Evaluating bee habitat provisioning within agricultural landscapes

Morgan Mackert

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View the bee data.

## Date Site TotalBees   
## 5/12/2016: 2 Bowman : 5 Min. : 0.00   
## 5/15/2016: 2 Cretsinger: 5 1st Qu.: 21.50   
## 5/18/2016: 2 Kaldenberg: 5 Median : 41.50   
## 5/19/2016: 2 McClellan : 5 Mean : 65.67   
## 5/22/2016: 2 Peckumn : 5 3rd Qu.: 68.25   
## 5/29/2016: 2 Plunkett : 5 Max. :434.00   
## (Other) :28 (Other) :10

View the plant data.

## Date Site TotalPlants   
## 5/12/2016: 2 Bowman : 5 Min. : 0.0   
## 5/15/2016: 2 Cretsinger: 5 1st Qu.: 1.0   
## 5/18/2016: 2 Kaldenberg: 5 Median : 2.0   
## 5/19/2016: 2 McClellan : 5 Mean : 3.5   
## 5/22/2016: 2 Peckumn : 5 3rd Qu.: 6.0   
## 5/29/2016: 2 Plunkett : 5 Max. :13.0   
## (Other) :28 (Other) :10

Use "lubridate" to fix date formats in both bee and plant data.

library(lubridate)

##   
## Attaching package: 'lubridate'

## The following object is masked from 'package:base':  
##   
## date

simplebees$Date <- mdy(simplebees$Date)  
simpleplants$Date <- mdy(simpleplants$Date)

Add column to simplebees and simpleplants denoting which taxon group they belong to.

simplebees$Taxa <- "Bees"  
simpleplants$Taxa <- "Plants"

Name columns appropriately.

names(simplebees) <- c("Date", "Site", "TotalBees", "Taxa")  
names(simpleplants) <- c("Date", "Site", "TotalPlants", "Taxa")  
head(simplebees)

## Date Site TotalBees Taxa  
## 1 2016-05-03 Plunkett 11 Bees  
## 2 2016-05-03 Bowman 4 Bees  
## 3 2016-05-04 Kaldenberg 5 Bees  
## 4 2016-05-04 McClellan 0 Bees  
## 5 2016-05-12 Sheller 0 Bees  
## 6 2016-05-12 Sloan 4 Bees

head(simpleplants)

## Date Site TotalPlants Taxa  
## 1 2016-05-03 Plunkett 1 Plants  
## 2 2016-05-03 Bowman 0 Plants  
## 3 2016-05-04 Kaldenberg 0 Plants  
## 4 2016-05-04 McClellan 0 Plants  
## 5 2016-05-12 Sheller 2 Plants  
## 6 2016-05-12 Sloan 1 Plants

Aggregate by "Site" and calculate mean and standard deviation of bees collected at each site.

beesbysite <- simplebees  
beesbysitemean <- with(beesbysite, aggregate(TotalBees ~ Site, FUN = mean))  
beesbysiteSD <- with(beesbysite, aggregate(TotalBees ~ Site, FUN = sd))

Combine the two bee data frames (mean/sd), delete extra columns, and rename them.

beesbysitemeanSD <- cbind(beesbysitemean, beesbysiteSD)  
beesbysitemeanSD <- beesbysitemeanSD[,-3]  
beesbysitemeanSD$Taxa <- "Bees"  
names(beesbysitemeanSD) <- c("Site", "Mean", "SD", "Taxa")  
View(beesbysitemeanSD)

Aggregate by "Site" and calculate mean and standard deviation of plant species found at each site.

plantsbysite <- simpleplants  
plantsbysitemean <- with(plantsbysite, aggregate(TotalPlants ~ Site, FUN = mean))  
plantsbysiteSD <- with(plantsbysite, aggregate(TotalPlants ~ Site, FUN = sd))

Combine the two plant data frames (mean/sd), delete extra columns, and rename them.

plantsbysitemeanSD <- cbind(plantsbysitemean, plantsbysiteSD)  
plantsbysitemeanSD <- plantsbysitemeanSD[,-3]  
plantsbysitemeanSD$Taxa <- "Plants"  
names(plantsbysitemeanSD) <- c("Site", "Mean", "SD", "Taxa")

Use "rbind" to combine "beesbysitemeanSD" and "plantsbysitemeanSD"

bindbeesandplants <- rbind(beesbysitemeanSD, plantsbysitemeanSD)

Left with one data frame with all necessary information. Woo! Move to BeesVsPlantsAnalysisScripts.

head(bindbeesandplants)

## Site Mean SD Taxa  
## 1 Bowman 15.4 14.82565 Bees  
## 2 Cretsinger 73.4 63.02619 Bees  
## 3 Kaldenberg 61.0 63.27322 Bees  
## 4 McClellan 41.0 29.43637 Bees  
## 5 Peckumn 81.2 35.82876 Bees  
## 6 Plunkett 157.4 184.69921 Bees

tail(bindbeesandplants)

## Site Mean SD Taxa  
## 11 Kaldenberg 3.2 3.0331502 Plants  
## 12 McClellan 0.4 0.5477226 Plants  
## 13 Peckumn 5.4 4.8270074 Plants  
## 14 Plunkett 6.0 4.1833001 Plants  
## 15 Sheller 2.6 1.1401754 Plants  
## 16 Sloan 4.0 2.9154759 Plants