```
## Example R script for reproducible analysis

### Analysis of change in Pileated woodpecker abundance versus habitat
#### and variation over time (2000,2005, 2010)

### Script written 11/21/2017
### by Nathan Brouwer brouwern@gmail.com

# This is a bare-bones script to carry out the creation of the dataframe and begin the regression/ANOVA analysis.
# To be complete this script MUST have additional comment added.  Please see the associated vignette
#  in the widlifeR package for more infomation.

#load devtools
library(devtools)

#download wildlifeR from github
install_github("brouwern/wildlifeR")

#load wildlifeR into your current R sessions
library(wildlifeR)

### The USGS BBS data
data(BBS_PA)

### Selecting a focal bird species
#### Determining the numeric species code

data(AOU_species_codes)

library(dplyr)

AOU_species_codes %>% filter(alpha.code == "PIWO")

BBS_PA_PIWO <- BBS_PA %>% filter(Aou == "4050")

### Selecting a focal analysis question
### Formatting data for habitat analyses

#### Subsetting bird data
BBS_PA_PIWO_2 <- BBS_PA_PIWO %>% filter(Year == 2006)

#### Preparing habitat data
data(BBS_PA_landcover_1km)


BBS_PA_landcover_1km_2 <- BBS_PA_landcover_1km %>%
 select(Route, NLCD.41, NLCD.42, NLCD.43, SUM)



#### Calculating percentages of habitat
BBS_PA_landcover_1km_2$decid.percent <- BBS_PA_landcover_1km_2$NLCD.41/BBS_PA_landcover_1km_2$SUM

BBS_PA_landcover_1km_2$conifer.percent <- BBS_PA_landcover_1km_2$NLCD.42/BBS_PA_landcover_1km_2$SUM

BBS_PA_landcover_1km_2$mixed.forest.percent <- BBS_PA_landcover_1km_2$NLCD.42/BBS_PA_landcover_1km_2$SUM


#### Merging bird counts and habitat cover
```

```
BBS_PA_PIWO_3 <- full_join(BBS_PA_PIWO_2 ,
                 BBS_PA_landcover_1km_2,   by = "Route")

#### Filling in columns
BBS_PA_PIWO_3$Year <- 2006
BBS_PA_PIWO_3$Aou <- 6080
BBS_PA_PIWO_3$name <- "PIWO"

#### Filling in NAs
BBS_PA_PIWO_4 <- NA_to_zero(dat = BBS_PA_PIWO_3,
column = "SpeciesTotal")

#compare output
#with NAs
summary(BBS_PA_PIWO_3$SpeciesTotal)

#with NAs removed by set_NA_SpeciesTotal_to_zero()
summary(BBS_PA_PIWO_4$SpeciesTotal)

## Save data
write.csv(BBS_PA_PIWO_4, file = "PIWO_vs_forest_cover.csv")

### Formatting data for analysis of change over time
library(Hmisc)

PIWO_00_05_10 <- sample_BBS_routes(dat = BBS_PA_PIWO,
        years = c(2000,2005,2010), aou.code = 4050)

library(ggplot2)
library(ggpubr)

#### Plot
ggerrorplot(data = PIWO_00_05_10,
y = "SpeciesTotal",
x = "Year",
desc_stat = "mean_ci")


### save
write.csv(PIWO_00_05_10, file = "PIWO_00_05_10.csv")

## Data Exploration
### Exploring abundance-habitat data

#### Boxplots

## number of birds seen
plot1.spp.total <- ggboxplot(data = BBS_PA_PIWO_4,
  y = "SpeciesTotal",   xlab = "")

## Deciduous landcover
plot2.decid.percent <- ggboxplot(data = BBS_PA_PIWO_4,
  y = "decid.percent", xlab = "")

## Coniferous landcover
plot3.confir.percent <- ggboxplot(data = BBS_PA_PIWO_4,
  y = "conifer.percent", xlab = "")
```

```
## Mixed forest landcover
plot4.mixed.percent <- ggboxplot(data = BBS_PA_PIWO_4,
  y = "mixed.forest.percent", xlab = "")

###
library(cowplot)

plot_grid(plot1.spp.total,  plot2.decid.percent,
        plot3.confir.percent, plot4.mixed.percent,
     labels = c("A", "B","C","D"))

#### Histograms
## number of birds seen
plot1.spp.total <- gghistogram(data = BBS_PA_PIWO_4,
              x = "SpeciesTotal", xlab = "")

## Deciduous landcover
plot2.decid.percent <- gghistogram(data = BBS_PA_PIWO_4,
                x = "decid.percent", xlab = "")

## Coniferous landcover
plot3.confir.percent <- gghistogram(data = BBS_PA_PIWO_4,
               x = "conifer.percent", xlab = "")

## Mixed forest landcover
plot4.mixed.percent <- gghistogram(data = BBS_PA_PIWO_4,
               x = "mixed.forest.percent", xlab = "")

## Layout the four plots in a grid.
library(cowplot)

plot_grid(plot1.spp.total,  plot2.decid.percent,
     plot3.confir.percent,  plot4.mixed.percent,
     labels = c("A", "B", "C","D"))

#### Scatter plot
library(ggplot2)
library(ggpubr)

ggscatter(data = BBS_PA_PIWO_4,
     y = "SpeciesTotal", x = "conifer.percent") +
     geom_smooth(se = FALSE)


### Exploring abudance-time data

#### Boxplot
ggboxplot(data = PIWO_00_05_10,
     y = "SpeciesTotal", x = "Year")

#### Histograms
gghistogram(data = PIWO_00_05_10,
     x = "SpeciesTotal", facet.by = "Year")

#### Plotting means and error bars
ggerrorplot(data = PIWO_00_05_10,
     y = "SpeciesTotal", x = "Year",
     desc_stat = "mean_ci")
```

```
## Data modeling
### Modeling habitat

m.null    <- lm(SpeciesTotal ~ 1, BBS_PA_PIWO_4)
m.decid  <- lm(SpeciesTotal ~ decid.percent, BBS_PA_PIWO_4)
m.mixed  <- lm(SpeciesTotal ~ mixed.forest.percent, BBS_PA_PIWO_4)


### Present results
#### Regression summary
library(broom)
tidy(m.null)
tidy(m.decid)
tidy(m.mixed)

#### Significance test
anova(m.null, m.decid)
anova(m.null, m.mixed)


#### Model comparison
library(bbmle)
AICtab(m.null, m.decid, m.mixed)


### Modeling variation over time
PIWO_00_05_10$Year <- factor(PIWO_00_05_10$Year)
m.time.null <- lm(SpeciesTotal ~ 1 , data = PIWO_00_05_10)
m.time.year <- lm(SpeciesTotal ~ Year , data = PIWO_00_05_10)

### Regression summary
library(broom)
tidy(m.time.null)
tidy(m.time.year)

### Model comparison
library(bbmle)
AICtab(m.time.null,  m.time.year)

### Multiple comparisons
#### Refit model w/aov()
m.time.year.aov <- aov(SpeciesTotal ~ Year , data = PIWO_00_05_10)


TukeyHSD(m.time.year.aov)

tukey.out <- TukeyHSD(m.time.year.aov)

plotTukeysHSD(tukey.out)
```