



```

m_d <- ln( ln(450/2) / 90 )
sd_d <- 0.587405*2
d ~ dnLognorma(m_d,sd_d)
m_r <- ln( ln(450/2) / 90 )
sd_r <- 0.587405*2
r ~ dnLognorma(m_r,sd_r)
lambda := d + r
mu := r
root ~ dnNormal(90.0,6.0)
psi ~ dnBirthDeath( lambda, mu, root, taxa)

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)

m_alpha <- 5.0
sd_alpha <- 0.587405
alpha ~ dnLognormal( m_alpha, sd_alpha )
sr := fnDiscretizeGamma( alpha, alpha, 4, false )
log_clock ~ dnUniform(-6,1)
clock := 10^log_clock

seq ~ dnPhyloCTMC( tree=psi, Q=Q_mol, sr
                  branchRates=0.01, type="DNA" )
seq.clamp( data )

```