Week 6 Assignment

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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   3.4.4     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- 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)

These data are downloaded from the WHO and contain the amount of forest (sq. km) per country. 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))`.

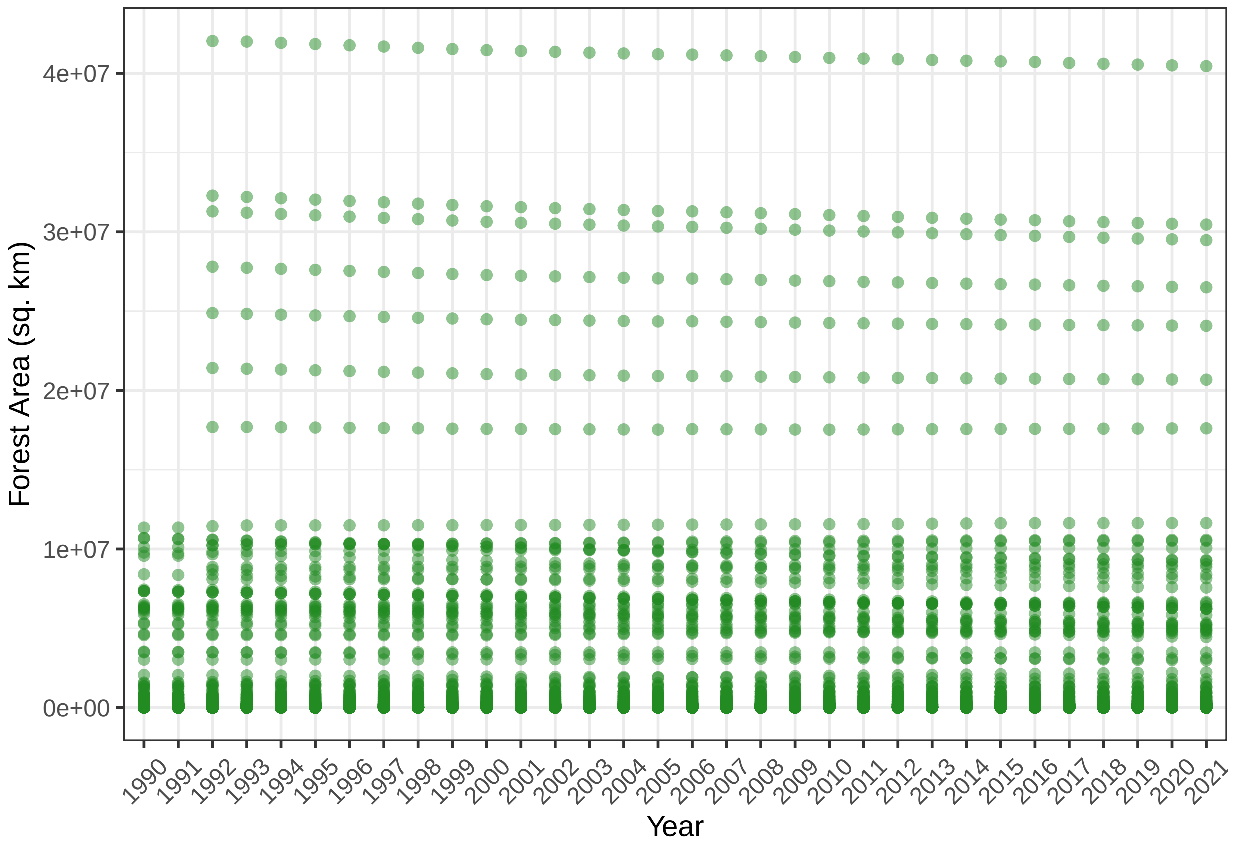
```
# a
forest <- forest %>%
  pivot_longer(`1990`:`2022`, names_to = "Year", values_to = "ForestArea_sqkm")
forest
```

```
## # 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
```

```r
# 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)

We have some 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.

Run this line of code to read in the file. Like the forest data, this data has a few rows of metadata at the top of the document that we need to skip.

```r
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>
```

a. Use the `fill()` function to fill in the values in the first column.
b. Use `pivot_longer()` to 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.

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

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

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.

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.

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.

```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, "?"))
```

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

```r
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).
b. Select the Site, Trap Location and Grouped Veg columns and save those as a new dataframe
c. Use an `inner_join()` to join those same 2 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.

a. Use the `separate()` function to split the date column into 3 separate columns.

b. Use `unite()` to bring them back together into 1 Date 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`.

```r
#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>
```

```r
#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>
```

```r
#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 5.

```
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),
                      mass = c(4.2, 5, 9.1, 8.6, 4.1, 8.7))
```

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:mass, names_to = "measurement", values_to = "value")

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

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