**##R codes for all model testing, analyses, tree building and ancestral character estimations**

library(ape)

library(geiger)

library(nlme)

library (phytools)

library(picante)

library(phylobase)

library(adephylo)

setwd("C:/Users/Rachael/Desktop/Comparative Ontogeny")

##Load the spider phylogeny, plot it

SpiderTree <- read.newick ("SToL")

plot(SpiderTree)

##Load the dataset (specific to each spigot for each instar)

library(readxl)

Females <- read\_excel("C:/Users/Rachael/Desktop/Comparative Ontogeny/Females.xlsx")

View(Females)

##Name check the tips and species data

rownames(Females) <- Females$Species

Females <- Females[match(SpiderTree$tip.label,rownames(Females)),]

name.check (SpiderTree, Females, data.names = NULL)

str(Females)

Species <- Females$Species

Average <- Females$Average

Strategy <- Females$Foraging\_Strategy

Specific <- Females$Specific\_Strategy

Type <- Females$Spigot\_Type

Silk <- Females$Type\_of\_Silk

**## Test for phylogenetic signal:**

##Pagel's lambda test for each variable

##Average (continuous)

trait <- Females [,5]

names(trait) <- rownames(Females)

phylosig(SpiderTree, trait, method="lambda", test = TRUE, nsim=999)

##Foraging\_Strategy

trait<- Females [,6]

phylosig(SpiderTree, trait, method="lambda", test = TRUE, nsim=999)

##Specific\_Strategy

trait<- Females [,7]

phylosig(SpiderTree, trait, method="lambda", test = TRUE, nsim=999)

##Type\_of\_Silk

trait<- Females [,8]

phylosig(SpiderTree, trait, method="lambda", test = TRUE, nsim=999)

##Spigot\_Type

trait <- Females [,9]

phylosig(SpiderTree, trait, method="lambda", test = TRUE, nsim=999)

##Blomberg's K test for each variable

##Average (continuous)

trait <- Females [,5]

phylosig(SpiderTree, trait, method="K", test = TRUE, nsim=999)

##Foraging\_Strategy

trait<- Females [,6]

phylosig(SpiderTree, trait, method="K", test = TRUE, nsim=999)

##Specific\_Strategy

trait<- Females [,7]

phylosig(SpiderTree, trait, method="K", test = TRUE, nsim=999)

##Type\_of\_Silk

trait<- Females [,8]

phylosig(SpiderTree, trait, method="K", test = TRUE, nsim=999)

##Spigot\_Type

trait <- Females [,9]

phylosig(SpiderTree, trait, method="K", test = TRUE, nsim=999)

**##Code for Model Selection for variables and modes of evolution:**

# call up the following installed packages-----------------

library(nlme)

library(MuMIn)

##Modes of evolution test:

pglsOU <- gls(Average ~ Instar, correlation = corPagel(1, phy = SpiderTree, fixed = FALSE), data = Females, method = "ML")

summary(pglsOU)

anova(pglsOU)

pglsMartins <- gls(Average ~ Instar, correlation = corMartins(1, phy = SpiderTree, fixed = FALSE), data = Females, method = "ML")

summary(pglsMartins)

anova(pglsMartins)

pglsBlomberg <- gls(Average ~ Instar, correlation = corBlomberg(1, phy = SpiderTree, fixed = TRUE), data = Females, method = "ML")

summary(pglsBlomberg)

anova(pglsBlomberg)

pglsGrafen <- gls(Average ~ Instar, correlation = corGrafen(1, phy = SpiderTree, fixed = FALSE), data = Females, method = "ML")

summary(pglsGrafen)

anova(pglsGrafen)

pglsBrownian <- gls(Average ~ Instar, correlation = corBrownian(1, phy = SpiderTree, fixed = FALSE), data = Females, method = "ML")

summary(pglsBrownian)

anova(pglsBrownian)

##Brownian mode of evolution had the best fit, so I then moved on to test the model variables, subsequently finding that single term models had the highest power/best fit leading to the final PGLS codes below.

##These are the variable models tested for each type of spigot (see details below in the PGLS codes).

pgls1 <- gls(Average ~ Instar, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls2 <- gls(Average ~ Type, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls3 <- gls(Average ~ Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls4 <- gls(Average ~ Specific, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls5 <- gls(Average ~ Strategy, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls6 <- gls(Average ~ Instar + Type, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls7 <- gls(Average ~ Instar + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls8 <- gls(Average ~ Silk + Type, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls9 <- gls(Average ~ Instar + Specific, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls10 <- gls(Average ~ Specific + Type, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls11 <- gls(Average ~ Specific + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls12 <- gls(Average ~ Instar + Strategy, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls13 <- gls(Average ~ Strategy + Type, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls14 <- gls(Average ~ Strategy + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls15 <- gls(Average ~ Strategy + Specific, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls16 <- gls(Average ~ Instar + Type + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls17 <- gls(Average ~ Specific + Type + Instar, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls18 <- gls(Average ~ Instar + Specific + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls19 <- gls(Average ~ Specific + Type + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls20 <- gls(Average ~ Instar + Type + Strategy, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls21 <- gls(Average ~ Instar + Strategy + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls22 <- gls(Average ~ Strategy + Type + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls23 <- gls(Average ~ Instar + Strategy + Specific, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls24 <- gls(Average ~ Strategy + Specific + Type, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls25 <- gls(Average ~ Strategy + Specific + Silk, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls26 <- gls(Average ~ Instar + Type + Silk + Strategy, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls27 <- gls(Average ~ Instar + Type + Specific + Strategy, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls28 <- gls(Average ~ Instar + Specific + Silk + Strategy, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls29 <- gls(Average ~ Specific + Type + Silk + Strategy, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls30 <- gls(Average ~ Instar + Type + Silk + Specific, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

pgls31 <- gls(Average ~ 1, correlation = corBrownian(phy = SpiderTree), data = Females, method = "ML")

**##Final Code for PGLS analyses**

##Adult female PMS aciniform spigot example

##PGLS with discrete variable, run pgls, then run anova

pglsModel <- gls(Average ~ Strategy, correlation = corBrownian(phy = SpiderTree),

 data = Females, method = "ML")

summary(pglsModel)

anova(pglsModel)

pglsModel1 <- gls(Average ~ Instar, correlation = corBrownian(phy = SpiderTree),

 data = Females, method = "ML")

summary(pglsModel1)

anova(pglsModel1)

pglsModel2 <- gls(Average ~ Specific, correlation = corBrownian(phy = SpiderTree),

 data = Females, method = "ML")

summary(pglsModel2)

anova(pglsModel2)

pglsModel3 <- gls(Average ~ Silk, correlation = corBrownian(phy = SpiderTree),

 data = Females, method = "ML")

summary(pglsModel3)

anova(pglsModel3)

pglsModel4 <- gls(Average ~ Type, correlation = corBrownian(phy = SpiderTree),

 data = Females, method = "ML")

summary(pglsModel4)

anova(pglsModel4)

##Adult female PMS minor ampullate spigot, female ALS major ampullate spigot, female ALS piriform spigot, female PMS cylindrical spigot, female ALS aciniform spigot, female PLS cylindrical spigot

##Run the data loading code again, but select the corresponding spreadsheet for this dataset

##Run the PGLS codes for each single term model

##Second instar data PGLS runs for 2nd instar ALS major ampullate spigot, 2nd instar ALS piriform spigot, 2nd instar PMS minor ampullate spigot, 2nd instar PMS aciniform spigot, 2nd instar PLS aciniform spigot:

##Run same start and data loading code, except select the second instar excel file and follow through the subsequent spreadsheets for each specific spigot.

##The PGLS code is the same and the renaming strings work, just name the second instar dataset, “Females” in R, so you don’t have to change the code.

**##Converting the Spider Tree (SToL) into an ultrametric tree, rather than one with equal branch lengths**

##Ultrametric tree conversion codes used:

## Quick and dirty method:

> library(ape)

> SpiderTree <- read.newick ("Final SToL")

> plot(SpiderTree)

> is.ultrametric(SpiderTree)

> timetree <- chronos (SpiderTree)

> is.ultrametric(timetree)

> plot(timetree)

> write.tree (timetree, file = "timetreeNewick.tre")

> tr$edge.length

> timetree$edge.length

### Setting tree to 1 and scaling branch lengths in a relaxed model (other easy way to convert to ultrametric with no prior knowledge for calibration (fossil) or a clock model (prior branch lengths/molecular rates of evolution)

> rel\_calib1 <- makeChronosCalib(SpiderTree, node = "root", age.min = 1, age.max = 1, interactive = FALSE, soft.bounds = FALSE)

> timetree2 <- chronos(SpiderTree, lambda = 0, model = "relaxed", calibration = rel\_calib1)

> plot(timetree2)

> timetree2$edge.length

**##Ancestral character estimation for the specialized spigot on the PLS**

##Final ACE with deeper taxon sampling, change of none to loss to better delineate having none to begin with, versus loosing a spigot

> library(ape)

> library(geiger)

> library(nlme)

> library (phytools)

> setwd("C:/Users/Rachael/Desktop/Comparative Ontogeny")

> SpiderTree <- read.newick ("SpiderTree")

> plot(SpiderTree)

> is.ultrametric (SpiderTree)

> library(readxl)

> Females <- read\_excel("C:/Users/Rachael/Desktop/Comparative Ontogeny/PLS.xlsx",

+ sheet = "PLS Other")

> View(Females)

> rownames(Females) <- Females$Species

> Females <- Females[match(SpiderTree$tip.label,rownames(Females)),]

> name.check (SpiderTree, Females, data.names = NULL)

> PLS <- Females$Spigot

> PLS

> fit <- ace(x = PLS, phy = SpiderTree, type = "discrete", method = "ML", CI = TRUE, model = matrix(c(0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0), nrow = 5, ncol = 5 , byrow = TRUE), use.expm = TRUE, use.eigen = FALSE, marginal = FALSE)

> fit

> round(fit$lik.anc, 3)

> plotTree(SpiderTree, type = "phylogram", fsize = 0.8, ftype = "i", label.offset = 1, jitter = 1)

> tiplabels(pie=to.matrix (PLS, sort(unique(PLS))), piecol = c("red", "black", "green", "blue", "yellow"), cex = 0.2)

> nodelabels(node=1:SpiderTree$Nnode+Ntip(SpiderTree), pie=fit$lik.anc, piecol= c("red", "black", "green", "blue", "yellow"), cex = 0.6)

> add.simmap.legend (leg = "Flagelliform", colors = c("red"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "Loss", colors = c("yellow"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "Modified", colors = c("black"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "None", colors = c("green"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "Pseudoflagelliform", colors = c("blue"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

**##Ancestral character estimation for four of the independent variables: foraging strategy, specific foraging strategy, type of silk utilized, variety of spigots possessed by spider species**

*##Ancestral character estimation for foraging strategy*

> library(ape)

> library(geiger)

> library(nlme)

> library (phytools)

> setwd("C:/Users/Rachael/Desktop/Comparative Ontogeny")

> SpiderTree <- read.newick ("ACE newick")

> plot(SpiderTree)

> is.ultrametric (SpiderTree)

> rel\_calib1 <- makeChronosCalib(SpiderTree, node = "root", age.min = 1, age.max = 1, interactive = FALSE, soft.bounds = FALSE)

> timetree2 <- chronos(SpiderTree, lambda = 0, model = "relaxed", calibration = rel\_calib1)

> plot(timetree2)

> is.ultrametric(timetree2)

> write.tree (timetree2, "ACE Charles")

> SpiderTree <- read.newick ("ACE Charles")

> plot(SpiderTree)

##Load Females dataset (updated version)

> rownames(Females) <- Females$Species

> Females <- Females[match(SpiderTree$tip.label,rownames(Females)),]

> name.check (SpiderTree, Females, data.names = NULL)

> PLS <- Females$Foraging

> PLS

> fit <- ace(x = PLS, phy = SpiderTree, type = "discrete", method = "ML", CI = TRUE, model = matrix(c(0, 1, 0, 0), nrow = 2, ncol = 2 , byrow = TRUE), use.expm = TRUE, use.eigen = FALSE, marginal = FALSE)

> fit

> round(fit$lik.anc, 3)

> plotTree(SpiderTree, type = "phylogram", fsize = 0.8, ftype = "i", label.offset = 1, jitter = 1)

> tiplabels(pie=to.matrix (PLS, sort(unique(PLS))), piecol = c("red", "blue"), cex = 0.2)

> nodelabels(node=1:SpiderTree$Nnode+Ntip(SpiderTree), pie=fit$lik.anc, piecol= c("red", "blue"), cex = 0.6)

> add.simmap.legend (leg = "0", colors = c("red"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "1", colors = c("blue"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

*##Ancestral character estimation for Specific foraging strategy*

> library(ape)

> library(geiger)

> library(nlme)

> library (phytools)

> setwd("C:/Users/Rachael/Desktop/Comparative Ontogeny")

> SpiderTree <- read.newick ("ACE newick")

> plot(SpiderTree)

> is.ultrametric (SpiderTree)

> rel\_calib1 <- makeChronosCalib(SpiderTree, node = "root", age.min = 1, age.max = 1, interactive = FALSE, soft.bounds = FALSE)

> timetree2 <- chronos(SpiderTree, lambda = 0, model = "relaxed", calibration = rel\_calib1)

> plot(timetree2)

> is.ultrametric(timetree2)

> write.tree (timetree2, "ACE Charles")

> SpiderTree <- read.newick ("ACE Charles")

> plot(SpiderTree)

##Load Females dataset (updated version)

> rownames(Females) <- Females$Species

> Females <- Females[match(SpiderTree$tip.label,rownames(Females)),]

> name.check (SpiderTree, Females, data.names = NULL)

> PLS <- Females$Specific

> PLS

> fit <- ace(x = PLS, phy = SpiderTree, type = "discrete", method = "ML", CI = TRUE, model = matrix(c(0, 1, 1, 2, 2, 0, 0, 0, 0, 1, 0, 1, 2, 2, 0, 0, 0, 0, 1, 1, 0, 1, 1, 0, 0, 0, 0, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 1, 2, 2, 3, 0, 1, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 2, 2, 3, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0), nrow = 9, ncol = 9 , byrow = TRUE), use.expm = TRUE, use.eigen = FALSE, marginal = FALSE)

> fit

> round(fit$lik.anc, 3)

> plotTree(SpiderTree, type = "phylogram", fsize = 0.8, ftype = "i", label.offset = 1, jitter = 1)

> tiplabels(pie=to.matrix (PLS, sort(unique(PLS))), piecol = c("red", "blue", "green", "yellow", "orange", "purple", "pink", "turquoise", "black"), cex = 0.2)

> nodelabels(node=1:SpiderTree$Nnode+Ntip(SpiderTree), pie=fit$lik.anc, piecol= c("red", "blue", "green", "yellow", "orange", "purple", "pink", "turquoise", "black"), cex = 0.6)

> add.simmap.legend (leg = "1", colors = c("red"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "1.5", colors = c("blue"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "2", colors = c("green"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "2.5", colors = c("yellow"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "3", colors = c("orange"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "4", colors = c("purple"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "4.5", colors = c("pink"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "5", colors = c("turquoise"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "5.5", colors = c("black"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

*##Ancestral character estimation for main Type of Silk utilized by the spider species*

> library(ape)

> library(geiger)

> library(nlme)

> library (phytools)

> setwd("C:/Users/Rachael/Desktop/Comparative Ontogeny")

> SpiderTree <- read.newick ("ACE newick")

> plot(SpiderTree)

> is.ultrametric (SpiderTree)

> rel\_calib1 <- makeChronosCalib(SpiderTree, node = "root", age.min = 1, age.max = 1, interactive = FALSE, soft.bounds = FALSE)

> timetree2 <- chronos(SpiderTree, lambda = 0, model = "relaxed", calibration = rel\_calib1)

> plot(timetree2)

> is.ultrametric(timetree2)

> write.tree (timetree2, "ACE Charles")

> SpiderTree <- read.newick ("ACE Charles")

> plot(SpiderTree)

##Load Females dataset (updated version)

> rownames(Females) <- Females$Species

> Females <- Females[match(SpiderTree$tip.label,rownames(Females)),]

> name.check (SpiderTree, Females, data.names = NULL)

> PLS <- Females$Type

> PLS

> fit <- ace(x = PLS, phy = SpiderTree, type = "discrete", method = "ML", CI = TRUE, model = matrix(c(0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0), nrow = 5, ncol = 5 , byrow = TRUE), use.expm = TRUE, use.eigen = FALSE, marginal = FALSE)

> fit

> round(fit$lik.anc, 3)

> plotTree(SpiderTree, type = "phylogram", fsize = 0.8, ftype = "i", label.offset = 1, jitter = 1)

> tiplabels(pie=to.matrix (PLS, sort(unique(PLS))), piecol = c("red", "blue", "green", "yellow", "black"), cex = 0.2)

> nodelabels(node=1:SpiderTree$Nnode+Ntip(SpiderTree), pie=fit$lik.anc, piecol= c("red", "blue", "green", "yellow", "black"), cex = 0.6)

> add.simmap.legend (leg = "1.0", colors = c("red"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "1.5", colors = c("blue"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "2.0", colors = c("green"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "3.0", colors = c("yellow"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "4.0", colors = c("black"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

*##Ancestral character estimation for variety of Spigot Types possessed by the spider species*

> library(ape)

> library(geiger)

> library(nlme)

> library (phytools)

> setwd("C:/Users/Rachael/Desktop/Comparative Ontogeny")

> SpiderTree <- read.newick ("ACE newick")

> plot(SpiderTree)

> is.ultrametric (SpiderTree)

> rel\_calib1 <- makeChronosCalib(SpiderTree, node = "root", age.min = 1, age.max = 1, interactive = FALSE, soft.bounds = FALSE)

> timetree2 <- chronos(SpiderTree, lambda = 0, model = "relaxed", calibration = rel\_calib1)

> plot(timetree2)

> is.ultrametric(timetree2)

> write.tree (timetree2, "ACE Charles")

> SpiderTree <- read.newick ("ACE Charles")

> plot(SpiderTree)

##Load Females dataset (updated version)

> rownames(Females) <- Females$Species

> Females <- Females[match(SpiderTree$tip.label,rownames(Females)),]

> name.check (SpiderTree, Females, data.names = NULL)

> PLS <- Females$Variety

> PLS

> fit <- ace(x = PLS, phy = SpiderTree, type = "discrete", method = "ML", CI = TRUE, model = matrix(c(0, 1, 2, 2, 2, 2, 2, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 2, 0, 1, 0, 0, 2, 0, 2, 0, 0, 1, 0, 3, 1, 1, 1, 0, 0, 0, 0, 0, 2, 0, 2, 1, 1, 2, 0), nrow = 7, ncol = 7 , byrow = TRUE), use.expm = TRUE, use.eigen = FALSE, marginal = FALSE)

> fit

> round(fit$lik.anc, 3)

> plotTree(SpiderTree, type = "phylogram", fsize = 0.8, ftype = "i", label.offset = 1, jitter = 1)

> tiplabels(pie=to.matrix (PLS, sort(unique(PLS))), piecol = c("red", "blue", "green", "yellow", "orange", "purple", "black"), cex = 0.2)

> nodelabels(node=1:SpiderTree$Nnode+Ntip(SpiderTree), pie=fit$lik.anc, piecol= c("red", "blue", "green", "yellow", "orange", "purple", "black"), cex = 0.6)

> add.simmap.legend (leg = "1", colors = c("red"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "1.5", colors = c("blue"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "2", colors = c("green"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "2.5", colors = c("yellow"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "2.75", colors = c("orange"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "3", colors = c("purple"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)

> add.simmap.legend (leg = "4", colors = c("black"), vertical = TRUE, prompt = TRUE, PLS=0.9\*par()$usr[1], fsize=0.7)