

Set working directory, load packages

```
setwd("~/GitHub/GroupProject")  
rm(list=ls())
```

```
library(vegan)
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.5-3
```

```
library(psych)
```

```
library(ggplot2)
```

```
##
```

```
## Attaching package: 'ggplot2'
```

```
## The following objects are masked from 'package:psych':
```

```
##
```

```
##      %+%, alpha
```

```
library(forcats)
```

```
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      intersect, setdiff, setequal, union
```

```
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```
library(indicspecies)
```

SPECIES RICHNESS CODE, WITHOUT FORAGING GUILDS

Load, manipulate data

```
data.without.guilds <- read.csv("hf085-01-bird.csv", header = TRUE)
```

```
data.num <- data.without.guilds[,3:51]
```

Write functions

```
S.obs <- function(x = ""){
  rowSums(x > 0) * 1
}

S.chao2 <- function(site = "", SbyS = ""){
  SbyS = as.data.frame(SbyS)
  x = SbyS[site, ]
  SbyS.pa <- (SbyS > 0) * 1
  Q1 = sum(colSums(SbyS.pa) == 1)
  Q2 = sum(colSums(SbyS.pa) == 2)
  S.chao2 = S.obs(x) + (Q1^2)/(2*Q2)
  return(S.chao2)
}

sem <- function(x){
  sd(na.omit(x))/sqrt(length(na.omit(x)))
}
```

Determine observed and estimated species richness

```
obs.rich <- S.obs(data.num)
obs.rich

## [1] 10 10 6 9 8 4 14 13 13 10 3 11 16 5 13 8 6 13 13 9 8 9 8
## [24] 10 7 5 9 9 10 11 6 7 7 5 5 9 8 14 9 8

est.rich <- S.chao2(1:40, data.num)
est.rich

## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
## 13.6 13.6 9.6 12.6 11.6 7.6 17.6 16.6 16.6 13.6 6.6 14.6 19.6 8.6 16.6
## 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
## 11.6 9.6 16.6 16.6 12.6 11.6 12.6 11.6 13.6 10.6 8.6 12.6 12.6 13.6 14.6
## 31 32 33 34 35 36 37 38 39 40
## 9.6 10.6 10.6 8.6 8.6 12.6 11.6 17.6 12.6 11.6
```

Make species richness plot

```
data.rich <- cbind(data.without.guilds, est.rich)

m1 <- lm(est.rich ~ mortality.class, data = data.rich)
summary(m1)

##
## Call:
## lm(formula = est.rich ~ mortality.class, data = data.rich)
##
## Residuals:
```

```
##      Min      1Q  Median      3Q      Max
## -6.5455 -1.5841  0.0875  1.7273  6.4545
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      13.3000     0.9745  13.648 8.45e-16 ***
## mortality.classHi-B -0.1545     1.3465  -0.115  0.909
## mortality.classLow  -1.4273     1.3465  -1.060  0.296
## mortality.classMed  -1.5750     1.4618  -1.077  0.288
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.082 on 36 degrees of freedom
## Multiple R-squared:  0.05531,    Adjusted R-squared:  -0.02342
## F-statistic: 0.7026 on 3 and 36 DF,  p-value: 0.5567

mortality <- factor(data.rich$mortality.class, levels = c("Low", "Med", "Hi-A", "Hi-B"))
mortality

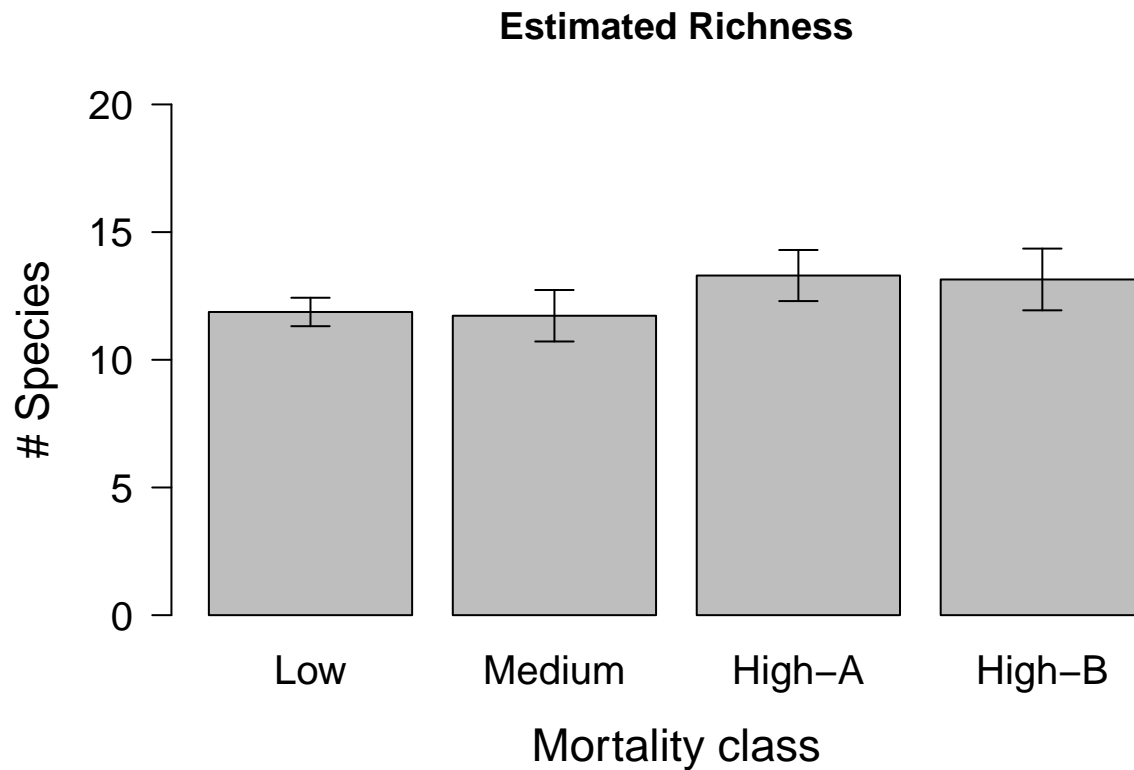
## [1] Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-B Hi-B Hi-B Hi-B
## [15] Hi-B Hi-B Hi-B Hi-B Hi-B Hi-B Hi-B Low Low Low Low Low Low Low
## [29] Low Low Low Low Med Med Med Med Med Med Med Med
## Levels: Low Med Hi-A Hi-B

data.means <- tapply(data.rich$est.rich, mortality, mean)

data.sem <- tapply(data.rich$est.rich, mortality, sem)

bp1 <- barplot(data.means, ylim = c(0, round(max(data.rich$est.rich), digits = 0)),
  pch = 15, cex = 1.25, las = 1, cex.lab = 1.4, cex.axis = 1.25,
  xlab = "Mortality class",
  ylab = "# Species",
  names.arg = c("Low", "Medium", "High-A", "High-B"), main = "Estimated Richness")

arrows(x0 = bp1, y0 = data.means, y1 = data.means - data.sem, angle = 90,
  length = 0.1, lwd = 1)
arrows(x0 = bp1, y0 = data.means, y1 = data.means + data.sem, angle = 90,
  length = 0.1, lwd = 1)
```



Run Anova

```
fitanova <- aov(est.rich ~ mortality, data = data.rich)
fitanova
```

```
## Call:
## aov(formula = est.rich ~ mortality, data = data.rich)
##
## Terms:
##             mortality Residuals
## Sum of Squares    20.0159  341.8841
## Deg. of Freedom      3      36
##
## Residual standard error: 3.081685
## Estimated effects may be unbalanced
```

```
summary(fitanova)
```

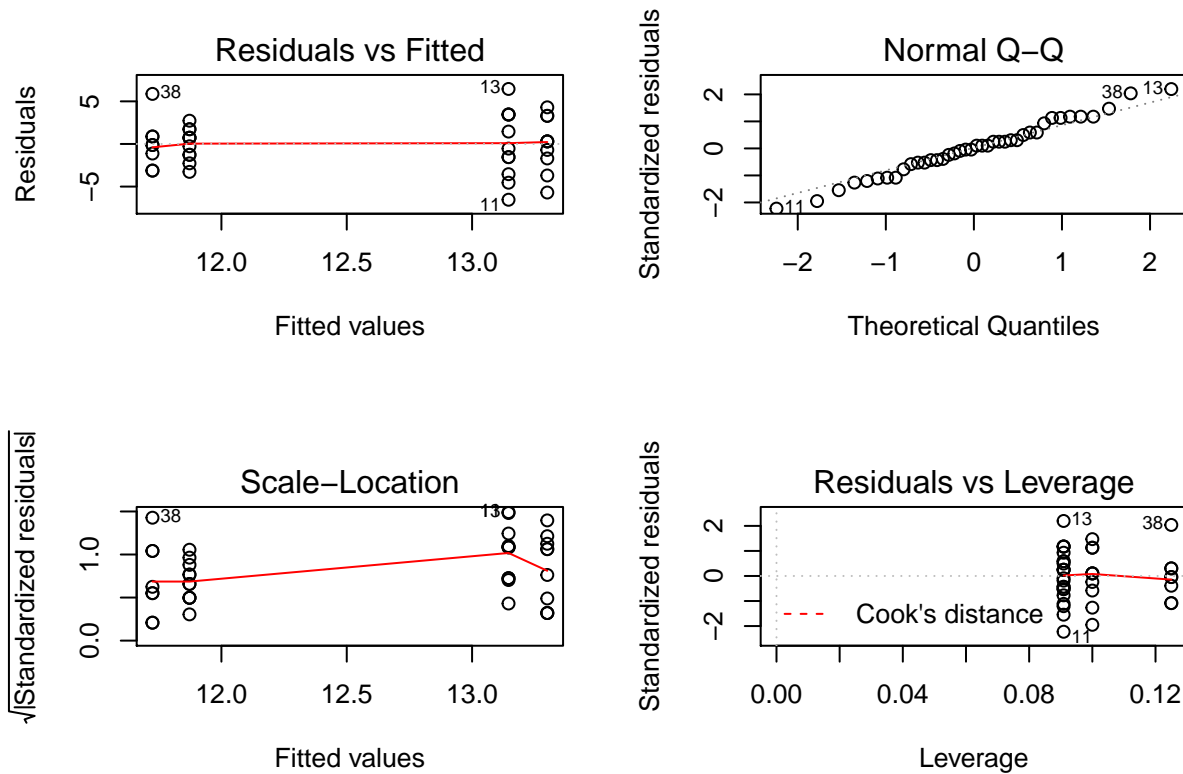
```
##           Df Sum Sq Mean Sq F value Pr(>F)
## mortality   3   20.0   6.672   0.703  0.557
## Residuals  36  341.9   9.497
```

```
TukeyHSD(fitanova)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = est.rich ~ mortality, data = data.rich)
##
```

```
## $mortality
##           diff      lwr      upr      p adj
## Med-Low   -0.1477273 -4.004257  3.708802 0.9995992
## Hi-A-Low    1.4272727 -2.199117  5.053663 0.7156092
## Hi-B-Low    1.2727273 -2.266267  4.811721 0.7679856
## Hi-A-Med    1.5750000 -2.361882  5.511882 0.7052768
## Hi-B-Med    1.4204545 -2.436075  5.276984 0.7548832
## Hi-B-Hi-A  -0.1545455 -3.780935  3.471844 0.9994486

par(mfrow = c(2,2), mar = c(5.1, 4.1, 4.1, 2.1))
plot(fitanova)
```



Mean abundance

Open data

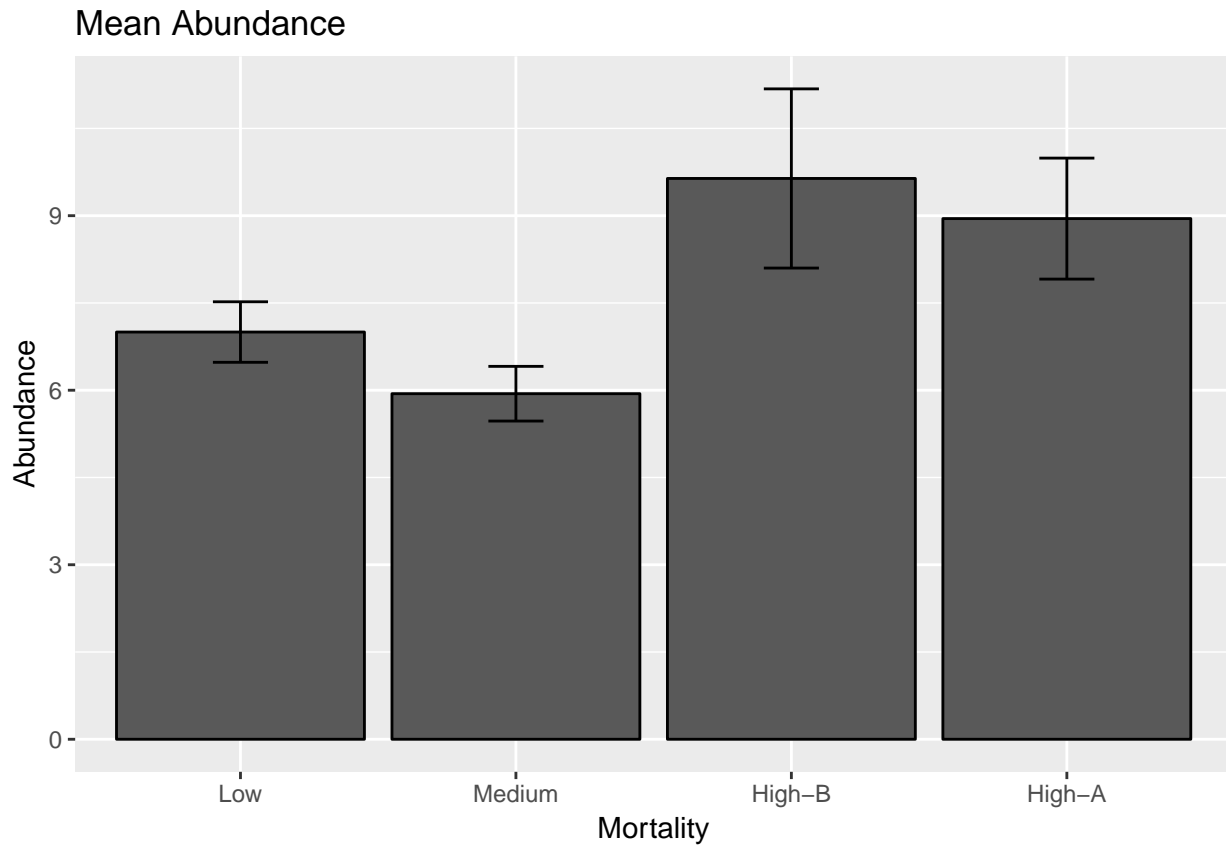
```
MeanAbundMort <- read.csv("MortalityMeanAbund.csv")
```

Reorder labels on x axis

```
MeanAbundMort$mortality <- fct_relevel(MeanAbundMort$mortality, "Low", "Medium", "High-B", "High-A")
```

Plot

```
ggplot(MeanAbundMort, aes(x=Mortality, y = Abundance)) +  
  geom_bar(position=position_dodge(), stat = "identity", colour = 'black') + geom_errorbar(aes(ymin=Abund
```



FORAGING GUILDS CODE

Species Richness

Open species richness foraging guilds file

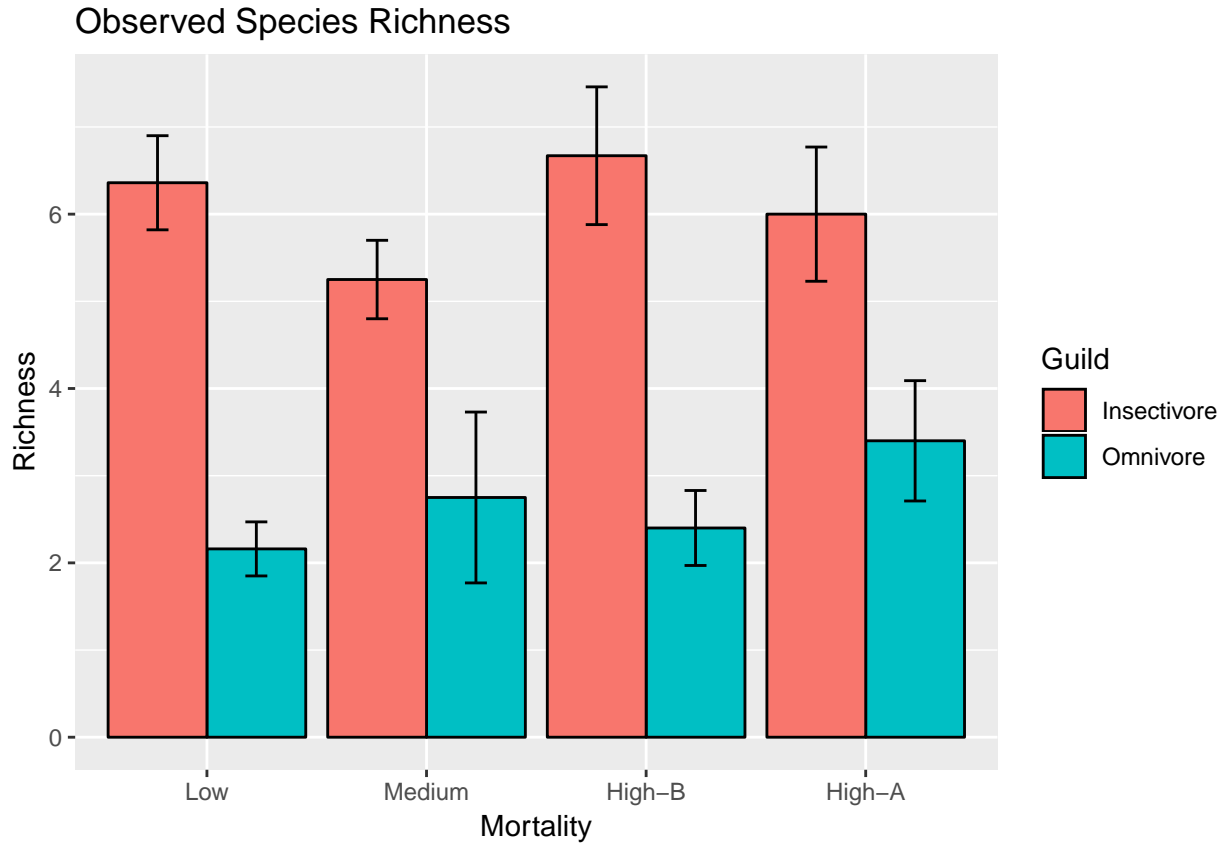
```
Spec.Rich.Guilds <- read.csv("GuildsClusteredRich.csv")  
Spec.Rich.Guilds <- read.csv("GuildsClusteredRich.csv")
```

Reorder labels on x axis

```
Spec.Rich.Guilds$Mortality <- fct_relevel(Spec.Rich.Guilds$Mortality, "Low", "Medium", "High-B", "High-A")
```

Plot

```
ggplot(Spec.Rich.Guilds, aes(x=Mortality, y = Richness, fill = Guild)) +  
  geom_bar(position=position_dodge(), stat = "identity", colour = 'black') + geom_errorbar(aes(ymin=Richn
```



Mean Abundance (Guilds)

Load Data

```
Guilds <- read.csv("ForagingGuildsDataFile.csv")  
  
str(Guilds)  
  
## 'data.frame': 40 obs. of 7 variables:  
## $ sample.point : Factor w/ 40 levels "P184","P187",...: 8 9 10 1 2 3 4 5 6 7 ...  
## $ mortality.class: Factor w/ 4 levels "HiA","HiB","Low",...: 1 1 1 2 2 2 2 2 2 2 ...  
## $ Car_2 : int 0 0 0 0 0 0 0 0 0 0 ...  
## $ Omn_16 : num 0.5 4 3 1 3 5 1 2 2 3 ...  
## $ Ins_29 : num 7 9 3 2 12 16 5 4.5 6 5 ...  
## $ Gra_1 : num 0 0 0 0 0 1 0 0.5 0 0 ...  
## $ Verm_1 : num 0 0 0 0 0 0 0 0 0 0 ...  
  
summary(Guilds)
```

```
## sample.point mortality.class Car_2 Omn_16 Ins_29
## P184 : 1 HiA:10 Min. :0 Min. :0.00 Min. : 2.000
## P187 : 1 HiB:11 1st Qu.:0 1st Qu.:1.00 1st Qu.: 4.000
## P188 : 1 Low:11 Median :0 Median :2.00 Median : 4.750
## P189 : 1 Med: 8 Mean :0 Mean :2.25 Mean : 5.475
## P195 : 1 3rd Qu.:0 3rd Qu.:3.00 3rd Qu.: 6.500
## P196 : 1 Max. :0 Max. :7.50 Max. :16.000
## (Other):34
## Gra_1 Verm_1
## Min. :0.0000 Min. :0.0000
## 1st Qu.:0.0000 1st Qu.:0.0000
## Median :0.0000 Median :0.0000
## Mean :0.1125 Mean :0.0625
## 3rd Qu.:0.0000 3rd Qu.:0.0000
## Max. :1.0000 Max. :1.5000
##
```

Compute means for omnivores and insectivores in the different mortality classes

```
Omnivores.Mean <- tapply(Guilds$Omn_16, Guilds$mortality.class, mean)
Omnivores.Mean
```

```
## HiA HiB Low Med
## 3.350000 2.636364 1.045455 2.000000
```

```
Insectivores.Mean <- tapply(Guilds$Ins_29, Guilds$mortality.class, mean)
Insectivores.Mean
```

```
## HiA HiB Low Med
## 5.250000 6.545455 5.818182 3.812500
```

Compute standard errors for those means

```
Omnivores.SE <- tapply(Guilds$Omn_16, Guilds$mortality.class, sem)
Omnivores.SE
```

```
## HiA HiB Low Med
## 0.6238322 0.3636364 0.1712859 0.6477985
```

```
Insectivores.SE <- tapply(Guilds$Ins_29, Guilds$mortality.class, sem)
Insectivores.SE
```

```
## HiA HiB Low Med
## 0.7610300 1.2200122 0.5651739 0.3651993
```

Omnivore bar plot

```
OmnivorePlot <- barplot(Omnivores.Mean, ylim = c(0, round(1.5*max(Omnivores.Mean), digits = 0)),
  pch = 15, cex = 1.25, las = 1, cex.lab = 1.4, cex.axis = 1.25,
```

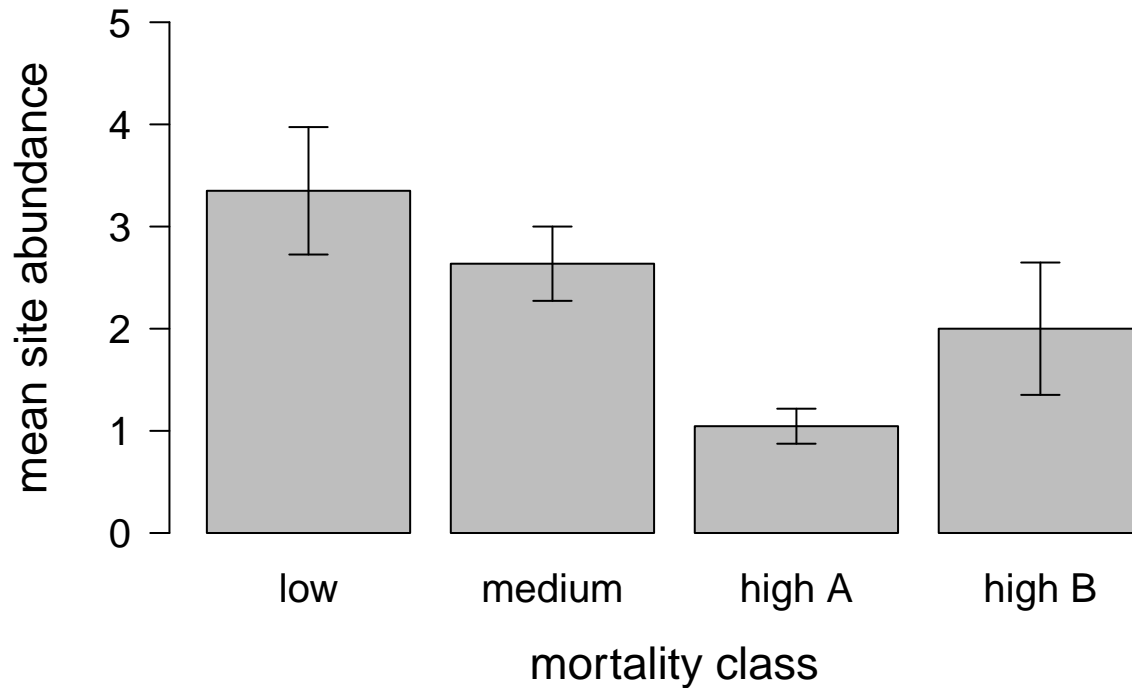


```

xlab = "mortality class",
ylab = "mean site abundance",
names.arg = c("low", "medium", "high A", "high B"))

arrows(x0 = OmnivorePlot, y0 = Omnivores.Mean, y1 = Omnivores.Mean - Omnivores.SE, angle = 90,
length = 0.1, lwd = 1)
arrows(x0 = OmnivorePlot, y0 = Omnivores.Mean , y1 = Omnivores.Mean + Omnivores.SE, angle = 90,
length = 0.1, lwd = 1)

```



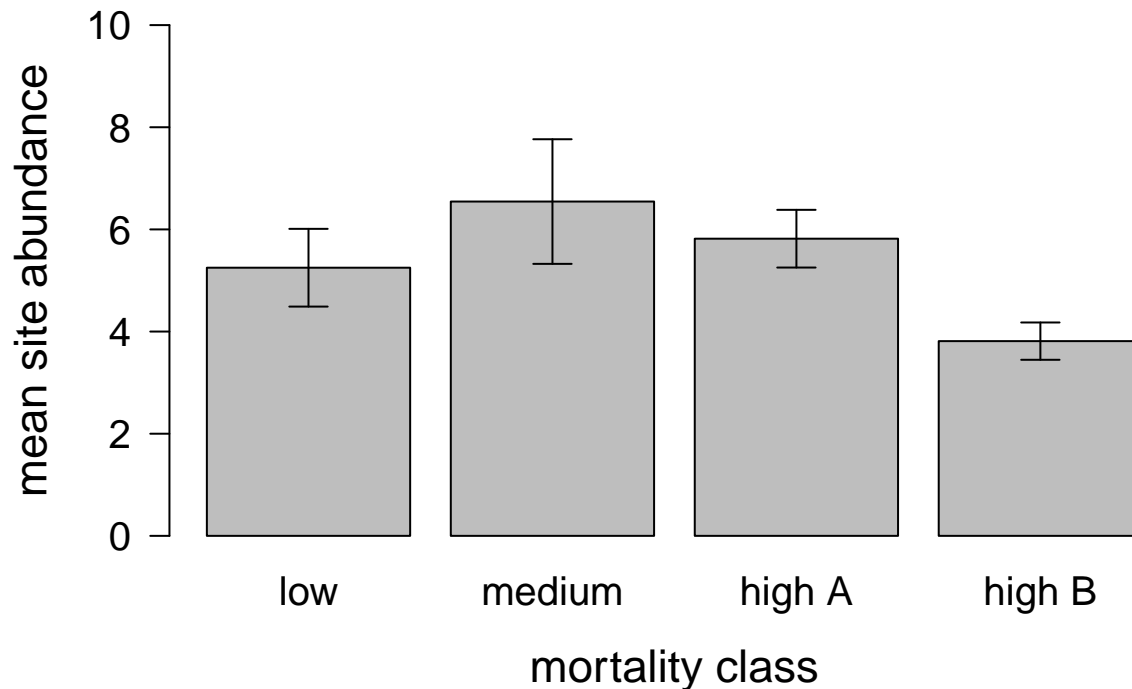
Insectivore bar plot

```

InsectivorePlot <- barplot(Insectivores.Mean, ylim = c(0, round(1.5*max(Insectivores.Mean), digits = 0)),
pch = 15, cex = 1.25, las = 1, cex.lab = 1.4, cex.axis = 1.25,
xlab = "mortality class",
ylab = "mean site abundance",
names.arg = c("low", "medium", "high A", "high B"))

arrows(x0 = InsectivorePlot, y0 = Insectivores.Mean, y1 = Insectivores.Mean - Insectivores.SE, angle = 90,
length = 0.1, lwd = 1)
arrows(x0 = InsectivorePlot, y0 = Insectivores.Mean , y1 = Insectivores.Mean + Insectivores.SE, angle = 90,
length = 0.1, lwd = 1)

```



Get omnivore and insectivore bars on same plot

#Load excel file with means and S.E.s for both guilds at each mortality class

```
ClusteredBar <- read.csv("GuildsClusteredBar.csv", header = TRUE)
ClusteredBar
```

```
## Mortality      Guild Mean S.E.
## 1    High-A    Omnivore 3.35 0.62
## 2    High-A  Insectivore 5.25 0.76
## 3    High-B    Omnivore 2.64 0.36
## 4    High-B  Insectivore 6.55 1.22
## 5      Low    Omnivore 1.05 0.17
## 6      Low  Insectivore 5.82 0.57
## 7    Medium    Omnivore 2.00 0.65
## 8    Medium  Insectivore 3.81 0.37
```

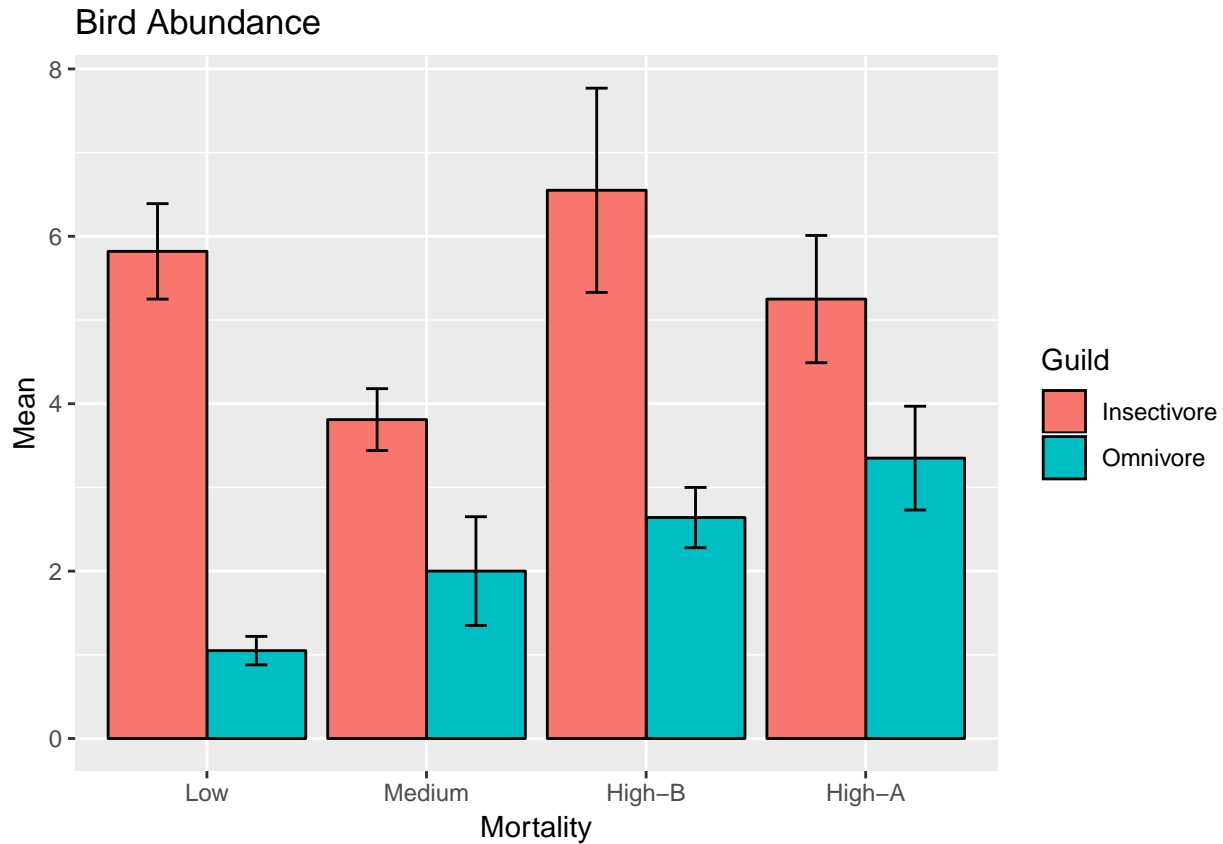
```
str(ClusteredBar)
```

```
## 'data.frame': 8 obs. of 4 variables:
## $ Mortality: Factor w/ 4 levels "High-A","High-B",...: 1 1 2 2 3 3 4 4
## $ Guild : Factor w/ 2 levels "Insectivore",...: 2 1 2 1 2 1 2 1
## $ Mean : num 3.35 5.25 2.64 6.55 1.05 5.82 2 3.81
## $ S.E. : num 0.62 0.76 0.36 1.22 0.17 0.57 0.65 0.37
```

Reorder x axis

```
ClusteredBar$Mortality <- fct_relevel(ClusteredBar$Mortality, "Low", "Medium", "High-B", "High-A")
```

```
ggplot(ClusteredBar, aes(x=Mortality, y = Mean, fill = Guild)) +
  geom_bar(position=position_dodge(), stat = "identity", colour = 'black') + geom_errorbar(aes(ymin=Mean
```



Run Omnivore Anova

```
OmnivoreAnova <- aov(Guilds$Omn_16~Guilds$mortality.class, data = Guilds)
OmnivoreAnova
```

```
## Call:
## aov(formula = Guilds$Omn_16 ~ Guilds$mortality.class, data = Guilds)
##
## Terms:
## Guilds$mortality.class Residuals
## Sum of Squares 30.20227 76.29773
## Deg. of Freedom 3 36
##
## Residual standard error: 1.45581
## Estimated effects may be unbalanced
```

```
summary(OmnivoreAnova)
```

```
## Df Sum Sq Mean Sq F value Pr(>F)
## Guilds$mortality.class 3 30.2 10.067 4.75 0.00683 **
## Residuals 36 76.3 2.119
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(OmnivoreAnova)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Guilds$Omn_16 ~ Guilds$mortality.class, data = Guilds)
##
## $`Guilds$mortality.class`
##           diff           lwr           upr           p adj
## HiB-HiA -0.7136364 -2.4267684  0.99949569 0.6786033
## Low-HiA -2.3045455 -4.0176775 -0.59141340 0.0047289
## Med-HiA -1.3500000 -3.2098109  0.50981093 0.2239469
## Low-HiB -1.5909091 -3.2627548  0.08093661 0.0670524
## Med-HiB -0.6363636 -2.4582152  1.18548797 0.7832371
## Med-Low  0.9545455 -0.8673062  2.77639707 0.5008378
```

Run Insectivore ANOVA

```
InsectivoreAnova <- aov(Guilds$Ins_29~Guilds$mortality.class, data = Guilds)
```

```
summary(InsectivoreAnova)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Guilds$mortality.class  3  36.52  12.173    1.695  0.185
## Residuals              36 258.46    7.179
```

```
TukeyHSD(InsectivoreAnova)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Guilds$Ins_29 ~ Guilds$mortality.class, data = Guilds)
##
## $`Guilds$mortality.class`
##           diff           lwr           upr           p adj
## HiB-HiA  1.2954545 -1.857586  4.4484948 0.6878842
## Low-HiA  0.5681818 -2.584858  3.7212221 0.9618696
## Med-HiA -1.4375000 -4.860504  1.9855045 0.6730776
## Low-HiB -0.7272727 -3.804325  2.3497795 0.9194970
## Med-HiB -2.7329545 -6.086094  0.6201854 0.1439617
## Med-Low -2.0056818 -5.358822  1.3474581 0.3854354
```

PCoA

```
bird <- read.csv("hf085-01-bird.csv", header = TRUE)
over <- read.csv("hf085-02-overstory.csv", header = TRUE)
under <- read.csv("hf085-03-understory.csv", header = TRUE)

bird.num <- bird[3:51]
```

```

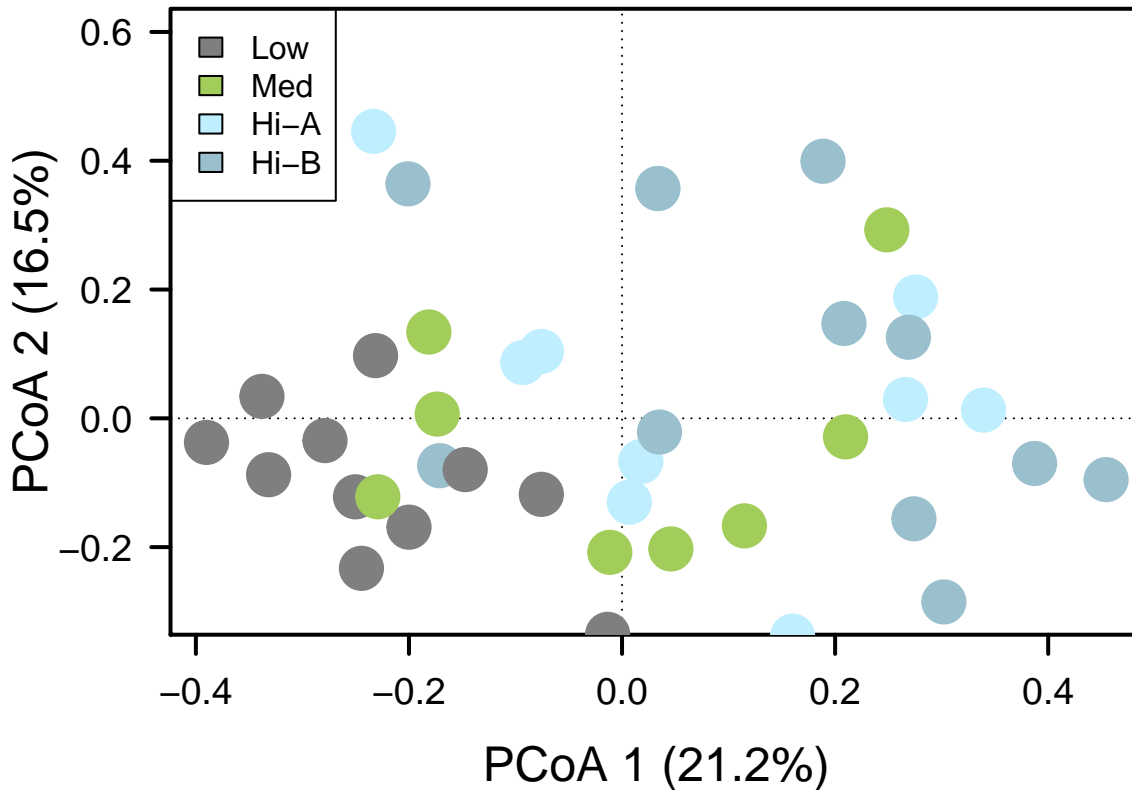
over.num <- over[3:23]
under.num <- under[3:20]

# Sorenson & PCoA
bird.rm <- vegdist(bird.num, method = "bray", binary = TRUE)
bird.pcoa <- cmdscale(bird.rm, eig = TRUE, k = 3)

explainvar1 <- round(bird.pcoa$eig[1] / sum(bird.pcoa$eig), 3) * 100
explainvar2 <- round(bird.pcoa$eig[2] / sum(bird.pcoa$eig), 3) * 100
explainvar3 <- round(bird.pcoa$eig[3] / sum(bird.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

# Plotting PCoA
palette(c('lightblue1', 'lightblue3', 'gray50', 'darkolivegreen3'))
par(mar = c(5, 5, 1, 2) + 0.1)
plot(bird.pcoa$points[,1], bird.pcoa$points[,2], ylim = c(-0.3, 0.6),
      xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
      ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
      pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)
points(bird.pcoa$points[,1], bird.pcoa$points[,2],
       pch = 19, cex = 3, bg = bird$mortality.class, col = bird$mortality.class)
legend("topleft", legend=c("Low", "Med", "Hi-A", "Hi-B"), fill=c('gray50', 'darkolivegreen3', 'lightblue1', 'darkolivegreen3'))

```



Phi coefficient of association

```
mortality <- c(rep("Hi-A", 10), rep("Hi-B", 11), rep("Low", 11), rep("Med", 8))

bird.rel <- decostand(bird.num, method = "total")
phi <- multipatt(bird.rel, cluster = mortality, func = "r.g", control = how(nperm=10000))
summary(phi)

##
## Multilevel pattern analysis
## -----
##
## Association function: r.g
## Significance level (alpha): 0.05
##
## Total number of species: 49
## Selected number of species: 6
## Number of species associated to 1 group: 5
## Number of species associated to 2 groups: 0
## Number of species associated to 3 groups: 1
##
## List of species associated to each combination:
##
## Group Hi-A #sps. 1
##      stat p.value
## bhco 0.541 0.0026 **
##
## Group Hi-B #sps. 2
##      stat p.value
## howa 0.582 0.0027 **
## eawp 0.414 0.0373 *
##
## Group Low #sps. 2
##      stat p.value
## btnw 0.741 1e-04 ***
## blbw 0.448 0.0494 *
##
## Group Hi-A+Hi-B+Med #sps. 1
##      stat p.value
## etti 0.502 0.0071 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mantel test

```
bird.dist <- vegdist(bird.num, method = "bray")
over.dist <- vegdist(over.num, method = "bray")

bird2.dist <- vegdist(bird.num[-29,], method = "bray")
under.dist <- vegdist(under.num[-29,], method = "bray")

## Warning in vegdist(under.num[-29, ], method = "bray"): you have empty rows:
```

```

## their dissimilarities may be meaningless in method "bray"
mantel(bird.dist, over.dist)

##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = bird.dist, ydis = over.dist)
##
## Mantel statistic r: 0.1311
##      Significance: 0.013
##
## Upper quantiles of permutations (null model):
##      90%      95%    97.5%      99%
## 0.0704 0.0896 0.1107 0.1349
## Permutation: free
## Number of permutations: 999
mantel(bird2.dist, under.dist)

##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = bird2.dist, ydis = under.dist)
##
## Mantel statistic r: 0.05738
##      Significance: 0.113
##
## Upper quantiles of permutations (null model):
##      90%      95%    97.5%      99%
## 0.0616 0.0795 0.0971 0.1108
## Permutation: free
## Number of permutations: 999

```