

Molecular Dating

The global molecular clock model

The molecular sequence data was used to estimate the relationships between extant species of bears and relative speciation times was inferred using a global clock model. Attempts were made for different exercises on molecular dating tutorial using RevBayes. So far, I was able to do exercise 1 but got stocked on exercise 2 and could not proceed forward with the exercises. In exercise 1, program Tracer was used to load the output log file and FigTree was used to visualize the tree file.

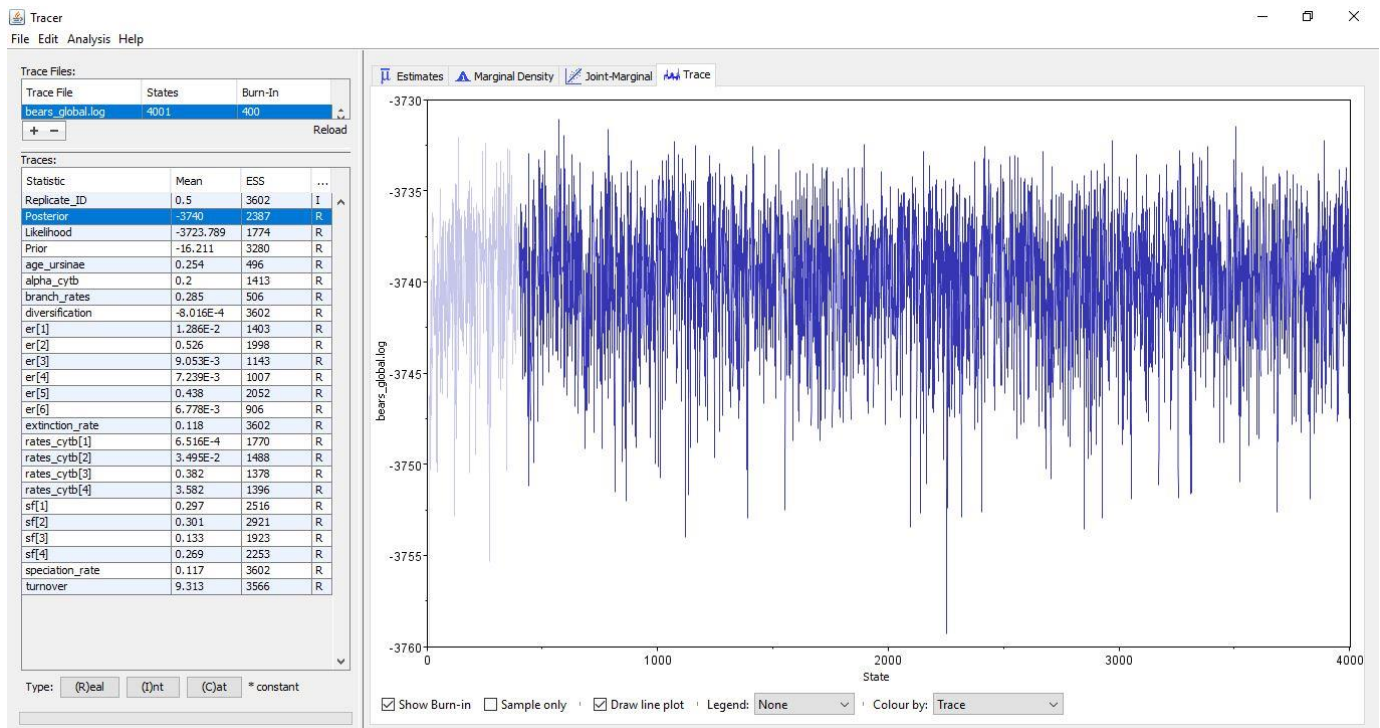


Figure: Program Tracer used to evaluate the mixing and convergence of MCMC analysis

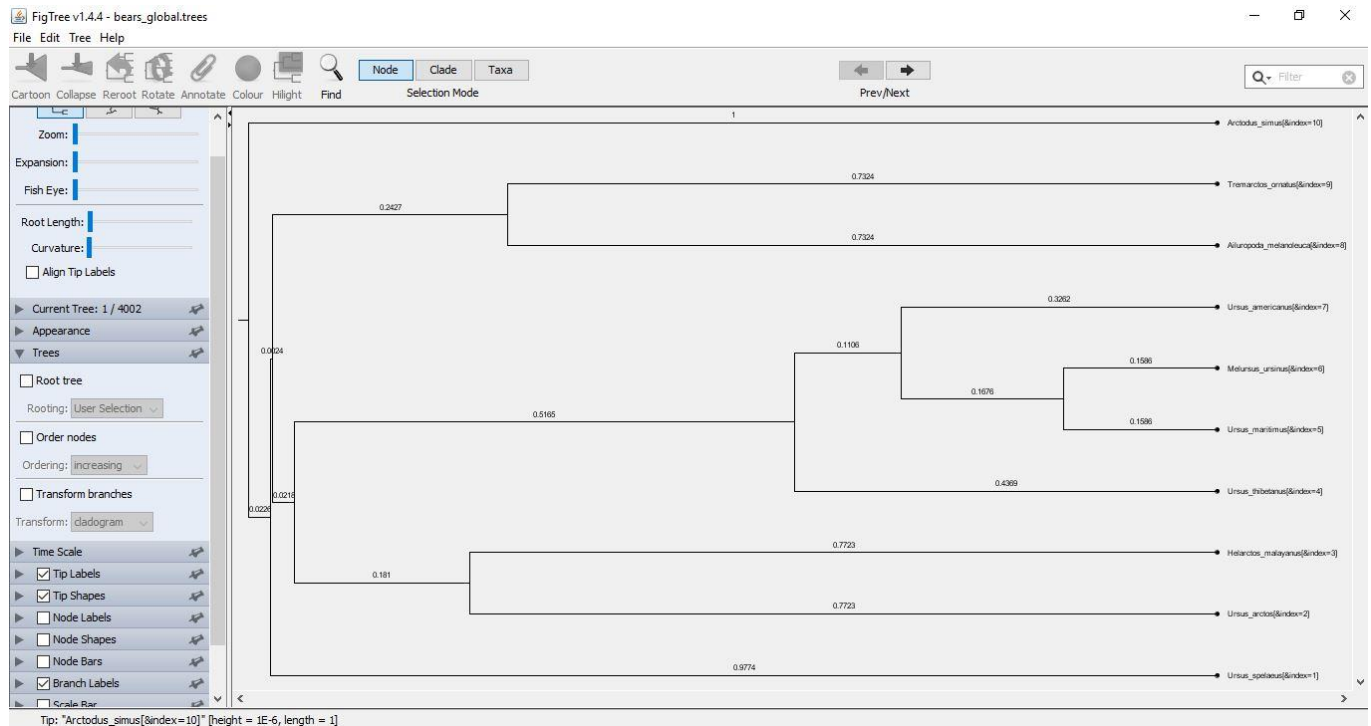


Figure: Program FigTree was used to visualize the output MCC tree file

The following scripts were used during the exercises:

```
setwd ()

setwd ("C:\\Users\\ssapkot1\\Desktop\\RevBayes_Win_v1.0.13\\Data")

cytb <- readDiscreteCharacterData("Data/bears_cytb.nex")

n_taxa <- cytb.size()

taxa <- cytb.taxa()

moves = VectorMoves()

monitors = VectorMonitors()

speciation_rate ~ dnExponential(10)

extinction_rate ~ dnExponential(10)

moves.append( mvScale(speciation_rate, lambda=0.5, tune=true, weight=3.0) )

moves.append( mvScale(extinction_rate, lambda=0.5, tune=true, weight=3.0) )
```

```

diversification := speciation_rate - extinction_rate

turnover := extinction_rate/speciation_rate

rho <- 1.0

extant_mrca <- 1.0

tree_dist      =      dnBDP(lambda=speciation_rate,      mu=extinction_rate,      rho=rho,
rootAge=extant_mrca, samplingStrategy="uniform", condition="nTaxa", taxa=taxa)

clade_ursinae   =   clade("Melursus_ursinus",      "Ursus_arctos",      "Ursus_maritimus",
"Helarctos_malayanus", "Ursus_americanus", "Ursus_thibetanus")

constraints = v(clade_ursinae)

timetree ~ dnConstrainedTopology(tree_dist, constraints=constraints)

moves.append( mvNarrow(timetree, weight=n_taxa) )

moves.append( mvFNPR(timetree, weight=n_taxa/4) )

moves.append( mvNodeTimeSlideUniform(timetree, weight=n_taxa) )

moves.append( mvSubtreeScale(timetree, weight=n_taxa/5.0) )

age_ursinae := tmrca(timetree, clade_ursinae)

branch_rates ~ dnExponential(10.0)

moves.append( mvScale(branch_rates, lambda=0.5, tune=true, weight=3.0) )

sf_hp <- v(1,1,1,1)

sf ~ dnDirichlet(sf_hp)


er_hp <- v(1,1,1,1,1,1)

er ~ dnDirichlet(er_hp)

moves.append( mvSimplexElementScale(er, alpha=10.0, weight=3.0) )

moves.append( mvSimplexElementScale(sf, alpha=10.0, weight=2.0) )

Q_cytb := fnGTR(er,sf)

alpha_cytb ~ dnUniform(0.0,1E6)

alpha_cytb.setValue( 1.0 )


moves.append( mvScale(alpha_cytb, lambda=0.5, tune=true, weight=2.0) )

```

```

rates_cytb := fnDiscretizeGamma(alpha_cytb, alpha_cytb, 4)

phySeq      ~      dnPhyloCTMC(tree=timetree,      Q=Q_cytb,      siteRates=rates_cytb,
branchRates=branch_rates, type="DNA")

phySeq.clamp(cytb)

source("C:\Users\ssapkot1\Desktop\RevBayes_Win_v1.0.13\Data\scripts\tree_BD.Rev")
source("C:\Users\ssapkot1\Desktop\RevBayes_Win_v1.0.13\Data\scripts\clock_global.Rev")
source("C:\Users\ssapkot1\Desktop\RevBayes_Win_v1.0.13\Data\scripts\scripts\sub_GTR.Rev"
)

mymodel = model(sf)

monitors.append( mnModel(filename="output/bears_global.log", printgen=10) )
monitors.append( mnFile(filename="output/bears_global.trees", printgen=10, timetree) )
monitors.append( mnScreen(printgen=10, extant_mrca, diversification, branch_rates) )

mymcmc = mcmc(mymodel, monitors, moves, nruns=2, combine="mixed")
mymcmc.run(generations=20000, tuningInterval=200)

trace = readTreeTrace("output\bears_global.trees")
mccTree(trace, file="output\bears_global.mcc.tre")

```

```

branch_rates_mean ~ dnExponential(10.0)

moves.append( mvScale(branch_rates_mean, lambda=0.5, tune=true, weight=3.0) )

n_branches <- 2 * n_taxa - 2

for(i in 1:n_branches){
  branch_rates(i) <- dnExp(1/branch_rates_mean)
  moves.append( mvScale(branch_rates(i), lambda=0.5, tune=true, weight=1.0) )
}

```

Got the error
here and could
not proceed
forward

```

moves.append( mvVectorScale(branch_rates, lambda=0.5, tune=true, weight=4.0) )

moves.append( mvRateAgeBetaShift(tree=timetree, rates=branch_rates, tune=true,
weight=n_taxa) )

source("C:\Users\ssapkot1\Desktop\RevBayes_Win_v1.0.13\Data\scripts\clock_relaxed_expo
nential.Rev")

monitors.append( mnModel(filename="output/bears_relaxed_exponential.log", printgen=10) )

```

```
monitors.append( mnFile(filename="output/bears_relaxed_exponential.trees", printgen=10,  
timetree) )  
  
trace = readTreeTrace("output/bears_relaxed_exponential.trees")  
  
mccTree(trace, file="output/bears_relaxed_exponential.mcc.tre" )
```