

# Bill's Drills Book

William McDonald

2020-04-18



# Contents

<b>1 Drills: Part of Every Healthy Intellectual Diet</b>	<b>5</b>
<b>2 Data Exploration</b>	<b>7</b>
2.1 Counting things. The naming of parts. . . . .	7
2.2 Summarize is another very useful function: . . . . .	10
2.3 Referencing other parts of the document . . . . .	11
2.4 Referencing citations: . . . . .	11
<b>3 Sampling</b>	<b>13</b>
3.1 Think about throwing a bunch of dice. . . . .	13
3.2 A keen way to divide up a dataset into testing and training components. . . . .	13
<b>4 Factor Practice</b>	<b>17</b>
<b>5 Crossing Trial</b>	<b>19</b>
<b>6 By Any Other Name</b>	<b>23</b>
<b>7 Correlation Plots</b>	<b>27</b>
<b>8 if_else() and case_when(): Comparison</b>	<b>35</b>
8.1 case_when() . . . . .	35
8.2 Compare this with if_else() . . . . .	37
<b>9 Subsetting</b>	<b>39</b>
9.1 Subsetting using brackets . . . . .	39
9.2 Subset using brackets by omitting the rows and columns we don't want . . . . .	40
9.3 Subset using brackets in combination with the which() function and the %in% operator . . . . .	40
9.4 Subset using the subset() function . . . . .	41
9.5 Subset using dplyr's filter() and select() . . . . .	41



# Chapter 1

## Drills: Part of Every Healthy Intellectual Diet

The goal of this book is to organize my R drills into reasonable chunks, the better to understand my strengths and weaknesses, and to plan new forays into data science.

Notes on **bookdown**:

- the `_bookdown.yml` file contains a snippet that is important to inserting the word “Chapter” before the chapter number in each of the Rmd files.
- packages are indicated in bold, like **dplyr**
- inline code and filenames are indicated in typewriter face using backticks, like `_bookdown.yml`
- `_output.yml` is modified from that used by Xie in his `bookdown-demo` (Xie, 2020); it evokes `style.css`, `toc.css`, `preamble.tex`, which are also borrowed from Xie.



## Chapter 2

# Data Exploration

Data exploration is one of the most important aspects of data science and forms the cornerstone of my drills. Nonetheless, I have lots of room for improvement.

I like Hadely Wickham's writing and find his approach exceptionally clear. Therefore, I'll use the **tidyverse**.

```
library(tidyverse)
```

### 2.1 Counting things. The naming of parts.

```
starwars %>%  
  filter(!is.na(species)) %>%  
  count(species = fct_lump(species, 5), sort = TRUE) %>%  
  mutate(species = fct_reorder(species, n)) %>%  
  ggplot(aes(species, n)) +  
  geom_col() + coord_flip()
```

I like stacked bars for their economy, but it's easy to over do it. Supperimposing gender onto the columns seems easy...

```
starwars %>%  
  filter(!is.na(species)) %>%  
  count(species = fct_lump(species, 5), gender = fct_lump(gender, 2), sort = TRUE) %>%  
  mutate(species = fct_reorder(species, n)) %>%  
  ggplot(aes(species, n, fill = gender)) +  
  geom_col() + coord_flip()
```

```
## Warning: Factor `gender` contains implicit NA, consider using  
## `forcats::fct_explicit_na`
```

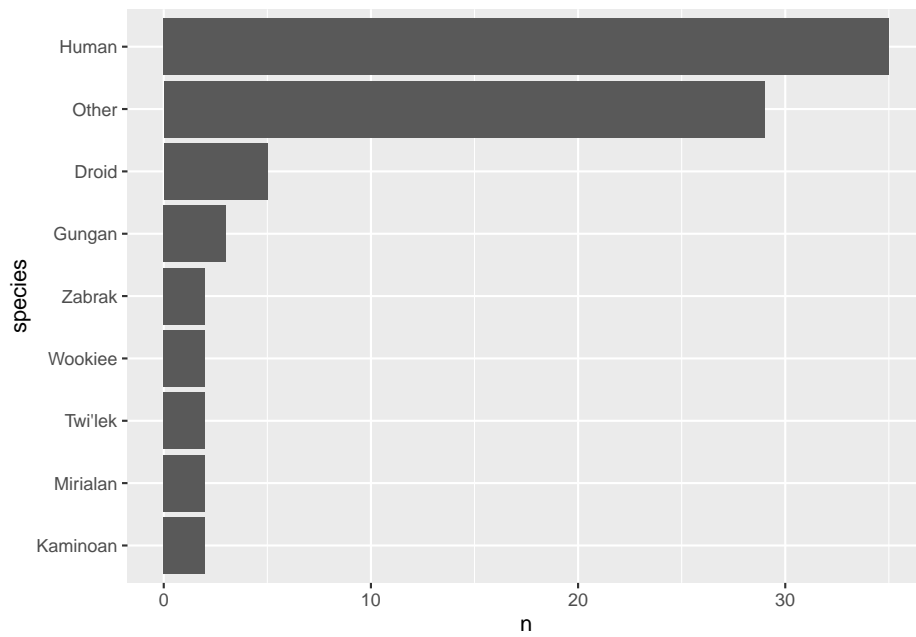
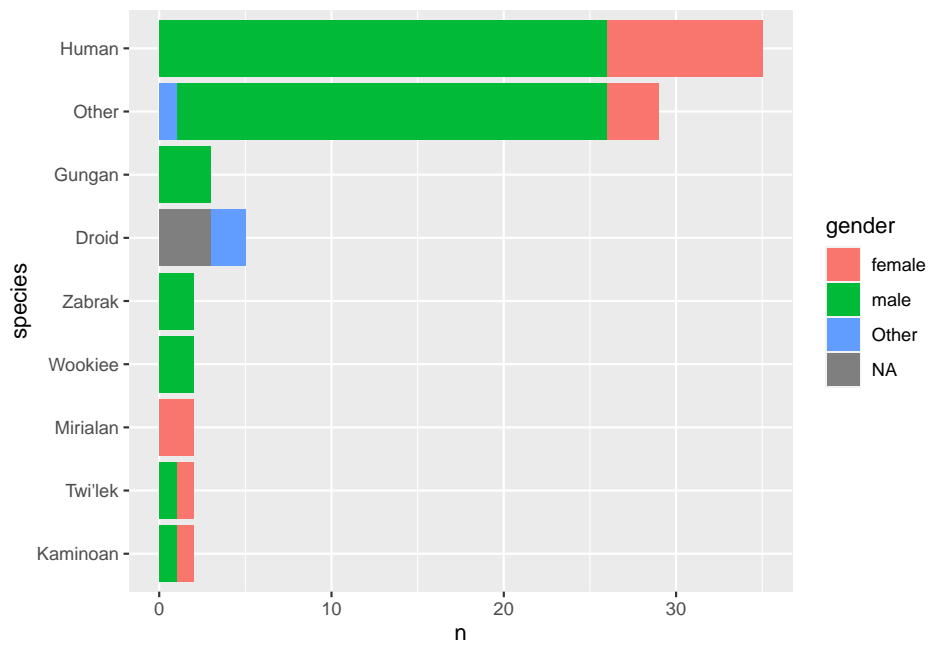


Figure 2.1: Starwars Figure 1



But note that I've got a problem: the Droids, which outnumber the Gungans, are now reordered to *after* the Gungans. This happens because the  $n$  that we're

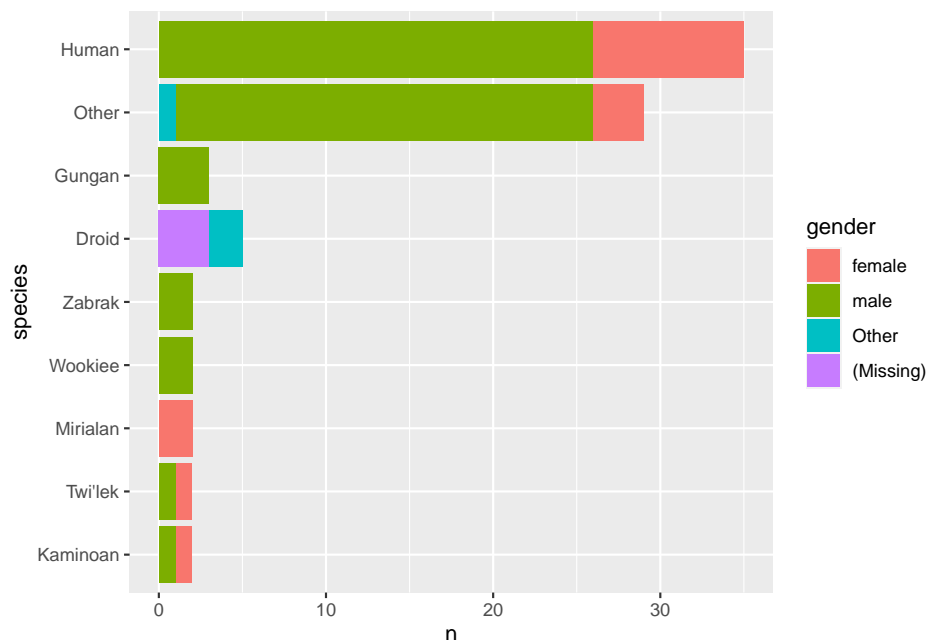


counting comprises subcategories of species *and* gender. Only three Gungan males exist (and no females), but that is enough to tie the Droid NA category. The Droid NA category come after the Gungan category, presumably because *male* comes before *NA*, or because *NA* comes last (more likely).

Exploring this, I see that I'm getting warning messages about the implicit NA's in gender. Note that the following renders a slightly different plot. I *still* have not fixed the order of the species.

```
starwars %>%
  filter(!is.na(species)) %>%
  count(species = fct_lump(species, 5), gender = fct_lump(gender, 2), sort = TRUE) %>%
  mutate(gender = fct_explicit_na(gender),
         species = fct_reorder(species, n)) %>%
  ggplot(aes(species, n, fill = gender)) +
  geom_col() + coord_flip()
```

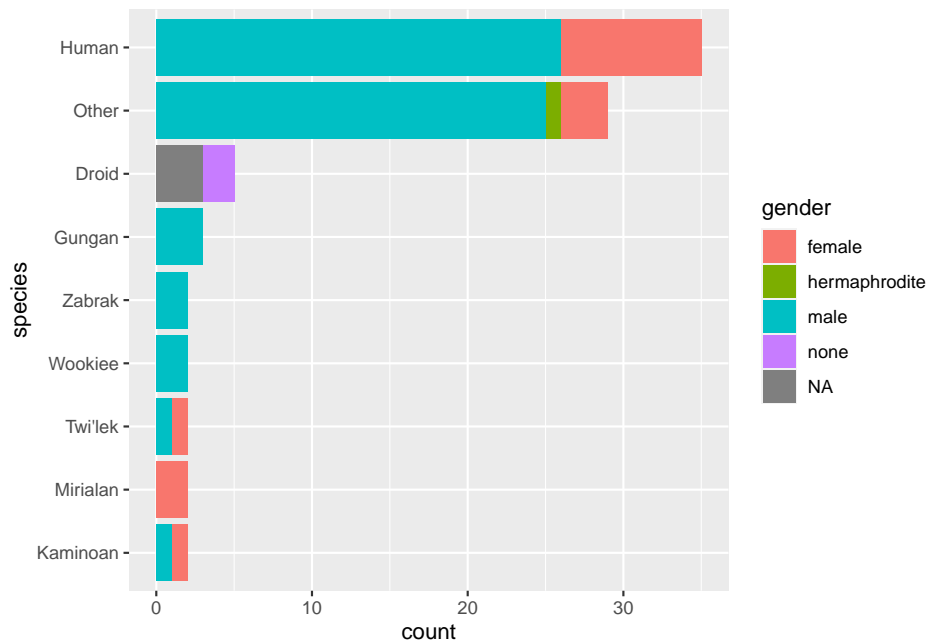
```
## Warning: Factor `gender` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```



The trick here is to use `group_by()` and `ungroup()` wisely.

```
starwars %>% filter(!is.na(species)) %>%
  mutate(species = fct_lump(species, 5)) %>%
  group_by(species) %>%
  mutate(typeCount = n()) %>%
  ungroup() %>%
```

```
mutate(species = fct_reorder(species, typeCount)) %>%
  ggplot()+
  geom_bar(aes(species, fill = gender))+
  coord_flip()
```



As opposed to using `count()`, which progressively narrows the information available to be used, by using `group_by()/mutate()/ungroup()` with `geom_bar()` we have all of the variables still available for plotting.

## 2.2 Summarize is another very useful function:

```
starwars %>%
  filter(!is.na(species)) %>%
  group_by(species) %>%
  summarize(n=n(), mean = mean(height, na.rm = TRUE)) %>%
  arrange(desc(n))
```

```
## # A tibble: 37 x 3
##   species      n mean
##   <chr>    <int> <dbl>
## 1 Human      35 177.
## 2 Droid       5 140
## 3 Gungan      3 209.
```

```
## 4 Kaminoan      2 221
## 5 Mirialan      2 168
## 6 Twi'lek       2 179
## 7 Wookiee       2 231
## 8 Zabrak        2 173
## 9 Aleena        1  79
## 10 Besalisk     1 198
## # ... with 27 more rows
```

## 2.3 Referencing other parts of the document

This is a good place to practice referencing figures. Say that I want to refer the reader back to my first starwars figure. See Figure 2.1.

I can reference other pages in a similar fashion. See Chapter 9. Note that this works by referencing a `{#label}` placed in the chapter title.

See Chapter 1

See Chapter 2

Note that the `{#label}` uses a single run-together word. It does not tolerate spaces and this cannot be overcome by ‘quoting’ it.

## 2.4 Referencing citations:

In order to insert citations, one needs a `.bib` file in the project. I’ve included one in this project as *book.bib*. The `yml` header in Chapter 1 needs to have a *bibliography* : and *biblio — style* : line added.

To insert a citation, use the **citr** Addin from RStudio. **bookdown**, for instance, is cited thusly (Xie, 2020). Note that I need to figure out an adequate workflow of references. The convenience of Endnote in MS Word will not be available. Nonetheless, if I populate the `book.bib` and `packages.bib` files carefully, with `.txt` files generated in Endnote, I should be OK.

For instance, a recent dump of my Endnote library is in `bookFromEndnote.txt`. This can be opened in RStudio, and I can copy-and-paste references from the `.txt` file to my `book.bib`. For instance, if I have a breast paper that I want to cite here (Stevens and Parekh, 2016), I’d copy-and-paste the reference from `bookFromEndnot.txt` to `book.bib`.

Of note, Yihui Xie includes a nifty bit of code to automatically generate a `bib` database for R packages:

```
knitr::write_bib(c(.packages(), 'bookdown', 'knitr', 'rmarkdown', 'tidyverse', 'Comple
```

References appear automatically at the end of a chapter.

## Chapter 3

# Sampling

### 3.1 Think about throwing a bunch of dice.

```
sample(1:6, size=100, replace=TRUE)
```

```
## [1] 3 4 6 6 4 2 5 3 4 1 1 6 2 5 1 3 2 4 1 5 2 5 4 4 2 1 4 4 2 4 1 3 5 3 2 5 3
## [38] 3 2 6 2 6 3 2 1 4 4 2 6 3 3 6 6 4 1 6 6 6 2 1 2 1 3 6 3 5 5 2 4 1 3 4 5 1
## [75] 1 4 5 4 2 2 2 3 5 3 2 1 1 1 4 4 4 3 2 4 4 3 4 4 5 5
```

```
sample(1:6, size=100, replace=TRUE) %>% table()
```

```
## .
## 1 2 3 4 5 6
## 22 14 12 15 18 19
```

```
sample(1:6, size=100, replace=TRUE) %>% table() %>% prop.table()
```

```
## .
## 1 2 3 4 5 6
## 0.12 0.18 0.18 0.18 0.15 0.19
```

### 3.2 A keen way to divide up a dataset into testing and training components.

```
x <- 1:50
y <- 51:100
```

```
df <- data.frame(x,y)
df
```

```
##      x  y
## 1    1 51
## 2    2 52
## 3    3 53
## 4    4 54
## 5    5 55
## 6    6 56
## 7    7 57
## 8    8 58
## 9    9 59
## 10   10 60
## 11   11 61
## 12   12 62
## 13   13 63
## 14   14 64
## 15   15 65
## 16   16 66
## 17   17 67
## 18   18 68
## 19   19 69
## 20   20 70
## 21   21 71
## 22   22 72
## 23   23 73
## 24   24 74
## 25   25 75
## 26   26 76
## 27   27 77
## 28   28 78
## 29   29 79
## 30   30 80
## 31   31 81
## 32   32 82
## 33   33 83
## 34   34 84
## 35   35 85
## 36   36 86
## 37   37 87
## 38   38 88
## 39   39 89
## 40   40 90
## 41   41 91
```

### 3.2. A KEEN WAY TO DIVIDE UP A DATASET INTO TESTING AND TRAINING COMPONENTS.15

```
## 42 42 92
## 43 43 93
## 44 44 94
## 45 45 95
## 46 46 96
## 47 47 97
## 48 48 98
## 49 49 99
## 50 50 100
```

```
set.seed(0)
train_indexes = sample(1:nrow(df), .7 * nrow(df))

train_set <- df[train_indexes,]
test_set <- df[-train_indexes,]

train_set
```

```
##      x  y
## 14 14 64
## 4   4 54
## 39 39 89
## 1   1 51
## 34 34 84
## 23 23 73
## 43 43 93
## 50 50 100
## 18 18 68
## 33 33 83
## 21 21 71
## 40 40 90
## 10 10 60
## 7   7 57
## 9   9 59
## 15 15 65
## 48 48 98
## 25 25 75
## 44 44 94
## 5   5 55
## 31 31 81
## 2   2 52
## 38 38 88
## 41 41 91
## 12 12 62
## 35 35 85
## 47 47 97
```

```
## 20 20 70
## 3 3 53
## 6 6 56
## 28 28 78
## 45 45 95
## 46 46 96
## 27 27 77
## 49 49 99
```

```
test_set
```

```
##      x  y
## 8      8 58
## 11     11 61
## 13     13 63
## 16     16 66
## 17     17 67
## 19     19 69
## 22     22 72
## 24     24 74
## 26     26 76
## 29     29 79
## 30     30 80
## 32     32 82
## 36     36 86
## 37     37 87
## 42     42 92
```



## Chapter 4

# Factor Practice

```
cups <- c("small", "medium", "large")
manyCups <- sample(cups, size = 100, replace = TRUE)
sizesCups <- factor(manyCups, levels = c("small", "medium", "large"))
sizesCups
```

```
## [1] medium small large medium small small large medium medium large
## [11] large medium medium medium medium small medium medium medium medium
## [21] small large large medium large large medium large large small
## [31] small small small large medium large small small medium small
## [41] small small small large medium small small large large large
## [51] medium medium medium large medium medium large large large small
## [61] medium medium small large large medium large medium small medium
## [71] small large large small medium small large medium large large
## [81] small small medium medium medium small small small medium small
## [91] large medium large large medium large large small small medium
## Levels: small medium large
```



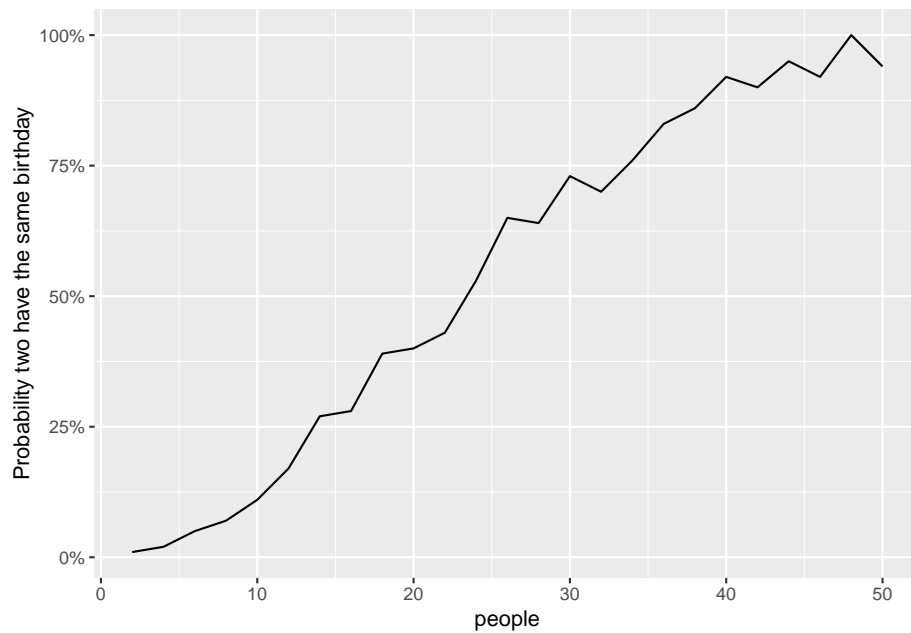
## Chapter 5

# Crossing Trial

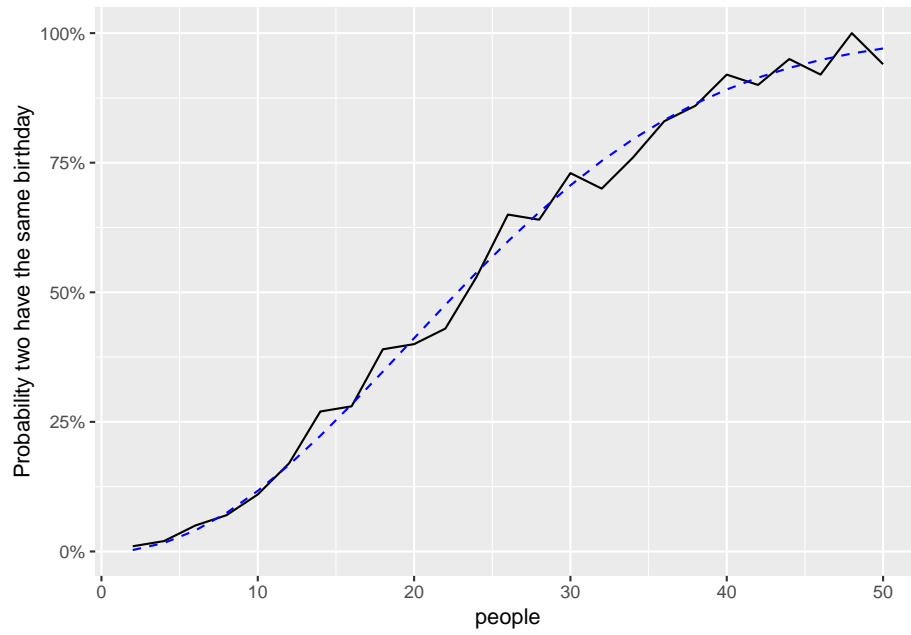
From David Robinson birthday paradox Rblogger at <https://www.r-bloggers.com/the-birthday-paradox-puzzle-tidy-simulation-in-r/>

```
summarized <- crossing(people = seq(2, 50, 2),
                      trial = 1:100) %>%
  mutate(birthday = map(people, ~ sample(365, .x, replace = TRUE)),
         multiple = map_lgl(birthday, ~ any(duplicated(.x)))) %>%
  group_by(people) %>%
  summarize(chance = mean(multiple))

ggplot(summarized, aes(people, chance)) +
  geom_line() +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(y = "Probability two have the same birthday")
```



```
# Checking the work with pbirthday function
summarized %>%
  mutate(exact = map_dbl(people, pbirthday)) %>%
  ggplot(aes(people, chance)) +
  geom_line() +
  geom_line(aes(y = exact), lty = 2, color = "blue") +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(y = "Probability two have the same birthday")
```





## Chapter 6

# By Any Other Name

This deceptively simple-seeming idea gets complex quickly. The following YouTube was a nice description of the process: <https://www.youtube.com/watch?v=Okc0IL5uTnA>

```
my.data <- data.frame(colOne=1:3, column2=4:6, column_3=7:9)
rownames(my.data) <- c("ant", "bee", "cat")
names(my.data)
```

```
## [1] "colOne" "column2" "column_3"
```

```
colnames(my.data)
```

```
## [1] "colOne" "column2" "column_3"
```

```
#make some changes
```

```
names(my.data) <- c("col_1", "col_2", "col_3")
my.data
```

```
##      col_1 col_2 col_3
## ant      1     4     7
## bee      2     5     8
## cat      3     6     9
```

```
names(my.data)[3] <- "col.3"
my.data
```

```
##      col_1 col_2 col.3
## ant      1     4     7
## bee      2     5     8
## cat      3     6     9
```

```
names(my.data)[names(my.data)=="col_2"]
```

```
## [1] "col_2"
```

```
my.data["col_2"]
```

```
##      col_2
```

```
## ant      4
```

```
## bee      5
```

```
## cat      6
```

```
my.data$col_2
```

```
## [1] 4 5 6
```

```
my.data[,2]
```

```
## [1] 4 5 6
```

```
names(my.data)[names(my.data)=="col_2"] <- "col.2"
```

```
my.data
```

```
##      col_1 col.2 col.3
```

```
## ant      1      4      7
```

```
## bee      2      5      8
```

```
## cat      3      6      9
```

```
names(my.data) <- gsub("_", ".", names(my.data))
```

```
my.data
```

```
##      col.1 col.2 col.3
```

```
## ant      1      4      7
```

```
## bee      2      5      8
```

```
## cat      3      6      9
```

```
rownames(my.data)
```

```
## [1] "ant" "bee" "cat"
```

```
my.data$species <- rownames(my.data)
```

```
my.data
```

```
##      col.1 col.2 col.3 species
```

```
## ant      1      4      7      ant
```

```
## bee      2      5      8      bee
```

```
## cat      3      6      9      cat
```

```
rownames(my.data) <- NULL
```

```
my.data
```

```
##      col.1 col.2 col.3 species
```

```
## 1      1      4      7      ant
```

```
## 2      2      5      8      bee
```



```
## 3      3      6      9      cat
colnames(my.data) <- c("good", "better", "best", "species")
my.data
```

```
##   good better best species
## 1     1      4     7      ant
## 2     2      5     8      bee
## 3     3      6     9      cat
```

```
keep <- 2:ncol(my.data)
my.data[,keep]
```

```
##   better best species
## 1      4     7      ant
## 2      5     8      bee
## 3      6     9      cat
```



## Chapter 7

# Correlation Plots

```
head(iris)
```

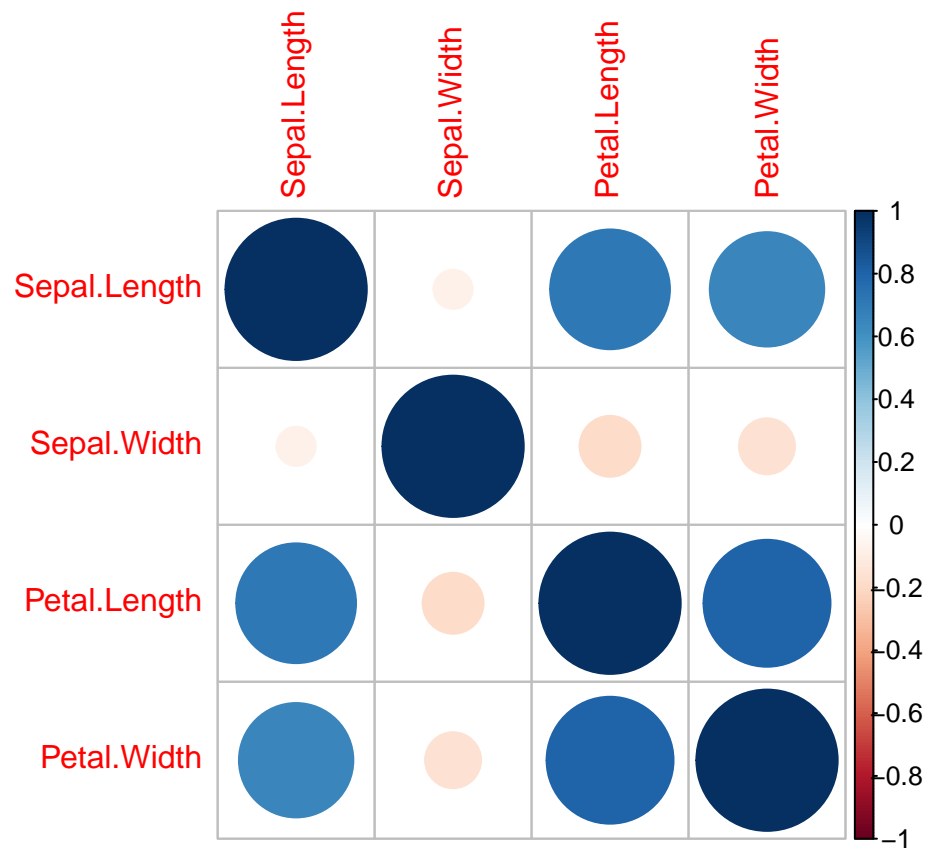
```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
## 4         4.6         3.1         1.5         0.2   setosa
## 5         5.0         3.6         1.4         0.2   setosa
## 6         5.4         3.9         1.7         0.4   setosa
```

```
iris %>% select(-Species) %>% cor()
```

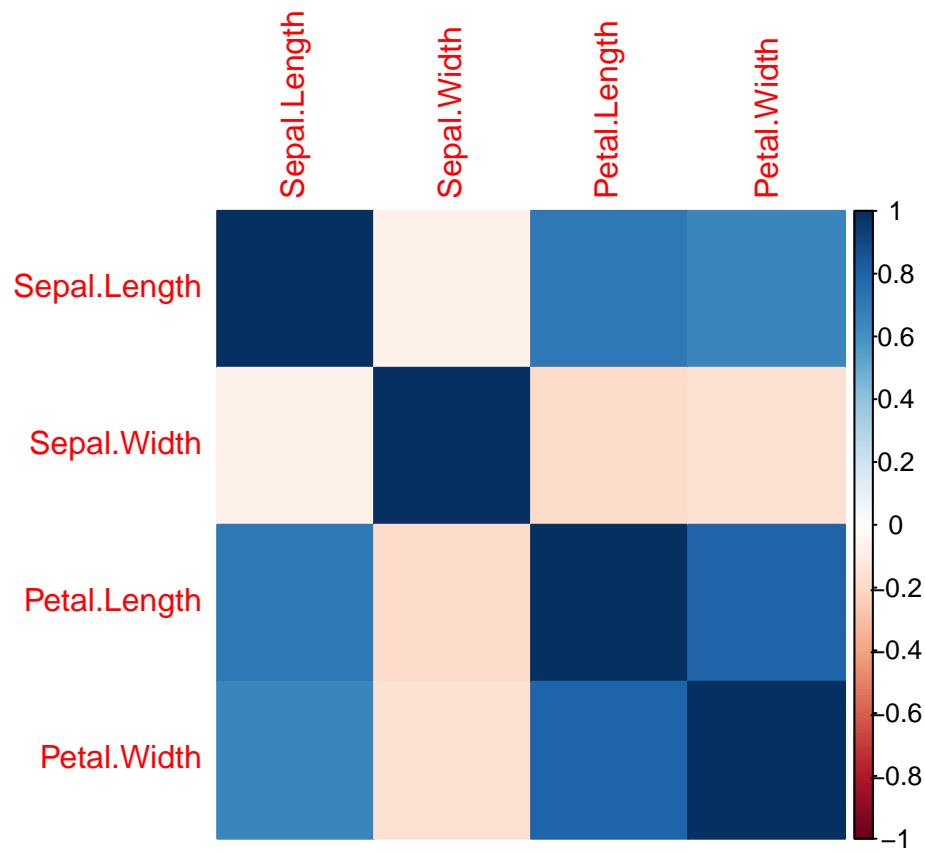
```
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## Sepal.Length    1.0000000 -0.1175698   0.8717538   0.8179411
## Sepal.Width     -0.1175698   1.0000000  -0.4284401  -0.3661259
## Petal.Length     0.8717538  -0.4284401   1.0000000   0.9628654
## Petal.Width      0.8179411  -0.3661259   0.9628654   1.0000000
```

```
M <- iris %>% select(-Species) %>% cor(method = "kendall")
```

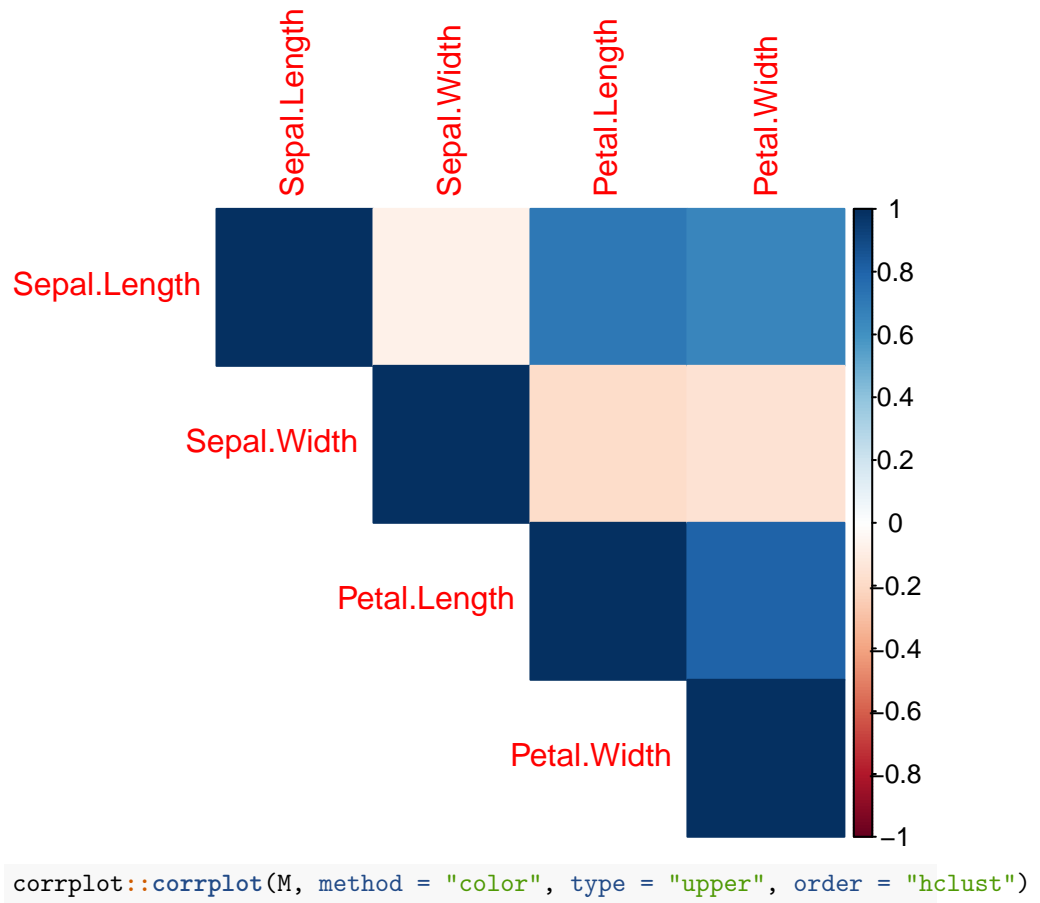
```
corrplot::corrplot(M)
```

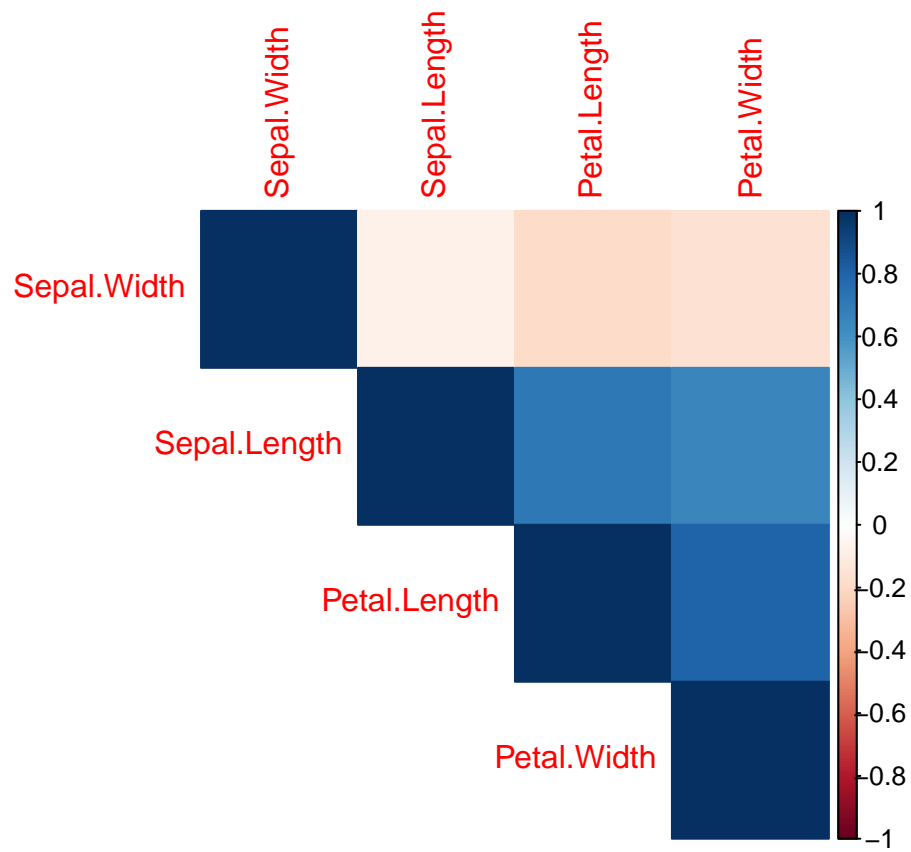


```
corrplot::corrplot(M, method = "color")
```

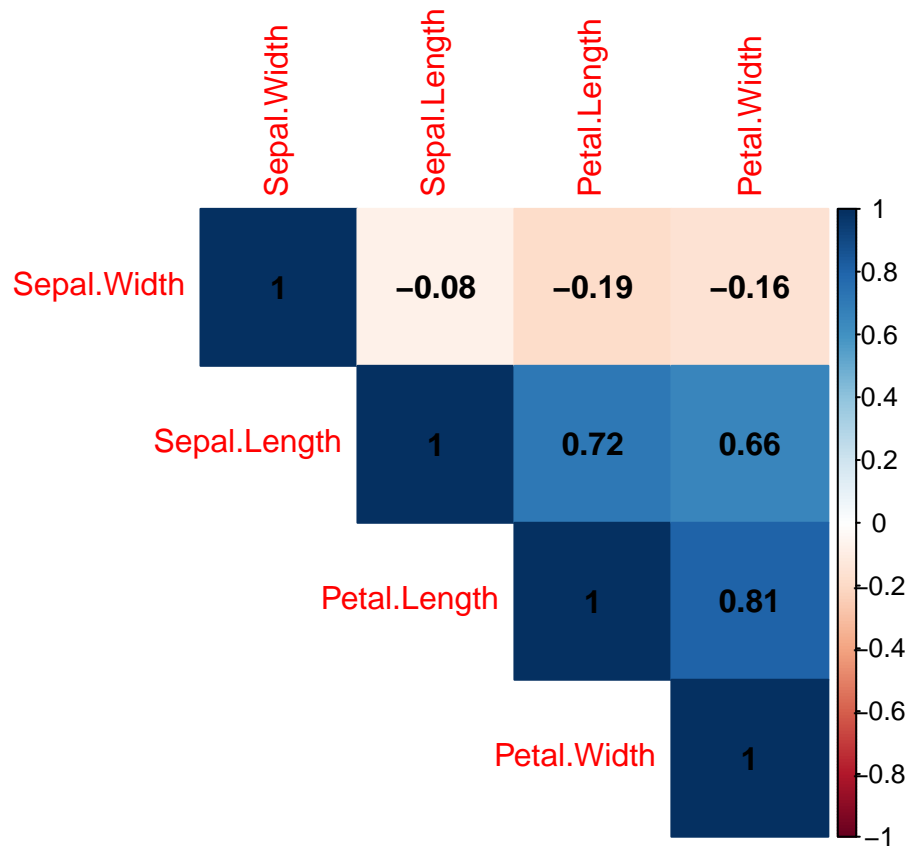


```
corrplot::corrplot(M, method = "color", type = "upper")
```



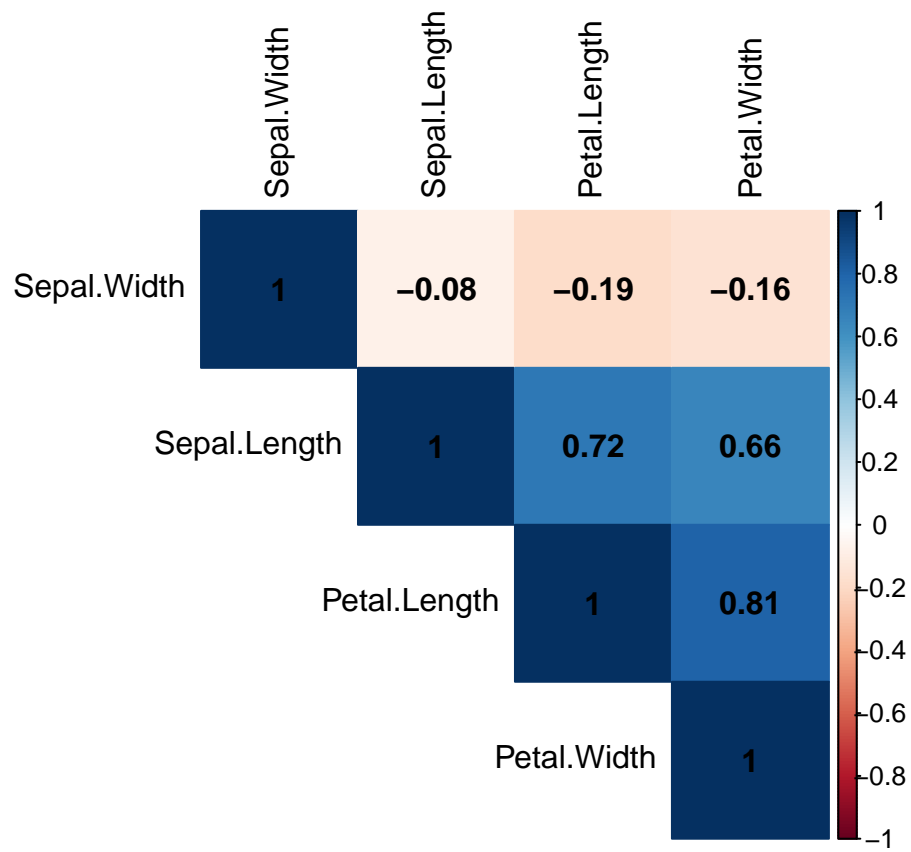


```
corrplot::corrplot(M, method = "color", type = "upper", order = "hclust", addCoef.col = "black")
```

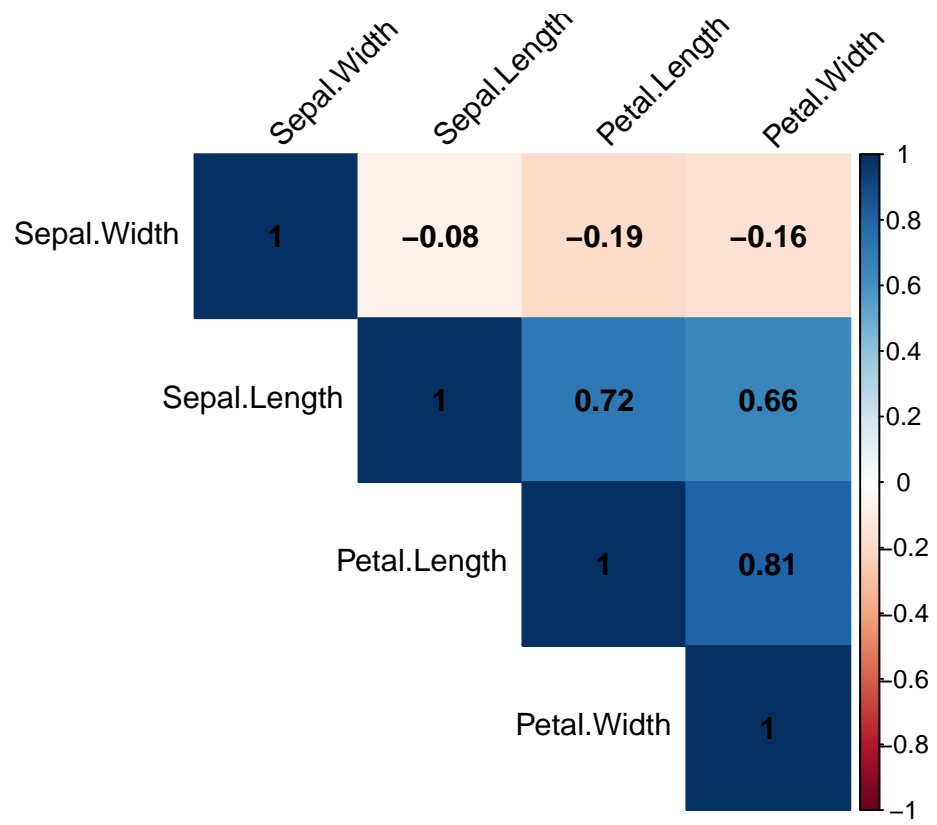


```
corrplot::corrplot(M, method = "color", type = "upper", order = "hclust", addCoef.col = TRUE)
```





```
corrplot::corrplot(M, method = "color", type = "upper", order = "hclust", addCoef.col = "black",
```



## Chapter 8

# if\_\_else() and case\_\_when(): Comparison

### 8.1 case\_\_when()

case\_\_when() from [https://www.rdocumentation.org/packages/dplyr/versions/0.7.8/topics/case\\_\\_when](https://www.rdocumentation.org/packages/dplyr/versions/0.7.8/topics/case__when)

```
x <- 1:50  
y <- 51:100
```

```
df <- data.frame(x,y)  
df
```

```
##      x  y  
## 1    1 51  
## 2    2 52  
## 3    3 53  
## 4    4 54  
## 5    5 55  
## 6    6 56  
## 7    7 57  
## 8    8 58  
## 9    9 59  
## 10 10 60  
## 11 11 61  
## 12 12 62  
## 13 13 63  
## 14 14 64  
## 15 15 65
```

```
## 16 16 66
## 17 17 67
## 18 18 68
## 19 19 69
## 20 20 70
## 21 21 71
## 22 22 72
## 23 23 73
## 24 24 74
## 25 25 75
## 26 26 76
## 27 27 77
## 28 28 78
## 29 29 79
## 30 30 80
## 31 31 81
## 32 32 82
## 33 33 83
## 34 34 84
## 35 35 85
## 36 36 86
## 37 37 87
## 38 38 88
## 39 39 89
## 40 40 90
## 41 41 91
## 42 42 92
## 43 43 93
## 44 44 94
## 45 45 95
## 46 46 96
## 47 47 97
## 48 48 98
## 49 49 99
## 50 50 100
```

```
case_when(
  x %% 35 == 0 ~ "fizz buzz",
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz",
  TRUE ~ as.character(x)
)
```

```
## [1] "1"      "2"      "3"      "4"      "fizz"   "6"
## [7] "buzz"   "8"      "9"      "fizz"   "11"     "12"
## [13] "13"     "buzz"   "fizz"   "16"     "17"     "18"
```

```
## [19] "19"      "fizz"     "buzz"     "22"      "23"      "24"
## [25] "fizz"    "26"      "27"      "buzz"    "29"      "fizz"
## [31] "31"      "32"      "33"      "34"      "fizz buzz" "36"
## [37] "37"      "38"      "39"      "fizz"    "41"      "buzz"
## [43] "43"      "44"      "fizz"     "46"      "47"      "48"
## [49] "buzz"    "fizz"
```

## 8.2 Compare this with if\_else()

```
if_else(x %% 2 == 0, "even", "odd")
```

```
## [1] "odd" "even" "odd" "even" "odd" "even" "odd" "even" "odd" "even"
## [11] "odd" "even" "odd" "even" "odd" "even" "odd" "even" "odd" "even"
## [21] "odd" "even" "odd" "even" "odd" "even" "odd" "even" "odd" "even"
## [31] "odd" "even" "odd" "even" "odd" "even" "odd" "even" "odd" "even"
## [41] "odd" "even" "odd" "even" "odd" "even" "odd" "even" "odd" "even"
```



## Chapter 9

# Subsetting

From <https://www.r-bloggers.com/5-ways-to-subset-a-data-frame-in-r/>

Note: since this is down for maintenance, I will turn off evaluation on these chunks:

```
education <- read.csv("https://vincentarelbundock.github.io/Rdatasets/csv/robustbase/education.csv")
colnames(education) <- c("X", "State", "Region", "Urban.Population", "Per.Capita.Income", "Minor.Population", "Education.Expenditures")
glimpse(education)
```

```
## Rows: 50
## Columns: 7
## $ X               <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 1...
## $ State           <chr> "ME", "NH", "VT", "MA", "RI", "CT", "NY", "N...
## $ Region          <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, ...
## $ Urban.Population <int> 508, 564, 322, 846, 871, 774, 856, 889, 715, ...
## $ Per.Capita.Income <int> 3944, 4578, 4011, 5233, 4780, 5889, 5663, 57...
## $ Minor.Population <int> 325, 323, 328, 305, 303, 307, 301, 310, 300, ...
## $ Education.Expenditures <int> 235, 231, 270, 261, 300, 317, 387, 285, 300, ...
```

### 9.1 Subsetting using brackets

```
education[c(10:21), c(2, 6:7)]
```

```
##      State Minor.Population Education.Expenditures
## 10    OH                324                    221
## 11    IN                329                    264
## 12    IL                320                    308
```

```
## 13    MI                337                379
## 14    WI                328                342
## 15    MN                330                378
## 16    IA                318                232
## 17    MO                309                231
## 18    ND                333                246
## 19    SD                330                230
## 20    NB                318                268
## 21    KS                304                337
```

## 9.2 Subset using brackets by omitting the rows and columns we don't want

```
education[-c(1:9,22:50),-c(1,3:5)]
```

```
##      State Minor.Population Education.Expenditures
## 10     OH                324                221
## 11     IN                329                264
## 12     IL                320                308
## 13     MI                337                379
## 14     WI                328                342
## 15     MN                330                378
## 16     IA                318                232
## 17     MO                309                231
## 18     ND                333                246
## 19     SD                330                230
## 20     NB                318                268
## 21     KS                304                337
```

## 9.3 Subset using brackets in combination with the which() function and the %in% operator

```
education[which(education$Region == 2),names(education) %in% c("State", "Minor.Population")]
```

```
##      State Minor.Population Education.Expenditures
## 10     OH                324                221
## 11     IN                329                264
## 12     IL                320                308
## 13     MI                337                379
## 14     WI                328                342
## 15     MN                330                378
```



## 16	IA	318	232
## 17	MO	309	231
## 18	ND	333	246
## 19	SD	330	230
## 20	NB	318	268
## 21	KS	304	337

## 9.4 Subset using the subset() function

```
subset(education, Region == 2, select = c("State", "Minor.Population", "Education.Expenditures"))
```

##	State	Minor.Population	Education.Expenditures
## 10	OH	324	221
## 11	IN	329	264
## 12	IL	320	308
## 13	MI	337	379
## 14	WI	328	342
## 15	MN	330	378
## 16	IA	318	232
## 17	MO	309	231
## 18	ND	333	246
## 19	SD	330	230
## 20	NB	318	268
## 21	KS	304	337

## 9.5 Subset using dplyr's filter() and select()

```
select(filter(education, Region == 2), c(State, Minor.Population: Education.Expenditures))
```

##	State	Minor.Population	Education.Expenditures
## 1	OH	324	221
## 2	IN	329	264
## 3	IL	320	308
## 4	MI	337	379
## 5	WI	328	342
## 6	MN	330	378
## 7	IA	318	232
## 8	MO	309	231
## 9	ND	333	246
## 10	SD	330	230
## 11	NB	318	268
## 12	KS	304	337



# Bibliography

Stevens, T. M. and Parekh, V. (2016). Mammary analogue secretory carcinoma. *Arch Pathol Lab Med.*, 140(9):997–1001. doi: 10.5858/arpa.2015-0075-RS.

Xie, Y. (2020). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.18.