```
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)


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