R Training 5

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R Markdown

Loading packages & data

```
# Load packages
library(here)
```

```
## here() starts at /Users/rachelkenny/Documents/IRC/R Code/IRC_R_Training
```

```
library(readxl)
library(readr)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.1     v dplyr   1.0.0
## v tibble  3.0.1     v stringr 1.4.0
## v tidyr   1.1.0     v forcats 0.5.0
## v purrr   0.3.4
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(janitor)
```

```
##
## Attaching package: 'janitor'
```

```
## The following objects are masked from 'package:stats':
##
##     chisq.test, fisher.test
```

```
# Load agua chinon veg data
ac_data_raw <- read_excel(here("data", "OCWR_AC_2019_Data.xlsx"))
ac_data <- clean_names(ac_data_raw)
ac_data$polygon_id[which(ac_data$polygon_id=="5M Buffer")] <- "5M BUFFER"

# Load weir oak restoration data
oak_data_raw <- read_csv(here("data", "Weir_Oak_Restoration_Data_winter19_2.csv"))
```

```
## Parsed with column specification:
## cols(
##   `Short ID` = col_character(),
##   Survival = col_logical(),
```

```
##   Quantity = col_double(),
##   `Height (cm)` = col_double(),
##   `Open Closed` = col_character(),
##   `Location UML` = col_character(),
##   `Water Yes No` = col_character(),
##   `Sampling Group` = col_character()
## )
```

```
oak_data <- clean_names(oak_data_raw)

# Load arthropod data
arth_data <- read_csv(here("data", "IRC_restoration_arthropod_data.csv")) %>%
  clean_names()
```

```
## Parsed with column specification:
## cols(
##   Type = col_character(),
##   Management = col_character(),
##   year_restoration = col_double(),
##   Year = col_double(),
##   Transect = col_character(),
##   `Evenness - functional` = col_double(),
##   `Richness - taxa` = col_double(),
##   `Richness - ant` = col_double(),
##   detritivores = col_double(),
##   `herb chew` = col_double(),
##   `herb suck` = col_double(),
##   parasitoid = col_double(),
##   pollinator = col_double(),
##   predator = col_double(),
##   scavenger = col_double()
## )
```

```
# Load cougar example data
cougar <- read_csv(here("data", "example_cougars.csv")) %>%
  clean_names
```

```
## Parsed with column specification:
## cols(
##   Location = col_character(),
##   Camera = col_character(),
##   `2017` = col_double(),
##   `2018` = col_double(),
##   `2019` = col_double()
## )
```

Review

```
# Show how you would refer to the 4th-6th rows of the oak dataframe using square brackets


# Using the arthropod data, write an ifelse statement to create a new column which assigns a 0 if the p

# Next, using the oak restoration data write an ifelse statement to create a new column based on locati
```

```
# Show me the mean and standard deviation of pin number in the agua chinon dataset. How can I check whe
```

Long and wide format data

It is sometimes necessary to rearrange the format of data in order to suit the needs of the analysis or data visualization.

Data is sometimes arranged in wide or long format. In wide format, categorical data is grouped. Wide data if often easier to read and interpret, but can sometimes lead to issues in conducting analyses or visualizing data in r. In long format (think long vertically), every row represents an observation belonging to a particular category.

Data is rearranged according to the key and the value. The key is an attribute and explains what the data describes. The value is the value of the observation described by the key.

Using the tidyr package, we can convert easily between long and wide format.

Spread

- Spread() is used to seperate data from two columns into many, based on the number of categories. In other words, go from long to wide format. The key column is used to assign categories to the header of each column, and the values get arranged by category.
- spread(data, key, value)

Gather

- Gather() is used to take more than one column, and consolidate them into two columns based on the key column attributes. In other words, go from wide to long. The key column contains the categorical data, and the value column contains the corresponding values.
- gather(data, key, value)

Check out these links for more information: https://github.com/rstudio/cheatsheets/blob/master/data-import.pdf https://garrettgman.github.io/tidying/

Spread and gather example 1

```
# What kind of data is the cougar?
View(cougar)

# How can we convert the data format?
cougar_gtr <- gather(cougar, "year", "total_cougars", 3:5)

View(cougar_gtr)

# Now how can we convert it back to its original format?
cougar_spd <- spread(cougar_gtr, "year", "total_cougars")
View(cougar_spd)
```

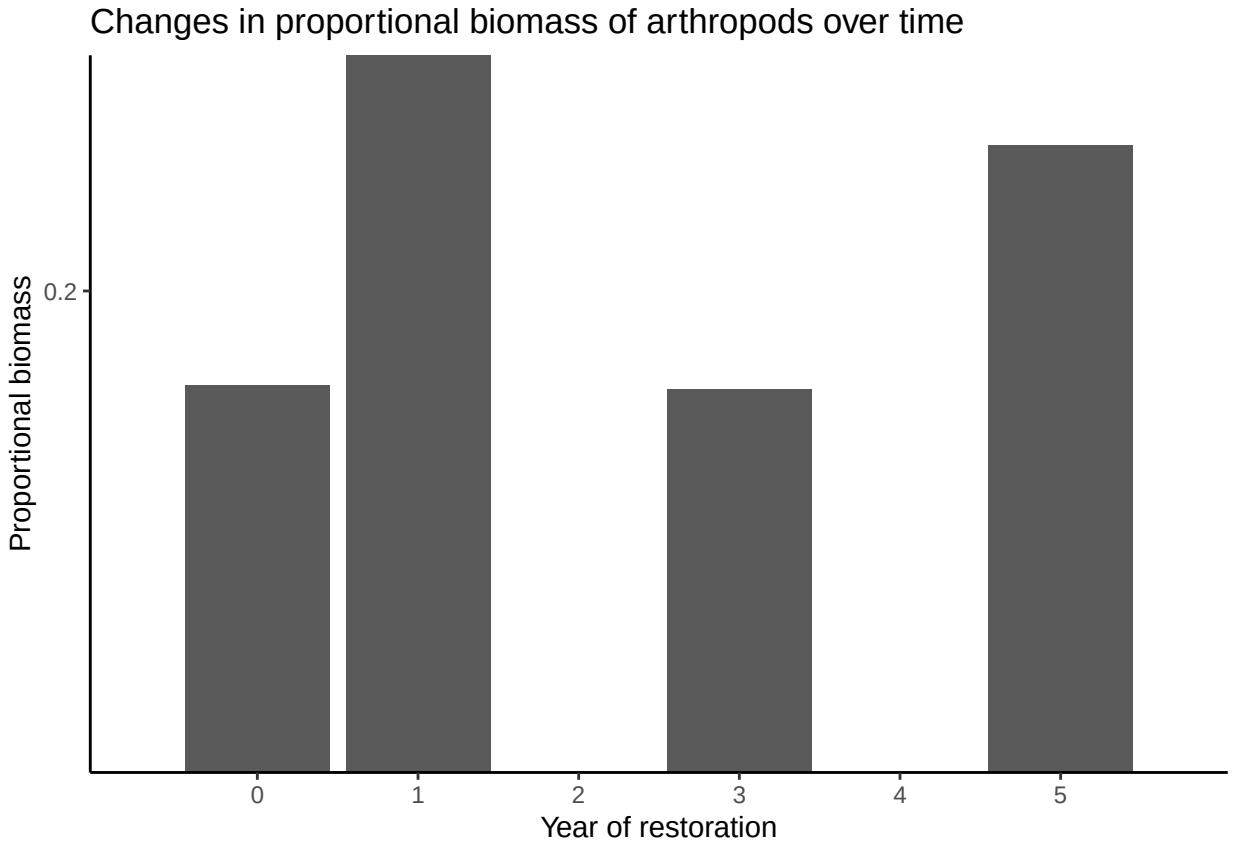
Spread and gather problem

```
# Problem - we want to create a plot showing the changes in proportional biomass of various functional

View(arth_data)

plot_det <- ggplot(arth_data) +
  geom_bar(aes(x = year_restoration, y = detritivores), stat = "summary", fun.y = "mean") +
  theme_classic() +
  ggtitle("Changes in proportional biomass of arthropods over time") +
  xlab("Year of restoration") +
  ylab("Proportional biomass") +
  scale_y_continuous(expand=c(0,0), breaks = c(.2,.4,.6,.8,1))+
  scale_x_continuous(expand=c(0.1,0), breaks = c(0,1,2,3,4,5))
```

```
## Warning: Ignoring unknown parameters: fun.y
```

```
plot_det
```

```
## No summary function supplied, defaulting to `mean_se()`
```



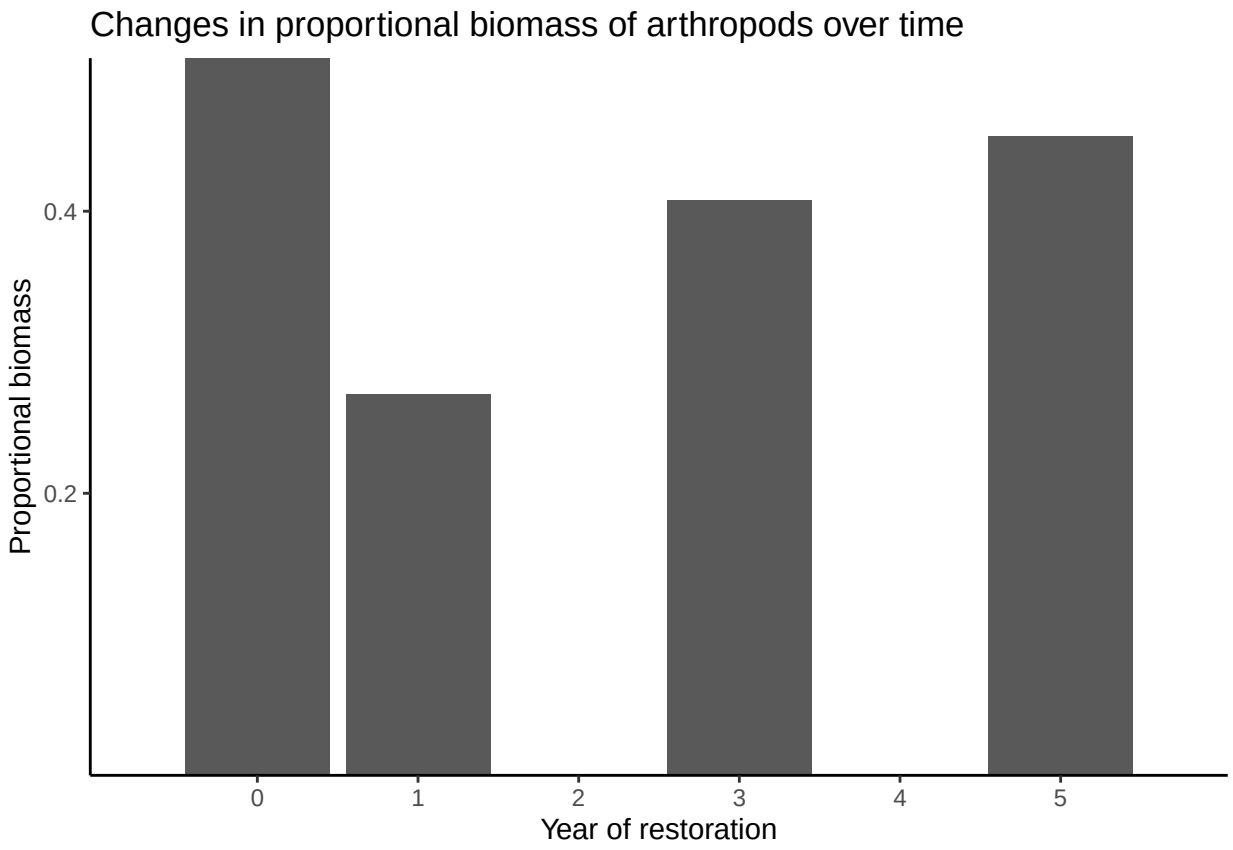

```
plot_pred <- ggplot(arth_data) +
  geom_bar(aes(x = year_restoration, y = predator), stat = "summary", fun.y = "mean") +
  theme_classic() +
  ggtitle("Changes in proportional biomass of arthropods over time") +
  xlab("Year of restoration") +
  ylab("Proportional biomass") +
  scale_y_continuous(expand=c(0,0), breaks = c(.2,.4,.6,.8,1))+
```

```
  scale_x_continuous(expand=c(0.1,0), breaks = c(0,1,2,3,4,5))
```

```
## Warning: Ignoring unknown parameters: fun.y
```

```
plot_pred
```

```
## No summary function supplied, defaulting to `mean_se()`
```

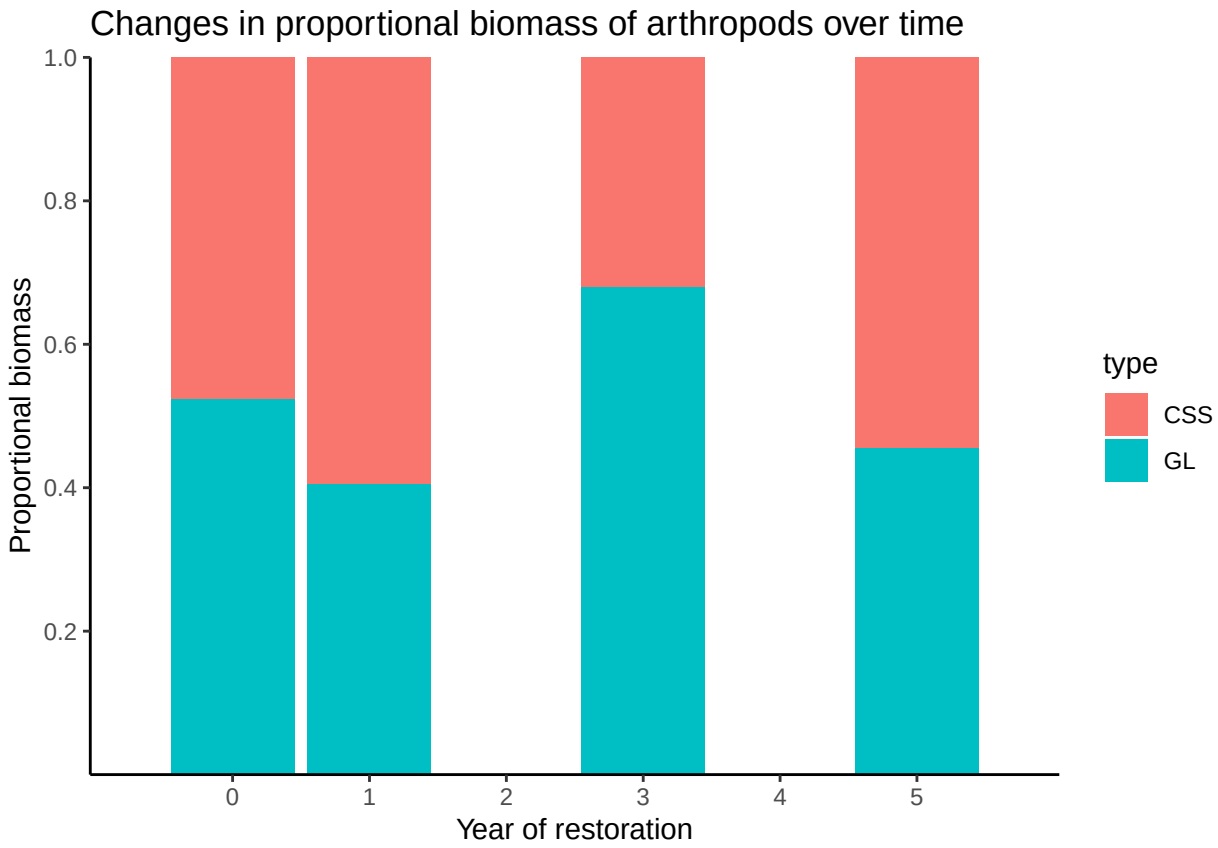



```
# In order to make a gpplot with grouping by functional group, we would need one column with all the va
plot_pred <- ggplot(arth_data) +
  geom_bar(aes(x = year_restoration, y = detritivores, fill = type), position = "fill", stat = "summary
  theme_classic() +
  ggtitle("Changes in proportional biomass of arthropods over time") +
  xlab("Year of restoration") +
  ylab("Proportional biomass") +
  scale_y_continuous(expand=c(0,0), breaks = c(.2,.4,.6,.8,1))+
  scale_x_continuous(expand=c(0.1,0), breaks = c(0,1,2,3,4,5))
```

```
## Warning: Ignoring unknown parameters: fun.y
```

```
plot_pred
```

```
## No summary function supplied, defaulting to `mean_se()`
```



Spread and gather example 2

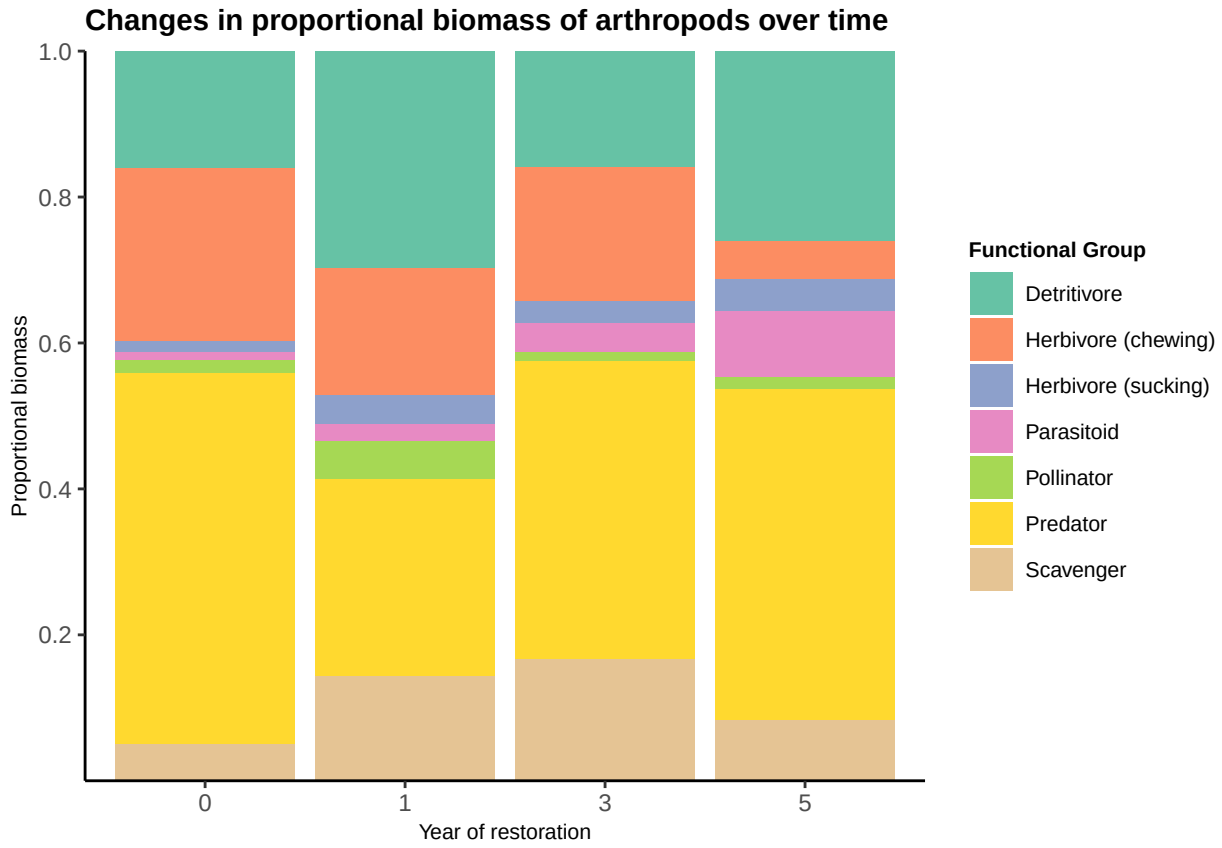
```
# Let's select the relevant columns. I always retain the ID (transect in this case) and then we want to
arth_data_2 <- arth_data %>%
  select(transect, year_restoration, detritivores, herb_chew, herb_suck, parasitoid, pollinator, predato

# Next we need to either spread or gather - which one?
arth_data_2 <- arth_data %>%
  select(transect, year_restoration, detritivores, herb_chew, herb_suck, parasitoid, pollinator, predato
  gather("functional_group", "proportional_biomass", 3:9)


View(arth_data_2)

# Then if we wanted to return the data to it's original format how would we do that?


# Now we're ready to plot! Use your long form dataframe for the ggplot. Note, we want to treat restorat

arth_data_2$year_restoration <- as.factor(arth_data_2$year_restoration)

# Create a ggplot
plot_arth <- ggplot(arth_data_2) +
  geom_bar(aes(x = year_restoration, y = proportional_biomass, fill = functional_group), position = "fi
  theme_classic() +
```

```
  ggtitle("Changes in proportional biomass of arthropods over time") +
  xlab("Year of restoration") +
  ylab("Proportional biomass") +
  scale_y_continuous(expand=c(0,0), breaks = c(.2,.4,.6,.8,1))+
  scale_x_discrete(expand=c(0.2,0))+
  scale_fill_brewer("Functional Group",palette="Set2", labels=c("Detritivore", "Herbivore (chewing)", "
  theme(plot.title = element_text(face="bold", size = 11),
        axis.title = element_text(size=8),
        legend.title = element_text(size=8, face="bold"),
        legend.text = element_text(size=8))
```

```
## Warning: Ignoring unknown parameters: fun.y
```

```
plot_arth
```

```
## No summary function supplied, defaulting to `mean_se()`
```



Aggregate function

```
# The aggregate function can help aggregate data according to grouping. In the example below, we want t

View(cougar)

cougar2 <- aggregate(cougar[3:5],list(cougar$location), mean)
```

```r
View(cougar2)
```

Understanding the mitigation code - calculating cover

```r
# Retain only the point-intercept data ("T.PI") and the columns for polygon ID, transect, pin number, a
ac_data_cvr <- ac_data %>%
  dplyr::filter(data_type == "T.PI") %>%
  select(polygon_id, transect, pin_number, native_non_native)

cover2 <- distinct(ac_data_cvr) %>%
  count(polygon_id, transect, native_non_native) %>%
  spread(native_non_native, n)

View(cover2)

#Reorder columns so that non-native comes before no native veg, and set any NA values equal to zero
cover2 <- cover2[,c(1,2,3,5,4)]
cover2[is.na(cover2)] = 0

# View(cover2)



# For polygons with multiple transects, average the values per polygon id, and then round all numbers
cover3 <- aggregate(cover2[3:5],list(cover2$polygon_id), mean)
colnames(cover3) <- c("polygon_id","avg_native_count", "avg_non_native_count", "avg_no_native_count")
cover3[,-1] <- round(cover3[,-1],1)

# View(cover3)



# ABSOLUTE COVER
# Multiply values by 100 and divide by 50 because there are 50 sample points (pins) per transect
cover3_table <- mutate(cover3, absolute_cover_native = avg_native_count*100/50)
cover3_table <- mutate(cover3_table, absolute_cover_non_native = avg_non_native_count*100/50)
cover3_table <- mutate(cover3_table, absolute_cover_no_native = avg_no_native_count*100/50)

# RELATIVE COVER
# To get relative native cover, take absolute native cover value and divide by absolute value native + 
cover3_table <- mutate(cover3_table, relative_cover_native = absolute_cover_native*100/(absolute_cover_
cover3_table <- mutate(cover3_table, relative_cover_non_native = absolute_cover_non_native*100/(absolut

# Round all values, and isolate only the relevant columns for the summary tables
cover3_table[,-1] <-round(cover3_table[,-1],1)
cover3_table <- cover3_table %>%
  select(polygon_id, absolute_cover_native, absolute_cover_non_native, absolute_cover_no_native, relati

# View(cover3_table)
```