

```
m_d < ln(ln(450/2) / 90)
sd_d <- 0.587405*2
d \sim dnLognorma(m_d,sd_d)
m_r < ln(ln(450/2) / 90)
sd_r <- 0.587405*2
r \sim dnLognorma(m_r,sd_r)
lambda := d + r
mu := r
root <- 90.0
psi \sim dnBirthDeath(lambda, mu, root, taxa)
alpha1 \leftarrow v(1,1,1,1,1,1)
alpha2 <- v(1,1,1,1)
er \sim dnDirichlet( alpha1 )
pi \sim dnDirichlet(alpha2)
Q_mol := fnGTR(er, pi)
m_alpha <- 5.0
sd_alpha <- 0.587405
alpha \sim dnLognormal( m_alpha, sd_alpha )
sr := fnDiscretizeGamma( alpha, alpha, 4, false )
log\_clock \sim dnUniform(-6,1)
clock := 10^log_clock
	ext{seq} \sim 	ext{dnPhyloCTMC(tree=psi, Q=Q_mol, sr}
                     branchRates=0.01, type="DNA")
seq.clamp( data )
```