```
root ~ dnUniform(0,1000.0)
psi ~ dnBirthDeath(lambda=2.0, mu=1.0,
                   rootAge=root, taxon_names)


alpha1 <- v(1,1,1,1,1,1)
alpha2 <- v(1,1,1,1)
er ~ dnDirichlet( alpha1 )
pi ~ dnDirichlet( alpha2 )
Q_mol := fnGTR(er, pi)
alpha ~ dnExponential(0.05)
gamma := fnDiscretizeGamma( rate=alpha, shape=alpha, numCats=4 )


seq ~ dnPhyloCTMC( tree=psi, Q=Q_mol, siteRates=gamma,
                   branchRates=0.01, type="DNA" )

seq.clamp( data )
```