

Assignment 3: Data Exploration

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OVERVIEW

This exercise accompanies the lessons in Environmental Data Analytics on Data Exploration.

Directions

1. Rename this file `<FirstLast>_A03_DataExploration.Rmd` (replacing `<FirstLast>` with your first and last name).
2. Change “Student Name” on line 3 (above) with your name.
3. Work through the steps, **creating code and output** that fulfill each instruction.
4. Assign a useful **name to each code chunk** and include ample **comments** with your code.
5. Be sure to **answer the questions** in this assignment document.
6. When you have completed the assignment, **Knit** the text and code into a single PDF file.
7. After Knitting, submit the completed exercise (PDF file) to the dropbox in Sakai.

TIP: If your code extends past the page when knit, tidy your code by manually inserting line breaks.

TIP: If your code fails to knit, check that no `install.packages()` or `View()` commands exist in your code.

Set up your R session

1. Check your working directory, load necessary packages (tidyverse, lubridate), and upload two datasets: the ECOTOX neonicotinoid dataset (ECOTOX_Neonicotinoids_Insects_raw.csv) and the Niwot Ridge NEON dataset for litter and woody debris (NEON_NIWO_Litter_massdata_2018-08_raw.csv). Name these datasets “Neonics” and “Litter”, respectively. Be sure to include the subcommand to read strings in as factors.

```
#checking directory  
getwd()
```

```
## [1] "/home/guest/ENV872/maia-g/EDE_Fall2023"
```

```
#loading packages  
library(tidyverse)  
library(lubridate)
```

```
#Import datasets
```

```

###ISSUE: using the './Data/' then tab to see the options yields nothing, but it was working when I had

Neonics <- read.csv("./Data/Raw/ECOTOX_Neonicotinoids_Insects_raw.csv", stringsAsFactors = T)
Litter <- read.csv("./Data/Raw/NEON_NIWO_Litter_massdata_2018-08_raw.csv", stringsAsFactors = T)

###QUESTION: Do I still need to call these out since it is enormous?
#Neonics
#Litter

```

Learn about your system

2. The neonicotinoid dataset was collected from the Environmental Protection Agency's ECOTOX Knowledgebase, a database for ecotoxicology research. Neonicotinoids are a class of insecticides used widely in agriculture. The dataset that has been pulled includes all studies published on insects. Why might we be interested in the ecotoxicology of neonicotinoids on insects? Feel free to do a brief internet search if you feel you need more background information.

Answer: Insecticides often kill all kinds of insects in an area, including beneficial ones, and can also harm other organisms that feed on the crop or the insects in that area. Pollinators like bees and butterflies for example are getting destroyed by this type of insecticide. Organisms like birds and fish are often one of the most impacted by insecticide use, especially since neonics stay in the environmental system (soil, water, fruit, etc) for many years.

Additional background info found here: <https://www.nrdc.org/stories/neonicotinoids-101-effects-humans-and-bees>

3. The Niwot Ridge litter and woody debris dataset was collected from the National Ecological Observatory Network, which collectively includes 81 aquatic and terrestrial sites across 20 ecoclimatic domains. 32 of these sites sample forest litter and woody debris, and we will focus on the Niwot Ridge long-term ecological research (LTER) station in Colorado. Why might we be interested in studying litter and woody debris that falls to the ground in forests? Feel free to do a brief internet search if you feel you need more background information.

Answer: Studying litter and woody debris in forests tells foresters about the rate of decay within that ecosystem as well as provides insights into fire likelihood and how big a fire would be. More debris, especially dry debris, means a higher likelihood of fires. Debris also helps calculate Aboveground Net Primary Productivity, biomass estimates, and carbon fluxes according to the NEON Litterfall User Guide.

4. How is litter and woody debris sampled as part of the NEON network? Read the NEON_Litterfall_UserGuide.pdf document to learn more. List three pieces of salient information about the sampling methods here:

Answer: 1. One elevated litter trap and one ground trap deployed per 400m² plot 2. Ground traps sampled once per year, elevated traps depends on vegetation type 3. Trap placement is randomized in places with 50% > cover and targeted in areas with less vegetation.

Obtain basic summaries of your data (Neonics)

5. What are the dimensions of the dataset?

```
dim(Neonics)
```

```
## [1] 4623 30
```

6. Using the `summary` function on the “Effect” column, determine the most common effects that are studied. Why might these effects specifically be of interest?

```
summary(Neonics$Effect)
```

```
##      Accumulation      Avoidance      Behavior      Biochemistry
##           12          102          360           11
##      Cell(s)      Development      Enzyme(s) Feeding behavior
##           9          136           62          255
##      Genetics      Growth      Histology      Hormone(s)
##          82           38           5           1
##      Immunological      Intoxication      Morphology      Mortality
##          16           12           22          1493
##      Physiology      Population      Reproduction
##           7          1803          197
```

Answer: Population (1803) and Mortality (1493) are by far the most common effects studied, probably because it is really important for biologists to know how big an insect population is in an area and how many die, especially when looking at impacts of an insecticide.

7. Using the `summary` function, determine the six most commonly studied species in the dataset (common name). What do these species have in common, and why might they be of interest over other insects? Feel free to do a brief internet search for more information if needed. [TIP: The `sort()` command can sort the output of the `summary` command...]

```
#Created a variable that will sort the common name data
sorted_common_name <- sort(summary(Neonics$Species.Common.Name))
sorted_common_name
```

```
##      Ant Family      Apple Maggot
##           9           9
##      Glasshouse Potato Wasp      Lacewing
##          10          10
##      Southern House Mosquito      Two Spotted Lady Beetle
##          10          10
##      Spotless Ladybird Beetle      Braconid Parasitoid
##          11          12
##      Common Thrip      Eastern Subterranean Termite
##          12          12
##      Jassid      Mite Order
##          12          12
##      Pea Aphid      Pond Wolf Spider
##          12          12
##      Armoured Scale Family      Diamondback Moth
##          13          13
##      Eulophid Wasp      Monarch Butterfly
##          13          13
```

##	Predatory Bug	Yellow Fever Mosquito
##	13	13
##	Corn Earworm	Green Peach Aphid
##	14	14
##	House Fly	Ox Beetle
##	14	14
##	Red Scale Parasite	Spined Soldier Bug
##	14	14
##	Western Flower Thrips	Hemlock Woolly Adelgid Lady Beetle
##	15	16
##	Hemlock Woolly Adelgid	Mite
##	16	16
##	Onion Thrip	Araneoid Spider Order
##	16	17
##	Bee Order	Egg Parasitoid
##	17	17
##	Insect Class	Moth And Butterfly Order
##	17	17
##	Oystershell Scale Parasitoid	Black-spotted Lady Beetle
##	17	18
##	Calico Scale	Fairyfly Parasitoid
##	18	18
##	Lady Beetle	Minute Parasitic Wasps
##	18	18
##	Mirid Bug	Mulberry Pyralid
##	18	18
##	Silkworm	Vedalia Beetle
##	18	18
##	Codling Moth	Flatheaded Appletree Borer
##	19	20
##	Horned Oak Gall Wasp	Leaf Beetle Family
##	20	20
##	Potato Leafhopper	Tooth-necked Fungus Beetle
##	20	20
##	Argentine Ant	Beetle
##	21	21
##	Mason Bee	Mosquito
##	22	22
##	Citrus Leafminer	Ladybird Beetle
##	23	23
##	Spider/Mite Class	Tobacco Flea Beetle
##	24	24
##	Chalcid Wasp	Convergent Lady Beetle
##	25	25
##	Stingless Bee	Ground Beetle Family
##	25	27
##	Rove Beetle Family	Tobacco Aphid
##	27	27
##	Scarab Beetle	Spring Tiphia
##	29	29
##	Thrip Order	Ladybird Beetle Family
##	29	30
##	Parasitoid	Braconid Wasp
##	30	33

```
##          Cotton Aphid          Predatory Mite
##                33                33
##      Sweetpotato Whitefly      Aphid Family
##                37                38
##          Cabbage Looper      Buff-tailed Bumblebee
##                38                39
##      True Bug Order      Sevenspotted Lady Beetle
##                45                46
##          Beetle Order      Snout Beetle Family, Weevil
##                47                47
##      Erythrina Gall Wasp      Parasitoid Wasp
##                49                51
##      Colorado Potato Beetle      Parastic Wasp
##                57                58
##      Asian Citrus Psyllid      Minute Pirate Bug
##                60                62
##      European Dark Bee      Wireworm
##                66                69
##      Euonymus Scale      Asian Lady Beetle
##                75                76
##      Japanese Beetle      Italian Honeybee
##                94                113
##          Bumble Bee      Carniolan Honey Bee
##                140                152
##      Buff Tailed Bumblebee      Parasitic Wasp
##                183                285
##          Honey Bee      (Other)
##                667                670
```

```
#Then created a variable to hold and show me the top 6 most commonly studied species
top_6 <- sorted_common_name[95:100]
top_6
```

```
##          Bumble Bee      Carniolan Honey Bee Buff Tailed Bumblebee
##                140                152                183
##      Parasitic Wasp      Honey Bee      (Other)
##                285                667                670
```

Answer: While the largest category is **Other**, the others in the top 6 are all pollinators. If we ignore the **Other** category and include the next most common species, then we still get all bees and one wasp. As key pollinators, these organisms help maintain healthy ecosystems and are therefore of high interest for conservation, especially since they are one of the most negatively impacted groups as I mentioned in Question 2.

8. Concentrations are always a numeric value. What is the class of `Conc.1..Author.` column in the dataset, and why is it not numeric?

```
class(Neonics$Conc.1..Author.)
```

```
## [1] "factor"
```

Answer: The class is “factor” because when we imported the dataset we made all the data into factors using the `stringAsFactors = T` command.

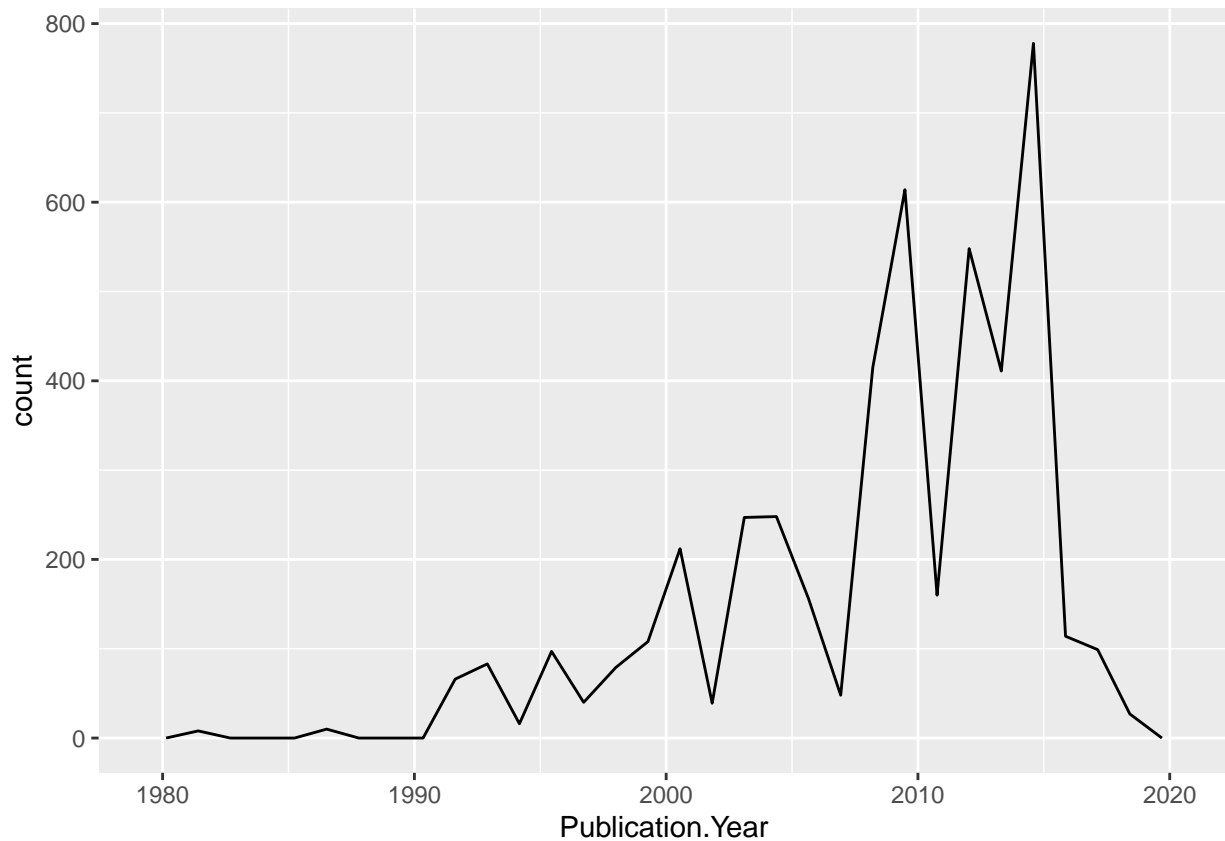
Explore your data graphically (Neonics)

9. Using `geom_freqpoly`, generate a plot of the number of studies conducted by publication year.

###QUESTION: Do I need to somehow call out each plot so it shows when I knit or does it automatically s

```
ggplot(Neonics) +  
  geom_freqpoly(aes(x = Publication.Year))
```

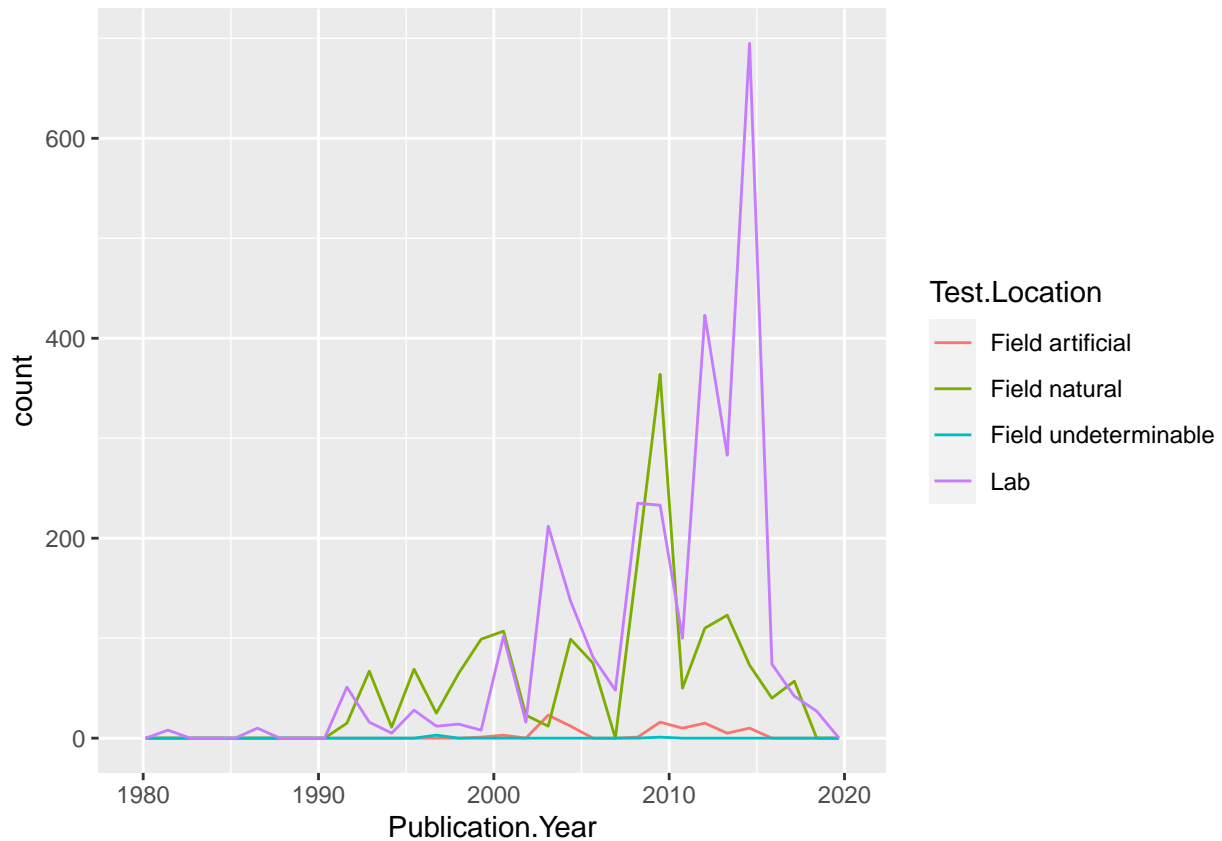
'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.



10. Reproduce the same graph but now add a color aesthetic so that different Test.Location are displayed as different colors.

```
ggplot(Neonics) +  
  geom_freqpoly(aes(x = Publication.Year, color = Test.Location))
```

'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.



Interpret this graph. What are the most common test locations, and do they differ over time?

Answer: The most common test locations are Lab and Field natural, although Lab definitely increases between 2010 and 2020, perhaps because field work is generally more expensive than lab work. The overall number of studies increased as time went on as well.

11. Create a bar graph of Endpoint counts. What are the two most common end points, and how are they defined? Consult the ECOTOX_CodeAppendix for more information.

[TIP: Add `theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))` to the end of your plot command to rotate and align the X-axis labels...]

```
ggplot(Neonics) +
  geom_bar(aes(x = Endpoint)) +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```



Answer: The two most common end points are LOEL and NOEL, which are both terrestrial-based codes. LOEL is defined as the “Lowest-observable-effect-level” in the Code Appendix, meaning the lowest concentration of toxins that resulted in significant effects. NOEL is defined as “No-observable-effect-level” in the Code Appendix, meaning the highest concentration of toxins that DO NOT result in significant effects.

Explore your data (Litter)

- Determine the class of collectDate. Is it a date? If not, change to a date and confirm the new class of the variable. Using the `unique` function, determine which dates litter was sampled in August 2018.

```
class(Litter$collectDate) #The class is factor.
```

```
## [1] "factor"
```

```
#Determining what format the dates are currently written in.
Litter$collectDate[1] #This shows it is in year-month-day format
```

```
## [1] 2018-08-02
## Levels: 2018-08-02 2018-08-30
```



```
#Change into date class.
Litter$collectDate <- as.Date(Litter$collectDate, format = "%Y-%m-%d")
```

```
#Check to see if it changed.
class(Litter$collectDate) #this vector is now a Date class.
```

```
## [1] "Date"
```

```
#Using the `unique` function.
unique(Litter$collectDate) #shows Aug 2nd and 30th were sample dates.
```

```
## [1] "2018-08-02" "2018-08-30"
```

13. Using the `unique` function, determine how many plots were sampled at Niwot Ridge. How is the information obtained from `unique` different from that obtained from `summary`?

```
#Use the length AND unique functions together to return the number of plots sampled.
length(unique(Litter$plotID))
```

```
## [1] 12
```

```
#Comparing `summary` and `unique` functions.
summary(Litter$plotID)
```

```
## NIWO_040 NIWO_041 NIWO_046 NIWO_047 NIWO_051 NIWO_057 NIWO_058 NIWO_061
##      20      19      18      15      14      8      16      17
## NIWO_062 NIWO_063 NIWO_064 NIWO_067
##      14      14      16      17
```

```
unique(Litter$plotID)
```

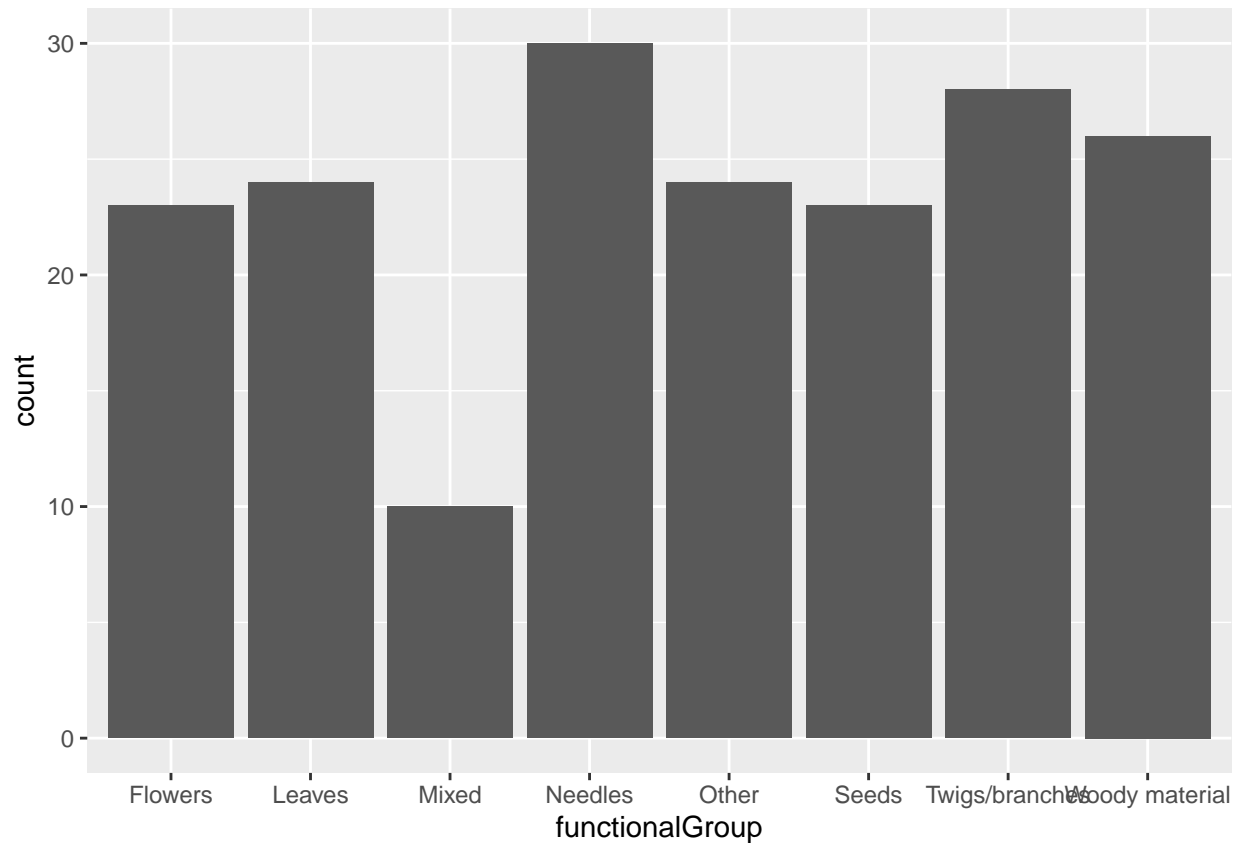
```
## [1] NIWO_061 NIWO_064 NIWO_067 NIWO_040 NIWO_041 NIWO_063 NIWO_047 NIWO_051
## [9] NIWO_058 NIWO_046 NIWO_062 NIWO_057
## 12 Levels: NIWO_040 NIWO_041 NIWO_046 NIWO_047 NIWO_051 NIWO_057 ... NIWO_067
```

```
###QUESTION: What are Levels? Google was not helpful...
```

Answer: Summary returns the plot IDs AND how many times each was sampled. Unique returns all the different plot IDs and excludes repeats. It also includes “Levels” which shows the plot IDs in ascending order.

14. Create a bar graph of functionalGroup counts. This shows you what type of litter is collected at the Niwot Ridge sites. Notice that litter types are fairly equally distributed across the Niwot Ridge sites.

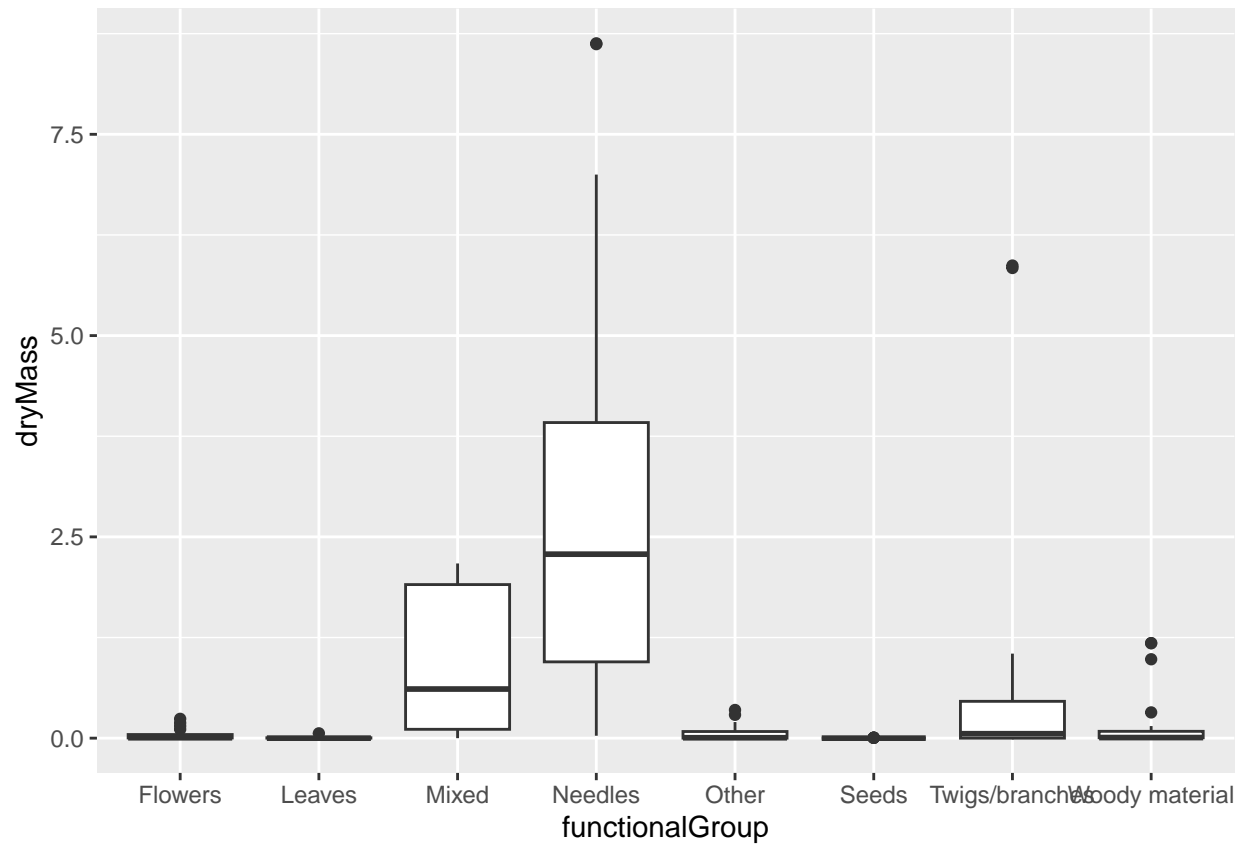
```
#Used ggplot and geom_bar to make the graph.
ggplot(Litter) +
  geom_bar(aes(x = functionalGroup))
```



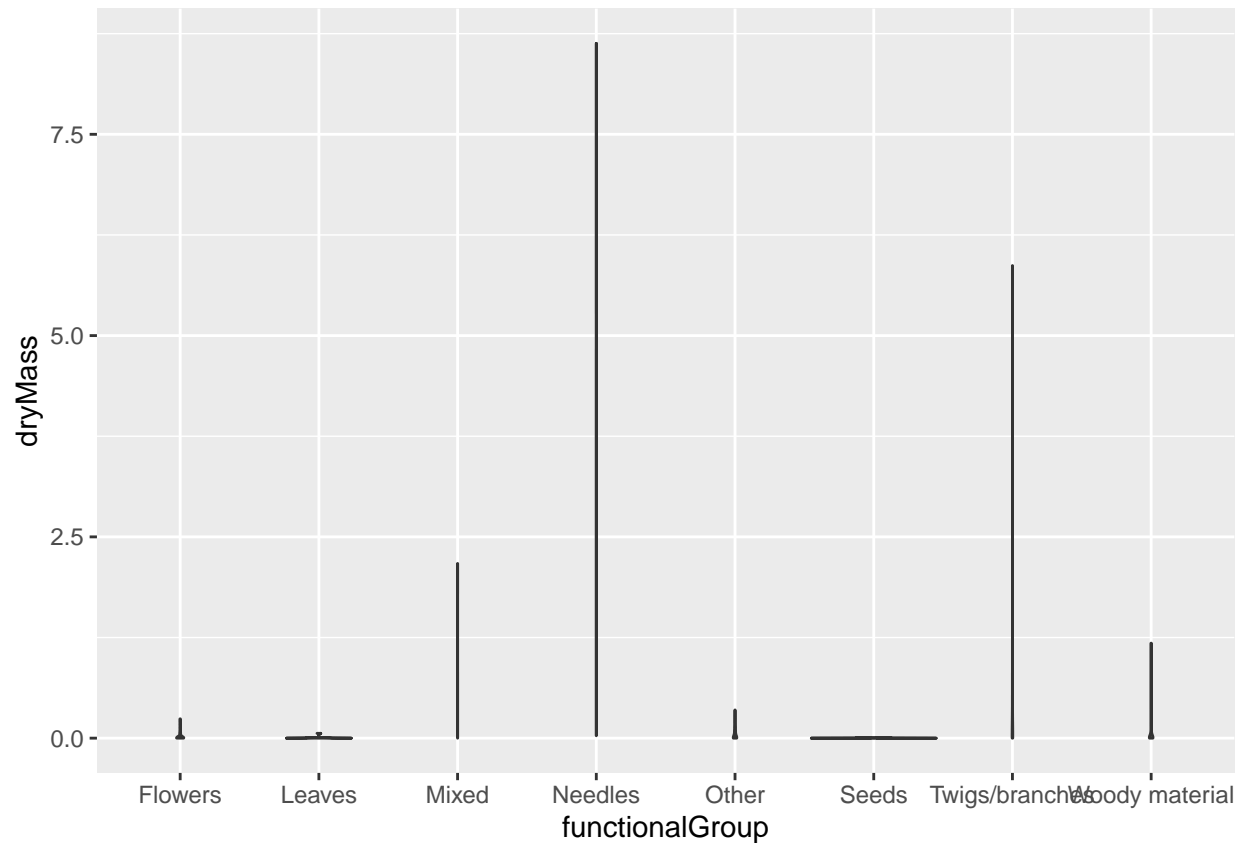
#the Functional Group "Mixed" has the least by quite a lot, but the others are fairly equally distributed

15. Using `geom_boxplot` and `geom_violin`, create a boxplot and a violin plot of `dryMass` by `functionalGroup`.

```
#First going to make the box plot with x-axis as functional group and y-axis as dryMass.
ggplot(Litter) +
  geom_boxplot(aes(x = functionalGroup, y = dryMass))
```



```
#Next going to create a violin plot with same axis.  
ggplot(Litter) +  
  geom_violin(aes(x = functionalGroup, y = dryMass))
```



#Violin plot does not look very good but I think I did it right.

`length(Litter$dryMass)` *#Wanted to know how many data points we had*

```
## [1] 188
```

Why is the boxplot a more effective visualization option than the violin plot in this case?

Answer: The boxplot is more effective in this case because there are not a huge amount of data points to show any visible distribution. When we used the USGS dataset in the lesson, there were thousands of data points so the width of the violin plots were actually discernable.

What type(s) of litter tend to have the highest biomass at these sites?

Answer: Needles and Mixed tend to have the highest biomass, with one outlier in Twigs/branches that is a very high value.