

Dustin Brewer ; Brooke Peckenpaugh

Set working directory, load packages

```
setwd("C:/Users/dusti/Box Sync/Personal Computer/Quantitative Biodiversity/Group Project/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
```

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)
data.rich
```

##	sample.point	mortality.class	acfl	amcr	amgo	amro	baww	bcch	bhco	blbw				
## 1	P37	Hi-A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0				
## 2	P69	Hi-A	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0				
## 3	P70	Hi-A	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0				
## 4	P719	Hi-A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0				
## 5	P721	Hi-A	0.0	0.0	1.5	0.0	0.0	2.5	0.0	0.0				
## 6	P724	Hi-A	0.0	0.0	1.5	0.0	0.5	1.5	0.0	0.0				
## 7	P727	Hi-A	0.0	1.0	0.5	0.0	0.5	1.0	1.0	0.0				
## 8	P728	Hi-A	0.0	0.0	0.5	0.0	0.5	0.5	0.5	0.0				
## 9	P734	Hi-A	0.0	0.0	1.0	0.0	0.0	2.5	1.0	0.0				
## 10	P735	Hi-A	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0				
## 11	P184	Hi-B	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0				
## 12	P187	Hi-B	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0				
## 13	P188	Hi-B	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0				
## 14	P189	Hi-B	0.0	0.0	0.0	0.0	1.0	2.0	0.0	0.0				
## 15	P195	Hi-B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0				
## 16	P196	Hi-B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0				
## 17	P197	Hi-B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0				
## 18	P707	Hi-B	1.0	0.0	0.0	1.5	0.0	0.5	0.0	0.0				
## 19	P710	Hi-B	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0				
## 20	P725	Hi-B	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0				
## 21	P730	Hi-B	0.0	0.0	1.5	0.0	0.0	2.5	0.0	0.0				
## 22	P703	Low	0.5	0.0	0.0	0.0	0.5	0.0	0.0	1.0				
## 23	P704	Low	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.5				
## 24	P705	Low	0.0	1.0	0.0	0.0	0.0	2.5	0.0	0.0				
## 25	P706	Low	0.0	0.5	0.0	0.0	0.0	1.0	0.0	0.0				
## 26	P708	Low	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0				
## 27	P711	Low	0.0	0.0	0.0	0.5	0.0	2.5	0.0	0.0				
## 28	P712	Low	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0				
## 29	P736	Low	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0				
## 30	P737	Low	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0				
## 31	P739	Low	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0				
## 32	P740	Low	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.5				
## 33	P713	Med	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0				
## 34	P714	Med	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0				
## 35	P715	Med	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0				
## 36	P716	Med	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0				
## 37	P717	Med	0.0	0.5	0.0	0.0	0.0	1.0	0.0	0.0				
## 38	P718	Med	0.0	0.0	0.5	0.0	0.0	0.5	0.0	0.0				
## 39	P720	Med	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0				
## 40	P723	Med	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0				
##	blja	brcr	btnw	cawa	cedw	cogr	dowo	eaki	eaph	eato	eawp	etti	gcfl	gcki
## 1	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.5	0.5	0.5	0.0
## 2	1.0	0.0	1.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	2.0	1.0	0.0
## 3	0.0	0.0	1.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0
## 4	0.5	0.0	0.5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0
## 5	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.5	2.5	0.0	0.0
## 6	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 7	0.0	0.0	0.0	0.0	0.0	1	0.5	0.0	0.0	0.0	0.0	3.5	0.5	0.0
## 8	1.0	0.5	0.5	0.5	0.0	0	1.0	0.0	0.0	0.0	0.0	0.5	0.0	1.0

## 9	0.5	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
## 10	2.0	0.0	0.0	0.0	0.5	0	0.5	0.0	0.0	0.0	0.0	0.0	1.0	0.0
## 11	1.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 12	0.0	0.0	0.0	1.0	2.0	0	0.0	0.0	0.0	0.0	3.0	0.0	0.0	0.0
## 13	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	1.0	0.0	1.0	1.0	0.0	0.0
## 14	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 15	0.5	0.5	0.0	0.0	0.0	0	0.5	0.0	0.0	0.0	0.5	1.0	0.5	0.0
## 16	0.0	0.0	1.0	0.0	0.0	0	1.0	0.0	0.0	0.0	1.0	1.0	1.0	0.0
## 17	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	2.0	2.0	0.0
## 18	0.0	0.0	0.0	0.0	1.0	0	0.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0
## 19	0.0	0.0	0.0	0.0	0.0	0	0.5	0.0	0.5	0.5	0.0	1.5	0.5	0.0
## 20	0.0	0.0	0.0	0.0	0.0	0	0.5	0.0	0.0	0.0	0.5	2.0	0.5	0.0
## 21	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.5	2.5	0.0	0.0
## 22	0.0	0.0	1.5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 23	0.0	0.0	1.5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 24	0.5	0.0	1.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0
## 25	0.5	0.0	2.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0
## 26	0.0	0.0	1.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 27	0.5	0.5	3.0	0.0	0.0	0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	1.0
## 28	0.5	1.0	1.5	0.0	0.0	0	0.5	1.0	0.0	0.0	0.0	0.0	0.0	0.0
## 29	0.5	0.0	1.0	0.0	0.0	0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0
## 30	0.5	0.0	1.5	0.0	0.0	0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.5
## 31	1.5	0.0	2.5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 32	1.0	0.0	2.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 33	0.0	0.0	0.5	0.0	1.0	0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0
## 34	0.0	0.0	0.5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.5	0.5	0.0
## 35	0.0	0.0	1.5	0.0	0.5	0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0
## 36	1.0	0.0	0.5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.5	1.0	1.0	0.0
## 37	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0
## 38	0.5	0.0	0.5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
## 39	0.5	0.5	0.5	0.0	0.5	0	0.0	0.0	0.0	0.0	0.0	2.5	0.0	0.0
## 40	0.0	0.0	0.0	0.0	0.0	0	0.5	0.0	0.0	0.0	0.0	1.5	0.0	0.0
##	grca	hawo	heth	howa	modo	noca	oven	piwa	piwo	rbgr	rbnu	revi	rphe	rsha
## 1	0.0	0.5	0.5	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	1.5	0.0	0.0
## 2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0
## 3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
## 4	0.5	0.5	0.0	0.0	0.0	0.5	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.5
## 5	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.5	0.0	0.0	0.0	0.0	0.0	1.0
## 6	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 7	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0
## 8	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 9	0.0	1.0	0.0	0.0	0.5	1.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0
## 10	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0
## 11	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 12	0.0	1.0	0.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0
## 13	0.0	2.0	1.0	1.0	1.0	1.0	0.0	0.0	2.0	0.0	0.0	2.0	0.0	0.0
## 14	0.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 15	0.5	0.5	0.0	0.5	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 16	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 17	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
## 18	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0
## 19	1.0	0.0	0.0	1.0	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 20	0.0	0.0	0.0	0.0	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 21	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.5	0.0	0.0	0.0	0.0	0.0	1.0

## 22	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0
## 23	0.0	0.0	0.5	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 24	0.0	0.5	0.0	0.0	0.0	0.0	0.5	0.0	0.5	0.0	0.5	0.0	0.5	0.0
## 25	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 26	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
## 27	0.0	0.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 28	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 29	0.0	0.0	0.0	0.0	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0
## 30	0.0	0.5	1.0	0.0	0.0	0.0	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0
## 31	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0
## 32	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.5	0.0	0.0	0.0	0.0
## 33	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
## 34	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 35	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0
## 36	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0
## 37	0.5	0.0	0.5	0.0	0.5	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 38	1.0	0.5	0.5	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0
## 39	0.0	0.0	0.0	0.0	0.0	0.5	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
## 40	0.0	0.5	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.5	0.5	0.0	0.0
##	rtha	rthu	scju	scta	sovi	veer	wbnu	wewa	witu	wiwr	woth	ysfl	ytvi	
## 1	0.0	0.0	0	1.5	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.5	
## 2	0.0	0.0	0	2.0	1.0	0.0	2.0	0.0	0.0	0.0	1.0	0.0	0.0	
## 3	1.0	0.0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 4	0.0	0.0	0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 5	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	
## 6	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 7	0.0	0.0	0	0.5	0.0	0.5	0.5	0.0	0.0	0.0	0.0	0.0	0.0	
## 8	0.0	0.0	0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 9	0.0	0.0	0	1.0	0.0	0.0	1.5	0.0	0.0	0.0	0.5	0.0	0.5	
## 10	0.0	0.0	0	0.0	0.0	0.0	0.0	0.5	1.0	0.0	0.5	1.5	0.0	
## 11	0.0	0.0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 12	0.0	0.0	0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	
## 13	0.0	0.0	0	1.0	1.0	3.0	2.0	1.0	0.0	0.0	0.0	0.0	0.0	
## 14	0.0	0.0	1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 15	0.0	0.0	0	0.5	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	
## 16	0.0	0.0	0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 17	0.0	0.0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	
## 18	0.0	0.5	0	1.5	1.5	0.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0	
## 19	0.0	0.0	0	0.5	0.5	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 20	0.0	0.0	0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	
## 21	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	
## 22	0.0	0.0	0	0.5	1.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 23	0.0	0.0	0	0.0	1.0	0.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0	
## 24	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 25	0.0	0.0	0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 26	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	0.0	0.0	
## 27	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 28	0.5	0.0	0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 29	0.0	0.0	0	0.5	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	
## 30	0.0	0.0	0	1.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 31	0.0	0.0	0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	
## 32	0.0	0.0	0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
## 33	0.0	0.0	0	0.5	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	
## 34	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

```
## 35 0.0 0.0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
## 36 0.0 0.0 0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
## 37 0.0 0.0 0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
## 38 0.0 0.0 0 0.5 0.0 0.5 0.0 0.0 0.5 0.0 0.5 0.0 0.0
## 39 0.0 0.0 0 0.0 0.0 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0
## 40 0.0 0.0 0 0.0 0.0 0.0 0.5 0.0 0.0 0.0 0.0 0.0 0.0
```

```
## est.rich
```

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

```
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
```

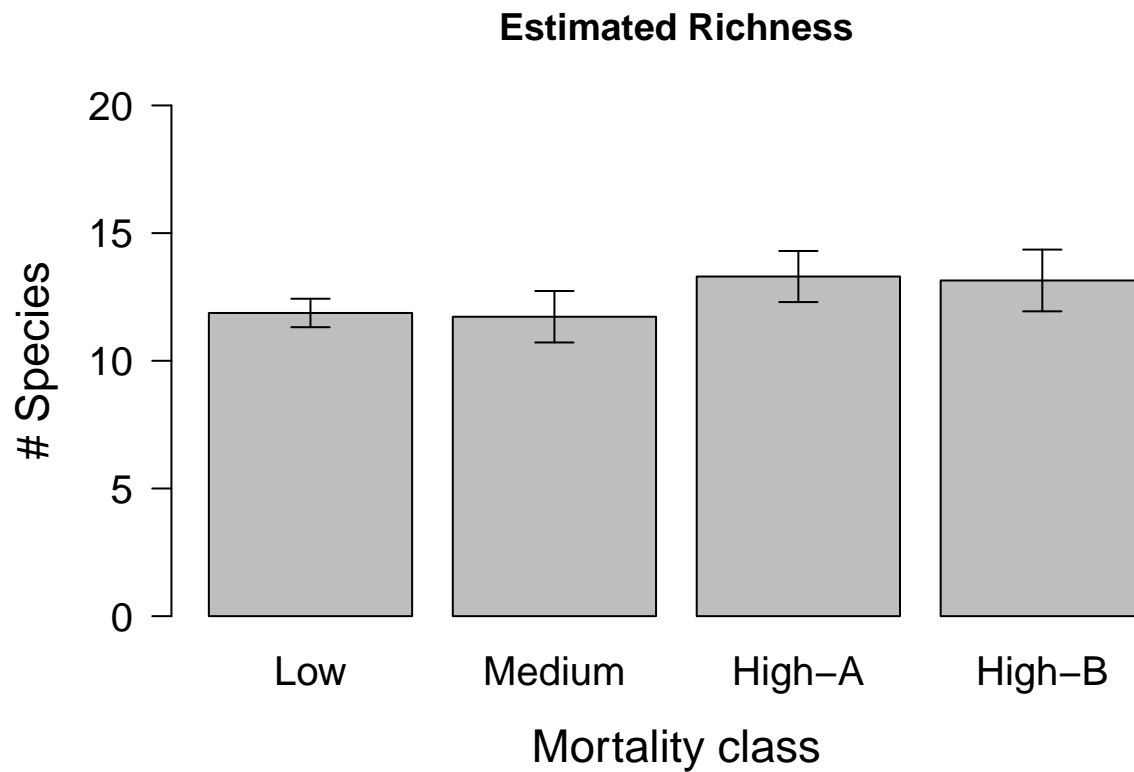
```
## [1] Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-A Hi-B Hi-B Hi-B Hi-B
## [15] Hi-B Hi-B Hi-B Hi-B Hi-B Hi-B Hi-B Low Low Low Low Low Low Low
## [29] Low Low Low Low Med Med Med Med Med Med Med Med
## Levels: Low Med Hi-A Hi-B
```

```
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)
```

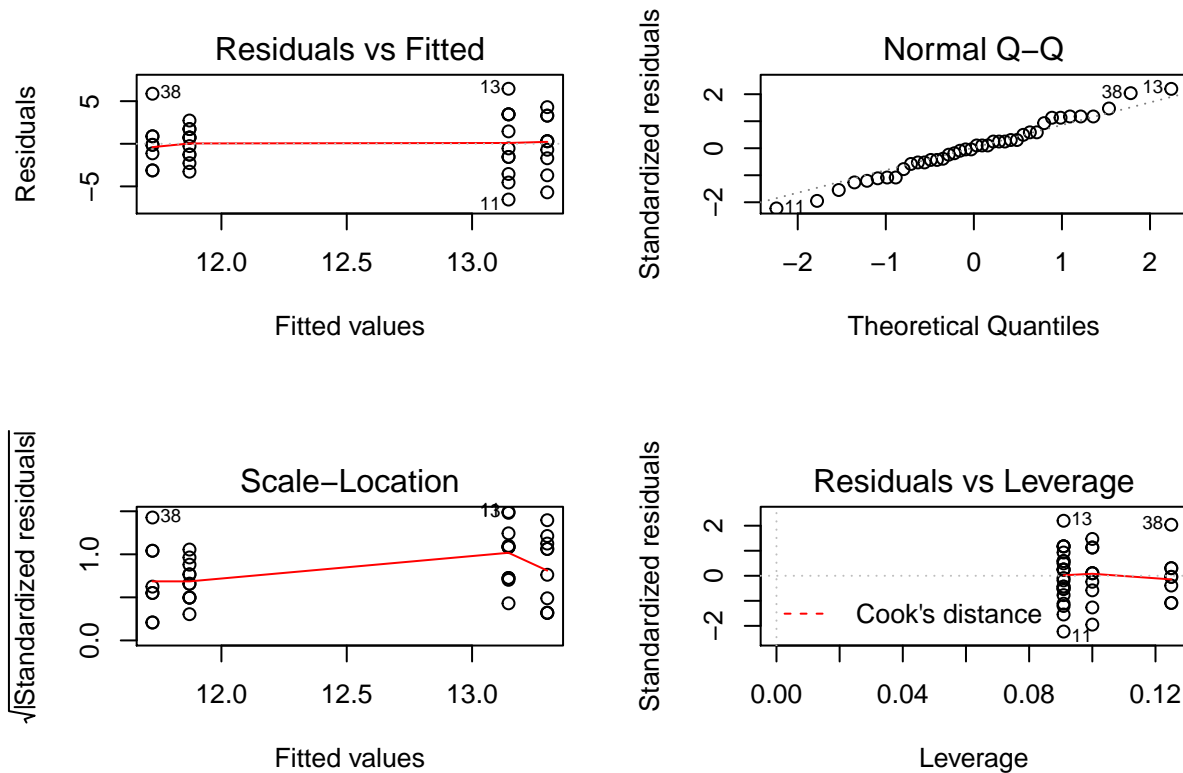
```
##           Df Sum Sq Mean Sq F value Pr(>F)
## mortality   3   20.0   6.672   0.703  0.557
## Residuals  36  341.9   9.497
```



```
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

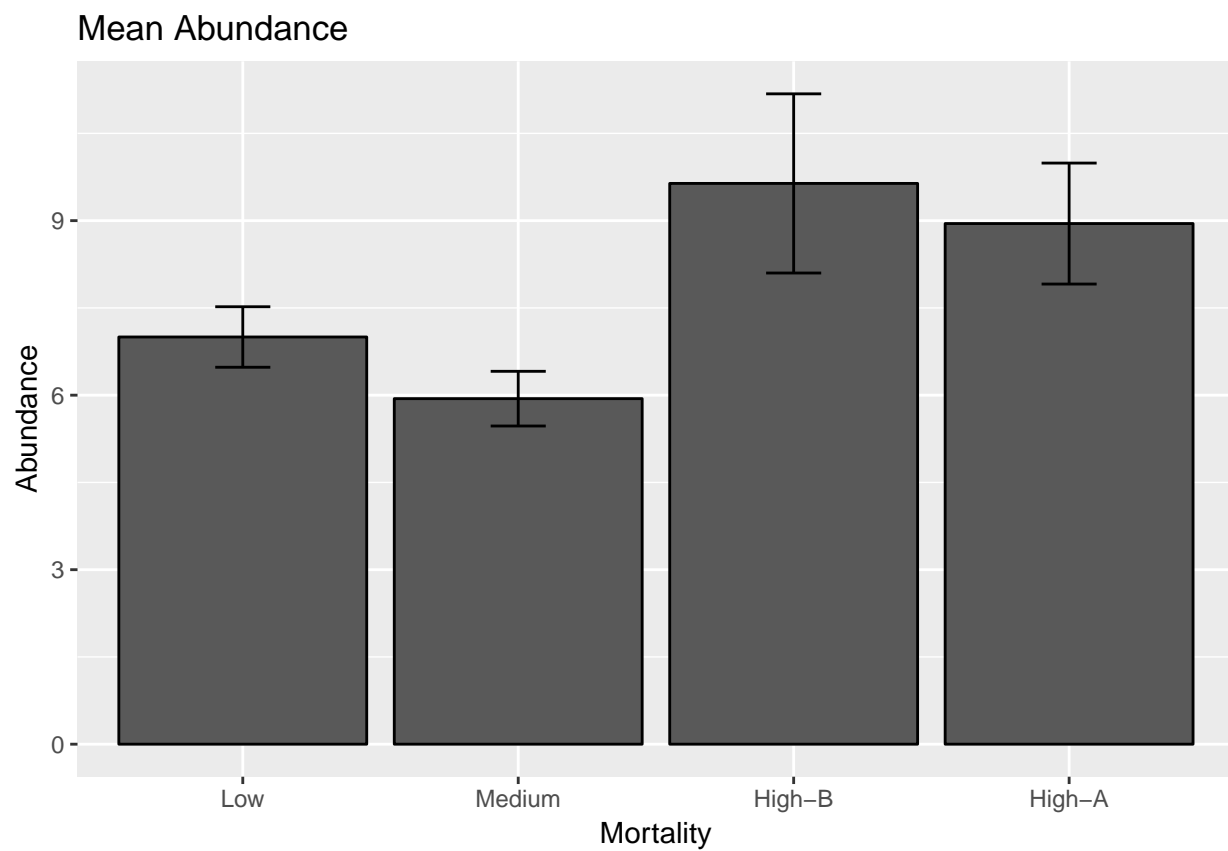
```
MeanAbundMort <- read.csv("MortalityMeanAbund.csv")
```

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")
```

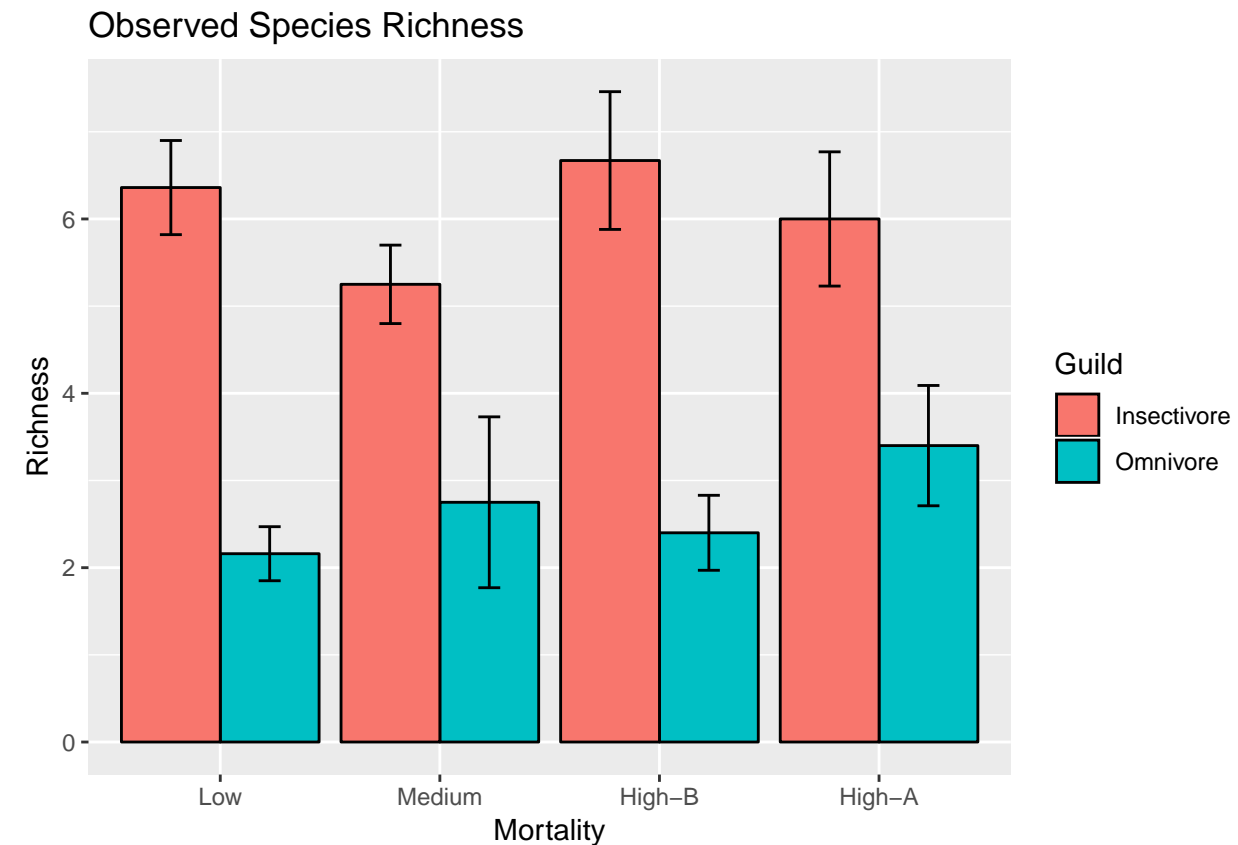
```
Spec.Rich.Guilds <- read.csv("GuildsClusteredRich.csv")
```

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=Richness - 1, ymax=Richness + 1))
```



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
```

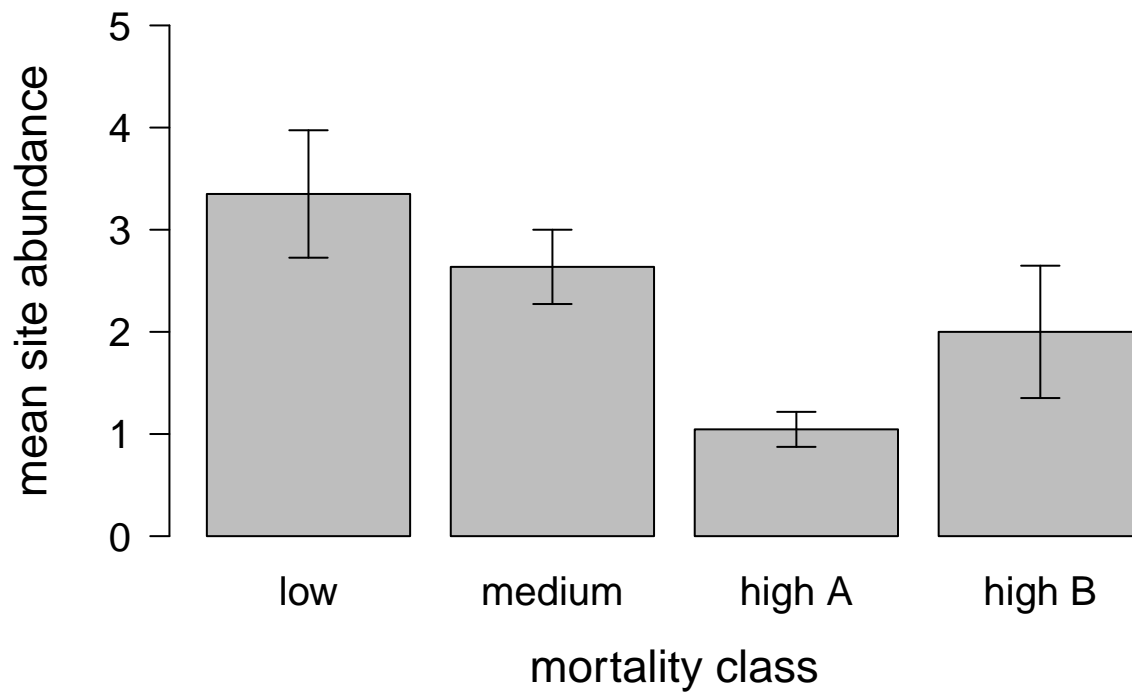
```
Insectivores.SE <- tapply(Guilds$Ins_29, Guilds$mortality.class, sem)
Insectivores.SE
```

```
##      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"))

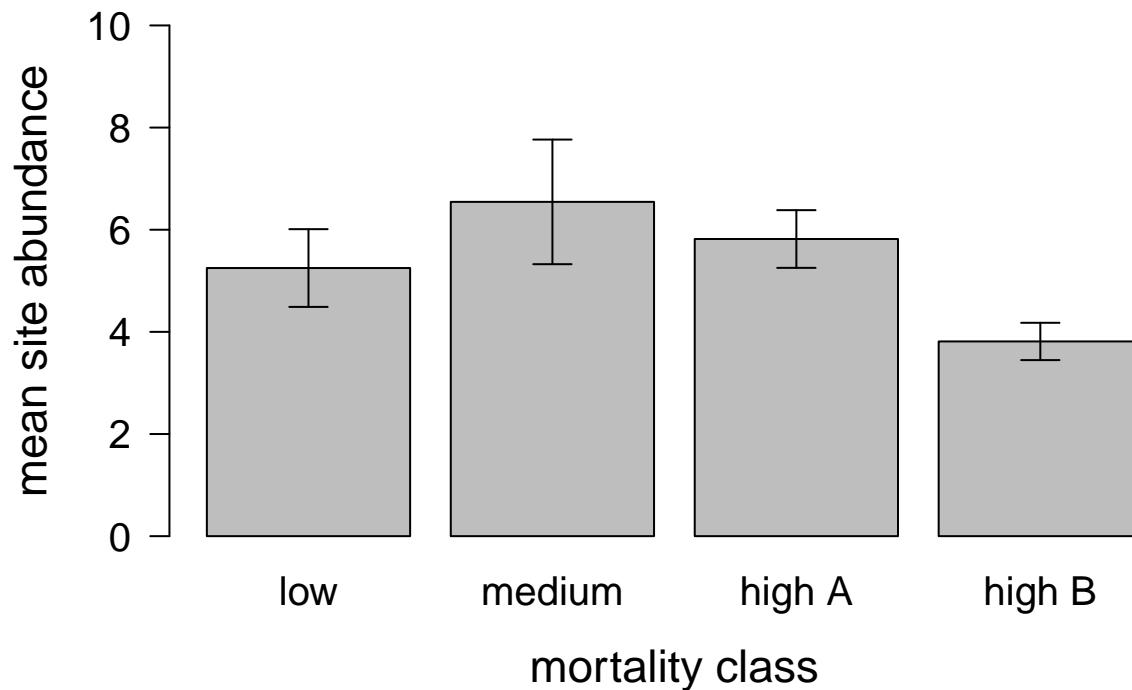
arrows(x0 = OmnivorePlot, y0 = Omnivores.Mean, y1 = Omnivores.Mean - Omnivores.SE, angle = 90,
  length = 0.1, lwd = 1)
arrows(x0 = OmnivorePlot, y0 = Omnivores.Mean, y1 = Omnivores.Mean + Omnivores.SE, angle = 90,
  length = 0.1, lwd = 1)
```



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
```

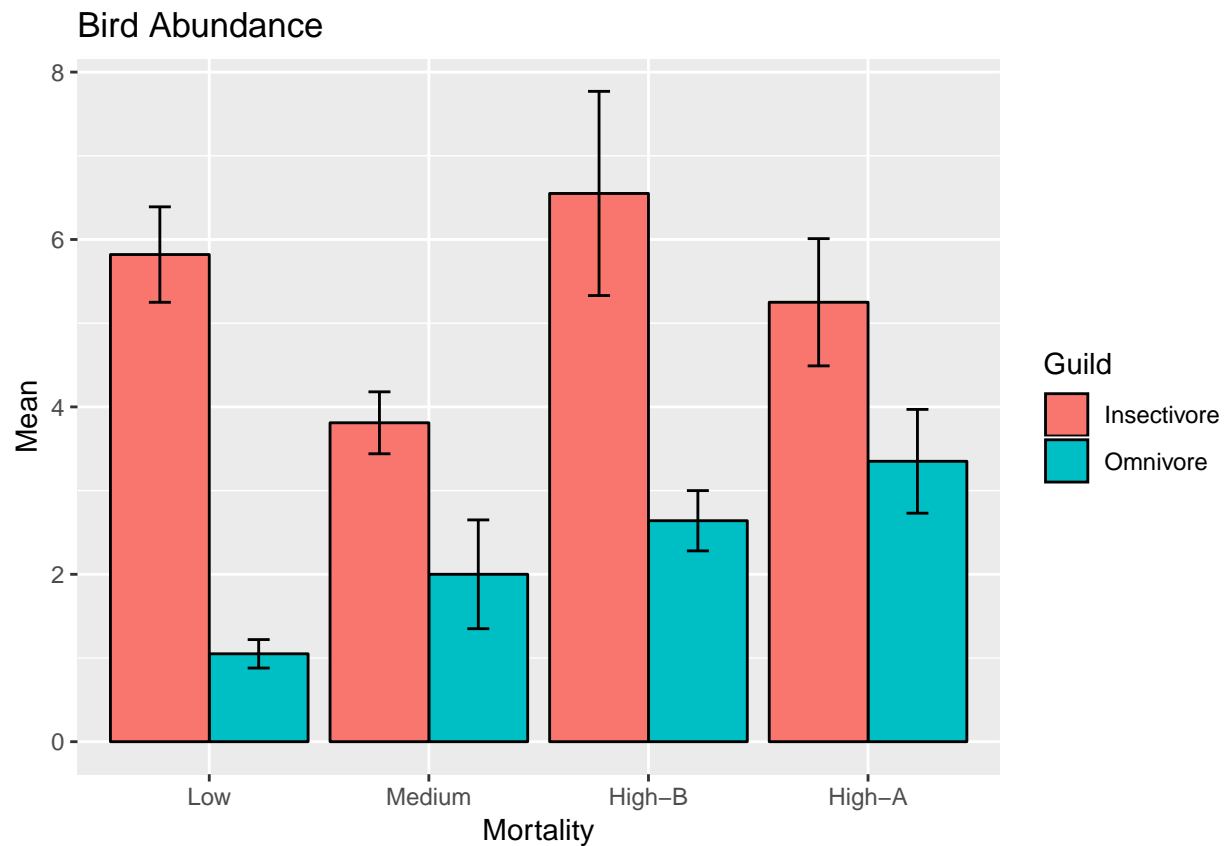
```
str(ClusteredBar)
```

```
## '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
```