```
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 <- 90.0
psi ~ dnBirthDeath( lambda, mu, root, taxa)


Q_mol <- fnJC(4)


log_clock ~ dnUniform(-6,1)
clock := 10^log_clock


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

seq.clamp( data )
```