



```

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=phylogeny,
  siteRates=rates_morpho, Q=Q_morpho,
  type="Standard", coding="variable" )
phyMorpho.clamp( data )

```