



```
psi ~ dnUniformTopologyBranchLength(names, dnExponential(10))
```

```
Q_morpho <- fnJC(2)
```

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

```
phyMorpho.clamp( data )
```