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

alpha1 <- v(1,1,1,1,1,1)
alpha2 <- v(1,1,1,1)
er ~ dnDirichlet( alpha1 )
pi ~ dnDirichlet( alpha2 )
Q := fnGTR(er, pi)

m_alpha <- ln(5.0)
sd_alpha <- 0.587405
alpha ~ dnLognormal( m_alpha, sd_alpha )
sr := fnDiscretizeGamma( alpha, alpha, 4, false )

p_inv ~ dnBeta(1,1)

seq ~ dnPhyloCTMC( tree=psi, Q=Q, pInv=p_invar,
                   siteRates=sr, type="DNA" )

seq.clamp( data )
```