

# Contents

BEMA supplemental fungal figures

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## BEMA supplemental fungal figures

Make figures for brief fungal analysis. The goal is to show that the study bias, combined with too few studies makes combined analysis goofy.

```
library(wesanderson)
library(scales)
```

```
# setwd('~/.Dropbox/BEMA/bacteriaHTS/closed_ref_pickedOTUs/R/fungalSupp')
pcAll <- read.delim('binary_sorensen_dice_pc.txt', head=TRUE, row.names=1)
pcNoAA <- read.delim('binary_sorensen_dice_pcNoAmend.txt', head=TRUE, row.names=1)
map <- read.delim('map.txt', head=TRUE, row.names=1)[-1, ]
```

```
head(map) # Description
```

```
##          BarcodeSequence  LinkerPrimerSequence  Geolocation
## Adamsresdust1    ACGAGTGC GTTGGTCATTAGAGGAAGTAA Albany_CA_USA
## Adamsresdust2    ACGCTCGACA GTTGGTCATTAGAGGAAGTAA Albany_CA_USA
## Adamsresdust3    AGACGCACTC GTTGGTCATTAGAGGAAGTAA Albany_CA_USA
## Adamsresdust4    AGCACTGTAG GTTGGTCATTAGAGGAAGTAA Albany_CA_USA
## Adamsresdust5    ATCAGACACG GTTGGTCATTAGAGGAAGTAA Albany_CA_USA
## Adamsresdust6    ATATCGCGAG GTTGGTCATTAGAGGAAGTAA Albany_CA_USA
##          Building_Type Building_Type2 Room_Function
## Adamsresdust1    apt_bulding apt_bulding kitchen
## Adamsresdust2    apt_bulding apt_bulding living_room
## Adamsresdust3    apt_bulding apt_bulding bathroom
## Adamsresdust4    apt_bulding apt_bulding bedroom
## Adamsresdust5    apt_bulding apt_bulding balcony
## Adamsresdust6    apt_bulding apt_bulding kitchen
##          Sequencing_Technology Target_Region Primer_name
## Adamsresdust1    454_GS_FLX_Titanium ITS1 ITS1F_ITS2
## Adamsresdust2    454_GS_FLX_Titanium ITS1 ITS1F_ITS2
## Adamsresdust3    454_GS_FLX_Titanium ITS1 ITS1F_ITS2
## Adamsresdust4    454_GS_FLX_Titanium ITS1 ITS1F_ITS2
## Adamsresdust5    454_GS_FLX_Titanium ITS1 ITS1F_ITS2
## Adamsresdust6    454_GS_FLX_Titanium ITS1 ITS1F_ITS2
##          Sampling_Method Matrix Specific_Matrix Extraction_method
## Adamsresdust1    settle_plate air air chloroform_powersoil
## Adamsresdust2    settle_plate air air chloroform_powersoil
## Adamsresdust3    settle_plate air air chloroform_powersoil
## Adamsresdust4    settle_plate air air chloroform_powersoil
## Adamsresdust5    settle_plate air air chloroform_powersoil
## Adamsresdust6    settle_plate air air chloroform_powersoil
##          Description
## Adamsresdust1 Adams_res_dust
## Adamsresdust2 Adams_res_dust
## Adamsresdust3 Adams_res_dust
```

```
## Adamsresdust4 Adams_res_dust
## Adamsresdust5 Adams_res_dust
## Adamsresdust6 Adams_res_dust
```

```
map$Description <- factor(map$Description)
table(map$Description)
```

```
##
##      Adams_res_dust  Adams_res_surfaces Adams_univ_classroom
##              94              160              28
##      Amend_global      Dann_Chamacos      Hoisington_retail
##              118              46              23
```

```
cols <- c(wes.palette(5, 'Darjeeling2')[-3], wes.palette(5, 'Darjeeling')[c(1,4)])
cols <- cols[c(6,3,4,2,5,1)]
map$col <- ''
```

```
for(i in 1:nlevels(map$Description)) {
  these <- which(map$Description == levels(map$Description)[i])
  map$col[these] <- cols[i]
}
```

```
perExplAll <- pcAll['% variation explained', ]
perExplNoAA <- pcNoAA['% variation explained', ]
perExplAll[c(1,2)]; perExplNoAA[c(1,2)]
```

```
##              X1      X2
## % variation explained 9.626 4.508
```

```
##              X1      X2
## % variation explained 8.466 4.182
```

```
sum(perExplAll)
```

```
## [1] 100
```

```
dim(pcAll)
```

```
## [1] 375 373
```

```
pcAll <- pcAll[-c(nrow(pcAll), nrow(pcAll)-1), c(1,2)]
pcNoAA <- pcNoAA[-c(nrow(pcNoAA), nrow(pcNoAA)-1), c(1,2)]
```

```
all(row.names(pcAll) %in% row.names(map))
```

```
## [1] TRUE
```

```
all(row.names(pcNoAA) %in% row.names(map))
```

```
## [1] TRUE
```

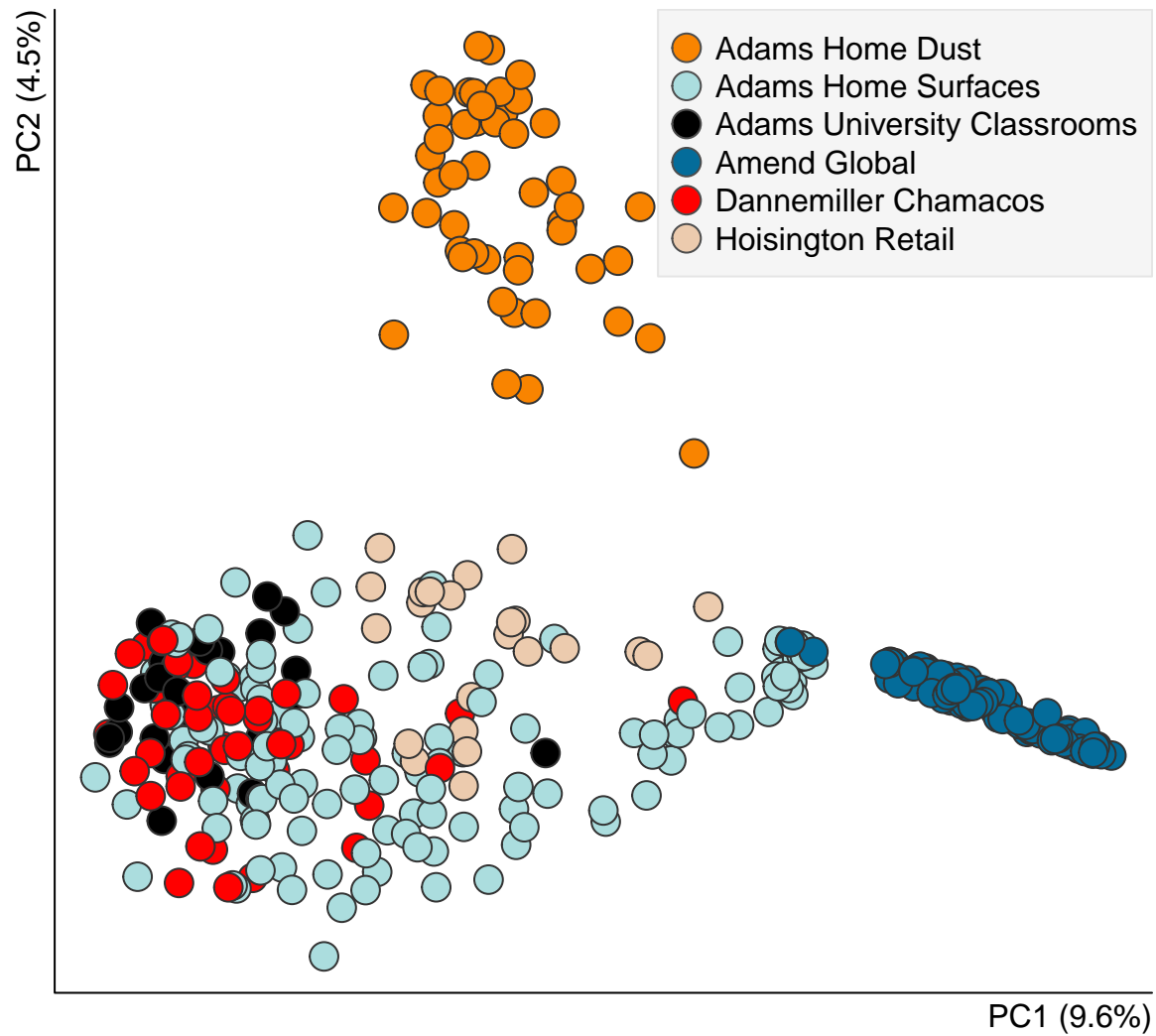
```
mapAll <- map[row.names(pcAll), ]  
mapNoAA <- map[row.names(pcNoAA), ]
```

```
leg <- data.frame(levs = levels(mapAll$Description), cols=cols)
```

```
leg$legend <- 'Adams Home Dust'  
leg$legend[leg$levs == 'Adams_res_surfaces'] <- 'Adams Home Surfaces'  
leg$legend[leg$levs == 'Adams_univ_classroom'] <- 'Adams University Classrooms'  
leg$legend[leg$levs == 'Amend_global'] <- 'Amend Global'  
leg$legend[leg$levs == 'Dann_Chamacos'] <- 'Dannemiller Chamacos'  
leg$legend[leg$levs == 'Hoisington_retail'] <- 'Hoisington Retail'
```

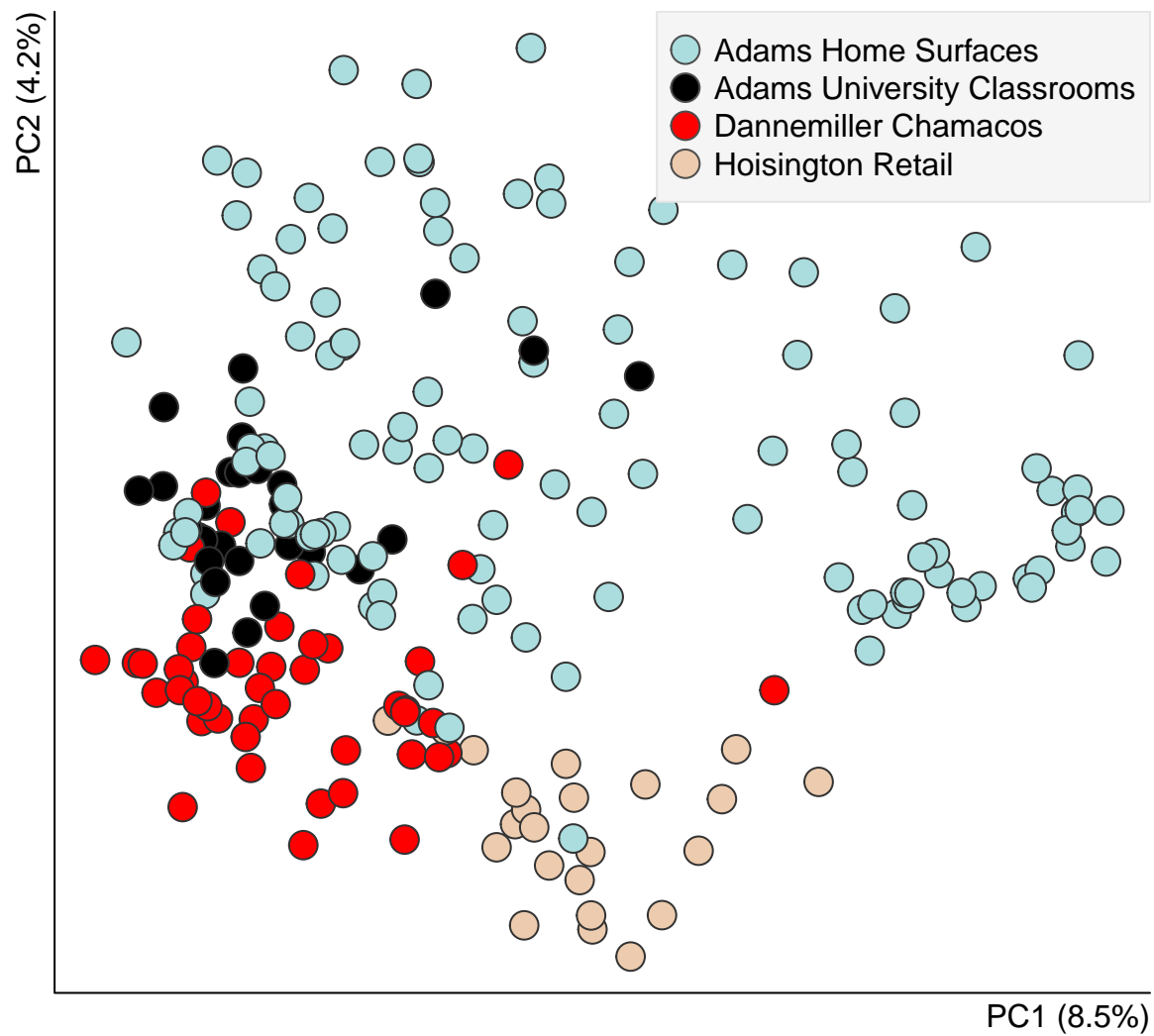
```
legNoAA <- leg[-c(1, 4), ]  
ch <- function(x) {as.character(x)}
```

```
#pdf('pcAllFungal.pdf', useDingbats=FALSE)  
plot(pcAll, pch=21, col='gray20', bg=alpha(mapAll$col, alpha=1), cex=2,  
     bty='l', ann=FALSE, xaxt='n', yaxt='n')  
legend('topright', legend=leg$legend,  
      pch=21, pt.bg=ch(leg$cols), col='gray30', pt.cex=2, cex=1,  
      bg='gray96', box.col='gray90')  
mtext('PC1 (9.6%)', side=1, adj=1, line=.1)  
mtext('PC2 (4.5%)', side=2, adj=1, line=.2)
```



```
#dev.off()
```

```
#pdf('pcNoAAFungal.pdf', useDingbats=FALSE)
plot(pcNoAA, pch=21, col='gray20', bg=alpha(mapNoAA$col, alpha=1), cex=2,
     bty='l', ann=FALSE, xaxt='n', yaxt='n')
legend('topright', legend=legNoAA$legend,
     pch=21, pt.bg=ch(legNoAA$cols), col='gray30', pt.cex=2, cex=1,
     bg='gray96', box.col='gray90')
mtext('PC1 (8.5%)', side=1, adj=1, line=.1)
mtext('PC2 (4.2%)', side=2, adj=1, line=.2)
```



*#dev.off()*