

# GRSM wildfire and bird species diversity and richness

```
# Load all libraries that will be used during analysis
library(readr)
library(tidyverse)
library(vegan)
library(stringr)
library(ggplot2)
library(FSA)

# Import all bird and per_plot data
june_16 <- read_csv("NEON.D07.GRSM.DP1.10003.001.brd_countdata.2016-06.expanded.20180418T200555Z.csv")
may_17 <- read_csv("NEON.D07.GRSM.DP1.10003.001.brd_countdata.2017-05.expanded.20180418T200734Z.csv")
june_17 <- read_csv("NEON.D07.GRSM.DP1.10003.001.brd_countdata.2017-06.expanded.20180418T200639Z.csv")
may_18 <- read_csv("NEON.D07.GRSM.DP1.10003.001.brd_countdata.2018-05.expanded.20181206T143246Z.csv")

#####
# DATA MANIPULATION
#####

# Combine all date from both years into one bird file
# Then add a column for year from startDate
brd_dat_all <- bind_rows(june_16, june_17, may_17, may_18)
brd_dat_all$Year <- str_sub(brd_dat_all$startDate, 1, 4)

# Filter plotID values to include only plots that were sampled
# before and after the fire
brd_dat <- filter(brd_dat_all, plotID %in% c("GRSM_001", "GRSM_002", "GRSM_003", "GRSM_004",
      "GRSM_006", "GRSM_007", "GRSM_010", "GRSM_013", "GRSM_015", "GRSM_020"))

# Convert plotID and taxonID to factors
brd_dat$plotID <- as.factor(brd_dat$plotID)
brd_dat$taxonID <- as.factor(brd_dat$taxonID)

# Remove columns where targetTaxaPresent = N
# No data associated with them
brd_dat <- filter(brd_dat, targetTaxaPresent=="Y")

#####
# CREATE DATA INPUT FOR VEGAN
#####

# First filter by year to get the pre- and post-burn datasets separate
bird_16 <- filter(brd_dat, Year==2016)
bird_17 <- filter(brd_dat, Year==2017)
bird_18 <- filter(brd_dat, Year==2018)

# Then create a matrix of plotID by species using the piping function (%>%)
# to carry out multiple steps at a time using the date in the step before

# Number of each species detected per plot in 2016
brd_matrix_16 <- bird_16 %>% group_by(plotID, taxonID) %>%
```

```

summarise(count=n()) %>%
spread(taxonID,count)

# Convert NAs to 0
brd_matrix_16[is.na(brd_matrix_16)] <- 0

# Vegan package does not like first column of plotID, so get rid of it!
brd_matrix_16 <- brd_matrix_16[,-1]

# Look at it - does it look ok?
brd_matrix_16

## # A tibble: 10 x 56
##   ACFL AMCR AMGO AMRO BADO BAWW BEKI BGGN BHCO BHVI BLJA BRTH
##   <int> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <int> <dbl> <dbl>
## 1     3     3     0     0     0     1     0     5     1     5     1     0
## 2     1     7     1     0     0     5     0     1     0     4     1     0
## 3     1     2     0     1     0     6     0     0     0    10     0     0
## 4     9     3     0     9     0     0     1     3     1    15     3     1
## 5     4     8     4     0     0     3     0     1     0     6     0     0
## 6     1     4     1     3     0     6     0     1     0     4     1     0
## 7     7     6     1     0     0     0     0     0     0     5     1     0
## 8     6     4     4     0     0     0     0     1     0     4     0     0
## 9     1     3     1     0     0     3     0     2     0     2     8     0
## 10    1     0     0     0     2     0     0     1     0     5     1     0
## # ... with 44 more variables: BTBW <dbl>, BTNW <dbl>, BWHA <dbl>,
## #   CACH <int>, CARW <dbl>, CEDW <dbl>, CHSP <dbl>, CHSW <dbl>,
## #   COGR <dbl>, DOWO <dbl>, EAPH <dbl>, EASO <dbl>, EATO <dbl>,
## #   EAWP <dbl>, GBHE <dbl>, HAWO <dbl>, HOWA <int>, INBU <dbl>,
## #   KEWA <dbl>, LOWA <dbl>, NOCA <dbl>, NOPA <dbl>, OVEN <dbl>,
## #   PIWA <dbl>, PIWO <dbl>, RBNU <dbl>, RBWO <dbl>, REVI <int>,
## #   RTHA <dbl>, RTHU <dbl>, RUGR <dbl>, SCTA <dbl>, SOVI <dbl>,
## #   SUTA <dbl>, TUTI <int>, UNBI <int>, UNWA <int>, UNWO <dbl>,
## #   UPCH <dbl>, WBNU <dbl>, WEWA <dbl>, WOTH <dbl>, YBCU <dbl>, YTWA <dbl>

# Repeat previous steps for 2017 and 2018 data
brd_matrix_17 <- bird_17 %>% group_by(plotID, taxonID) %>%
  summarise(count=n()) %>%
  spread(taxonID,count)
brd_matrix_17[is.na(brd_matrix_17)] <- 0
brd_matrix_17 <- brd_matrix_17[,-1]
brd_matrix_17

## # A tibble: 10 x 55
##   ACFL AMCR AMGO AMRO AMWO BADO BAWW BGGN BHCO BHVI BLJA BTNW
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <int> <dbl> <dbl> <int> <dbl> <int>
## 1     4     2     2     0     0     0     6     2     0     3     1    11
## 2     1     1     6     0     0     0     6     1     1     2     0    14
## 3     0     3     1     1     0     1     4     1     4    12     7    16
## 4    14     1     5     7     1     1     1     3     0     5     0     6
## 5     2     4     4     0     0     0     6     5     1     3     2     3
## 6     0     3     4     2     0     0     6     0     3     9     1     6
## 7     5     3     0     0     0     0     5     4     0     3     0    14

```

```
## 8      4      2      3      0      0      0      1      1      0      4      3      4
## 9      2      5      1      1      0      0      2      2      1      8      2     17
## 10     0      0      0      0      0      0      3      0      1      3      1     20
## # ... with 43 more variables: BWAH <dbl>, CACH <dbl>, CARW <dbl>,
## #   CEDW <dbl>, CHSP <dbl>, CHSW <dbl>, DOWO <dbl>, EABL <dbl>,
## #   EAPH <dbl>, EATO <dbl>, EAWP <dbl>, GCFL <dbl>, HAWO <dbl>,
## #   HOWA <dbl>, INBU <dbl>, LOWA <dbl>, NOCA <dbl>, NOFL <dbl>,
## #   NOPA <dbl>, OVEN <dbl>, PIWA <dbl>, PIWO <dbl>, RBNU <dbl>,
## #   RBWO <dbl>, RECR <dbl>, REVI <int>, RTHU <dbl>, SCTA <int>,
## #   SOVI <dbl>, TUTI <int>, UNBI <dbl>, UNNU <dbl>, UNTA <dbl>,
## #   UNWA <int>, UNWO <dbl>, WBNU <dbl>, WEVI <dbl>, WEWA <dbl>,
## #   WITU <dbl>, WOTH <dbl>, YBCU <dbl>, YTVI <dbl>, YTWA <dbl>
```

```
brd_matrix_18 <- bird_18 %>% group_by(plotID, taxonID) %>%
  summarise(count=n()) %>%
  spread(taxonID, count)
brd_matrix_18[is.na(brd_matrix_18)] <- 0
brd_matrix_18 <- brd_matrix_18[, -1]
brd_matrix_18
```

```
## # A tibble: 10 x 49
##   ACFL AMCR AMGO AMRO BAWW BGGN BHCO BHVI BLJA BTBW BTNW CACH
##   <dbl> <dbl> <dbl> <dbl> <int> <dbl> <dbl> <dbl> <dbl> <dbl> <int> <int>
## 1     2     0     0     0     2     2     0     2     1     0     5     4
## 2     0     3     2     1     4     0     0     0     0     0     5     1
## 3     0     0     0     0     3     0     0     3     0     3     6     1
## 4     6     1     2     3     1     4     2     3     1     0     3     3
## 5     1     4     2     0     2     1     0     4     0     0     4     5
## 6     0     0     1     0     6     2     0     3     0     0     3     1
## 7     3     1     0     0     1     1     0     1     0     0    10     3
## 8     0     0     1     0     4     1     0     3     1     0     3     2
## 9     1     2     0     0     1     1     0     1     0     0     7     2
## 10    0     0     0     0     2     0     0     0     1     0    13     1
## # ... with 37 more variables: CARW <dbl>, CEDW <dbl>, CHSW <dbl>,
## #   DEJU <dbl>, DOWO <dbl>, EABL <dbl>, EAPH <dbl>, EATO <dbl>,
## #   EAWP <dbl>, FISP <dbl>, GCKI <dbl>, HAWO <dbl>, HOWA <int>,
## #   INBU <dbl>, LOWA <dbl>, MODO <dbl>, NOCA <dbl>, NOFL <dbl>,
## #   NOPA <dbl>, OVEN <dbl>, PIWA <dbl>, PIWO <dbl>, RBWO <dbl>,
## #   REVI <int>, RTHU <dbl>, SCTA <dbl>, SWTH <dbl>, TUTI <int>,
## #   UNBI <dbl>, UNWO <dbl>, WBNU <dbl>, WEWA <dbl>, WITU <dbl>,
## #   WOTH <dbl>, YBCU <dbl>, YTVI <dbl>, YTWA <dbl>
```

```
# Now we are ready to calculate some diversity indices for each plot
# http://cc.oulu.fi/~jarioksa/softhelp/vegan/html/diversity.html
```

```
# Calculate shannon diversity and richness for each plot in each year
shd_16 <- diversity(brd_matrix_16, index = "shannon", MARGIN = 1, base = exp(1))
shd_17 <- diversity(brd_matrix_17, index = "shannon", MARGIN = 1, base = exp(1))
shd_18 <- diversity(brd_matrix_18, index = "shannon", MARGIN = 1, base = exp(1))

rich_16 <- specnumber(brd_matrix_16, MARGIN = 1)
rich_17 <- specnumber(brd_matrix_17, MARGIN = 1)
rich_18 <- specnumber(brd_matrix_18, MARGIN = 1)
```

```
#####
# Create dataset for running ANOVA to test hypotheses about
# changes in richness or diversity pre- and post-fire
#####

# Create a new dataframe for each year (x_16 and x_17) with the above vectors from vegan
# and a few more created below. Make the column names the same in both data frames so
# we can combine them
plotID <- c("GRSM_001","GRSM_002","GRSM_003","GRSM_004","GRSM_006","GRSM_007",
            "GRSM_010","GRSM_013","GRSM_015", "GRSM_020")
burn <- c("y","n","y","n","n","y","n","n","n","n")
year <- rep(2016, 10)
year2 <- rep(2017, 10)
year3 <- rep(2018, 10)
x_16 <- data.frame(plotID, year, burn, shd_16, rich_16)
#make the column names the same in both so we can combine
colnames(x_16)<- c("plotID","year","burn","shd", "rich")
x_17 <- data.frame(plotID, year2, burn, shd_17, rich_17)
colnames(x_17)<- c("plotID","year", "burn","shd", "rich")
x_18 <- data.frame(plotID, year3, burn, shd_18, rich_18)
colnames(x_18)<- c("plotID","year", "burn","shd", "rich")

#combine x_16 and x_17 and x_18 into one dataframe and make year a factor
x <- bind_rows(x_16, x_17, x_18)
x$year <- as.factor(x$year)

# Run ANOVA to see if treatment (burn), year, or an interaction of burn and year affect
# richness and shannon diversity
fit_rich <- aov(rich ~ burn*year, x)
summary(fit_rich)
```

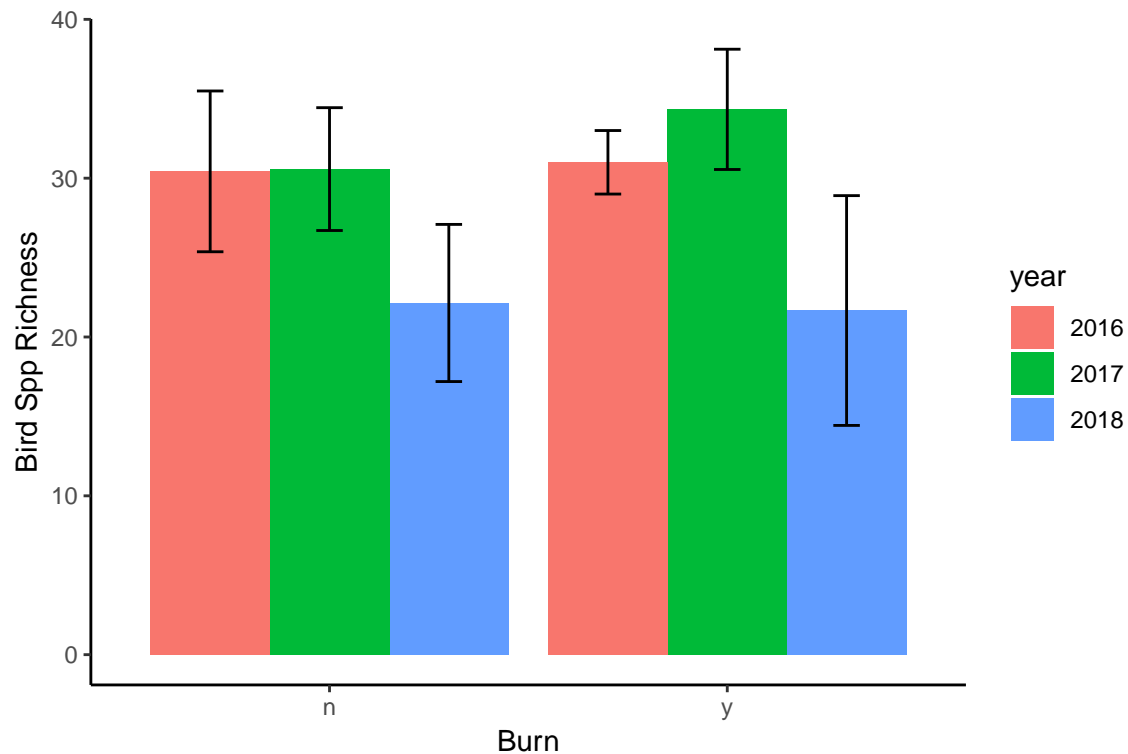
```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## burn       1   10.4    10.41    0.470 0.49949
## year       2  564.2   282.10   12.735 0.00017 ***
## burn:year   2   20.5    10.23    0.462 0.63552
## Residuals  24  531.6    22.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
fit_shd <- aov(shd ~ burn*year, x)
summary(fit_shd)
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## burn      1  0.0005   0.0005    0.007 0.9336
## year      2  0.6594   0.3297    4.825 0.0173 *
## burn:year  2  0.0157   0.0079    0.115 0.8917
## Residuals 24  1.6401   0.0683
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#to calculate Standard Deviation of estimates
rich_means <- Summarize(rich ~ burn + year, data=x)
diversity_means <- Summarize(shd ~ burn + year, data=x)
```

```
# Plot the data to visualize differences
ggplot(rich_means, aes(x=burn, y=mean, fill=year))+
  geom_bar(stat="identity", position=position_dodge()) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=0.2, position=position_dodge(0.9))+
  xlab("Burn") +
  ylab("Bird Spp Richness")+
  theme_classic()
```



```
ggplot(quality_means, aes(x=burn, y=mean, fill=year)) +
  geom_bar(stat="identity", position=position_dodge()) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=0.2, position=position_dodge(0.9)) +
  xlab("Burn") +
  ylab("Bird Spp Diversity") +
  theme_classic()
```

