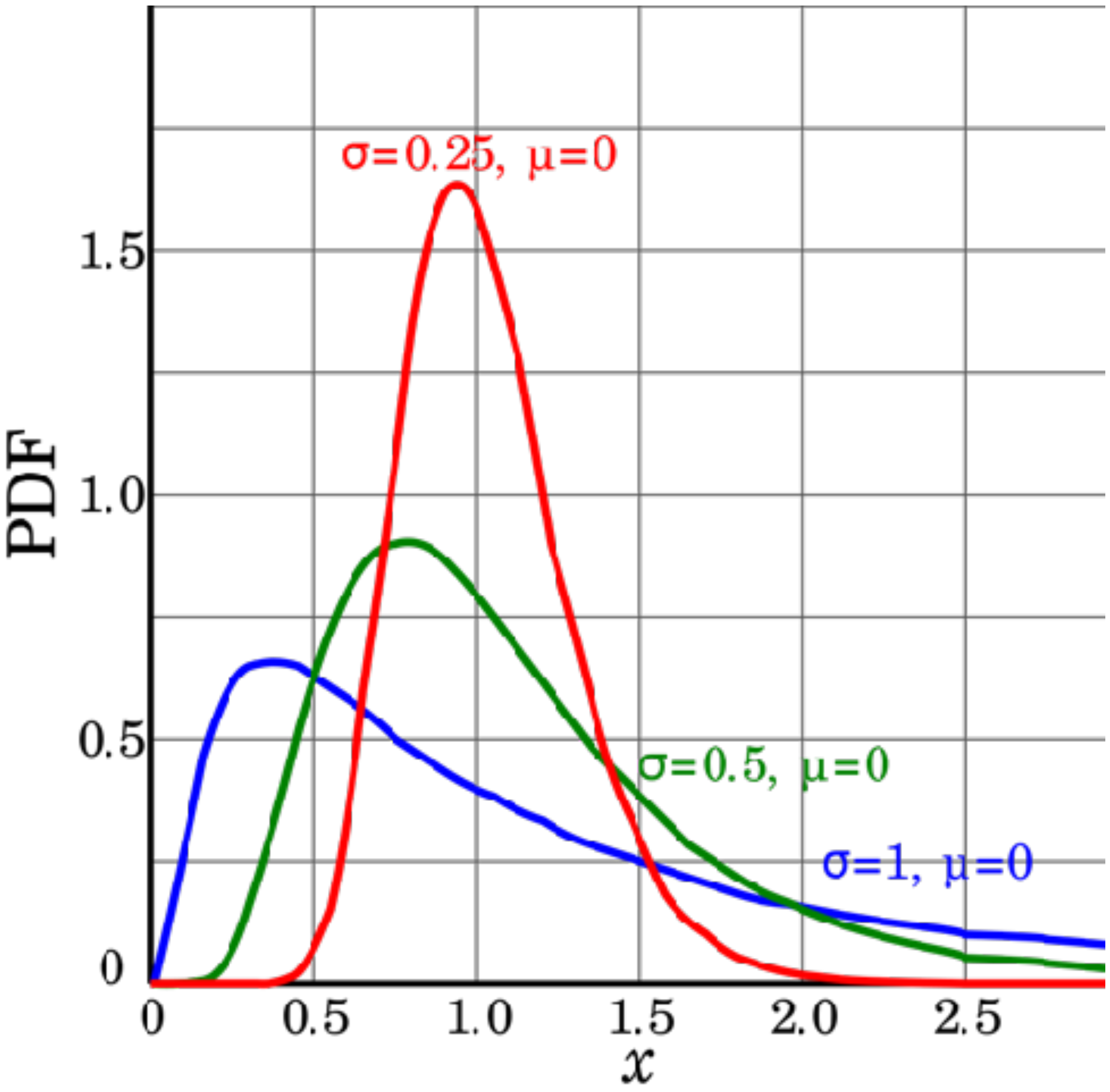
Jukes-Cantor

(Compound Dirichlet tree- and branch-length prior)

```
data = readDiscreteCharacterData(“myData.nex”)
taxa <- data.taxa()

alpha <- 2
beta <- 4

TL ~ dnGamma(alpha,beta)

alpha_bl <- 1.0

rel_branch_lengths ~ dnDirichlet( rep(alpha_bl,num_branches) )

br_lens := rel_branch_lengths * TL

topology ~ dnUniformTopology(taxa)

Q <- fnJC(4)

psi := treeAssembly(topology, br_lens)

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

seq.clamp(data)
```

Compound Dirichlet

Log-Normal Distribution

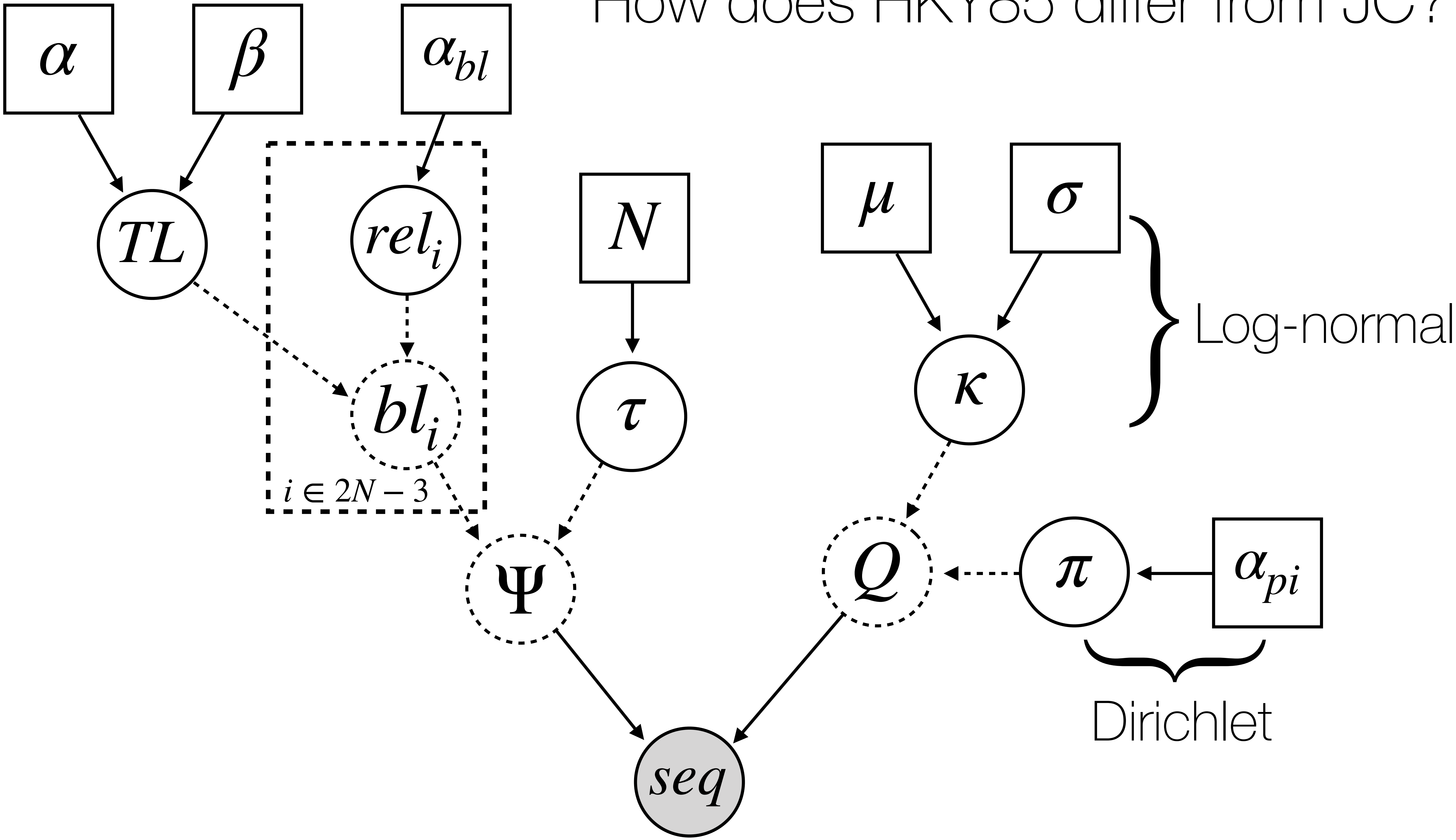


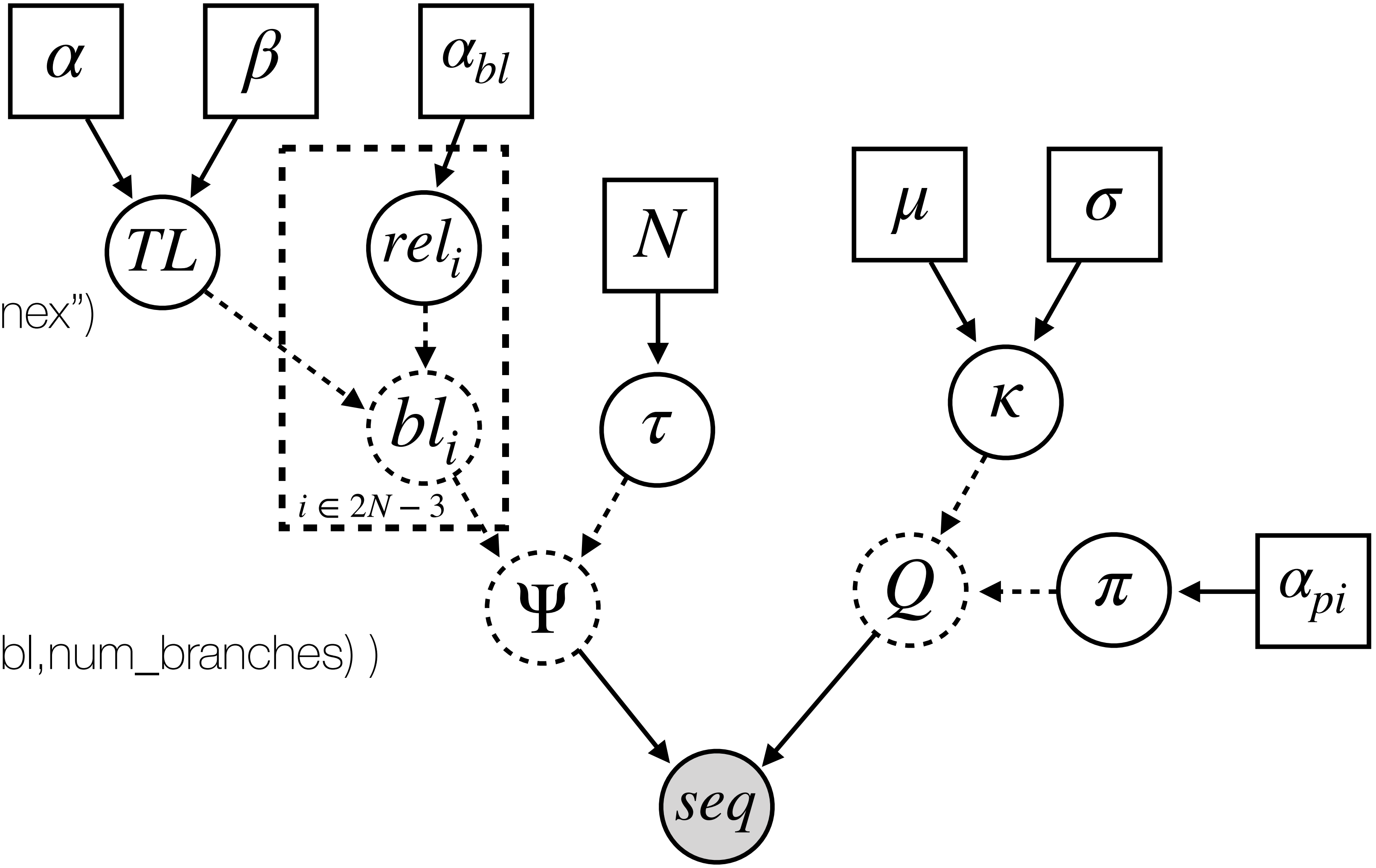
In probability theory, a log-normal (or lognormal) distribution is a continuous probability distribution of a random variable whose logarithm is normally distributed.

https://en.wikipedia.org/wiki/Log-normal_distribution

HKY85

How does HKY85 differ from JC?





```
data = readDiscreteCharacterData(“myData.nex”)
taxa <- data.taxa()
alpha <- 2
beta <- 4
TL ~ dnGamma(alpha,beta)
alpha_bl <- 1.0
rel_branch_lengths ~ dnDirichlet( rep(alpha_bl,num_branches) )
br_lens := rel_branch_lengths * TL
topology ~ dnUniformTopology(taxa)
psi := treeAssembly(topology, br_lens)
```

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

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

Q <- fnHKY(kappa,pi)
```

HKY85

```
seq ~ dnPhyloCTMC(tree=psi,Q=Q,type=“DNA”)
seq.clamp(data)
```

Things to Remember

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

Vectors modeled with a Dirichlet need to 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.

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 all the models that don't include +Gamma or +I. (we'll get to those shortly)

Keep your .rev files and inferred clade probabilities. Before next week, once you've worked through all the models, submit your .rev files and inferred probabilities to the homework folder on GitHub.