

Thalictrum Scent: Phylogenetic Signal

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The following script accompanies the manuscript ‘Scent Matters: Repeated loss of insect attraction by floral scent accompanies transition to wind Pollination.’

Test for phylogenetic signal by Bloomburgs K under Brownian motion are tested with the Thalictrum Floral Scent data and the Phylogeny. test for phylogenetic signal under Brownian motion in Thalictrum flora scent data.

Set Working Directory

Load libraries and data

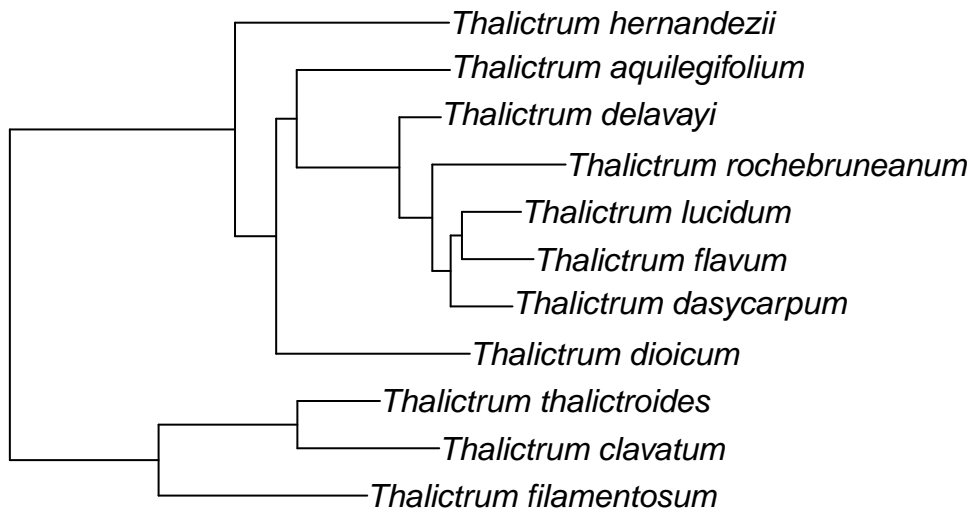
```
#Load Libraries
library(phytools)
library(adephylo)
library(picante)
library(phylocurve)
library(geomorph)

#Import Data
scent <- read.csv("data.csv")
#Scent dataframe
tree <- read.nexus('THALICTRUM86.tre')
#Read in pre-cooked Maximum A Posterior Phylogeny (MAP)
```

Data Wrangle

Prune Tree down to 11 Species in Study

```
keepSpecies <- unique(as.character(scent$Species_Name_Full))
trimmedTree<-drop.tip(tree,tree$tip.label[!match(keepSpecies, tree$tip.label)])
plot(trimmedTree) # Plot trimmed tree
```



Extract Relvant Information from Scent Dataframe

- 1) Extract scent emission data
- 2) Average across taxa
- 3) Formate for Phylogenetic Signal functions

```

#1)
scentCompounds <- scent[,9:63] # extract only scent data including mass*time column
scentCompounds$Species_Name_Full <- scent$Species_Name_Full

#2) Average Scent Data across
avgScentCompounds <- aggregate( scentCompounds,
                                by=list(scentCompounds$Species_Name_Full),
                                FUN = mean,
                                na.rm=TRUE)

#3)
avgScentCompounds$Species_Name_Full <- NULL
row.names(avgScentCompounds) <- avgScentCompounds$Group.1
avgScentCompounds$Group.1 <- NULL
avgScentCompounds <- as.matrix(avgScentCompounds)

```

Test for Phylogenetic Signal

Test for Phylogenetic Signal Individualy

Bloombergs K for each Individual

```

# Picante
multiPhylosignal(avgScentCompounds, tree)

```

Multivariate Bloombergs K

Two implementation of multivarite Bloombergs K:

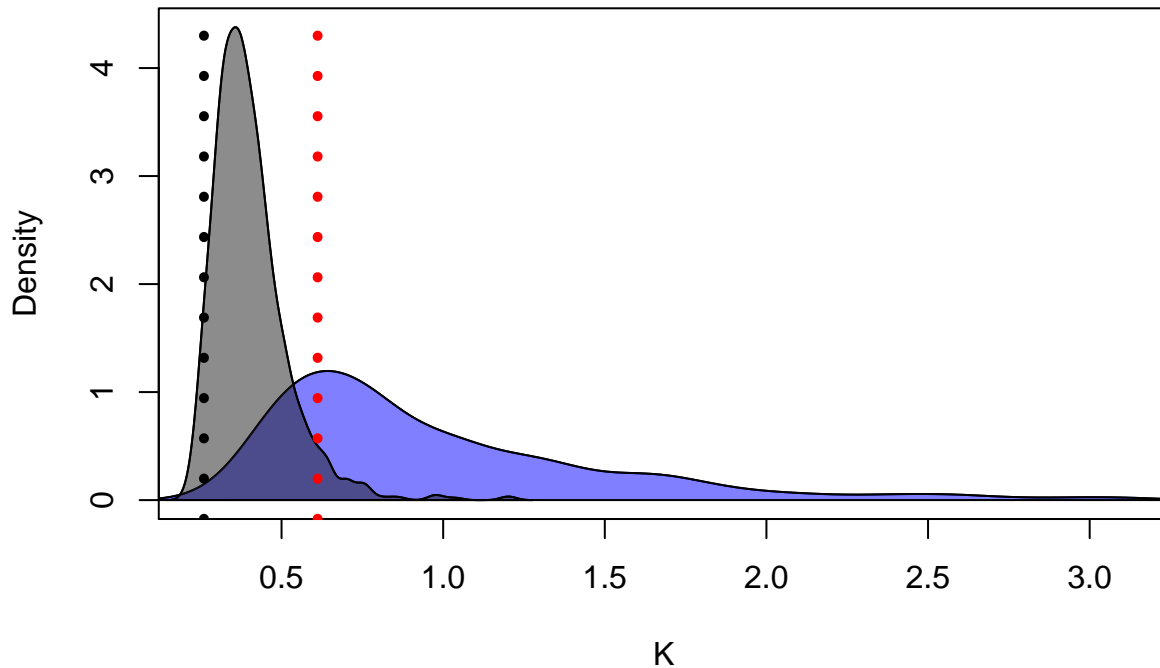
Phylocurve Library

Significance is assessed by simulating a brownian motion on a star phylogeny.

```
model <- evo.model(trimedTree, avgScentCompounds)
K.mult(model, nsim = 1000, plot = TRUE)
```

```
##
## Bootstrapping under null model.
```

Null vs Alt. Distribution



```
##
## *****Simulation results*****
## Test statistic (K)      0.2599050
## Critical test statistic 0.6116004
## Estimated Power        0.7410000
##
## P-value: 0.958
```

Figure Interpretation: Black density plot is null distribution of K values from 1000 simulations of Brownian motion under a star phylogeny. Blue is a distribution of K values from 1000 simulation on the true phylogeny. Black dotted line is observed K value from Bloombergs K analysis. This value falls well within the null distribution of simulation, indicating that there is no phylogenetic signal. I am not sure what the red line is.

Geomorph Implementation

Significance is assessed by permutating the shape data among the tips of the phylogeny.

```
physignal(avgScentCompounds, trimedTree)
```

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##
## Call:
## physignal(A = avgScentCompounds, phy = trimmedTree)
##
##
##
## Observed Phylogenetic Signal (K): 0.2618
##
## P-value: 0.818
##
## Based on 1000 random permutations

```