Week 4 Assignment

Grace Adams

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Assignment Details

Purpose

The goal of this assignment is to work with data aggregation and joining data frames together using `dplyr` functions.

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

Feb 12 at midnight MST

Assignment Exercises

1. Set-Up (5 pts)

Load the `readr` and `dplyr` packages.

Read in the following data sets using `read_csv()`. Even if they already exist in your current working environment, you will need to have the code to read them in this document to successfully `Knit`.

- `surveys.csv`
- `species.csv`
- `plots.csv`

```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     1.3.0
## 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
```

```
surveys <- read_csv("surveys.csv")
```

```
## Rows: 35549 Columns: 9
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (2): species_id, sex
## dbl (7): record_id, month, day, year, plot_id, hindfoot_length, weight
##
## 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.
```

```
species <- read_csv("species.csv")
```

```
## Rows: 54 Columns: 4
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (4): species_id, genus, species, taxa
##
## 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.
```

```
plots <- read_csv("plots.csv")
```

```
## Rows: 24 Columns: 2
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (1): plot_type
## dbl (1): plot_id
##
## 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.
```

2. Portal Data Aggregation (10 pts)

Using the `surveys` data frame, complete the following:

a. Use the `group_by()` and `summarize()` functions to get a count of the number of individuals in each species ID.
b. Use the `group_by()` and `summarize()` functions to get a count of the number of individuals in each species ID in each year.
c. Use the `filter()`, `group_by()`, and `summarize()` functions to get the mean mass of species `DO` in each year.

```
question2a <- surveys %>%
  group_by(species_id) %>%
  summarize(abundance = n())
question2a
```

```
## # A tibble: 49 x 2
##    species_id abundance
##    <chr>          <int>
##  1 AB               303
##  2 AH               437
##  3 AS                 2
##  4 BA                46
##  5 CB                50
##  6 CM                13
##  7 CQ                16
##  8 CS                 1
##  9 CT                 1
## 10 CU                 1
## # i 39 more rows
```

```
question2b <- surveys %>%
  group_by(species_id, year) %>%
  summarize(abundance = n())
```

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

```
question2b
```

```
## # A tibble: 535 x 3
## # Groups:   species_id [49]
##    species_id  year abundance
##    <chr>      <dbl>     <int>
##  1 AB          1980         5
##  2 AB          1981         7
##  3 AB          1982        34
##  4 AB          1983        41
##  5 AB          1984        12
##  6 AB          1985        14
##  7 AB          1986         5
##  8 AB          1987        35
##  9 AB          1988        39
## 10 AB          1989        31
## # i 525 more rows
```

```
question2c <- surveys %>%
  filter(species_id == "DO") %>%
  group_by(year) %>%
  summarize(mean_mass = mean(weight, na.rm=TRUE))
question2c
```

```
## # A tibble: 26 x 2
##     year mean_mass
##    <dbl>     <dbl>
##  1  1977      42.7
##  2  1978      45
##  3  1979      45.9
##  4  1980      48.1
##  5  1981      49.1
##  6  1982      47.9
##  7  1983      47.2
##  8  1984      48.4
##  9  1985      48.0
## 10  1986      49.4
## # i 16 more rows
```

3. Shrub Volume Aggregation (10 pts)

This is a follow-up to Shrub Volume Data Basics (from a previous assignment).

Dr. Morales wants some summary data of the plants at her sites and for her experiments. If the file shrub-volume-data.csv is not already in your work space download it.

This code calculates the average height of a plant at each site:

```
shrub_dims <- read_csv('shrub-volume-data.csv')
```

```
## Rows: 15 Columns: 5
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## dbl (5): site, experiment, length, width, height
##
## 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.
```

```
shrub_dims %>%
  group_by(experiment) %>%
  summarize(avg_height = mean(height, na.rm=TRUE), max_height = max(height, na.rm=TRUE))
```

```
## # A tibble: 3 x 3
##   experiment avg_height max_height
##        <dbl>      <dbl>      <dbl>
## 1          1       4.7         9.6
## 2          2       5.12        7.6
## 3          3       3.85        7.5
```

Modify the code to calculate and print the average height of a plant in each experiment.

Add a line of code to use `max()` to determine the maximum height of a plant at each experiment.

Also, remember to modify the code so that there are no NAs produced in the final output.

4. Portal Data Joins (15 pts)

Using the Portal data sets, do the following:

a. Use `inner_join()` to create a table that contains the information from both the surveys table and the species table.
b. Use `inner_join()` twice to create a table that contains the information from all three tables.
c. Use `inner_join()` and `filter()` to get a data frame with the information from the surveys and plots tables where the plot_type is Control.

```
number4_a <- inner_join(surveys, species, join_by(species_id))
number4_a
```

```
## # A tibble: 34,786 x 12
##    record_id month   day  year plot_id species_id sex   hindfoot_length weight
##        <dbl> <dbl> <dbl> <dbl>   <dbl> <chr>      <chr>           <dbl>  <dbl>
##  1         1     7    16  1977       2 NL         M                  32     NA
##  2         2     7    16  1977       3 NL         M                  33     NA
##  3         3     7    16  1977       2 DM         F                  37     NA
##  4         4     7    16  1977       7 DM         M                  36     NA
##   5          5     7    16  1977       3 DM         M                    35     NA
##   6          6     7    16  1977       1 PF         M                    14     NA
##   7          7     7    16  1977       2 PE         F                    NA     NA
##   8          8     7    16  1977       1 DM         M                    37     NA
##   9          9     7    16  1977       1 DM         F                    34     NA
## 10         10     7    16  1977       6 PF         F                    20     NA
## # i 34,776 more rows
## # i 3 more variables: genus <chr>, species <chr>, taxa <chr>
```

```
number4_b <- number4_a %>%
  inner_join(., plots, join_by(plot_id))
number4_b
```

```
## # A tibble: 34,786 x 13
##    record_id month   day  year plot_id species_id sex   hindfoot_length weight
##        <dbl> <dbl> <dbl> <dbl>   <dbl> <chr>      <chr>           <dbl>  <dbl>
##   1          1     7    16  1977       2 NL         M                    32     NA
##   2          2     7    16  1977       3 NL         M                    33     NA
##   3          3     7    16  1977       2 DM         F                    37     NA
##   4          4     7    16  1977       7 DM         M                    36     NA
##   5          5     7    16  1977       3 DM         M                    35     NA
##   6          6     7    16  1977       1 PF         M                    14     NA
##   7          7     7    16  1977       2 PE         F                    NA     NA
##   8          8     7    16  1977       1 DM         M                    37     NA
##   9          9     7    16  1977       1 DM         F                    34     NA
## 10         10     7    16  1977       6 PF         F                    20     NA
## # i 34,776 more rows
## # i 4 more variables: genus <chr>, species <chr>, taxa <chr>, plot_type <chr>
```

```
number4_c <- surveys %>%
  inner_join(., plots, join_by(plot_id)) %>%
  filter(plot_type == "Control")
number4_c
```

```
## # A tibble: 15,660 x 10
##    record_id month   day  year plot_id species_id sex   hindfoot_length weight
##        <dbl> <dbl> <dbl> <dbl>   <dbl> <chr>      <chr>           <dbl>  <dbl>
##   1          1     7    16  1977       2 NL         M                    32     NA
##   2          3     7    16  1977       2 DM         F                    37     NA
##   3          7     7    16  1977       2 PE         F                    NA     NA
##   4         14     7    16  1977       8 DM         <NA>                 NA     NA
##   5         16     7    16  1977       4 DM         F                    36     NA
##   6         18     7    16  1977       2 PP         M                    22     NA
##   7         19     7    16  1977       4 PF         <NA>                 NA     NA
##   8         20     7    17  1977      11 DS         F                    48     NA
##   9         21     7    17  1977      14 DM         F                    34     NA
## 10         28     7    17  1977      11 DM         M                    38     NA
## # i 15,650 more rows
## # i 1 more variable: plot_type <chr>
```

5. Portal Data `dplyr` Review (20 pts)

We want to do an analysis comparing the size of individuals on the Control plots to the Long-term Krat Exclosures.

Create a data frame with the `year`, `genus`, `species`, `weight` and `plot_type` for all cases where the plot type is either Control or Long-term Krat Exclosure. Only include cases where Taxa is Rodent. Remove any records where the weight is missing.

```
head(number4_b)
```

```
## # A tibble: 6 x 13
##   record_id month   day  year plot_id species_id sex   hindfoot_length weight
##       <dbl> <dbl> <dbl> <dbl>   <dbl> <chr>      <chr>           <dbl>  <dbl>
## 1         1     7    16  1977       2 NL         M                  32     NA
## 2         2     7    16  1977       3 NL         M                  33     NA
## 3         3     7    16  1977       2 DM         F                  37     NA
## 4         4     7    16  1977       7 DM         M                  36     NA
## 5         5     7    16  1977       3 DM         M                  35     NA
## 6         6     7    16  1977       1 PF         M                  14     NA
## # i 4 more variables: genus <chr>, species <chr>, taxa <chr>, plot_type <chr>
```

```
number5 <- number4_b %>%
  select(year, genus, species, weight, plot_type, taxa) %>%
  filter(plot_type == "Control" | plot_type == "Long-term Krat Exclosure", taxa == "Rodent", !is.na(wei
  select(year, genus, species, weight, plot_type)
number5
```

```
## # A tibble: 19,344 x 5
##     year genus       species  weight plot_type
##    <dbl> <chr>       <chr>     <dbl> <chr>
##  1  1977 Dipodomys   merriami     40 Long-term Krat Exclosure
##  2  1977 Dipodomys   merriami     29 Control
##  3  1977 Dipodomys   merriami     46 Control
##  4  1977 Dipodomys   ordii        52 Control
##  5  1977 Perognathus flavus        8 Control
##  6  1977 Onychomys   sp.          22 Long-term Krat Exclosure
##  7  1977 Perognathus flavus        7 Control
##  8  1977 Dipodomys   merriami     22 Control
##  9  1977 Perognathus flavus        8 Control
## 10  1977 Dipodomys   merriami     41 Control
## # i 19,334 more rows
```

6. Shrub Volumn Bind (10 pts)

First, run the following code chunk to produce a data frame with additional data related to the shrub volumn data (shrub_dims).

```
new_data <- data.frame(respiratory_rate = c(2.2, 4.0, 6.1, 2.3, 4.1, 6.2, 1.8, 3.5, 5.7, 1.9, 3.5, 5.8,
                      average_temp_C = c(15.1, 20.2, 24.7, 15.2, 22.0, 25.1, 14.2, 19.0, 23.6, 14.9, 2
```

Take a look at the new dataframe that has just been produced. Should this data be bound to the shrub volumn data by bind_rows() or bind_cols()? How do you know?

```
head(shrub_dims)
```

```
## # A tibble: 6 x 5
##    site experiment length width height
##   <dbl>      <dbl>  <dbl> <dbl>  <dbl>
## 1     1          1    2.2   1.3    9.6
## 2     1          2    2.1   2.2    7.6
## 3     1          3    2.7   1.5    2.2
## 4     2          1    3     4.5    1.5
## 5     2          2    3.1   3.1    4
## 6     2          3    2.5   2.8    3
```

```
head(new_data)
```

```
##   respiratory_rate average_temp_C
## 1              2.2           15.1
## 2              4.0           20.2
## 3              6.1           24.7
## 4              2.3           15.2
## 5              4.1           22.0
## 6              6.2           25.1
```

Answer: # It should be bound using bind_cols since there are two new columns of data, not new observations to add to existing columns.

Based on your answer above, bind the `shrub_dims` and `new_data` data frames together.

```
new_shrub_dims <- bind_cols(shrub_dims, new_data)
new_shrub_dims
```

```
## # A tibble: 15 x 7
##     site experiment length width height respiratory_rate average_temp_C
##    <dbl>      <dbl>  <dbl> <dbl>  <dbl>            <dbl>          <dbl>
##  1     1          1    2.2   1.3    9.6              2.2           15.1
##  2     1          2    2.1   2.2    7.6              4             20.2
##  3     1          3    2.7   1.5    2.2              6.1           24.7
##  4     2          1    3     4.5    1.5              2.3           15.2
##  5     2          2    3.1   3.1    4                4.1           22
##  6     2          3    2.5   2.8    3                6.2           25.1
##  7     3          1    1.9   1.8    4.5              1.8           14.2
##  8     3          2    1.1   0.5    2.3              3.5           19
##  9     3          3    3.5   2      7.5              5.7           23.6
## 10     4          1    2.9   2.7    3.2              1.9           14.9
## 11     4          2    4.5   4.8    6.5              3.5           20.3
## 12     4          3    1.2   1.8    2.7              5.8           24.1
## 13     5          1    2.6   0.8   NA                2             19.2
## 14     5          2    1.8  NA      5.2              4.7           22.7
## 15     5          3    3.1   2.2   NA                6.2           25
```

7. Shrub Volume Join (10 pts)

This is a follow-up to Shrub Volume Aggregation.

In addition to the main data table on shrub dimensions (`shrub_dims` from Q3), Dr. Morales has two additional data tables. The first describes the manipulation for each experiment. The second provides information about the different sites. Run the following code chunk to bring them into your environment.

```
experiments <- read_csv("https://datacarpentry.org/semester-biology/data/shrub-volume-experiments.csv")
```

```
## Rows: 3 Columns: 2
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (1): manipulation
## dbl (1): experiment
##
## 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.
```

```
sites <- read_csv("https://datacarpentry.org/semester-biology/data/shrub-volume-sites.csv")
```

```
## Rows: 4 Columns: 4
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## dbl (4): site, latitude, longitude, elevation
##
## 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.
```

Use `inner_join()` to combine `experiments` with the shrub dimensions data to add a manipulation column to the shrub data.

```
number7_a <- inner_join(shrub_dims, experiments, join_by(experiment))
number7_a
```

```
## # A tibble: 15 x 6
##     site experiment length width height manipulation
##    <dbl>      <dbl>  <dbl> <dbl>  <dbl> <chr>
##  1     1          1    2.2   1.3    9.6 control
##  2     1          2    2.1   2.2    7.6 burn
##  3     1          3    2.7   1.5    2.2 rainout
##  4     2          1    3     4.5    1.5 control
##  5     2          2    3.1   3.1    4   burn
##  6     2          3    2.5   2.8    3   rainout
##  7     3          1    1.9   1.8    4.5 control
##  8     3          2    1.1   0.5    2.3 burn
##  9     3          3    3.5   2      7.5 rainout
## 10     4          1    2.9   2.7    3.2 control
## 11     4          2    4.5   4.8    6.5 burn
## 12     4          3    1.2   1.8    2.7 rainout
## 13     5          1    2.6   0.8   NA   control
## 14     5          2    1.8  NA      5.2 burn
## 15     5          3    3.1   2.2   NA   rainout
```

Next, combine the `sites` data frame with both the data on shrub dimensions and the data on experiments to produce a single data frame that contains all of the data.

```
number7_b <- number7_a %>%
  inner_join(., sites, join_by(site))
number7_b
```

```
## # A tibble: 12 x 9
##     site experiment length width height manipulation latitude longitude
##    <dbl>      <dbl>  <dbl> <dbl>  <dbl> <chr>           <dbl>     <dbl>
##  1     1          1    2.2   1.3    9.6 control          29.6     -82.3
##  2     1          2    2.1   2.2    7.6 burn             29.6     -82.3
##  3     1          3    2.7   1.5    2.2 rainout          29.6     -82.3
##  4     2          1    3     4.5    1.5 control          29.3     -82.4
##  5     2          2    3.1   3.1    4   burn             29.3     -82.4
##  6     2          3    2.5   2.8    3   rainout          29.3     -82.4
##  7     3          1    1.9   1.8    4.5 control          29.8     -82.2
##  8     3          2    1.1   0.5    2.3 burn             29.8     -82.2
##  9     3          3    3.5   2      7.5 rainout          29.8     -82.2
## 10     4          1    2.9   2.7    3.2 control          30.0     -82.6
## 11     4          2    4.5   4.8    6.5 burn             30.0     -82.6
## 12     4           3    1.2   1.8    2.7 rainout          30.0     -82.6
## # i 1 more variable: elevation <dbl>
```

8. Extracting vectors from data frames (10 pts)

Using the `shrub_data` data frame you just created in Question 7:

a. Use `$` to extract the latitude column into a vector
b. Use `[]` to extract the manipulation column into a vector
c. Extract the `width` column into a vector and calculate the mean width, removing null values.

```r
number8_a <- number7_b$latitude
number8_a
```

```
##  [1] 29.65 29.65 29.65 29.26 29.26 29.26 29.80 29.80 29.80 29.99 29.99 29.99
```

```r
number8_b <- number7_b[["manipulation"]]
number8_b
```

```
##  [1] "control" "burn"    "rainout" "control" "burn"    "rainout" "control"
##  [8] "burn"    "rainout" "control" "burn"    "rainout"
```

```r
number8_c <- number7_b$width
number8_c
```

```
##  [1] 1.3 2.2 1.5 4.5 3.1 2.8 1.8 0.5 2.0 2.7 4.8 1.8
```

```r
number8_cp2 <- mean(number8_c, na.rm=TRUE)
number8_cp2
```

```
## [1] 2.416667
```

9. Building data frames from vectors (10 pts)

You have data on the length, width, and height of 10 individuals of the Foothills Palo Verde tree (*Cercidium microphyllum*) stored in the following vectors:

```r
length <- c(2.2, 2.1, 2.7, 3.0, 3.1, 2.5, 1.9, 1.1, 3.5, 2.9)
width <- c(1.3, 2.2, 1.5, 4.5, 3.1, NA, 1.8, 0.5, 2.0, 2.7)
height <- c(9.6, 7.6, 2.2, 1.5, 4.0, 3.0, 4.5, 2.3, 7.5, 3.2)
```

Make a data frame that contains these three vectors as columns along with a genus column containing the name “Cercidium” on all rows and a species column containing the word “microphyllum” on all rows.

```r
number9 <- data.frame(genus = "Cercidium",
                      species = "microphyllum",
                      length=length,
                      width=width,
                      height=height)
number9
```

```
##        genus      species length width height
## 1  Cercidium microphyllum    2.2   1.3    9.6
## 2  Cercidium microphyllum    2.1   2.2    7.6
## 3  Cercidium microphyllum    2.7   1.5    2.2
## 4  Cercidium microphyllum    3.0   4.5    1.5
## 5  Cercidium microphyllum    3.1   3.1    4.0
## 6  Cercidium microphyllum    2.5    NA    3.0
## 7  Cercidium microphyllum    1.9   1.8    4.5
## 8  Cercidium microphyllum    1.1   0.5    2.3
## 9  Cercidium microphyllum    3.5   2.0    7.5
## 10 Cercidium microphyllum    2.9   2.7    3.2
```