```
for (i in 1:n_branches) {
        bl[i] ~ dnExponential(10.0)
}
topology ~ dnUniformTopology(taxa)
psi := treeAssembly(topology, bl)


Q <- fnJC(4)


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

seq.clamp( data )
```