Day 8: Beta Diversity (Guerrero Negro)

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All of the code in this page is meant to be run in `R` unless otherwise specified.

Install biom package and vegan package if not installed.

```
install.packages(c('biom','vegan'),repo='http://cran.wustl.edu')
```

Load biom package, load data

```
library('biom')
library('vegan')

# load biom file
otus.biom <- read_biom('otu_table_json.biom')

# Extract data matrix (OTU counts) from biom table
otus <- as.matrix(biom_data(otus.biom))

# transpose so that rows are samples and columns are OTUs
otus <- t(otus)

# load mapping file
map <- read.table('map.txt', sep='\t', comment='', head=T, row.names=1)
```

It is extremely important to ensure that your OTU table and metadata table sample IDs are lined up correctly.

```
# see rownames of map and otus
rownames(map)
```

```
##  [1] "GN01P.484257"   "GN01P.o.484256" "GN02P.o.484250" "GN02P.484248"
##  [5] "GN03P.484253"   "GN03P.o.484249" "GN04P.484258"   "GN04P.o.484251"
##  [9] "GN05P.o.484260" "GN05P.484261"   "GN06P.o.484262" "GN06P.484247"
## [13] "GN07P.o.484246" "GN07P.484259"   "GN08P.484265"   "GN08P.o.484263"
## [17] "GN09P.484254"   "GN09P.o.484264" "GN10P.o.484252" "GN10P.484255"
```

```
rownames(otus)
```

```
##  [1] "GN01P.484257"   "GN07P.o.484246" "GN01P.o.484256" "GN06P.484247"
##  [5] "GN05P.484261"   "GN08P.484265"   "GN05P.o.484260" "GN06P.o.484262"
##  [9] "GN08P.o.484263" "GN07P.484259"   "GN04P.484258"   "GN04P.o.484251"
## [13] "GN09P.484254"   "GN09P.o.484264" "GN02P.484248"   "GN03P.484253"
## [17] "GN02P.o.484250" "GN03P.o.484249"
```

```
# find the overlap
common.ids <- intersect(rownames(map), rownames(otus))

# get just the overlapping samples
otus <- otus[common.ids,]
map <- map[common.ids,]
```

See dimensions of OTU table

```
dim(otus)
```

```
## [1]   18 1750
```

See dimensions of mapping file

```
dim(map)
```

```
## [1] 18 60
```

Get three different distances metrics

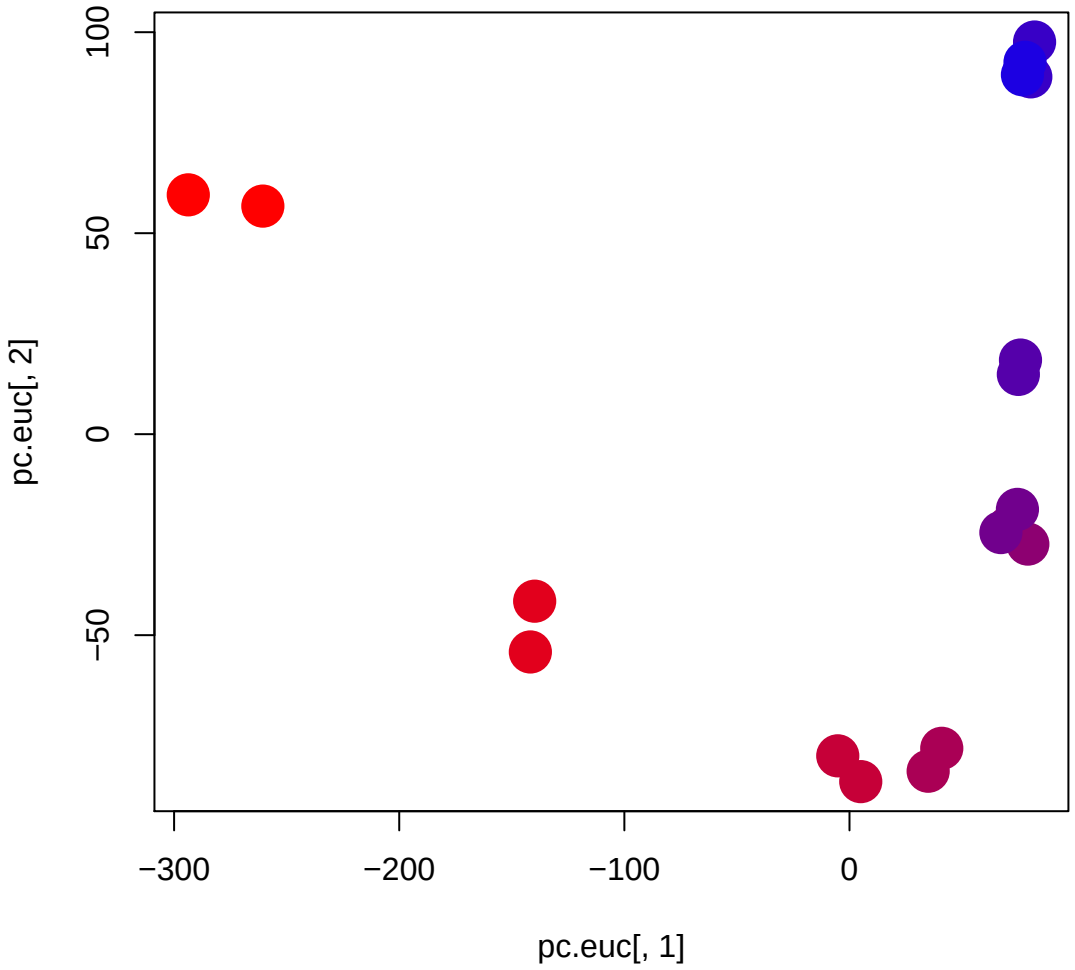
```
# get Euclidean distance
d.euc <- dist(otus)

# get Bray-Curtis distances (default for Vegan)
d.bray <- vegdist(otus)

# get Chi-square distances using vegan command
# we will extract chi-square distances from correspondence analysis
my.ca <- cca(otus)
```

Now run principal coordinates embedding on the distance metrics

```
# Run PCoA (not PCA)
pc.euc <- cmdscale(d.euc, k=2)

# Bray-Curtis principal coords
pc.bray <- cmdscale(d.bray,k=2)

# get first two dimensions of chi-square coordinates:
pc.chisq <- my.ca$CA$u[,1:2]
```

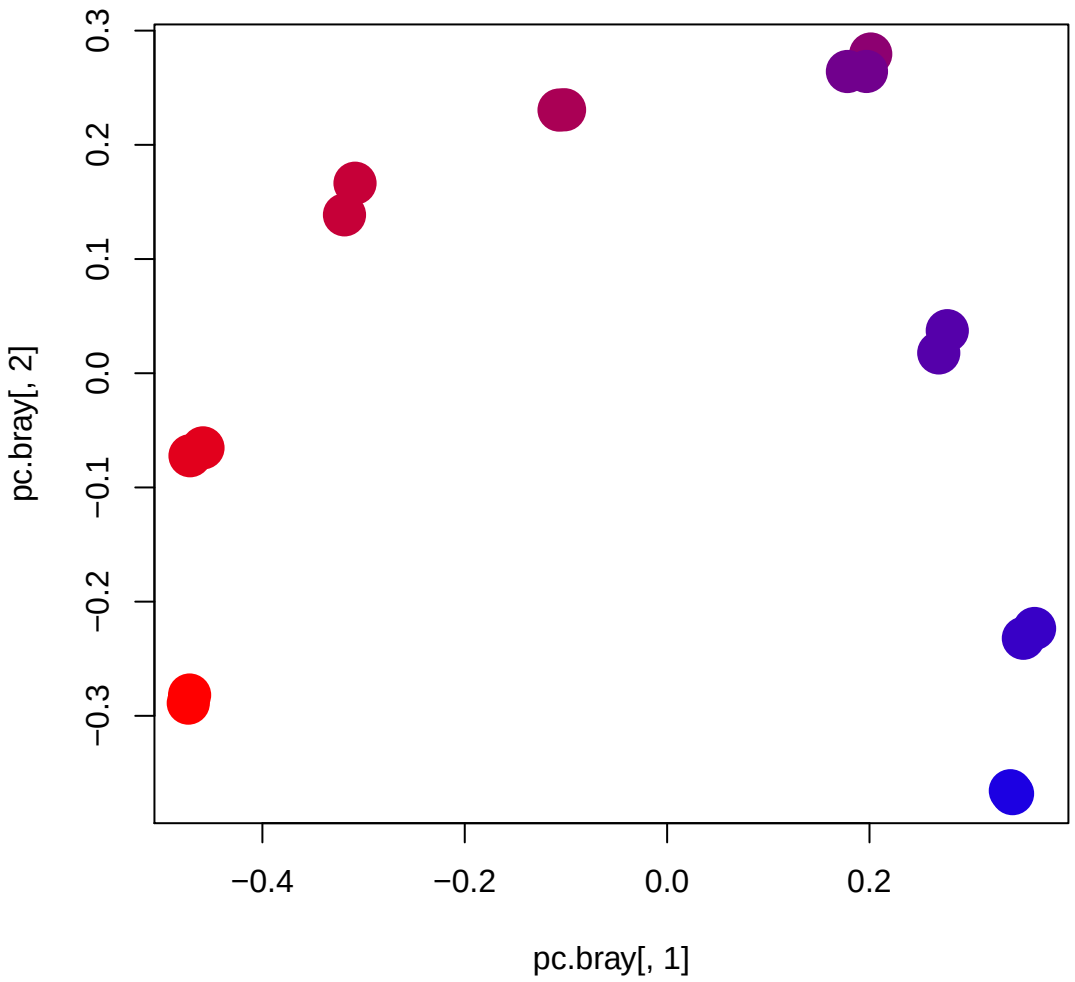
Plot Euclidean distances with gradient colors

```
# makes a gradient from red to blue
my.colors <- colorRampPalette(c('red','blue'))(10)

# plot Euclidean PCoA coords using color gradient
# based on layer (1...10)
layer <- map[,'LAYER']
plot(pc.euc[,1], pc.euc[,2], col=my.colors[layer], cex=3, pch=16)
```



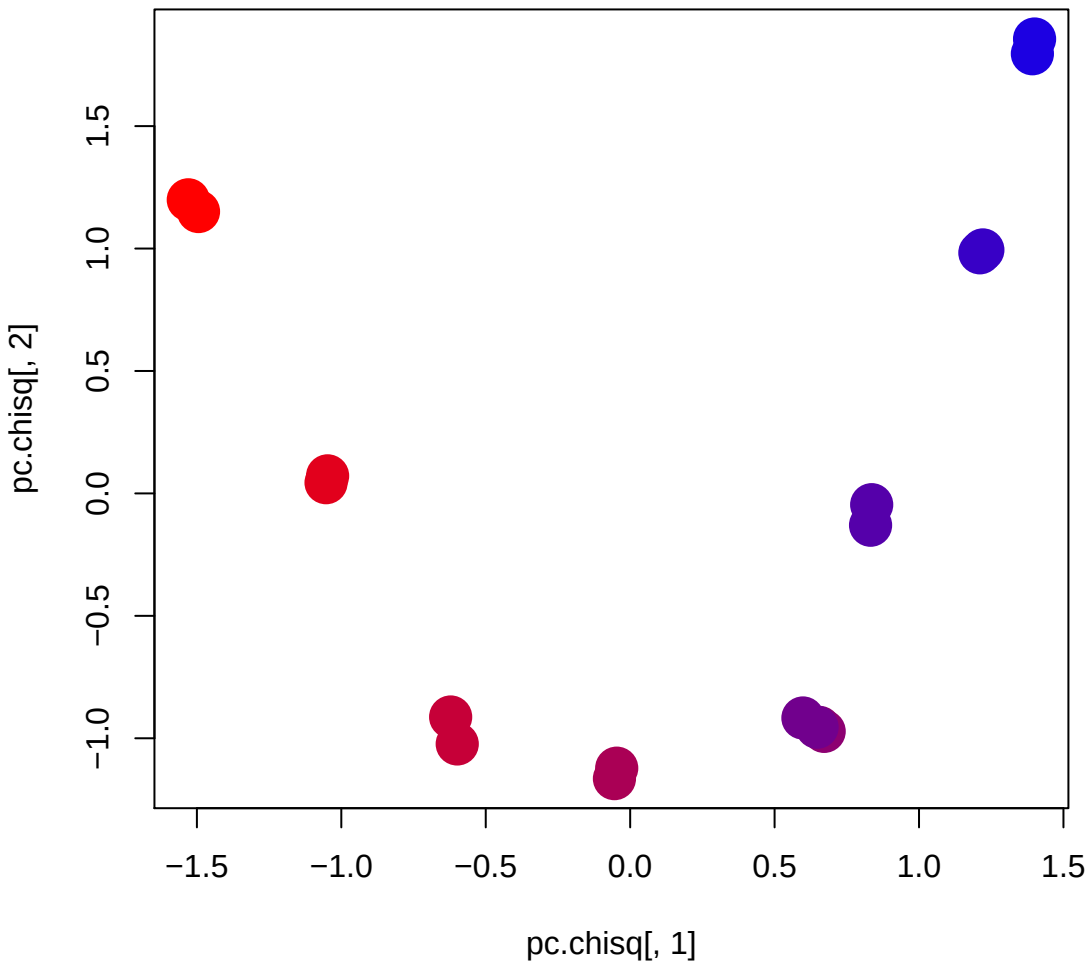
Plot Bray-Curtis distances with gradient colors

```
# Plot Bray-Curtis PCoA
plot(pc.bray[,1], pc.bray[,2], col=my.colors[layer], cex=3, pch=16)
```



Plot Chi-square distances with gradient colors

```
# Plot Chi-square PCoA
plot(pc.chisq[,1], pc.chisq[,2], col=my.colors[layer], cex=3, pch=16)
```



Note: to make a PDF:

```
pdf("chisq.pdf",width=5,height=5)
plot(pc.chisq[,1], pc.chisq[,2], col=my.colors[map[,'Layer']], cex=3, pch=16)
dev.off()
```