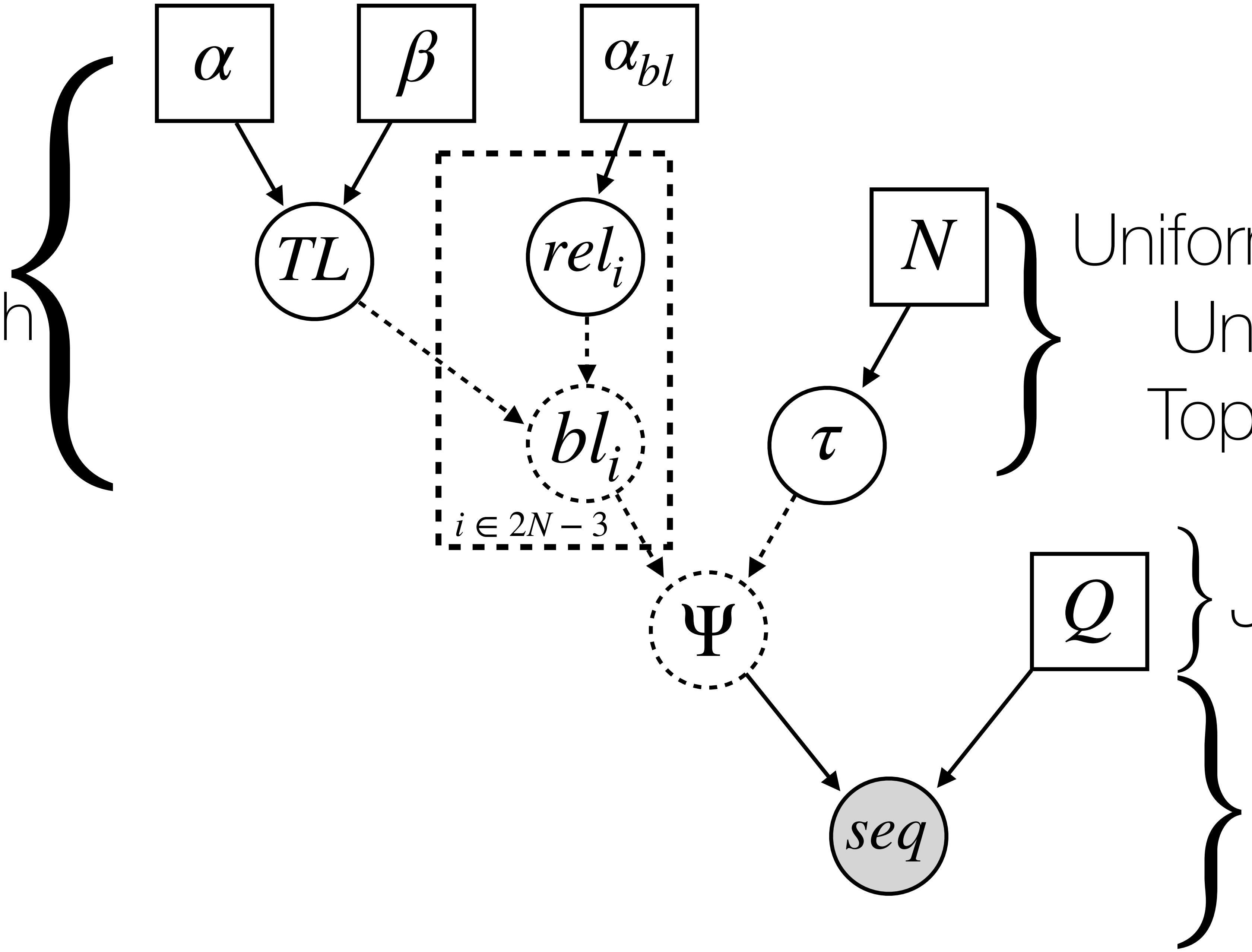
Phylogenetic Graphical Models

Jukes-Cantor



Compound Tree- and Branch-length Prior

Uniform Prior on Unrooted Topologies

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PhyloCTMC

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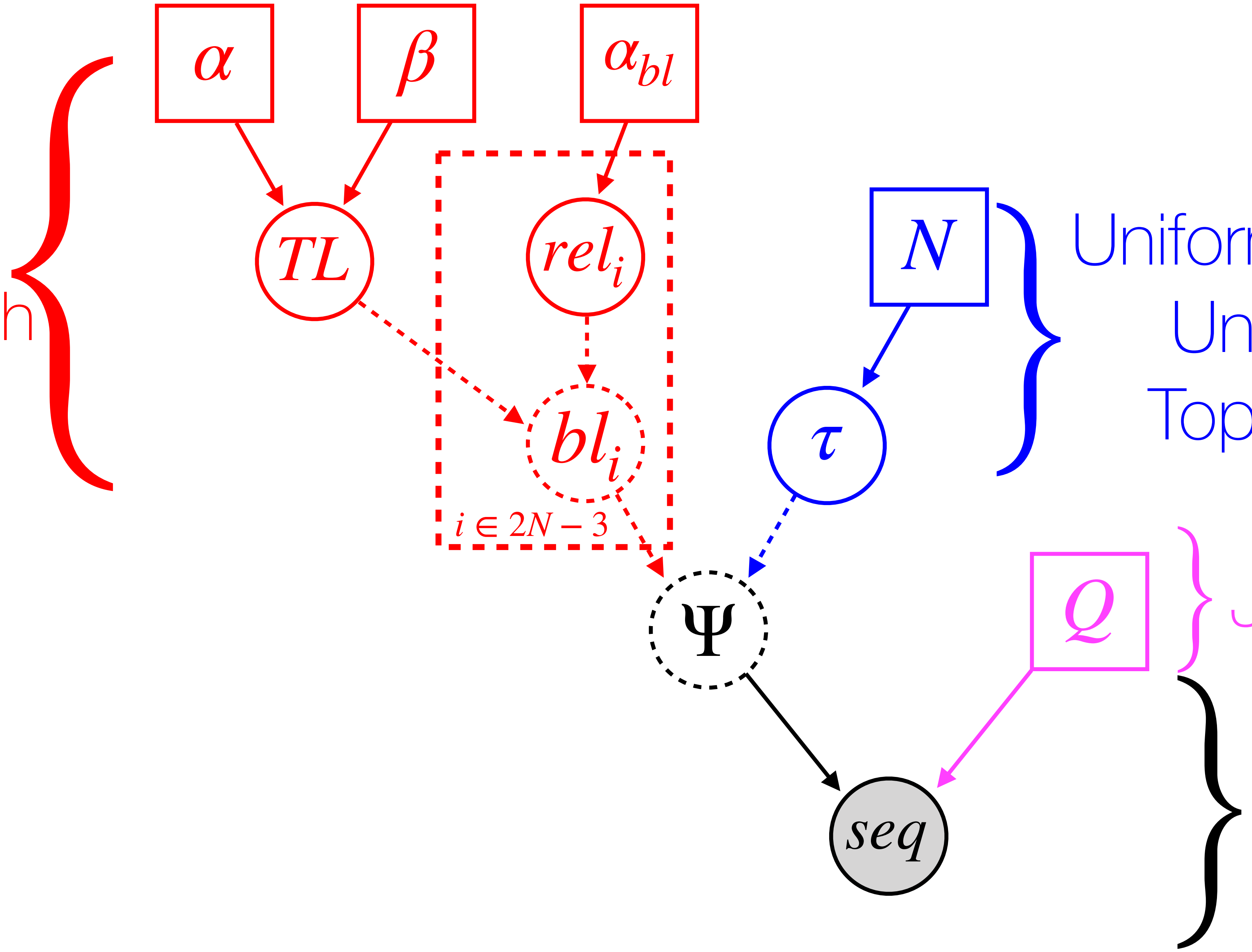

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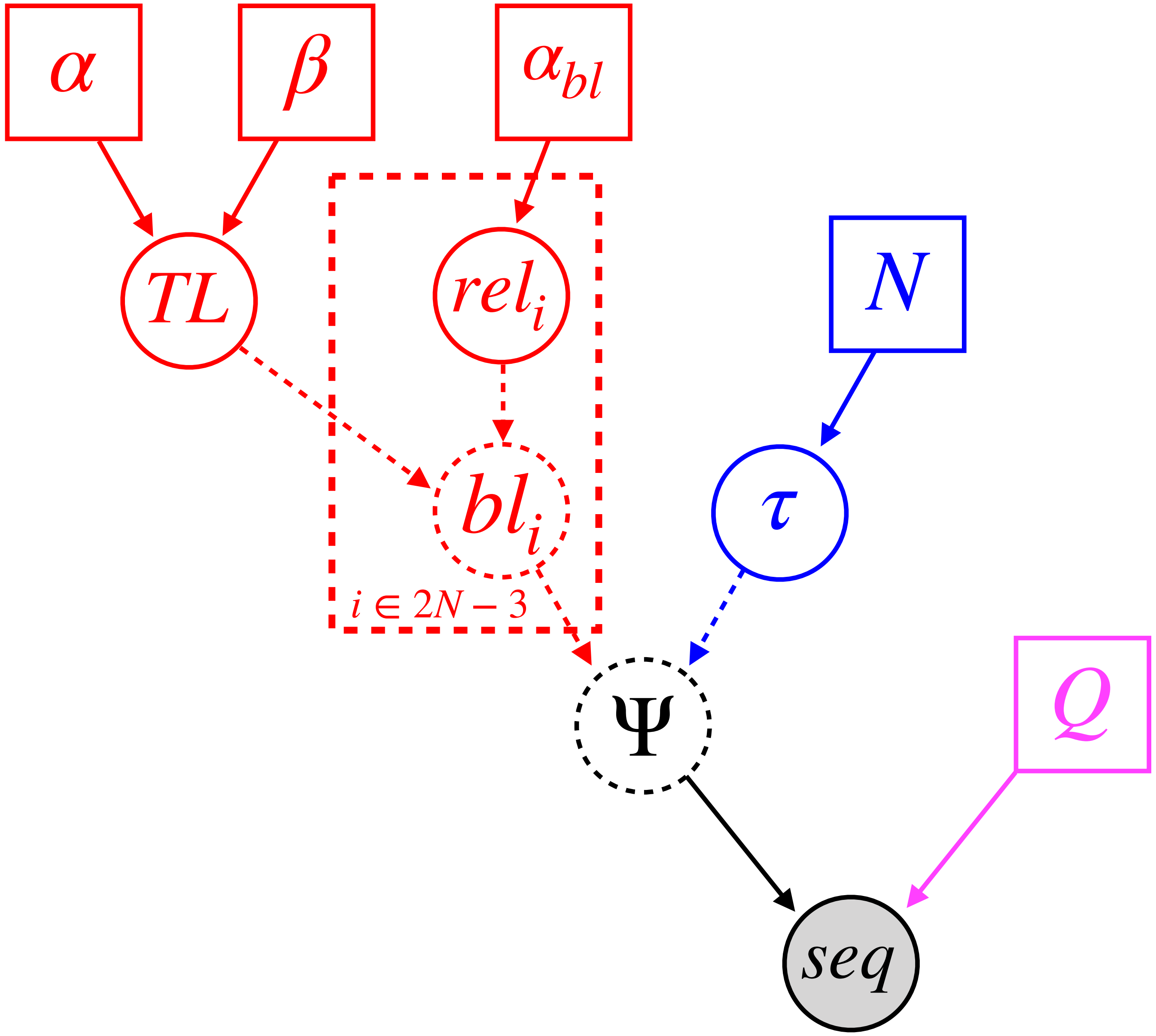

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taxa <- data.taxa()
n_taxa <- data.ntaxa()
n_branches <- 2 * n_taxa - 3

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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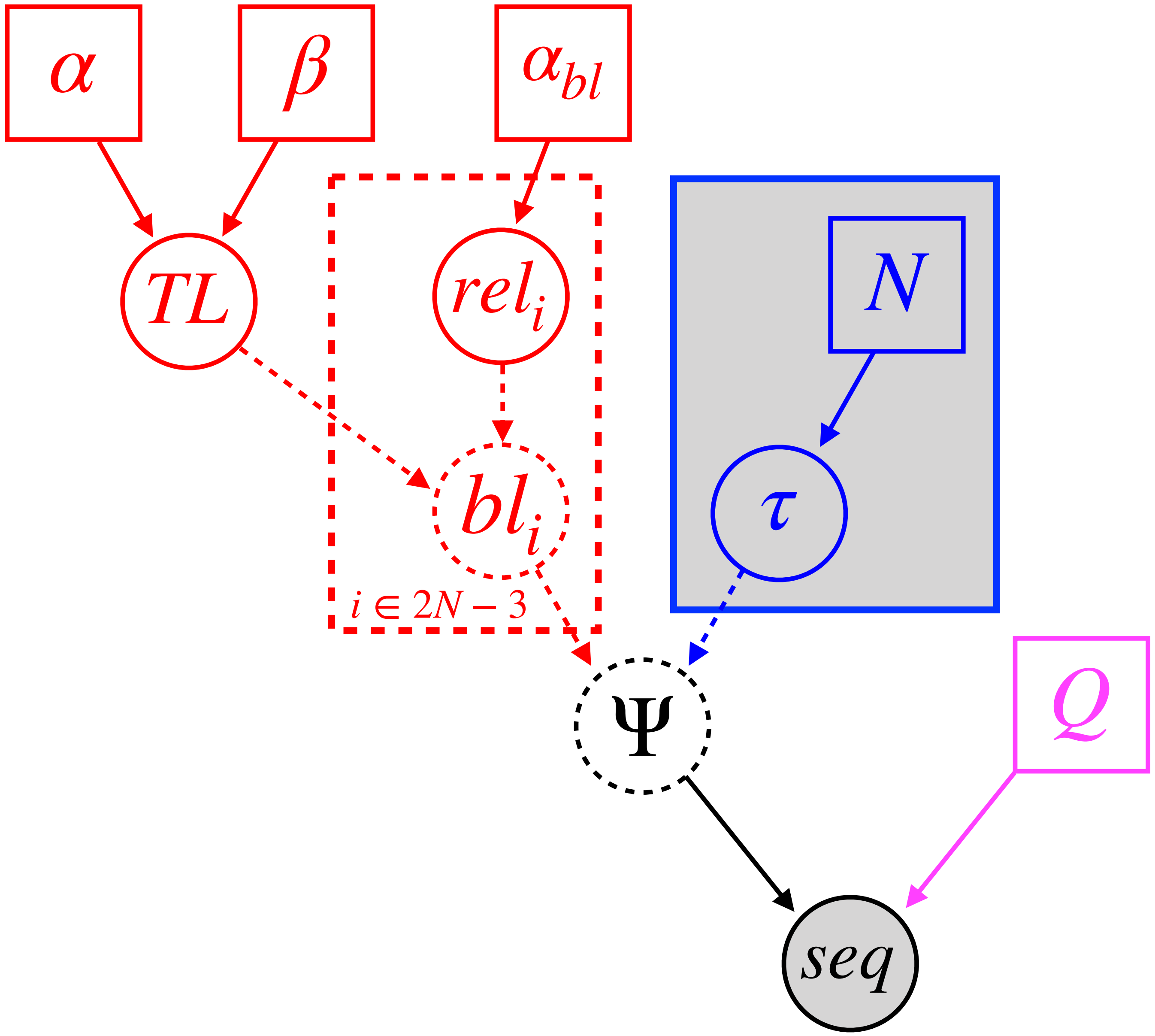

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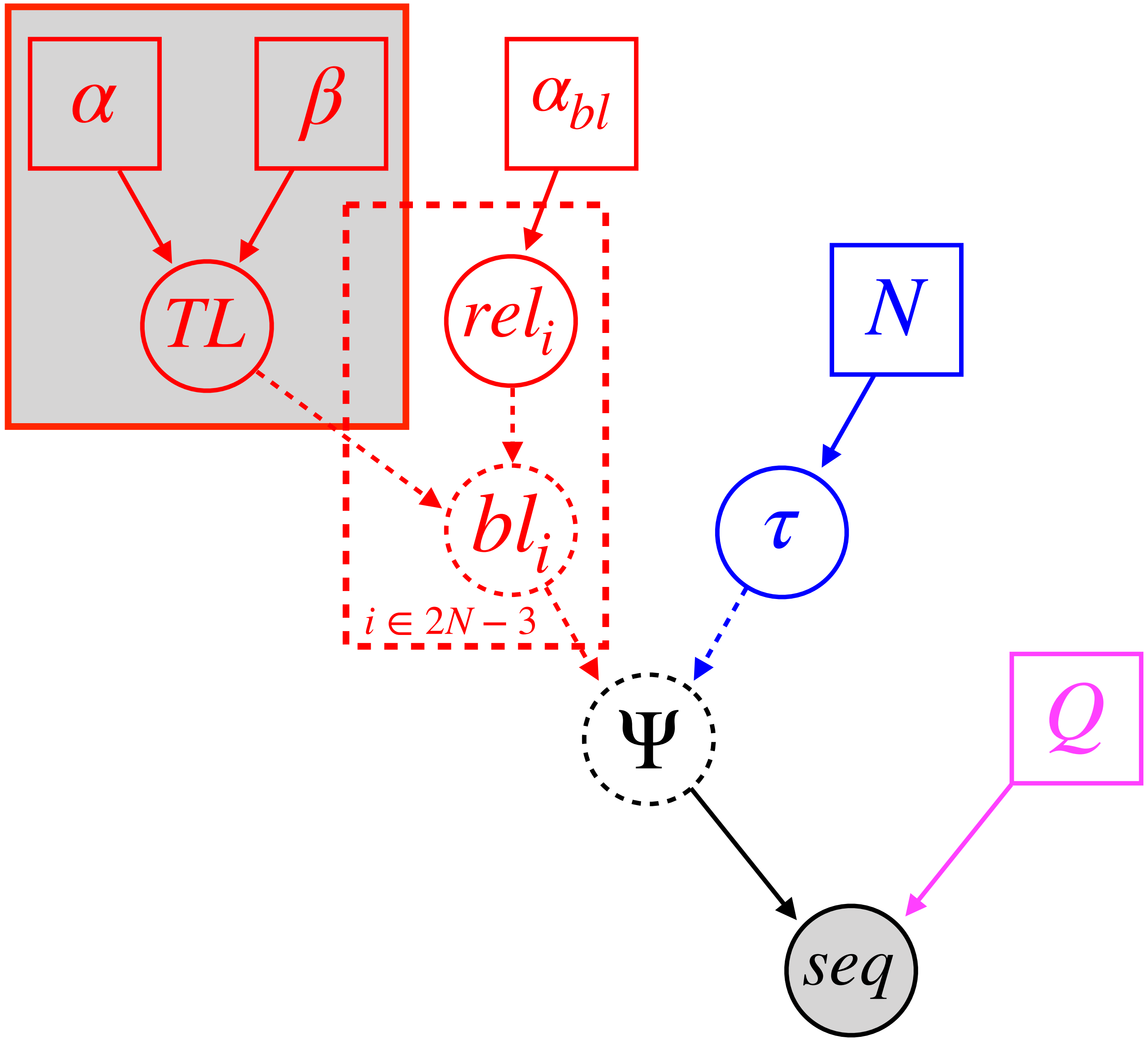
(Compound Dirichlet tree- and branch-length prior)



Tree Length

$Gamma(\alpha, \beta)$

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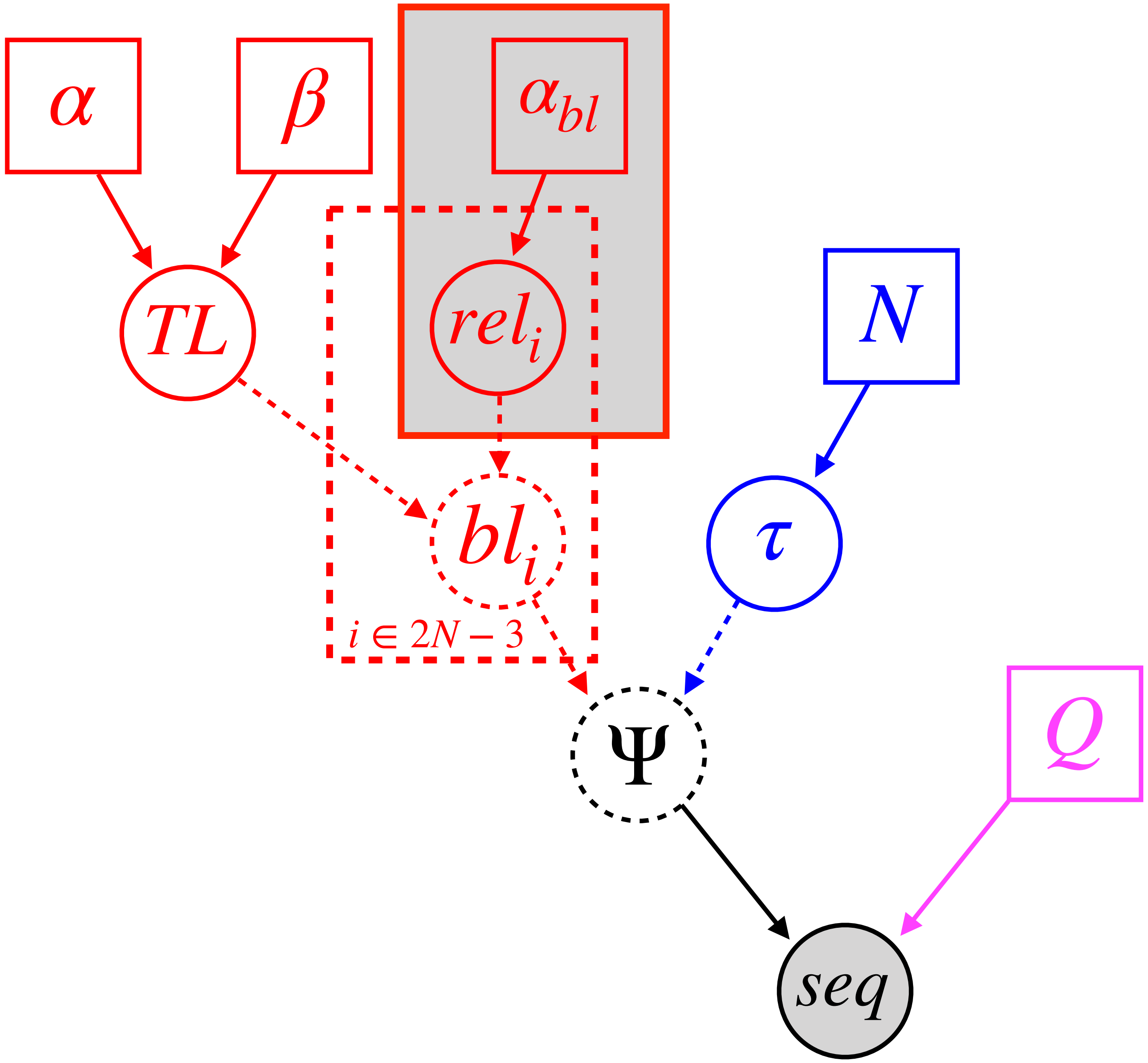

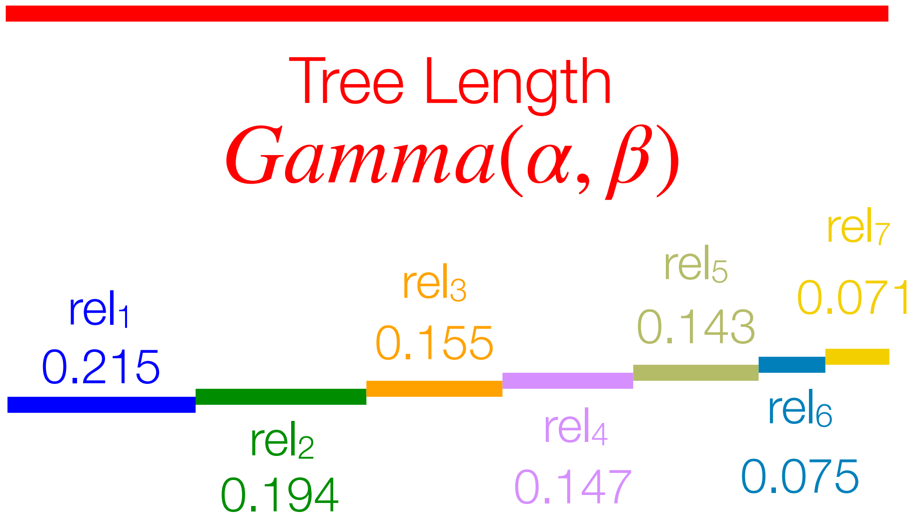

Tree Length
$Gamma(\alpha, \beta)$

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

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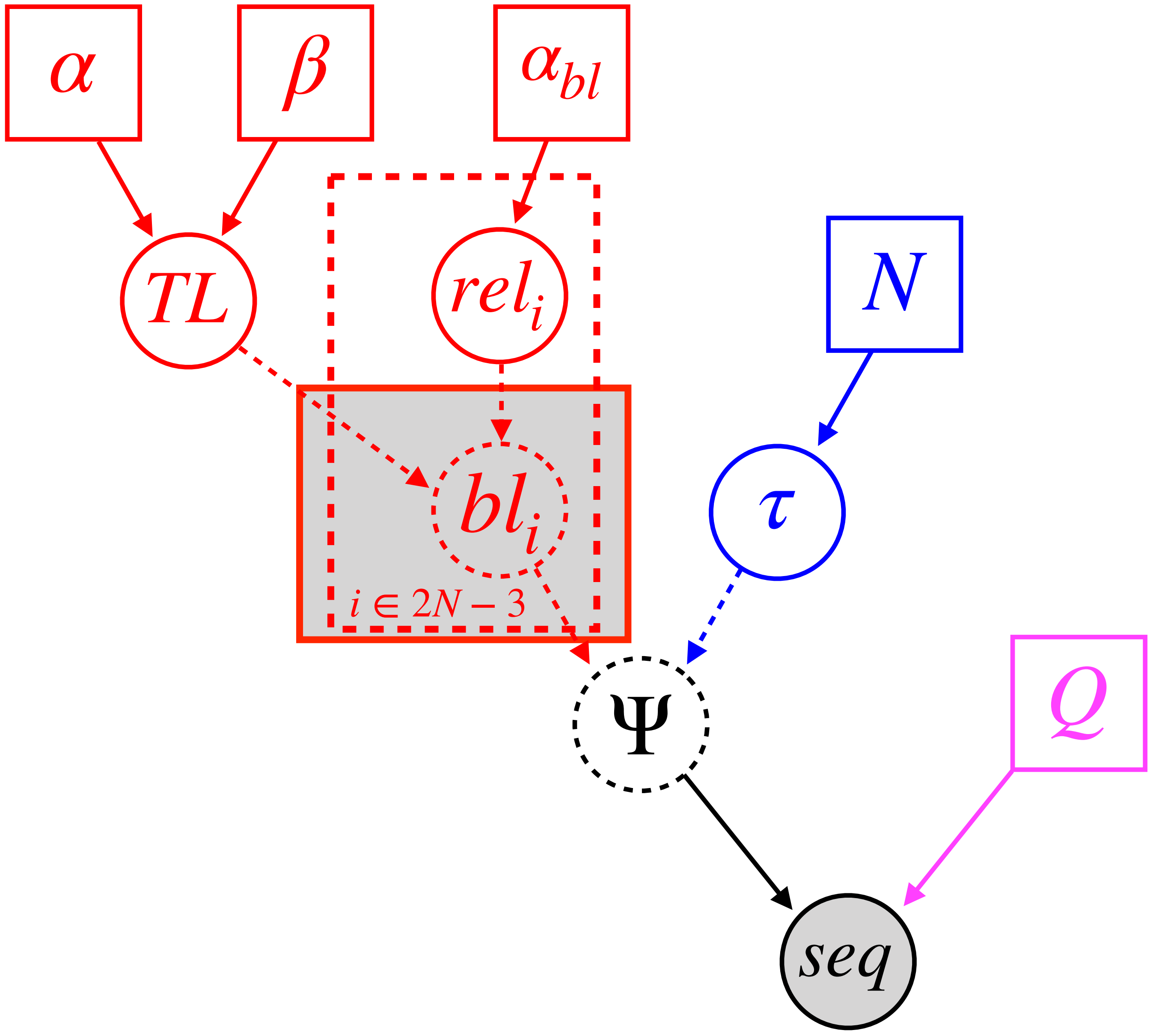
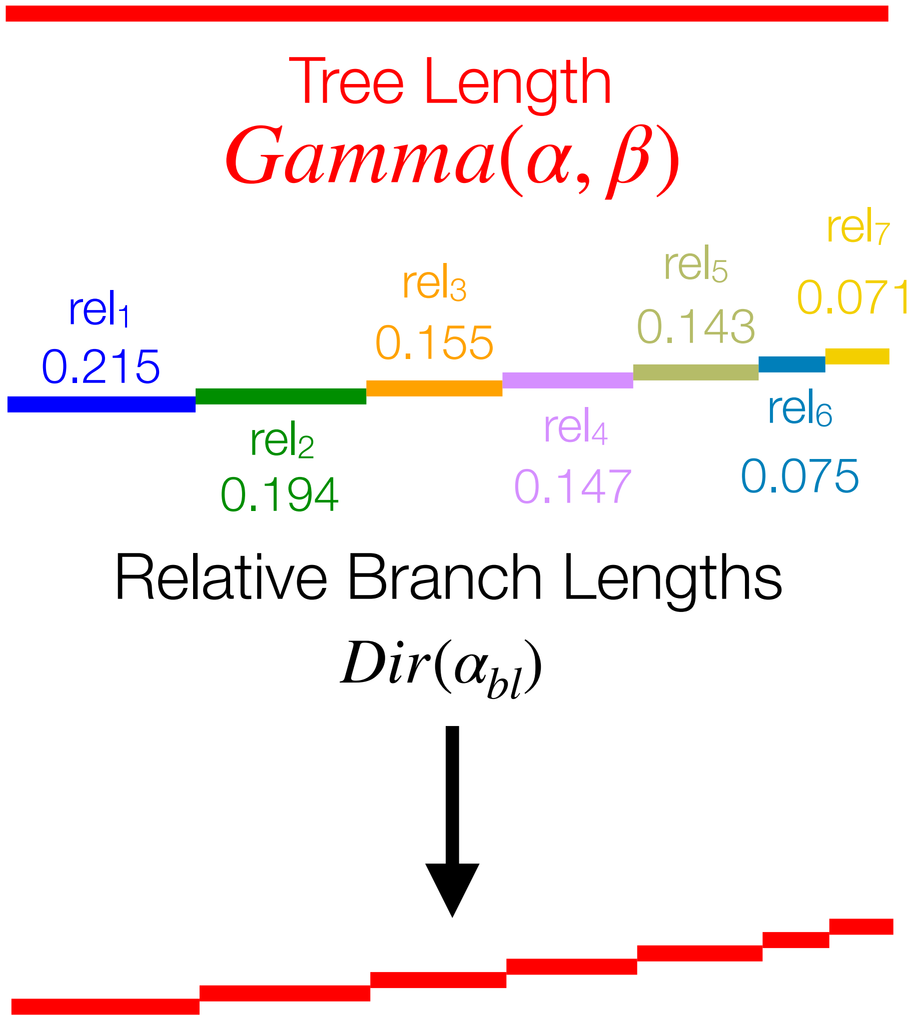
(Compound Dirichlet tree- and branch-length prior)





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

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

Branch Lengths

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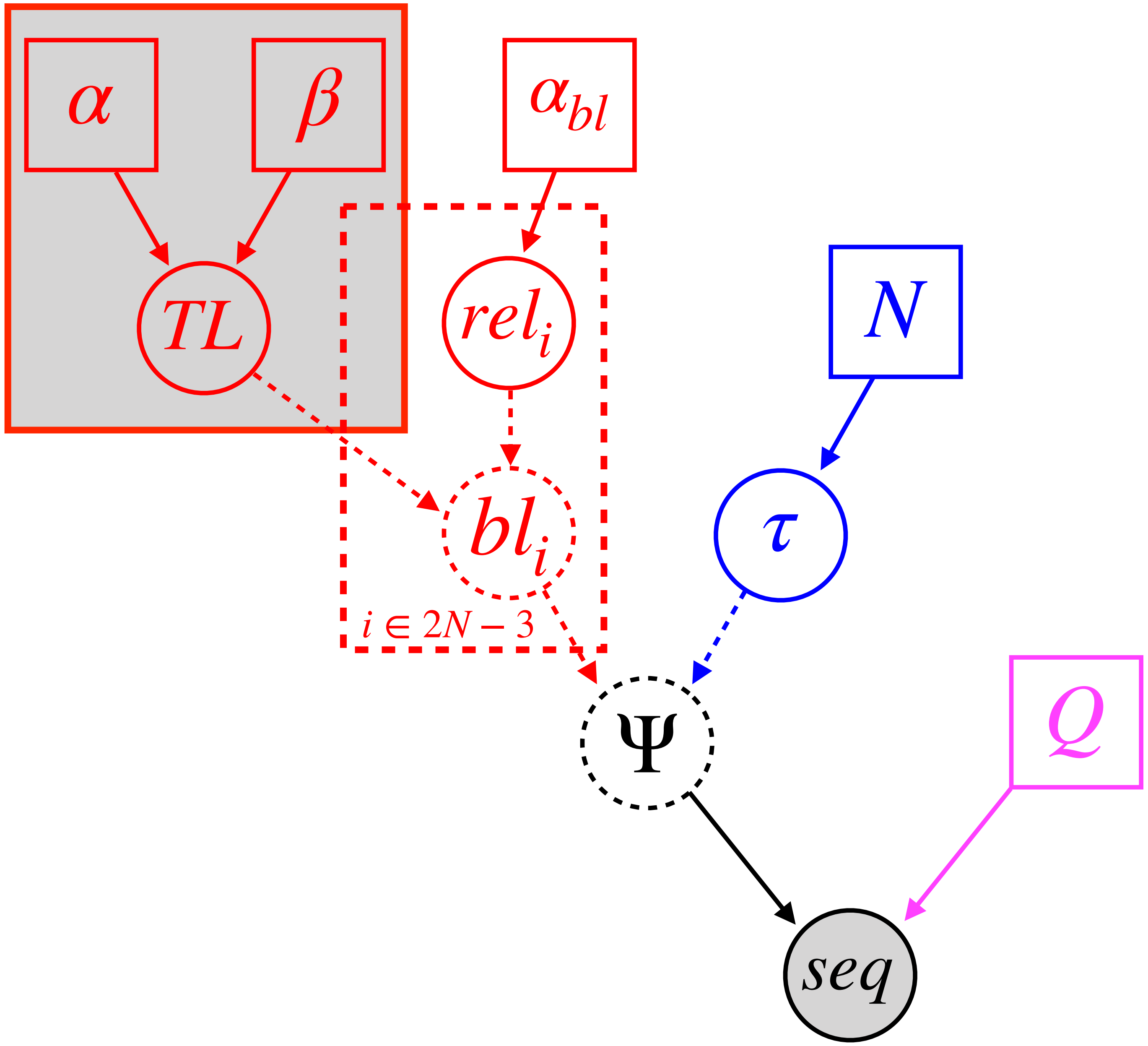

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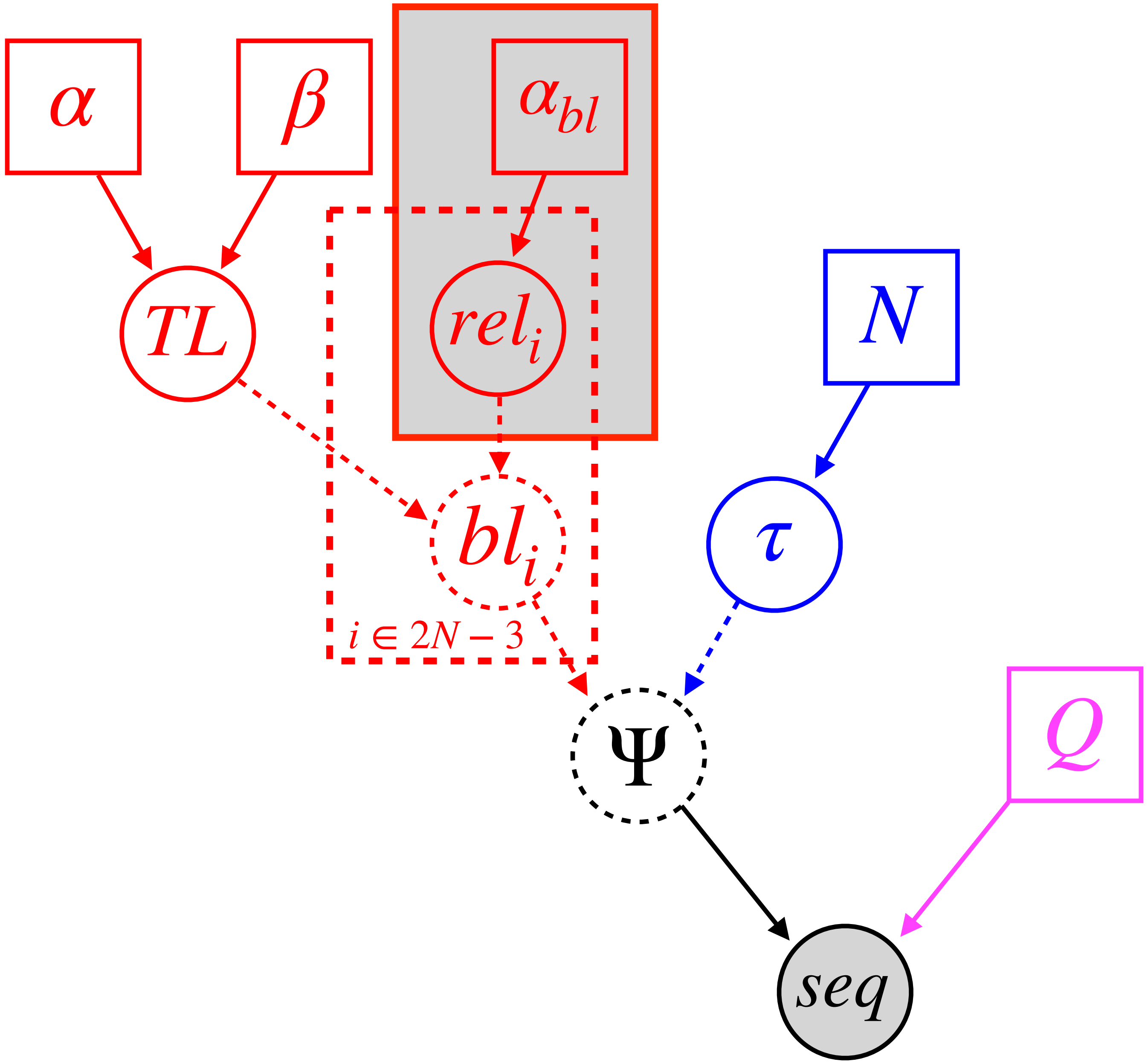

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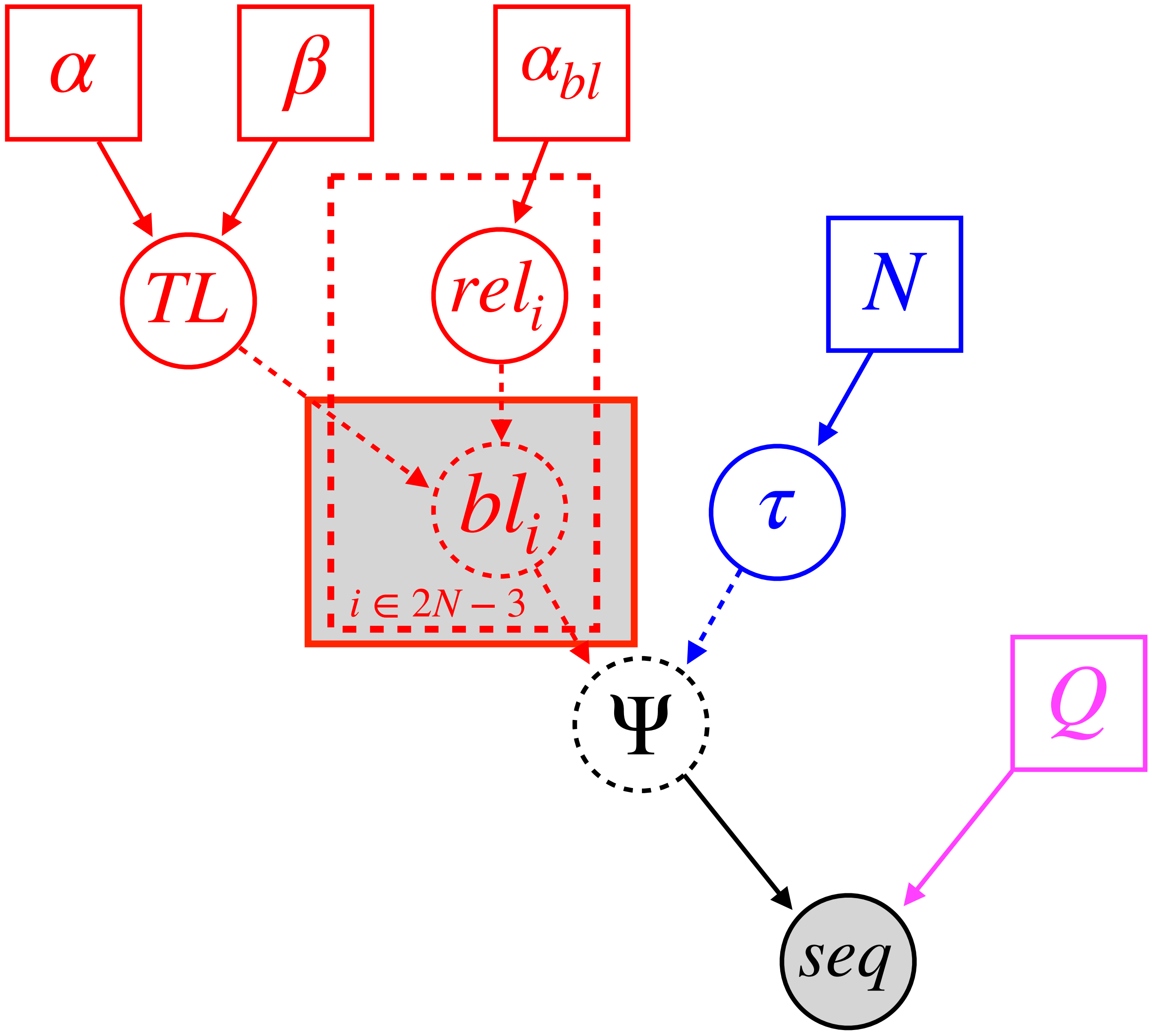

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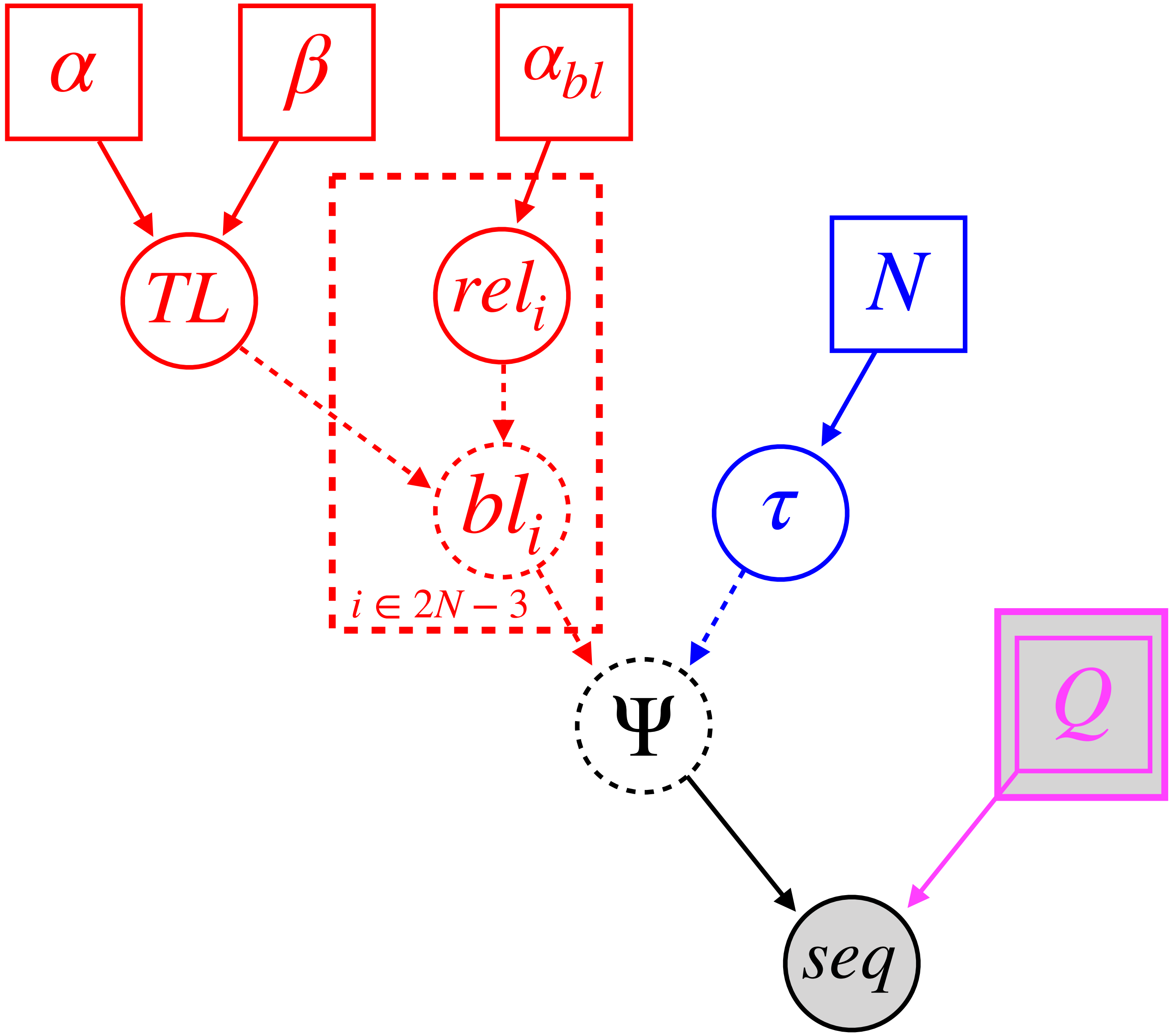

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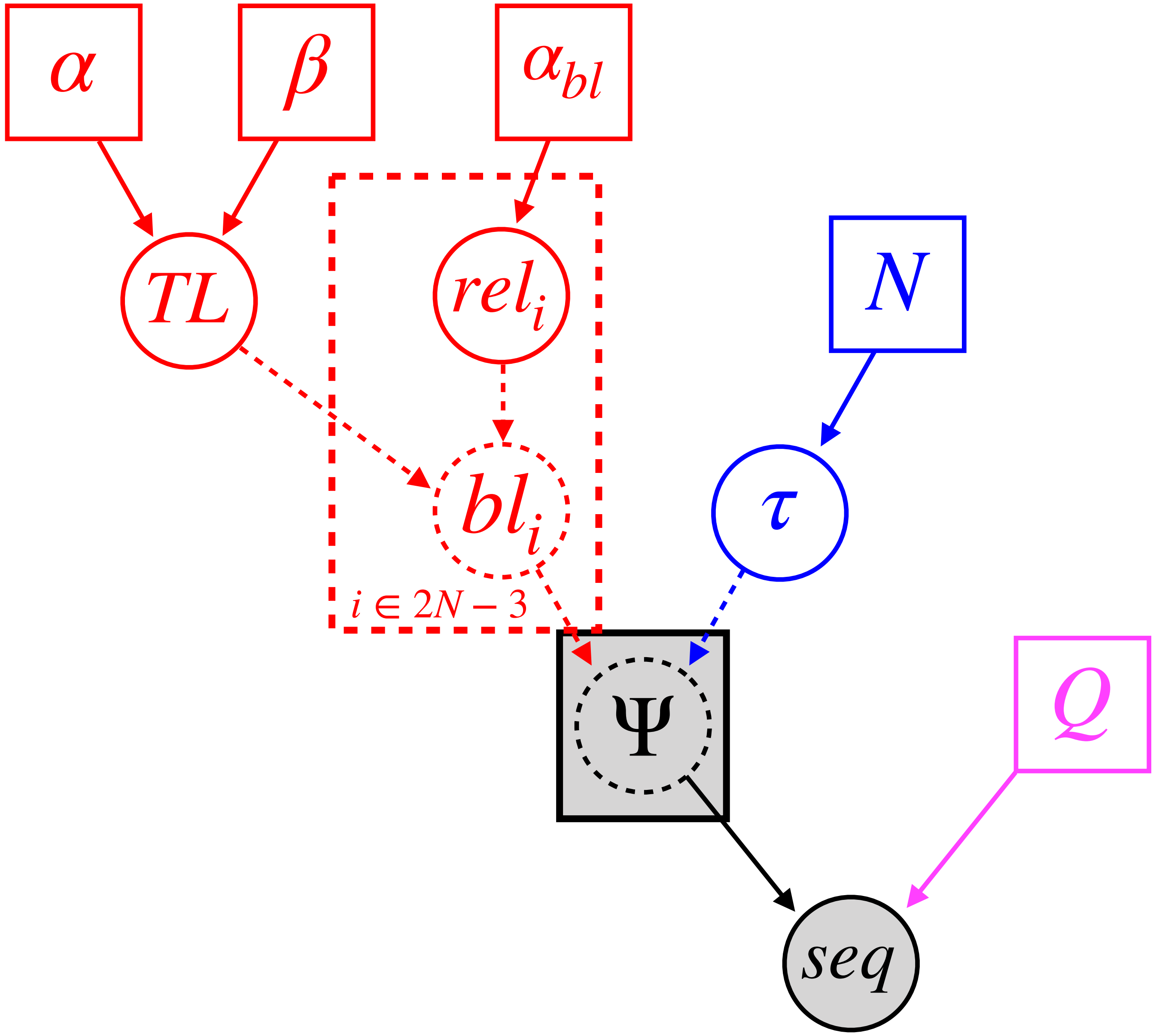

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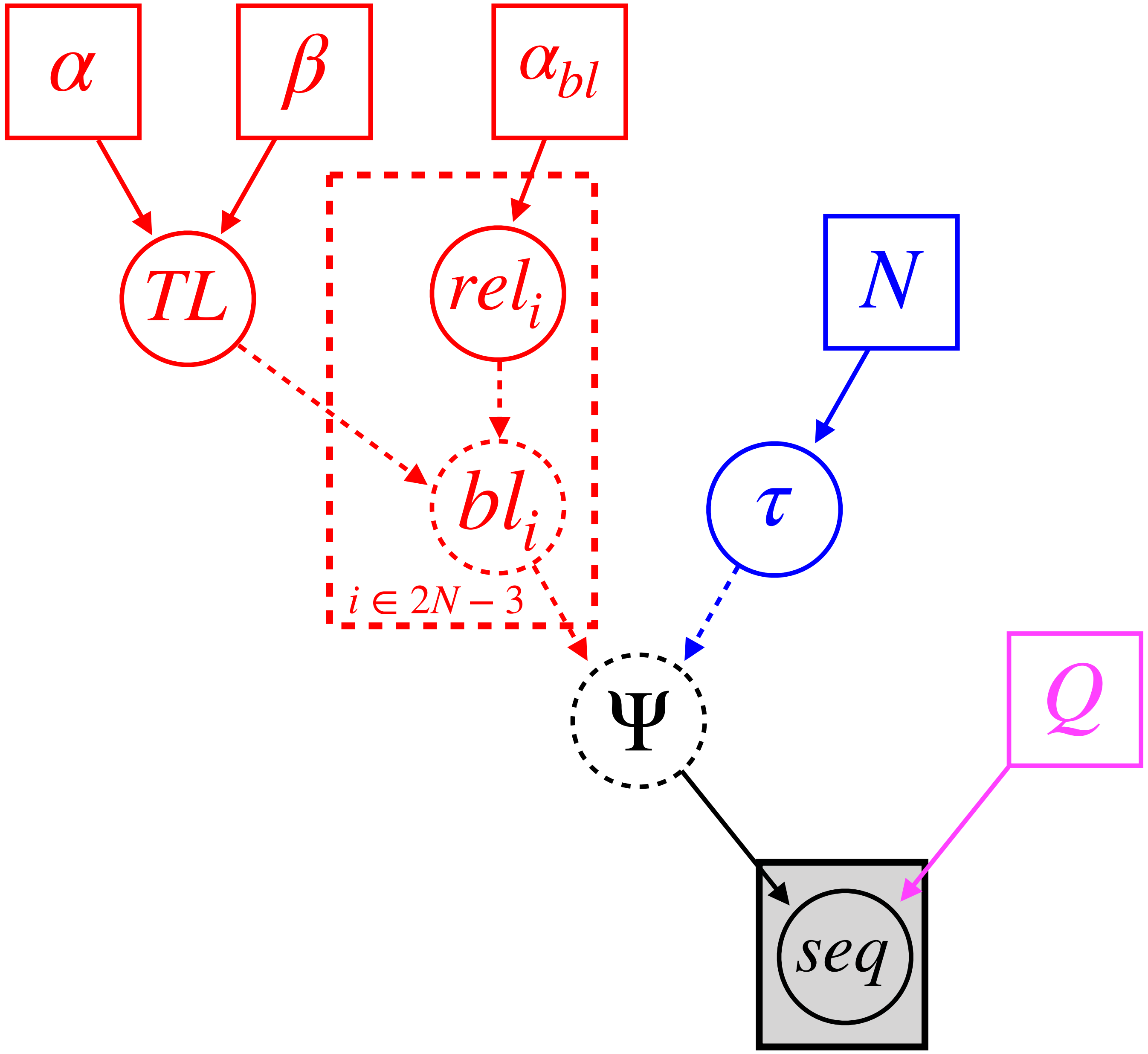

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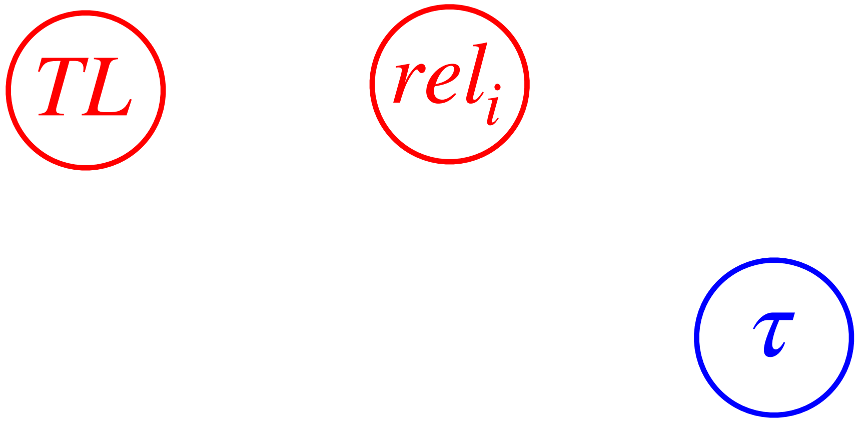
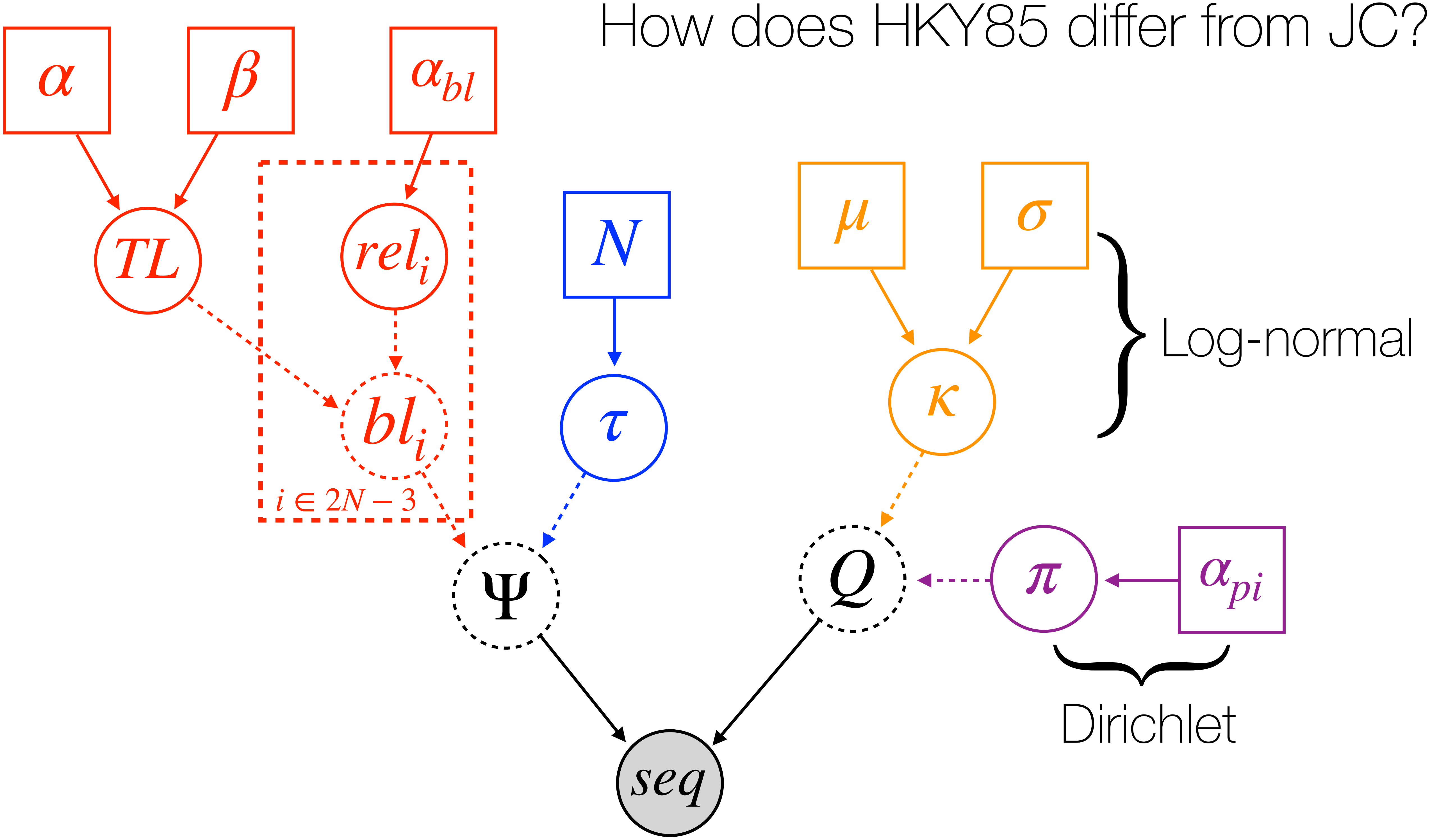


Inferring these parameters under Jukes-Cantor.

HKY85

How does HKY85 differ from JC?



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HKY85

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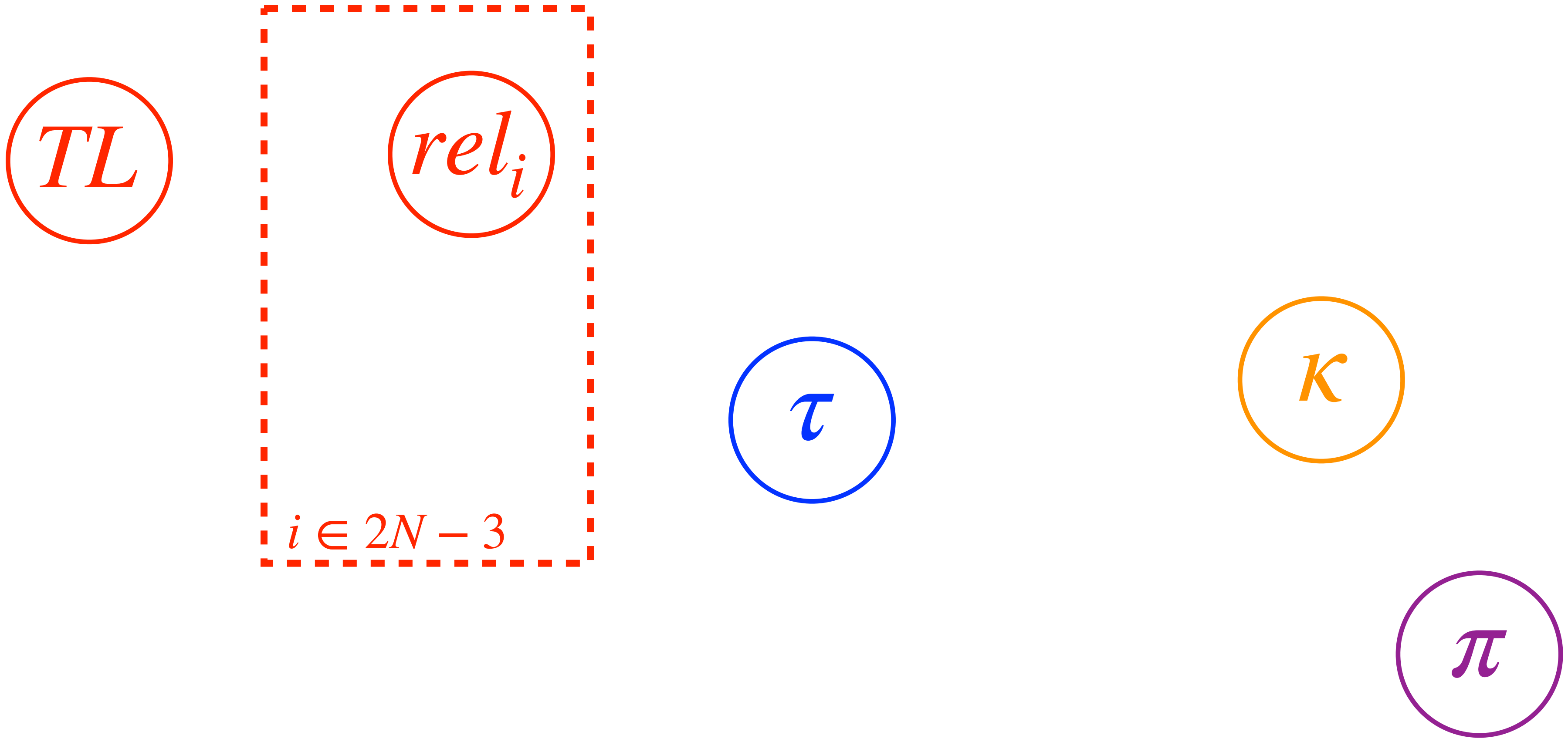


HKY85

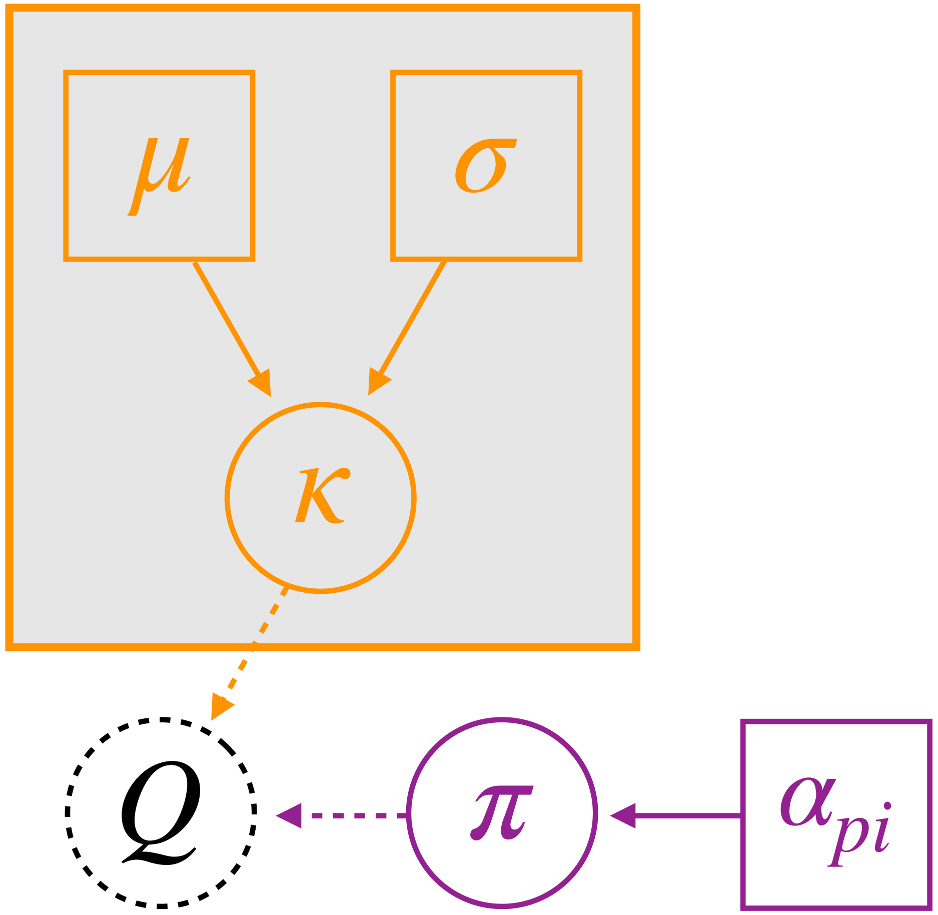
How does HKY85 differ from JC?

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)
```



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HKY85

How does HKY85 differ from JC?

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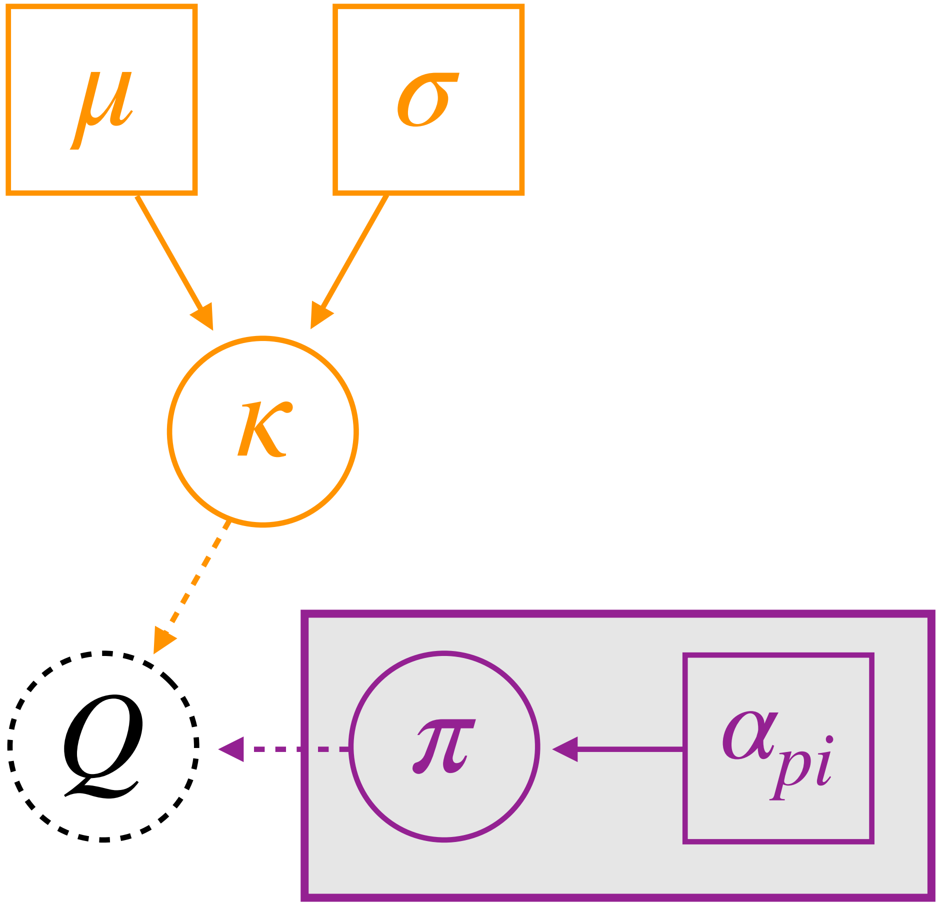
mu <- 0
sigma <- 1
kappa ~ dnLognormal(mu,sigma)
```

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

Variable Base Frequencies

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



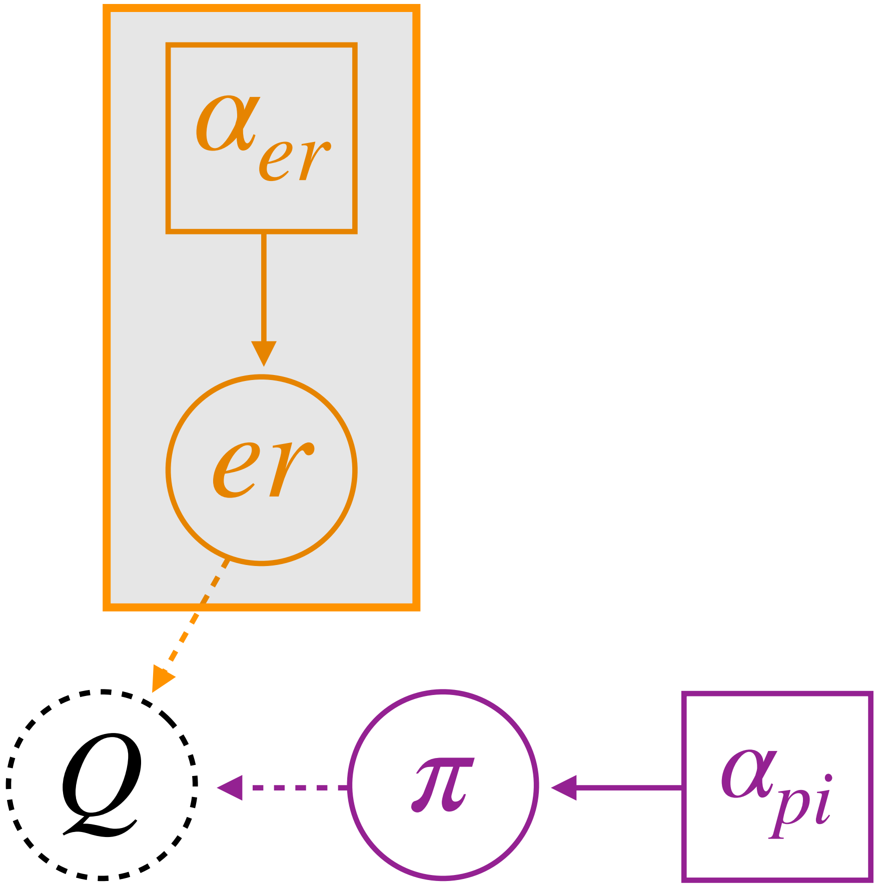
General Time Reversible (GTR)

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)
```



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Choose Your Own Model Adventure!

Now, **pick one of these models** (JC, HKY, or GTR), and run an MCMC analysis in RevBayes.

Scripts are available on GitHub for each of these models, along with an example dataset.

Choose a different model than your neighbor and **compare the resulting trees**. Does the tree vary?