

Data_Wrangling_Jacob_Chung_Joshua_Holt

```
#install.packages("tidyverse")  
## Load packages from library  
library("tidyverse")
```

Warning: package 'dplyr' was built under R version 4.2.3

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --  
v dplyr      1.1.4      v readr      2.1.6  
v forcats    1.0.1      v stringr    1.6.0  
v ggplot2    4.0.1      v tibble     3.3.0  
v lubridate  1.9.4      v tidyr      1.3.2  
v purrr      1.2.0  
-- 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
```

```
library(here)
```

here() starts at /Users/jacobchung/coding_projects/Data_Wrangling_1_Rows_Columns_JC_JH

```
fruits <- c("apple", "apple", "orange", "orange", "banana")
```

Start of code

```
fruits <- c("apple", "apple", "orange", "orange", "banana")  
unique(fruits)
```

```
[1] "apple" "orange" "banana"
```

length

```
length(unique(fruits))
```

```
[1] 3
```

```
#create intermediate data objects  
unique.fruits <- unique(fruits)  
length(unique.fruits)
```

```
[1] 3
```

Piping

```
# for instance:  
fruits %>% unique()
```

```
[1] "apple" "orange" "banana"
```

```
# is the same as:  
unique(fruits)
```

```
[1] "apple" "orange" "banana"
```

```
# Piping!  
fruits %>% unique() %>% length()
```

```
[1] 3
```

```
#Add lines  
fruits %>%  
  unique() %>%  
  length()
```

```
[1] 3
```

Importing data

```
# Import the data
cereal <- read_csv(here("cereal.csv"))
```

Rows: 77 Columns: 16

-- Column specification -----

Delimiter: ","

chr (3): name, mfr, type

dbl (13): calories, protein, fat, sodium, fiber, carbo, sugars, potass, vita...

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 first six rows
head(cereal)
```

A tibble: 6 x 16

	name <chr>	mfr <chr>	type <chr>	calories <dbl>	protein <dbl>	fat <dbl>	sodium <dbl>	fiber <dbl>	carbo <dbl>	sugars <dbl>	potass <dbl>
1	100% Bran	Nabi~	C	70	4	1	130	10	5	6	280
2	100% Natu~	Quak~	C	120	3	5	15	2	8	8	135
3	All-Bran	Kell~	C	70	4	1	260	9	7	5	320
4	All-Bran ~	Kell~	C	50	4	0	140	14	8	0	330
5	Almond De~	Rals~	C	110	2	2	200	1	14	8	-1
6	Apple Cin~	Gene~	C	110	2	2	180	1.5	10.5	10	70

i 5 more variables: vitamins <dbl>, shelf <dbl>, weight <dbl>, cups <dbl>,

rating <dbl>

```
# Start with the cereal dataframe
```

```
cereal %>%
```

```
# This line extracts the column names from the dataframe input and creates a vector
```

```
colnames() %>%
```

```
# This line calculates the "length" (the number) of those names from the vector input
```

```
length()
```

```
[1] 16
```

Select() columns

```
cereal %>%  
  select(name, calories, fiber)
```

```
# A tibble: 77 x 3  
  name                calories fiber  
  <chr>              <dbl> <dbl>  
1 100% Bran           70    10  
2 100% Natural Bran  120     2  
3 All-Bran           70     9  
4 All-Bran with Extra Fiber  50    14  
5 Almond Delight     110     1  
6 Apple Cinnamon Cheerios  110    1.5  
7 Apple Jacks        110     1  
8 Basic 4            130     2  
9 Bran Chex          90     4  
10 Bran Flakes       90     5  
# i 67 more rows
```

```
cereal_fiber <- cereal %>%  
  select(name, calories, fiber)  
  
#Excluding columns  
cereal %>%  
  select(-name, -mfr)
```

```
# A tibble: 77 x 14  
  type calories protein fat sodium fiber carbo sugars potass vitamins shelf  
  <chr>   <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>   <dbl> <dbl>  
1 C       70     4     1   130   10     5     6   280     25     3  
2 C      120     3     5    15     2     8     8   135      0     3  
3 C       70     4     1   260     9     7     5   320     25     3  
4 C       50     4     0   140    14     8     0   330     25     3  
5 C      110     2     2   200     1    14     8    -1     25     3  
6 C      110     2     2   180    1.5  10.5    10    70     25     1  
7 C      110     2     0   125     1    11    14    30     25     2  
8 C      130     3     2   210     2    18     8   100     25     3  
9 C       90     2     1   200     4    15     6   125     25     1  
10 C       90     3     0   210     5    13     5   190     25     3  
# i 67 more rows  
# i 3 more variables: weight <dbl>, cups <dbl>, rating <dbl>
```

Q1.1A:

```
cereal_sugar <- cereal %>%  
  select(name, mfr, sugars)
```

1.4 rename

```
cereal_sugar %>%  
  # Rename the mfr column to a more informative manufacturer  
  rename(manufacturer = mfr)
```

```
# A tibble: 77 x 3
```

	name <chr>	manufacturer <chr>	sugars <dbl>
1	100% Bran	Nabisco	6
2	100% Natural Bran	Quaker_Oats	8
3	All-Bran	Kelloggs	5
4	All-Bran with Extra Fiber	Kelloggs	0
5	Almond Delight	Ralston_Purina	8
6	Apple Cinnamon Cheerios	General_Mills	10
7	Apple Jacks	Kelloggs	14
8	Basic 4	General_Mills	8
9	Bran Chex	Ralston_Purina	6
10	Bran Flakes	Post	5

```
# i 67 more rows
```

```
#multiple columns
```

```
cereal_sugar %>%  
  rename(manufacturer = mfr,  
         cereal_name = name)
```

```
# A tibble: 77 x 3
```

	cereal_name <chr>	manufacturer <chr>	sugars <dbl>
1	100% Bran	Nabisco	6
2	100% Natural Bran	Quaker_Oats	8
3	All-Bran	Kelloggs	5
4	All-Bran with Extra Fiber	Kelloggs	0

5	Almond Delight	Ralston_Purina	8
6	Apple Cinnamon Cheerios	General_Mills	10
7	Apple Jacks	Kelloggs	14
8	Basic 4	General_Mills	8
9	Bran Chex	Ralston_Purina	6
10	Bran Flakes	Post	5

i 67 more rows

1.5 relocate()

```
cereal_sugar %>%
  relocate(mfr, .before = name)
```

```
# A tibble: 77 x 3
   mfr      name      sugars
  <chr>   <chr>      <dbl>
1 Nabisco 100% Bran      6
2 Quaker_Oats 100% Natural Bran 8
3 Kelloggs All-Bran      5
4 Kelloggs All-Bran with Extra Fiber 0
5 Ralston_Purina Almond Delight 8
6 General_Mills Apple Cinnamon Cheerios 10
7 Kelloggs Apple Jacks 14
8 General_Mills Basic 4 8
9 Ralston_Purina Bran Chex 6
10 Post Bran Flakes 5
# i 67 more rows
```

1.6 filter()

```
cereal_sugar %>%
  filter(sugars > 12)
```

```
# A tibble: 9 x 3
   name      mfr      sugars
  <chr>   <chr>      <dbl>
1 Apple Jacks Kelloggs 14
2 Cocoa Puffs General_Mills 13
```

3	Count Chocula	General_Mills	13
4	Froot Loops	Kelloggs	13
5	Golden Crisp	Post	15
6	Mueslix Crispy Blend	Kelloggs	13
7	Post Nat. Raisin Bran	Post	14
8	Smacks	Kelloggs	15
9	Total Raisin Bran	General_Mills	14

```
cereal_sugar %>%
  filter(mfr == "Kelloggs")
```

```
# A tibble: 23 x 3
  name                mfr      sugars
  <chr>              <chr>    <dbl>
1 All-Bran           Kelloggs     5
2 All-Bran with Extra Fiber Kelloggs     0
3 Apple Jacks        Kelloggs    14
4 Corn Flakes        Kelloggs     2
5 Corn Pops          Kelloggs    12
6 Cracklin' Oat Bran Kelloggs     7
7 Crispix            Kelloggs     3
8 Froot Loops        Kelloggs    13
9 Frosted Flakes     Kelloggs    11
10 Frosted Mini-Wheats Kelloggs     7
# i 13 more rows
```

Q1.2A:

```
cereal_sugar %>%
  filter(mfr == "Kelloggs",
         sugars > 12)
```

```
# A tibble: 4 x 3
  name                mfr      sugars
  <chr>              <chr>    <dbl>
1 Apple Jacks        Kelloggs    14
2 Froot Loops        Kelloggs    13
3 Mueslix Crispy Blend Kelloggs    13
4 Smacks             Kelloggs    15
```

Q1.3A:

```
cereal %>%  
  select(name, fat, potass) %>%  
  filter(potass < 30)
```

```
# A tibble: 8 x 3  
  name                fat potass  
  <chr>              <dbl> <dbl>  
1 Almond Delight      2     -1  
2 Corn Chex           0     25  
3 Corn Pops           0     20  
4 Cream of Wheat (Quick) 0     -1  
5 Frosted Flakes      0     25  
6 Fruity Pebbles      1     25  
7 Puffed Rice         0     15  
8 Trix                1     25
```

Q1.4A:

```
cereal %>%  
  filter(calories > 120) %>%  
  select(fiber, fat, sodium)
```

```
# A tibble: 8 x 3  
  fiber    fat sodium  
  <dbl> <dbl> <dbl>  
1     2      2   210  
2     2      1   170  
3     3      3    95  
4     3      3   150  
5     3      2   150  
6     3      2   220  
7    1.5      2   170  
8     4      1   190
```


arrange()

```
cereal %>%  
  arrange(calories)
```

```
# A tibble: 77 x 16
```

	name	mfr	type	calories	protein	fat	sodium	fiber	carbo	sugars	potass
	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	All-Bran~	Kell~	C	50	4	0	140	14	8	0	330
2	Puffed R~	Quak~	C	50	1	0	0	0	13	0	15
3	Puffed W~	Quak~	C	50	2	0	0	1	10	0	50
4	100% Bran	Nabi~	C	70	4	1	130	10	5	6	280
5	All-Bran	Kell~	C	70	4	1	260	9	7	5	320
6	Shredded~	Nabi~	C	80	2	0	0	3	16	0	95
7	Bran Chex	Rals~	C	90	2	1	200	4	15	6	125
8	Bran Fla~	Post	C	90	3	0	210	5	13	5	190
9	Nutri-gr~	Kell~	C	90	3	0	170	3	18	2	90
10	Raisin S~	Kell~	C	90	2	0	0	2	15	6	110

```
# i 67 more rows  
# i 5 more variables: vitamins <dbl>, shelf <dbl>, weight <dbl>, cups <dbl>,  
#   rating <dbl>
```

```
cereal %>%  
  # The desc() reverses the order, making it highest to lowest  
  arrange(desc(calories))
```

```
# A tibble: 77 x 16
```

	name	mfr	type	calories	protein	fat	sodium	fiber	carbo	sugars	potass
	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	Mueslix ~	Kell~	C	160	3	2	150	3	17	13	160
2	Muesli R~	Rals~	C	150	4	3	95	3	16	11	170
3	Muesli R~	Rals~	C	150	4	3	150	3	16	11	170
4	Just Rig~	Kell~	C	140	3	1	170	2	20	9	95
5	Nutri-Gr~	Kell~	C	140	3	2	220	3	21	7	130
6	Total Ra~	Gene~	C	140	3	1	190	4	15	14	230
7	Basic 4	Gene~	C	130	3	2	210	2	18	8	100
8	Oatmeal ~	Gene~	C	130	3	2	170	1.5	13.5	10	120
9	100% Nat~	Quak~	C	120	3	5	15	2	8	8	135
10	Cap'n'Cr~	Quak~	C	120	1	2	220	0	12	12	35

```
# i 67 more rows
```

```
# i 5 more variables: vitamins <dbl>, shelf <dbl>, weight <dbl>, cups <dbl>,
#   rating <dbl>
```

```
cereal %>%
  arrange(mfr, calories)
```

```
# A tibble: 77 x 16
```

	name <chr>	mfr <chr>	type <chr>	calories <dbl>	protein <dbl>	fat <dbl>	sodium <dbl>	fiber <dbl>	carbo <dbl>	sugars <dbl>	potass <dbl>
1	Maypo	Amer~	H	100	4	1	0	0	16	3	95
2	Crispy W~	Gene~	C	100	2	1	140	2	11	10	120
3	Multi-Gr~	Gene~	C	100	2	1	220	2	15	6	90
4	Raisin N~	Gene~	C	100	3	2	140	2.5	10.5	8	140
5	Total Wh~	Gene~	C	100	3	1	200	3	16	3	110
6	Wheaties	Gene~	C	100	3	1	200	3	17	3	110
7	Apple Ci~	Gene~	C	110	2	2	180	1.5	10.5	10	70
8	Cheerios	Gene~	C	110	6	2	290	2	17	1	105
9	Clusters	Gene~	C	110	3	2	140	2	13	7	105
10	Cocoa Pu~	Gene~	C	110	1	1	180	0	12	13	55

```
# i 67 more rows
```

```
# i 5 more variables: vitamins <dbl>, shelf <dbl>, weight <dbl>, cups <dbl>,
#   rating <dbl>
```

1.8 mutate()

```
cereal_carbs <- cereal %>%
  # Select just the name, carbs, and sugars columns, and store it as a new data object called
  select(name, carbo, sugars)

cereal_carbs %>%
  # in this case, the new sugars_total column is going to be 2 times the sugars column
  mutate(sugars_total = sugars*2)
```

```
# A tibble: 77 x 4
```

	name <chr>	carbo <dbl>	sugars <dbl>	sugars_total <dbl>
1	100% Bran	5	6	12
2	100% Natural Bran	8	8	16
3	All-Bran	7	5	10

```

4 All-Bran with Extra Fiber      8      0      0
5 Almond Delight                 14      8     16
6 Apple Cinnamon Cheerios       10.5    10     20
7 Apple Jacks                    11     14     28
8 Basic 4                       18      8     16
9 Bran Chex                     15      6     12
10 Bran Flakes                   13      5     10
# i 67 more rows

```

```

cereal_carbs %>%
  mutate(sugars = sugars*2)

```

```

# A tibble: 77 x 3
  name                carbo sugars
  <chr>              <dbl> <dbl>
1 100% Bran           5      12
2 100% Natural Bran   8      16
3 All-Bran            7      10
4 All-Bran with Extra Fiber 8      0
5 Almond Delight     14      16
6 Apple Cinnamon Cheerios 10.5    20
7 Apple Jacks        11      28
8 Basic 4            18      16
9 Bran Chex          15      12
10 Bran Flakes       13      10
# i 67 more rows

```

```

# Check that the original cereal_carbs data is unaltered
cereal_carbs

```

```

# A tibble: 77 x 3
  name                carbo sugars
  <chr>              <dbl> <dbl>
1 100% Bran           5      6
2 100% Natural Bran   8      8
3 All-Bran            7      5
4 All-Bran with Extra Fiber 8      0
5 Almond Delight     14      8
6 Apple Cinnamon Cheerios 10.5    10
7 Apple Jacks        11     14
8 Basic 4            18      8

```

```

  9 Bran Chex                15      6
10 Bran Flakes              13      5
# i 67 more rows

```

```

cereal_carbs %>%
  mutate(sugars_with_milk = sugars + 5)

```

```
# A tibble: 77 x 4
```

	name <chr>	carbo <dbl>	sugars <dbl>	sugars_with_milk <dbl>
1	100% Bran	5	6	11
2	100% Natural Bran	8	8	13
3	All-Bran	7	5	10
4	All-Bran with Extra Fiber	8	0	5
5	Almond Delight	14	8	13
6	Apple Cinnamon Cheerios	10.5	10	15
7	Apple Jacks	11	14	19
8	Basic 4	18	8	13
9	Bran Chex	15	6	11
10	Bran Flakes	13	5	10

```
# i 67 more rows
```

```

cereal_carbs %>%
  mutate(total_carbs = carbo + sugars) %>%
  mutate(sugars_with_milk = sugars + 5)

```

```
# A tibble: 77 x 5
```

	name <chr>	carbo <dbl>	sugars <dbl>	total_carbs <dbl>	sugars_with_milk <dbl>
1	100% Bran	5	6	11	11
2	100% Natural Bran	8	8	16	13
3	All-Bran	7	5	12	10
4	All-Bran with Extra Fiber	8	0	8	5
5	Almond Delight	14	8	22	13
6	Apple Cinnamon Cheerios	10.5	10	20.5	15
7	Apple Jacks	11	14	25	19
8	Basic 4	18	8	26	13
9	Bran Chex	15	6	21	11
10	Bran Flakes	13	5	18	10

```
# i 67 more rows
```

```
cereal_carbs %>%
  mutate(total_carbs = carbo + sugars,
         sugars_with_milk = sugars + 5)
```

A tibble: 77 x 5

	name <chr>	carbo <dbl>	sugars <dbl>	total_carbs <dbl>	sugars_with_milk <dbl>
1	100% Bran	5	6	11	11
2	100% Natural Bran	8	8	16	13
3	All-Bran	7	5	12	10
4	All-Bran with Extra Fiber	8	0	8	5
5	Almond Delight	14	8	22	13
6	Apple Cinnamon Cheerios	10.5	10	20.5	15
7	Apple Jacks	11	14	25	19
8	Basic 4	18	8	26	13
9	Bran Chex	15	6	21	11
10	Bran Flakes	13	5	18	10

i 67 more rows

BISON!

```
#install.packages("lterdatasampler")
library(lterdatasampler)
```

Q2.1A

```
knz_bison
```

A tibble: 8,325 x 8

	data_code <chr>	rec_year <dbl>	rec_month <dbl>	rec_day <dbl>	animal_code <chr>	animal_sex <chr>	animal_weight <dbl>
1	CBH01	1994	11	8	813	F	890
2	CBH01	1994	11	8	834	F	1074
3	CBH01	1994	11	8	B-301	F	1060
4	CBH01	1994	11	8	B-402	F	989
5	CBH01	1994	11	8	B-403	F	1062

```

6 CBH01      1994      11      8 B-502      F      978
7 CBH01      1994      11      8 B-503      F     1068
8 CBH01      1994      11      8 B-504      F     1024
9 CBH01      1994      11      8 B-601      F      978
10 CBH01     1994      11      8 B-602      F     1188
# i 8,315 more rows
# i 1 more variable: animal_yob <dbl>

```

calculating the age of the bison

```

bison_stats <- knz_bison %>%
  mutate(bison_age = rec_year - animal_yob,
         bison_weight_kg = animal_weight * 0.453592)
bison_stats

```

```

# A tibble: 8,325 x 10
  data_code rec_year rec_month rec_day animal_code animal_sex animal_weight
  <chr>      <dbl>    <dbl>   <dbl> <chr>      <chr>      <dbl>
1 CBH01      1994      11      8 813      F          890
2 CBH01      1994      11      8 834      F         1074
3 CBH01      1994      11      8 B-301    F          1060
4 CBH01      1994      11      8 B-402    F           989
5 CBH01      1994      11      8 B-403    F          1062
6 CBH01      1994      11      8 B-502    F           978
7 CBH01      1994      11      8 B-503    F         1068
8 CBH01      1994      11      8 B-504    F         1024
9 CBH01      1994      11      8 B-601    F           978
10 CBH01     1994      11      8 B-602    F         1188
# i 8,315 more rows
# i 3 more variables: animal_yob <dbl>, bison_age <dbl>, bison_weight_kg <dbl>

```

Q2.2A:

After looking at the data set, we came up with the research question, “Is there a case of sexual dimorphism in the bison based on the relationship between bison age and weight in the data provided?”

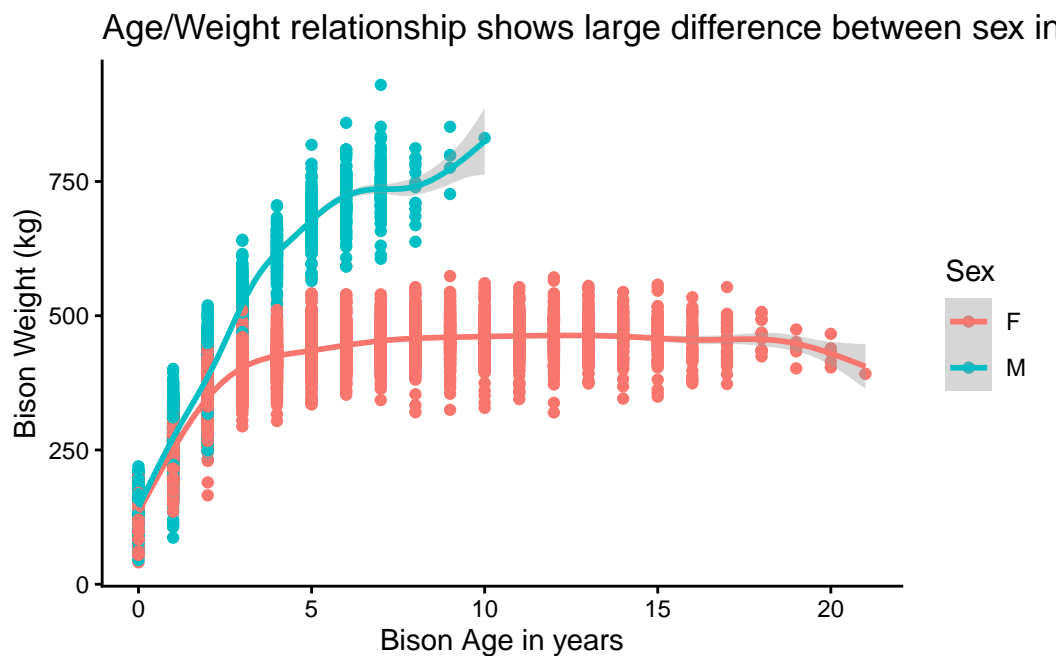
Q2.3A:

```
bison_graph <- ggplot(bison_stats, aes(x = bison_age, y = bison_weight_kg, color = animal_sex)) +  
  geom_point() +  
  geom_smooth() +  
  labs(x = "Bison Age in years",  
       y = "Bison Weight (kg)",  
       title = "Age/Weight relationship shows large difference between sex in American Bison") +  
  theme(plot.title = element_text(size = 10)) +  
  theme_classic()  
bison_graph
```

`geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'

Warning: Removed 252 rows containing non-finite outside the scale range
(`stat_smooth()`).

Warning: Removed 252 rows containing missing values or values outside the scale range
(`geom_point()`).



```
ggsave("Age_Weight_Relationship_DataWrangling.png")
```

```
Saving 5.5 x 3.5 in image
```

```
`geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
```

```
Warning: Removed 252 rows containing non-finite outside the scale range  
(`stat_smooth()`).
```

```
Removed 252 rows containing missing values or values outside the scale range  
(`geom_point()`).
```

Our sentences

After looking at our data, we noticed that there was a large dimorphism in weight between the sexes. A follow up research question is why do males disappear around age 10? Is it because of the way they were marking and recording the bison, or is there an ecological reason?