Week 6 Assignment

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Week 6 Assignment

Purpose

The goal of this assignment is to practice converting messy data into tidy data.

Task

Write R code to successfully answer each question below.

Criteria for Success

- Code is within the provided code chunks or new code chunks are created where necessary
- Code chunks run without errors
- Code chunks have brief comments indicating which code is answering which part of the question
- Code will be assessed as follows:
  - Produces the correct answer using the requested approach: 100%
  - Generally uses the right approach, but a minor mistake results in an incorrect answer: 90%
  - Attempts to solve the problem and makes some progress using the core concept, but returns the wrong answer and does not demonstrate comfort with the core concept: 50%
  - Answer demonstrates a lack of understanding of the core concept: 0%
- Any questions requiring written answers are answered with sufficient detail

Due Date

March 4 at 3:30 pm

Assignment Exercises

Set-up

Load the packages we will need. You can either load all of them individually (`readr`, `dplyr`, `tidyr`, `ggplot2`) or load the `tidyverse` package.

```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

1. Forest Area per Country (15 pts)

The data in `forest_per_country.csv` are downloaded from the WHO and contain the amount of forest (sq. km) per country.

First, click on the .csv file in the "Files" tab and select "View File." You might notice that the top of the document looks a bit odd.

The first 3 rows of the file are metadata or empty, which we do not want. I've added the arguments `skip = 4` and `col_names = TRUE` to the `read_csv` function to deal with this.

```r
forest <- read_csv("forest_per_country.csv", skip = 4, col_names = TRUE)
```

```
## Rows: 266 Columns: 35
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (2): Country Name, Country Code
## dbl (32): 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, ...
## lgl  (1): 2022
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

a. Currently, this data is in a wide format. We want to convert this to a longer format and make it tidy. Use the `pivot_longer` function to do so. Overwrite the `forest` dataframe so that it contains the long version of the data.

   Because the column names start with numbers, which R does not like, we need to put the column names either in backticks or quotation marks (e.g., "1990":"2022").

b. Remove any rows that have `NA` in the forest area column using the `drop_na()` function.

c. Let's remind ourselves how to plot the data. Make a scatterplot of the data with year on the x-axis and forest area on the y-axis. Make the points partially tranparent and the color "forestgreen." Add more descriptive axes labels and a theme.

   Add the following line of code to the end of your ggplot code so we can see the years along the x-axis: `theme(axis.text.x = element_text(angle = 45, vjust = 0.5))`.

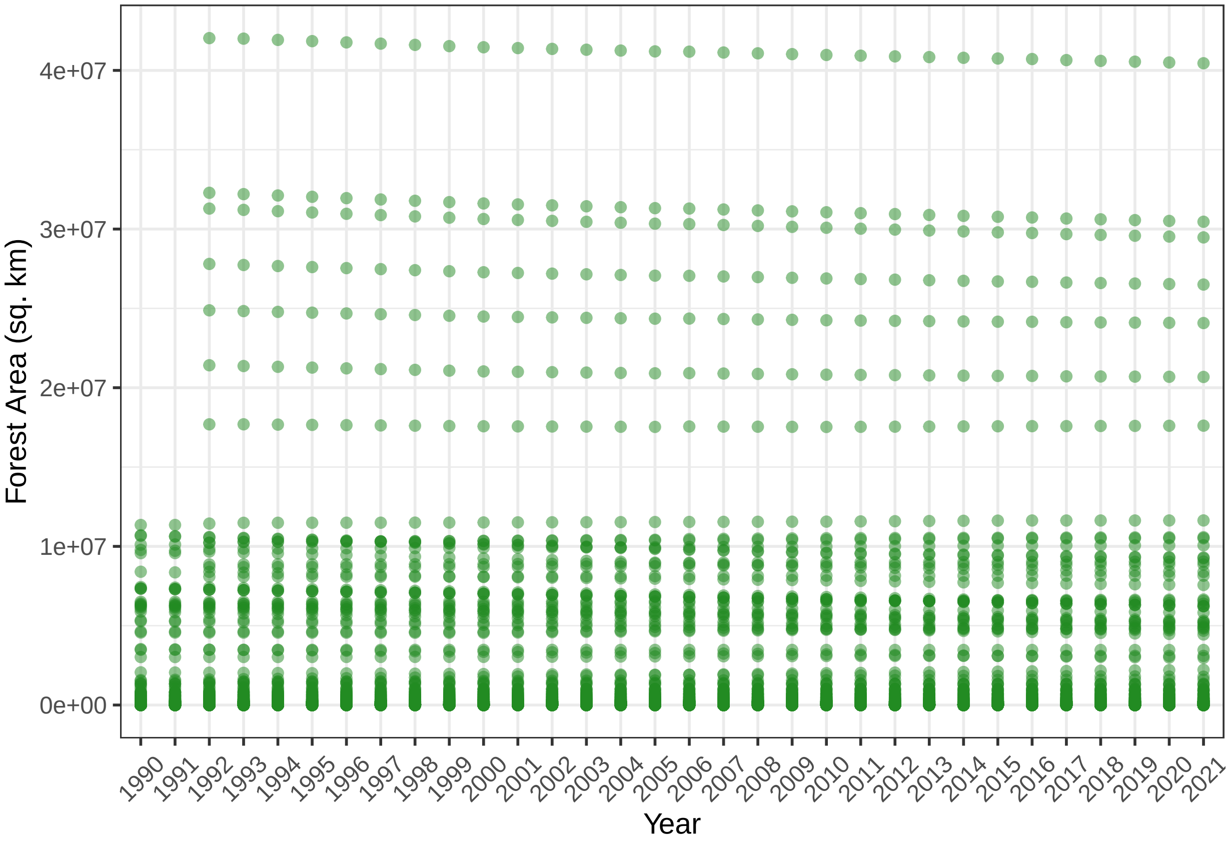
```r
# a
forest <- forest %>%
  pivot_longer(`1990`:`2022`, names_to = "Year", values_to = "ForestArea_sqkm")
forest
```

```
## # A tibble: 8,778 x 4
##    `Country Name` `Country Code` Year  ForestArea_sqkm
##    <chr>          <chr>          <chr>           <dbl>
##  1 Aruba          ABW            1990              4.2
##  2 Aruba          ABW            1991              4.2
##  3 Aruba          ABW            1992              4.2
##  4 Aruba          ABW            1993              4.2
##  5 Aruba          ABW            1994              4.2
##  6 Aruba          ABW            1995              4.2
##  7 Aruba          ABW            1996              4.2
##  8 Aruba          ABW            1997              4.2
##  9 Aruba          ABW            1998              4.2
## 10 Aruba          ABW            1999              4.2
## # i 8,768 more rows
```

```
# b.
forest <- forest %>%
  drop_na(ForestArea_sqkm)
forest
```

```
## # A tibble: 8,176 x 4
##    `Country Name` `Country Code` Year  ForestArea_sqkm
##    <chr>          <chr>          <chr>           <dbl>
##  1 Aruba          ABW            1990              4.2
##  2 Aruba          ABW            1991              4.2
##  3 Aruba          ABW            1992              4.2
##  4 Aruba          ABW            1993              4.2
##  5 Aruba          ABW            1994              4.2
##  6 Aruba          ABW            1995              4.2
##  7 Aruba          ABW            1996              4.2
##  8 Aruba          ABW            1997              4.2
##  9 Aruba          ABW            1998              4.2
## 10 Aruba          ABW            1999              4.2
## # i 8,166 more rows
```

```
# c
ggplot(forest, aes(Year, ForestArea_sqkm)) +
  geom_point(alpha = 0.5, color = "forestgreen") +
  labs(x = "Year",
       y = "Forest Area (sq. km)") +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 0.5))
```



2. OECD Data (10 pts)

The `oecd_annual_data.csv` contains data from the Organisation for Economic Co-operation and Development (OECD) about various global fishing economies and sustainability. This dataset has the area of protected marine reserves.

a. Like the forest data from Question 1, this data has a few rows of metadata at the top of the document that we need to skip. Use the same arguments as we did in Question 1 (same values, as well) when reading in the file.

```
oecd <- read_csv("oecd_annual_data.csv", skip = 4, col_names = TRUE)
```

```
## Rows: 127 Columns: 25
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (2): OECD_member, Country
## dbl (23): 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, ...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
head(oecd)
```

```
## # A tibble: 6 x 25
##   OECD_member Country    ‘2000‘ ‘2001‘ ‘2002‘ ‘2003‘ ‘2004‘ ‘2005‘ ‘2006‘ ‘2007‘
##   <chr>       <chr>       <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
## 1 OECD        Australia  3.77e5 3.77e5 4.00e5 4.00e5 4.02e5 4.06e5 4.12e5 4.17e5
## 2 OECD        Belgium    5.52e1 5.52e1 5.52e1 5.82e1 5.82e1 3.50e2 3.50e2 3.50e2
## 3 OECD        Canada     2.47e4 2.47e4 2.49e4 2.81e4 3.00e4 3.22e4 3.25e4 3.27e4
## 4 OECD        Chile      8.85e3 8.85e3 8.85e3 8.87e3 1.01e4 1.02e4 1.02e4 1.02e4
## 5 OECD        Colombia   2.94e4 2.94e4 2.94e4 2.94e4 2.94e4 6.09e4 6.09e4 6.09e4
## 6 OECD        Costa Rica 5.84e4 5.84e4 5.84e4 5.84e4 5.84e4 5.84e4 5.86e4 5.86e4
## # i 15 more variables: ‘2008‘ <dbl>, ‘2009‘ <dbl>, ‘2010‘ <dbl>, ‘2011‘ <dbl>,
## #   ‘2012‘ <dbl>, ‘2013‘ <dbl>, ‘2014‘ <dbl>, ‘2015‘ <dbl>, ‘2016‘ <dbl>,
## #   ‘2017‘ <dbl>, ‘2018‘ <dbl>, ‘2019‘ <dbl>, ‘2020‘ <dbl>, ‘2021‘ <dbl>,
## #   ‘2022‘ <dbl>
```

b. Use the `fill()` function to fill in the missing values in the first column. Save the output as an object to be used in (c).

c. Using the data frame you created in (b), put the data in a tidy format. You'll need to use the same trick with the year column names as you did in 1a. Save the output as an object.

d. Using the data frame you created in (c), only keep the rows for non-OECD members. Then, wrangle the data so that it is back in wide format. This time, however, each row should represent a year and each country will have its own column. Your final data frame should only have a year column and each country's column.

```
#b
oecd <- oecd %>%
  fill(OECD_member)
oecd
```

```
## # A tibble: 127 x 25
##    OECD_member Country    ‘2000‘ ‘2001‘ ‘2002‘ ‘2003‘ ‘2004‘ ‘2005‘ ‘2006‘ ‘2007‘
##    <chr>       <chr>       <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
##  1 OECD        Australia  3.77e5 3.77e5 4.00e5 4.00e5 4.02e5 4.06e5 4.12e5 4.17e5
##  2 OECD        Belgium    5.52e1 5.52e1 5.52e1 5.82e1 5.82e1 3.50e2 3.50e2 3.50e2
##  3 OECD        Canada     2.47e4 2.47e4 2.49e4 2.81e4 3.00e4 3.22e4 3.25e4 3.27e4
##  4 OECD        Chile      8.85e3 8.85e3 8.85e3 8.87e3 1.01e4 1.02e4 1.02e4 1.02e4
##  5 OECD        Colombia   2.94e4 2.94e4 2.94e4 2.94e4 2.94e4 6.09e4 6.09e4 6.09e4
##  6 OECD        Costa Ri~  5.84e4 5.84e4 5.84e4 5.84e4 5.84e4 5.84e4 5.86e4 5.86e4
##  7 OECD        Denmark    7.68e3 7.68e3 7.68e3 9.45e3 1.19e4 1.23e4 1.23e4 1.30e4
##  8 OECD        Estonia    5.81e2 5.81e2 5.81e2 5.81e2 6.47e3 6.53e3 6.53e3 6.54e3
##  9 OECD        Finland    7.17e3 7.22e3 7.22e3 7.22e3 7.25e3 7.45e3 7.46e3 7.46e3
## 10 OECD        France     7.88e4 7.88e4 7.88e4 7.89e4 7.89e4 8.09e4 8.12e4 8.47e4
## # i 117 more rows
## # i 15 more variables: ‘2008‘ <dbl>, ‘2009‘ <dbl>, ‘2010‘ <dbl>, ‘2011‘ <dbl>,
## #   ‘2012‘ <dbl>, ‘2013‘ <dbl>, ‘2014‘ <dbl>, ‘2015‘ <dbl>, ‘2016‘ <dbl>,
## #   ‘2017‘ <dbl>, ‘2018‘ <dbl>, ‘2019‘ <dbl>, ‘2020‘ <dbl>, ‘2021‘ <dbl>,
## #   ‘2022‘ <dbl>
```

```
#c
oecd <- oecd %>%
  pivot_longer(`2000`:`2022`, names_to = "Year", values_to = "MarineProtectedArea_sqkm")
oecd
```

```
## # A tibble: 2,921 x 4
##    OECD_member Country   Year  MarineProtectedArea_sqkm
##    <chr>       <chr>     <chr>                    <dbl>
##  1 OECD        Australia 2000                   376896.
##  2 OECD        Australia 2001                   377198.
##  3 OECD        Australia 2002                   399906.
##  4 OECD        Australia 2003                   399923 
##  5 OECD        Australia 2004                   402052.
##  6 OECD        Australia 2005                   406364.
##  7 OECD        Australia 2006                   412438.
##  8 OECD        Australia 2007                   417116.
##  9 OECD        Australia 2008                   417560.
## 10 OECD        Australia 2009                   442165.
## # i 2,911 more rows
```

```
#d
oecd |>
  filter(OECD_member == "Non-OECD Economies") |>
  pivot_wider(names_from = Country, values_from = MarineProtectedArea_sqkm) |>
  select(-OECD_member)
```

```
## # A tibble: 23 x 96
##    Year  ‘American Samoa‘ Anguilla ‘Antigua and Barbuda‘ Argentina Aruba Bahamas
##    <chr>            <dbl>    <dbl>                 <dbl>     <dbl> <dbl>   <dbl>
##  1 2000            35439        58                  53.5     4498.  0.25    698.
##  2 2001            35440.       58                  53.5     8085.  0.25    698.
##  3 2002            35440.       58                  53.5     8177.  0.25    921.
##  4 2003            35441.       58                  53.5     8177.  0.25    921.
##  5 2004            35441.       58                  53.5     8180.  0.25    921.
##  6 2005            35441        58                 177.      8635.  0.25    921.
##  7 2006            35441        58                 177.      8635.  0.25    921.
##  8 2007            35441        76.5               177.      8635.  0.25    921.
##  9 2008            35441        76.5               177.      8636   0.25   1126.
## 10 2009            35446        76.5               177.      9363   0.25   1257.
## # i 13 more rows
## # i 89 more variables: Barbados <dbl>, Belize <dbl>, Bermuda <dbl>,
## #   Bonaire <dbl>, ‘Bouvet Island‘ <dbl>, Brazil <dbl>,
## #   ‘British Indian Ocean Territory‘ <dbl>, ‘British Virgin Islands‘ <dbl>,
## #   ‘Brunei Darussalam‘ <dbl>, Bulgaria <dbl>, Cambodia <dbl>,
## #   ‘Cayman Islands‘ <dbl>, ‘China (People’s Republic of)‘ <dbl>,
## #   ‘Christmas Islands‘ <dbl>, ‘Cocos (Keeling) Islands‘ <dbl>, ...
```

3. Santa Cruz Rodents Data Cleaning (20 pts)

Start by reading in the rodent data from the Santa Cruz River, `capture_data.csv`.

```
rodents <- read_csv("capture_data.csv")
```

```
## Rows: 51 Columns: 15
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (10): Site, Trap ID, Species, Status (R/N), Sex, Tail length, Hair samp...
## dbl   (4): Total Weight, Bag weight, Animal Weight, Hind foot length
## date  (1): Date
##
## i Use ‘spec()‘ to retrieve the full column specification for this data.
## i Specify the column types or set ‘show_col_types = FALSE‘ to quiet this message.
```

Take a look at the data. You'll likely notice immediately that there are some issues to be fixed.

For this question, there isn't really a good way for me to show you the output in the answer key; you'll want to take a look at the data frame in R and/or make good use of the filter function to make sure the issue got fixed.

a. Rename any column that needs to be renamed and save the output. This is the data frame we will use for the remainder of the questions, and you'll want to continue overwriting the output to use in each subsequent step.

b. Next we need to fill in the missing values in the `Site` column.

c. In the `Species` column, there are 2 different species that have question marks next to their names. Using the `replace` function inside of a `mutate` function, remove the question marks (e.g., `SIOC?` should become `SIOC` and `DIME?` should become `DIME`.

   (This is just for practice. In reality, we might want to create a code for unknown species or a column for unclear ID).

d. If we look at the data classes for the columns, we can see that the column for tail length is character when it should be numeric. This usually indicates that there is a special character or letter somewhere in the column. As it turns out, in the last row, the value is `~15.5` instead of `15.5`. Use the `replace` function inside of `mutate` to convert that value to `15.5`.

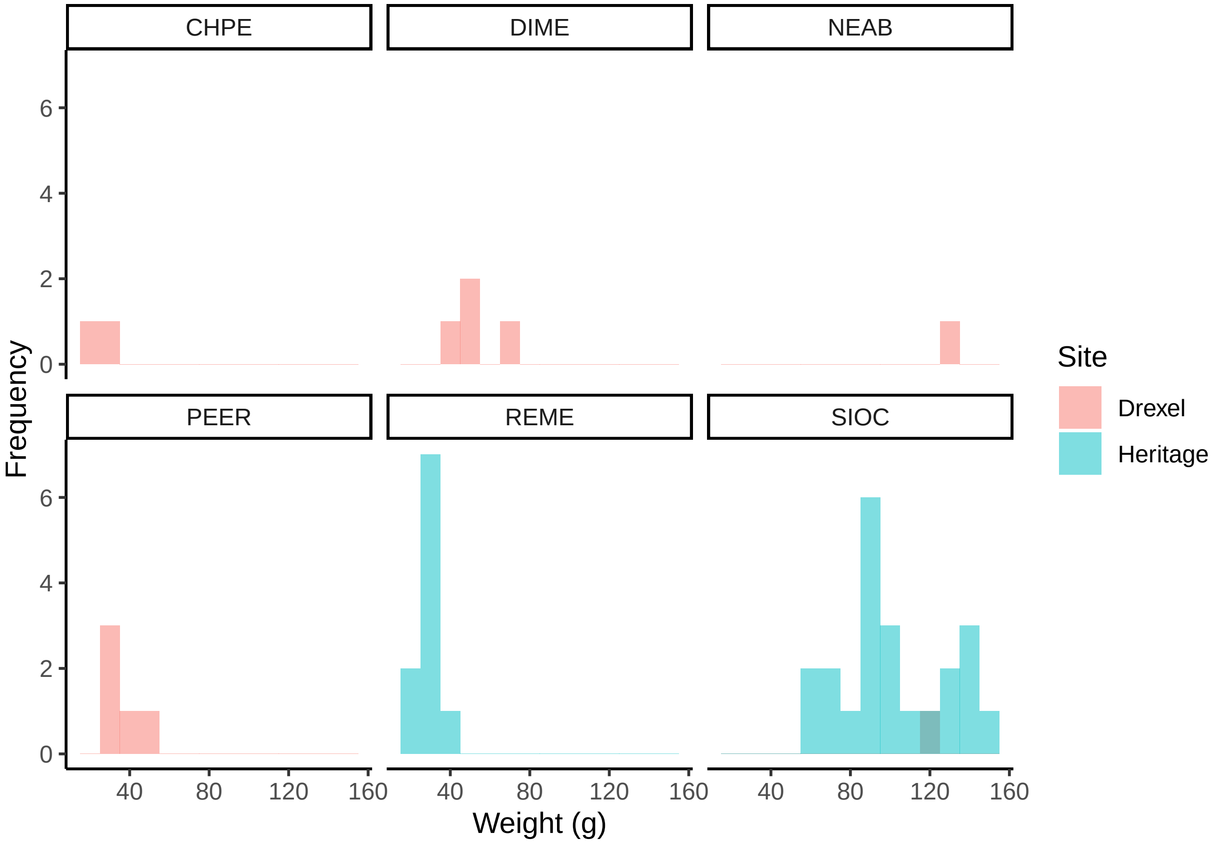
e. In both the "Hair Sample" and "Position" columns, there is a `?`. Use the `na_if` function inside a `mutate` function to convert those `?` to `NA` values.

f. Let's practice plotting again! Create a series of histograms (subplots within one larger plot) of the rodents' total weights, one histogram per species. Have the color of the histograms be determined by the site. Each histogram should be partially transparent, overlapping (not stacked), and the width of the bins should be 10. Finally, edit the axes labels and apply a theme.

```r
#a
rodents <- rodents %>%
  rename(TrapID = `Trap ID`, Status = `Status (R/N)`, TotalWeight = `Total Weight`,
         BagWeight = `Bag weight`, AnimalWeight = `Animal Weight`,
         HindfoodLength = `Hind foot length`, TailLength = `Tail length`,
         HairSample = `Hair sample (Y/N)`, Position = `Position (R/L)`)

#b
rodents <- rodents %>%
  fill(Site)

#c
rodents <- rodents %>%
  mutate(Species = replace(Species, Species == "SIOC?", "SIOC"),
         Species = replace(Species, Species == "DIME?", "DIME"))

#d
rodents <- rodents %>%
  mutate(TailLength = replace(TailLength, TailLength == "~15.5", "15.5"))
```

```
#e
rodents <- rodents %>%
  mutate(HairSample = na_if(HairSample, "?"),
         Position = na_if(Position, "?"))

#f
ggplot(rodents, aes(TotalWeight, fill = Site)) +
  geom_histogram(alpha = 0.5, position = "identity", binwidth = 10) +
  facet_wrap(~ Species) +
  labs(x = "Weight (g)", y = "Frequency") +
  theme_classic()
```

```
## Warning: Removed 6 rows containing non-finite outside the scale range
## (‘stat_bin()‘).
```



4. Remembering Joins (15 pts)

Let’s remind ourselves about joins from Week 4.

Read in the vegetation data that goes along with the Santa Cruz rodent data. The .csv file is called `microsite_grouped_veg.csv`

```
veg <- read_csv("microsite_grouped_veg.csv")
```

```
## New names:
## Rows: 80 Columns: 8
## -- Column specification
## -------------------------------------------------------- Delimiter: "," chr
## (4): Site, Trap Location, Type of Vegetation, Grouped_Veg dbl (4): ...1,
## Distance to Vegetation (m), Percent Veg Cover, Distance to Wa...
## i Use ‘spec()‘ to retrieve the full column specification for this data. i
## Specify the column types or set ‘show_col_types = FALSE‘ to quiet this message.
## * ‘‘ -> ‘...1‘
```

```
#a
veg <- veg %>%
  rename(RecordID = `...1`, TrapID = `Trap Location`, DistancetoVeg_m = `Distance to Vegetation (m)`,
         VegetationType = `Type of Vegetation`, PercentCover = `Percent Veg Cover`, DistancetoWater_m =

#b
veg <- veg %>%
  select(Site, TrapID, Grouped_Veg)

#c
inner_join(rodents, veg)
```

```
## Joining with ‘by = join_by(Site, TrapID)‘
```

```
## # A tibble: 51 x 16
##    Date       Site     TrapID Species Status Sex   TotalWeight BagWeight
##    <date>     <chr>    <chr>  <chr>   <chr>  <chr>       <dbl>     <dbl>
##  1 2022-11-14 Heritage 4C     SIOC    N      F             134        18
##  2 2022-11-14 Heritage 4D     SIOC    N      M             136        18
##  3 2022-11-14 Heritage 4I     SIOC    N      <NA>           90        18
##  4 2022-11-14 Heritage 2H     REME    N      M              38        26
##  5 2022-11-14 Heritage 4J     SIOC    N      <NA>           NA        NA
##  6 2022-11-14 Heritage 2F     REME    N      F              22        10
##  7 2022-11-15 Heritage 4C     SIOC    R      <NA>           NA        NA
##  8 2022-11-15 Heritage 4H     SIOC    N      F              95        11
##  9 2022-11-15 Heritage 1H     REME    N      <NA>           26         9
## 10 2022-11-15 Heritage 1B     REME    N      F              35         9
## # i 41 more rows
## # i 8 more variables: AnimalWeight <dbl>, HindfoodLength <dbl>,
## #   TailLength <chr>, HairSample <chr>, Position <chr>, Handler <chr>,
## #   Notes <chr>, Grouped_Veg <chr>
```

a. Rename the columns that should be renamed. Use a consistent structure (and make the Site and Trap Location column names match those from the rodents data frame in Question 3). Save the output.

b. Using the output from (a), select the Site, Trap Location and Grouped Veg columns and save those as a new data frame. Save the output.

c. Using the output from (b) and the final rodent data frame from Question 3, use an `inner_join()` to join those two data frames.

d. In your own words (~2-3 sentences), explain how the inner join in (c) worked.

5. Santa Cruz Rodents Wrangling (20 pts)

Let's practice splitting and combining columns as well as pivoting the Santa Cruz rodent data (from Question 3).

a. Use the `separate()` function to split the date column into three separate columns. Save your output.

b. Using the output from (a), rejoin the three date columns back together into one column.

c. Summarize the data so that we have a count of each species per site. Save this output as a new data frame (do not overwrite the rodents data frame)

d. Convert the data from (c) from long format to wide format. Use an argument in the `pivot_wider` function to have all blank cells filled with 0 instead of `NA`.

```
#a
rodents <- rodents %>%
  separate(Date, into = c("Year", "Month", "Day"), sep = "-")
rodents
```

```
## # A tibble: 51 x 17
##    Year  Month Day   Site     TrapID Species Status Sex   TotalWeight BagWeight
##    <chr> <chr> <chr> <chr>    <chr>  <chr>   <chr>  <chr>       <dbl>     <dbl>
##  1 2022  11    14    Heritage 4C     SIOC    N      F             134        18
##  2 2022  11    14    Heritage 4D     SIOC    N      M             136        18
##  3 2022  11    14    Heritage 4I     SIOC    N      <NA>           90        18
##  4 2022  11    14    Heritage 2H     REME    N      M              38        26
##  5 2022  11    14    Heritage 4J     SIOC    N      <NA>           NA        NA
##  6 2022  11    14    Heritage 2F     REME    N      F              22        10
##  7 2022  11    15    Heritage 4C     SIOC    R      <NA>           NA        NA
##  8 2022  11    15    Heritage 4H     SIOC    N      F              95        11
##  9 2022  11    15    Heritage 1H     REME    N      <NA>           26         9
## 10 2022  11    15    Heritage 1B     REME    N      F              35         9
## # i 41 more rows
## # i 7 more variables: AnimalWeight <dbl>, HindfoodLength <dbl>,
## #   TailLength <chr>, HairSample <chr>, Position <chr>, Handler <chr>,
## #   Notes <chr>
```

```
#b
rodents <- rodents %>%
  unite("Date", Year:Day, sep = "-")
rodents
```

```
## # A tibble: 51 x 15
##    Date     Site  TrapID Species Status Sex   TotalWeight BagWeight AnimalWeight
##    <chr>    <chr> <chr>  <chr>   <chr>  <chr>       <dbl>     <dbl>        <dbl>
##  1 2022-11~ Heri~ 4C     SIOC    N      F             134        18          116
##  2 2022-11~ Heri~ 4D     SIOC    N      M             136        18          118
##  3 2022-11~ Heri~ 4I     SIOC    N      <NA>           90        18           72
##  4 2022-11~ Heri~ 2H     REME    N      M              38        26           12
##  5 2022-11~ Heri~ 4J     SIOC    N      <NA>           NA        NA           NA
##  6 2022-11~ Heri~ 2F     REME    N      F              22        10           12
##  7 2022-11~ Heri~ 4C     SIOC    R      <NA>           NA        NA           NA
##  8 2022-11~ Heri~ 4H     SIOC    N      F              95        11           84
##  9 2022-11~ Heri~ 1H     REME    N      <NA>           26         9            17
## 10 2022-11~ Heri~ 1B     REME    N      F              35         9            26
## # i 41 more rows
## # i 6 more variables: HindfoodLength <dbl>, TailLength <chr>, HairSample <chr>,
## #   Position <chr>, Handler <chr>, Notes <chr>
```

```
#c
sp_by_site <- rodents %>%
  group_by(Site, Species) %>%
  summarize(Count = n())
```

```
## `summarise()` has grouped output by 'Site'. You can override using the
## `.groups` argument.
```

```
sp_by_site
```

```
## # A tibble: 7 x 3
## # Groups:   Site [2]
##   Site     Species Count
##   <chr>    <chr>   <int>
## 1 Drexel   CHPE        3
## 2 Drexel   DIME        5
## 3 Drexel   NEAB        1
## 4 Drexel   PEER        5
## 5 Drexel   SIOC        1
## 6 Heritage REME       10
## 7 Heritage SIOC       26
```

```
#d
sp_by_site %>%
  pivot_wider(names_from = Species,
              values_from = Count,
              values_fill = 0)
```

```
## # A tibble: 2 x 7
## # Groups:   Site [2]
##   Site      CHPE  DIME  NEAB  PEER  SIOC  REME
##   <chr>    <int> <int> <int> <int> <int> <int>
## 1 Drexel       3     5     1     5     1     0
## 2 Heritage     0     0     0     0    26    10
```

6. Mammals (20 pts)

The code chunk below has some made-up mammal data. Run the code chunk below to complete Question 6.

```
mammals <- data.frame(site = c(1,1,2,3,3,3),
                      taxon = c('Suncus etruscus', 'Sorex cinereus',
                                'Myotis nigricans', 'Notiosorex crawfordi',
                                'Suncus etruscus', 'Myotis nigricans'),
                      density = c(6.2, 5.2, 11.0, 1.2, 9.4, 9.6),
                      avg_mass = c(4.2, 5, 9.1, 8.6, 4.1, 8.7))
```

Like with many of the questions before, save your output from each task to use in the next task. You can overwrite the `mammals` object each time if you would like to.

a. Use the `separte()` function to create columns for the genus and species (from the taxon column).
b. Use `pivot_longer` so that `density` and `mass` end up in one column and the values end up in another column.
c. Even though the data from (b) is longer, it isn't tidier. Explain why not.
d. Use the `unite()` function to bring the genus and species column back together as one column with whatever separator you choose.
e. Use `pivot_wider()` to bring the data frame back to it's original state.

```r
mammals <- mammals %>%
  separate(taxon, c("genus", "species"), sep = " ")

mammals <- mammals %>%
  pivot_longer(density:avg_mass, names_to = "measurement", values_to = "value")

mammals <- mammals %>%
  unite("taxon", genus, species, sep = " ")

mammals <- mammals %>%
  pivot_wider(names_from = measurement, values_from = value)
```