

# PCOA phylogeny

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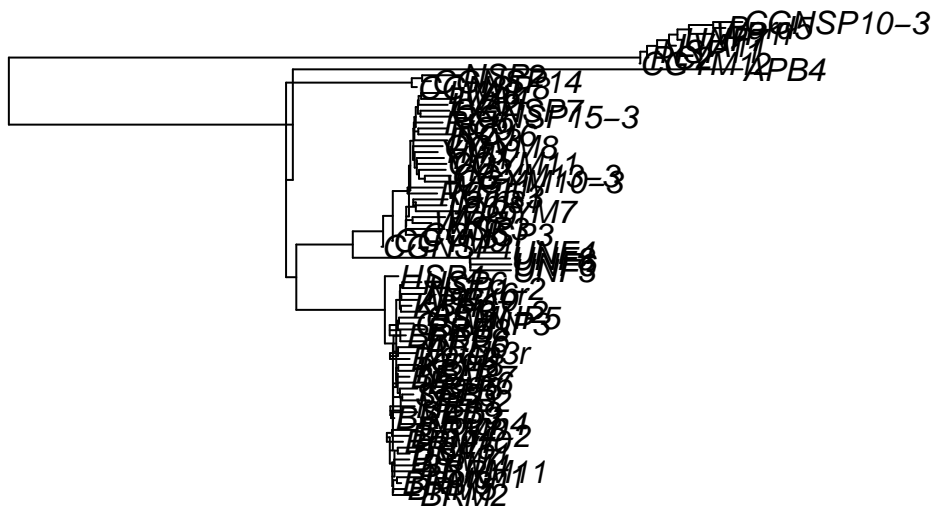
*2016-June-23*

```
library(ape)
library(geiger)
library(ade4)
library(adephylo)
```

```
##
## Attaching package: 'adephylo'
##
## The following object is masked from 'package:ade4':
##
##      orthogram
```

```
#read in NJ tree
KMtree<-read.tree("20160623_Katie_NJ_tree_N6_3SNP_ANBE_mod.nwk")

plot(KMtree)
```



```
#excluding
#ABP3, BRP7, BEAR4, CGYM12
length(KMtree$tip.label)
```

```
## [1] 81
```

```
KMtree2<-drop.tip(KMtree,c("ABP3", "BRP7", "BEAR4", "CGYM12"))
length(KMtree2$tip.label)
```

```
## [1] 80
```

```

#looks like only 1 tip dropped out
#ifelse(KMtree$tip.label=="ABP3",1,0)

# getting a distance matrix from branch lengths
bl<-cophenetic(KMtree2)

# pcoa of distance matrix
KMpcoa<-pcoa(bl)

#exploring the pcoa's
knitr::kable(KMpcoa$values[1:10,])

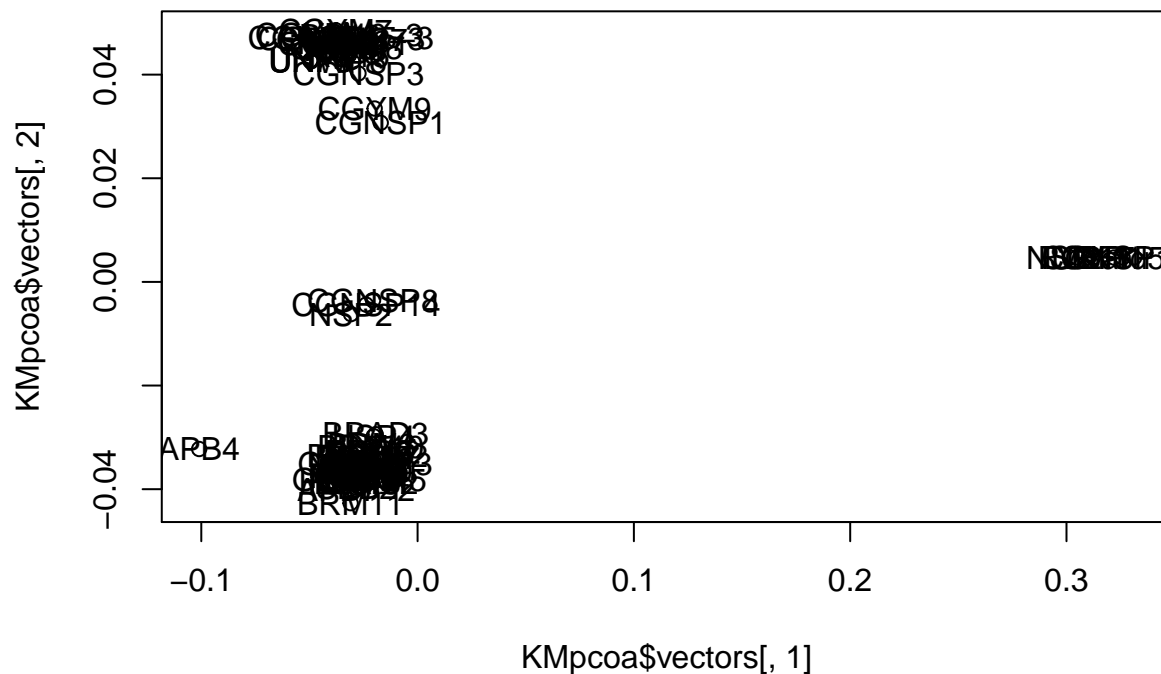
```

Eigenvalues	Relative_eig	Rel_corr_eig	Broken_stick	Cum_corr_eig	Cumul_br_stick
0.7726528	0.8065018	0.6015600	0.0633374	0.6015600	0.0633374
0.1121805	0.1170950	0.0901332	0.0505169	0.6916932	0.1138544
0.0311477	0.0325123	0.0273867	0.0441067	0.7190799	0.1579611
0.0190983	0.0199350	0.0180564	0.0398332	0.7371363	0.1977942
0.0162512	0.0169631	0.0158518	0.0366280	0.7529880	0.2344223
0.0007850	0.0008194	0.0038757	0.0340639	0.7568638	0.2684862
0.0005669	0.0005918	0.0037069	0.0319272	0.7605707	0.3004134
0.0004982	0.0005200	0.0036537	0.0300957	0.7642243	0.3305091
0.0004138	0.0004320	0.0035883	0.0284931	0.7678127	0.3590022
0.0003867	0.0004036	0.0035673	0.0270686	0.7713800	0.3860709

```

#plotting the first and second axis
plot(KMpcoa$vectors[,1],KMpcoa$vectors[,2])
text(KMpcoa$vectors[,1],KMpcoa$vectors[,2],labels=KMtree2$tip.label)

```



```

#the eigenvectors
#KMpcoa$vector[,1:10]
#write.csv(KMpcoa$vector[,1:10], "20160623_KM_eigenvectors.csv")

#code for merging eigenvectors into dataset
#setting as dataframe
pcoa.dat<-as.data.frame(KMpcoa$vector[,1:10])

##This is important, setting a new column with the names of tip labels
pcoa.dat$colony_id_name<-KMtree2$tip.label

knitr::kable(head(pcoa.dat[1:4,]))

```

	Axis.1	Axis.2	Axis.3	Axis.4	Axis.5	Axis.6	Axis.7	Axis.8	Axis.9
BRM2	-0.0255841	-0.0364679	-0.0058129	0.0035867	0.0005470	2.10e-06	-6.00e-07	-0.0013847	0.0002385
BRM5	-0.0223343	-0.0327471	-0.0018638	0.0010624	-0.0024723	7.70e-05	-2.10e-05	-0.0011582	-0.0006344
BRM3	-0.0211005	-0.0313486	-0.0003756	0.0001162	-0.0036118	1.02e-04	-2.74e-05	-0.0012288	-0.0008549
Notch1	-0.0265906	-0.0376323	-0.0070426	0.0043758	0.0014830	-2.16e-05	5.90e-06	-0.0016473	0.0005777

```

#merging dataset with ant_dat_clim

#Final.dat1<-inner_join(originaldata,pcoa.dat,by="colony_id_name")

```

```
sessionInfo()
```

```

## R version 3.2.4 (2016-03-10)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.11.5 (El Capitan)
##
## locale:
##  [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
##  [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
##  [1] adephylo_1.1-6 ade4_1.7-2      geiger_2.0.3  ape_3.2
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.11.6      subplex_1.1-6    mvtnorm_1.0-3    lattice_0.20-33
##  [5] deldir_0.1-9     assertthat_0.1   digest_0.6.8     foreach_1.4.2
##  [9] mime_0.4         R6_2.0.1         plyr_1.8.2       chron_2.3-47
## [13] Taxonstand_1.7   evaluate_0.8     coda_0.17-1     highr_0.5.1
## [17] httr_1.0.0       ggplot2_1.0.1    spdep_0.5-88     uuid_0.1-2
## [21] adegenet_2.0.0   rstudioapi_0.4.0 data.table_1.9.4 taxize_0.6.0
## [25] rpart_4.1-10     Matrix_1.2-4     RNeXML_2.0.3     rmarkdown_0.9.3
## [29] proto_0.3-10     splines_3.2.4    stringr_1.0.0    igraph_0.7.1
## [33] RCurl_1.95-4.7   munsell_0.4.2    shiny_0.13.2     httpuv_1.3.3
## [37] htmltools_0.3    codetools_0.2-14 XML_3.98-1.1     reshape_0.8.5
## [41] dplyr_0.4.1      MASS_7.3-45      bitops_1.0-6     grid_3.2.4

```

```
## [45] nlme_3.1-125      jsonlite_0.9.16  xtable_1.7-4     gtable_0.1.2
## [49] DBI_0.3.1         magrittr_1.5     formatR_1.2.1    scales_0.2.4
## [53] stringi_1.0-1     reshape2_1.4.1   LearnBayes_2.15  sp_1.1-0
## [57] phylobase_0.8.0   seqinr_3.1-3     boot_1.3-18      deSolve_1.12
## [61] iterators_1.0.7   tools_3.2.4      bold_0.2.6       rncl_0.6.0
## [65] parallel_3.2.4    yaml_2.1.13      colorspace_1.2-6 knitr_1.10.5
```