

Argyresthia_Host Plant_Stochastic_Character_Mapping

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```
library(phytools)
library(corHMM)
library(geiger)
```

1. Read in files (<5 seconds)

Read in life history data file containing Host Plant data (*Argyresthia_Hosts.csv*; this file contains the same matrix as Table S4), as well as iqtree phylogeny. Root tree based on outgroup node. Use function **drop.tip** to retain ingroup with host plant data and outgroup taxa, root, make ultrametric using function **chronos**.

```
#read in Host Plant data file
HPdata=read.csv("Argyresthia_Hosts.csv",header=TRUE,row.names=1)
rownames(HPdata)
head(HPdata)

#read in IQTREE phylogeny and use keep.tip to retain ingroup with host plant data
#and the outgroup taxa
iqtree=read.tree(file="Argyresthia_output_R1_taxa_removed.phy.contree.tre")
mrBayes=read.nexus(file="Argyresthia_Bayes_R2.tre")
#plot and identify node number for outgroup
plotTree(iqtree,node.numbers=TRUE,fsize=0.5)
#root based on node number of outgroup
iqtree=root(iqtree,node=222)
#plot to make sure tree is rooted properly
plotTree(iqtree,fsize=0.3)
#identify taxa not in tree and prune tree
HPchk=name.check(iqtree,HPdata)
HPtree=drop.tip(iqtree,HPchk$tree_not_data)
plotTree(HPtree,fsize=0.5)
#make tree ultrametric
HPtree=chronos(HPtree)
plotTree(HPtree,fsize=0.5)
```

2. Model selection for stochastic character mapping (~2 minutes)

Select models for use in stochastic character mapping based on Akaike information criterion (AIC) values.

```
HP=setNames(HPdata[,1],rownames(HPdata))
HP=as.factor(HP)

#social classification
fit.HP.ER=fitMk(HPtree,HP,model="ER")
fit.HP.SYM=fitMk(HPtree,HP,model="SYM")
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fit.HP.ARD=fitMk(HPtree,HP,model="ARD")

#extract AIC values for each model
aic.HP<-c(AIC(fit.HP.ER),AIC(fit.HP.ARD),AIC(fit.HP.SYM))
#print summary table
HP.mod.sel=data.frame(model.HP=c("ER","SYM","ARD"),
  logL.HP=c(logLik(fit.HP.ER),logLik(fit.HP.SYM),
    logLik(fit.HP.ARD)), AIC.HP=aic.HP,delta.AIC.HP=aic.HP-min(aic.HP))
HP.mod.sel
#use ER

#write model selection information to csv document
write.csv(HP.mod.sel,"model_selection.csv")

```

3. Stochastic character mapping (>2 hours)

Conduct stochastic character mapping for host plant, applying the model selected in section 2.

```

##social classification (levels = 8)
#set colors in accordance with levels
cols.HP=setNames(c("darkslategray", "cadetblue1", "lightcyan3","gray90","darkseagreen2",
  "darkseagreen4","navajowhite4","navajowhite1"),levels(HP))
#conduct stochastic character mapping using mcmc and model selected from section 3
mtrees.HP<-make.simmap(HPtree,HP,model="ER",
  nsim=1000,Q="mcmc",vQ=0.01, prior=list(use.empirical=TRUE),samplefreq=10)
#plot relative frequency vs. number of changes for each character state
#change from stochastic character mapping inference
dd.HP=density(mtrees.HP,bw=2)
plot(dd.HP)
#set a 10 x 10 grid to plot 100 stochastic map trees
par(mfrow=c(10,10))
#plot 100 stochastic map trees, sampled from set of 1000
null.HP<-sapply(mtrees.HP[seq(10,1000,by=10)],
  plot,colors=cols.HP,lwd=1,ftype="off")
#compute posterior probabilities at nodes
pd.HP<-summary(mtrees.HP)
pd.HP
pd.HP$ace
write.csv(pd.HP$ace,file="posterior_probabilities_by_node.csv")
#create a plot showing PP at all nodes of the tree and node labels
par(mfrow=c(1,1))
plot(pd.HP,colors=cols.HP,fsz=0.4,ftype="i",lwd=2,
  offset=0.4,ylim=c(-1,Ntip(HPtree)), cex=c(0.5,0.3))
nodelabels(bg="transparent",col="black",frame="none",
  adj=c(1.5,1.5),cex=0.7)
#add a legend
legend("bottomleft",legend=levels(HP),title="Host Plant",pch=22,
  pt.cex=1.5,pt.bg=cols.HP,bty="n",cex=0.8)
#create a plot showing PP at all nodes of the tree without node labels
pdf("Argyresthia_stochastic_host_plant.pdf") # starts writing a PDF to file
par(mfrow=c(1,1))
plot(pd.HP,colors=cols.HP,fsz=0.4,ftype="i",lwd=2,
  offset=0.4,ylim=c(-1,Ntip(HPtree)), cex=c(0.5,0.3))
#add a legend

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legend("bottomleft",legend=levels(HP),title="Host Plant",
      pch=22, pt.cex=1.5,pt.bg=cols.HP,bty="n",cex=0.8)
dev.off() # closes the PDF file
pdf("Argyresthia_stochastic_host_plant_node_numbers.pdf") # starts writing a PDF to file
par(mfrow=c(1,1))
plot(pd.HP,colors=cols.HP,fsi=0.4,ftype="i",lwd=2,
     offset=0.4,ylim=c(-1,Ntip(HPtree)), cex=c(0.5,0.3))
nodelabels(bg="transparent",col="black",frame="none",
           adj=c(1.5,1.5),cex=0.7)
#add a legend
legend("bottomleft",legend=levels(HP),title="Host Plant",
      pch=22, pt.cex=1.5,pt.bg=cols.HP,bty="n",cex=0.8)
dev.off() # closes the PDF file

```

4. Comparing results of phylogenetic inferences between IQTREE and MrBayes (<5 seconds)

```

pdf("Cophylo_IQTREE_MrBayes.pdf") # starts writing a PDF to file
#plot and identify node number for outgroup with MrBayes inference
plotTree(mrbayes,node.numbers=TRUE,fsi=0.5)
#root based on node number of outgroup with MrBayes inference
mrbayes=root(mrbayes,node=217)
plotTree(mrbayes,fsi=0.5)
#IQTREE with MrBayes
iqtree_mrbayes=cophylo(iqtree,mrbayes)
pdf("IQTREE_MrBayes_Cophylo.pdf") # starts writing a PDF to file
plot(iqtree_mrbayes,rotate=TRUE,print=TRUE,fsi=0.25)
dev.off() # closes the PDF file

```