HuGen2071 book

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October 2, 2022

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Preface

This is a Quarto book created from markdown and executable code using Quarto within RStudio.

Book web site: https://danieleweeks.github.io/HuGen2071/

Book source code: https://github.com/DanielEWeeks/HuGen2071

Created by Daniel E. Weeks

Website: https://www.publichealth.pitt.edu/home/directory/daniel-e-weeks

To learn more about Quarto books visit https://quarto.org/docs/books.

1 Preparation

The first part of our HuGen 2071 course aims to teach you R in the context of applied data wrangling in a genetic context. In our experience, if you have never programmed before, it moves kind of fast. As such, it would be useful to review these sources below.

1.1 Basic programming ideas

1.1.1 Introduction to Coding

This web page and two short videos discusses how computer programming is very similar to writing a recipe - you have to break a complex project down into precise smaller individual steps.

https://subjectguides.york.ac.uk/coding/introduction

1.2 R

1.2.1 PhD Training Workshop: Statistics in R

This online book has a nice introduction to the concepts of programming, RStudio, and R https://bookdown.org/animestina/R_Manchester/

See Chapters 1, 2, and 3

1.3 R and RStudio

1.3.1 R for the Rest of Us

Acquaint or refresh yourself with R and RStudio — including installing them on your computer with this "R for the Rest of Us course" (24 min of videos + exercises):

https://rfortherestofus.com/courses/getting-started/

Slides: https://rfortherestofus.github.io/getting-started/slides/slides.html

1.4 GitHub

To introduce yourself to GitHub:

https://guides.github.com/introduction/git-handbook/

https://guides.github.com/activities/hello-world/

1.5 R Markdown

To introduce yourself or refresh yourself on R Markdown:

https://rmarkdown.rstudio.com/ (click on Get Started)

1.6 Unix

And finally, to introduce yourself or refresh yourself with Unix (well, Linux in this case, but close enough), try Lessons 1–11 here:

https://www.webminal.org/

2 Introduction

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Book web site: https://danieleweeks.github.io/HuGen2071/

Book source code: https://github.com/DanielEWeeks/HuGen2071

Created by Daniel E. Weeks

Website: https://www.publichealth.pitt.edu/home/directory/daniel-e-weeks

3 Logistics

3.1 GitHub: Set up an account

Please go to https://github.com and set up a GitHub account.

Choose your GitHub user name carefully, as you may end up using it later in a professional context.

3.2 GitHub Classroom

As GitHub Classroom will be used to distribute course materials and to submit assignments, it would be best if you get git working on your own computer. The easiest way to do this is to install RStudio, R, and git on your computer.

Please follow the detailed instructions in https://github.com/jfiksel/github-classroom-for-students

In particular, see Step 5 re generating an ssh key so you don't need to login every time.

4 R Basics Group Exercise

4.1 Set up the data frame a

```
a <- data.frame(n = 1:4)
dim(a)

[1] 4 1

a

n
1 1
2 2
3 3
4 4</pre>
```

4.2 Exercise 1: recycling

This exercise should help answer this question: 'In what type of situations would "recycling" be useful?'

Use recycling to insert into the data frame a a column named rowNum1 that contains a 1 in even rows and a 2 in odd rows.

```
Tip

The R command

a$rowNum1 <- NA

would insert a new row into the data frame a full of NA values.
```

4.3 Exercise 2: vector addition

Use vector addition to construct a vector of length 4 that contains a 1 in even rows and a 2 in odd rows. Then insert this vector into the data frame a into a column named rowNum6.

```
    Tip
    What vector could you add to this vector so the sum is the vector (1, 2, 1, 2)?
    rep(1, 4)
    [1] 1 1 1 1
```

```
Pexpand to see the answer

r1 <- rep(1, times = 4)
 r2 <- rep(c(0,1), times = 2)
 r1

[1] 1 1 1 1

r2

[1] 0 1 0 1

r1 + r2

[1] 1 2 1 2</pre>
```

4.4 Exercise 3: for loops

Loops allow you to repeat actions on each item from a vector of items.

Here is an example for loop, iterating through the values of i from 1 to 3:

```
for (i in 1:3) {
    print(paste("i =",i))
}

[1] "i = 1"
[1] "i = 2"
[1] "i = 3"
```

This does the same thing as this repetitive code:

```
i.vector <- c(1,2,3)
i <- i.vector[1]
print(paste("i =",i))

[1] "i = 1"

i <- i.vector[2]
print(paste("i =",i))

[1] "i = 2"</pre>
```

```
i <- i.vector[3]
print(paste("i =",i))

[1] "i = 3"</pre>
```

Use a for loop to insert into the data frame a a column named rowNum2 that contains a 1 in even rows and a 2 in odd rows.



Think about how as i increments from 1 to nrow(a), how could we map that sequence (e.g. 1, 2, 3, 4) to the desired sequence of 1, 2, 1, 2.

```
? Expand to see the answer
  # Set value that we want to iterate 1, 2, 1, 2, ...
  j <- 1
  # Initialize rowNum2 to all missing values
  a$rowNum2 <- NA
  # Start the for loop, looping over the number of rows in a
  for (i in c(1:nrow(a))) {
     # Assign value j to row i
     a$rowNum2[i] <- j
     # Increment j
     j <- j + 1
     # If j is greater than 2, set it back to 1
     if (j > 2) {
       j <- 1
     }
  }
  n rowNum1 rowNum6 rowNum2
1 1
          1
                  1
2 2
          2
                  2
                          2
3 3
          1
                  1
                           1
4 4
          2
                  2
                           2
```

4.5 Exercise 4: while loops

Here's an example while loop:

```
i <- 1
while (i < 4) {
   print(paste("i =",i))
   i <- i + 1
}

[1] "i = 1"
[1] "i = 2"
[1] "i = 3"</pre>
```

Use a while loop to insert into the data frame a a column named rowNum3 that contains a 1 in even rows and a 2 in odd rows.

```
Expand to see the answer
  a$rowNum3 = NA
  i <- 1 #set index
  while(i <= nrow(a)){ #set conditions for while loop</pre>
    if ((i \% 2)) { #if statement for when "i" is odd
      a$rowNum3[i] <- 1
    else #else statement for when "i" is even
      a$rowNum3[i] <- 2
    i \leftarrow i + 1 #counter for "i", increments by 1 with each loop iteration
  }
  а
  n rowNum1 rowNum6 rowNum2 rowNum3
1 1
          1
                   1
                           1
                                    1
                           2
                                    2
2 2
          2
                   2
          1
3 3
                   1
                           1
                                    1
4 4
                   2
```

4.6 Exercise 5: repeat loops

Here's an example repeat loop:

```
i <- 1
repeat {
   print(paste("i =",i))
   i <- i + 1
   if (i > 3) break
}

[1] "i = 1"
[1] "i = 2"
[1] "i = 3"
```

Use a repeat loop to insert into the data frame a a column named rowNum4 that contains a 1 in even rows and a 2 in odd rows.

```
? Expand to see the answer
  a$rowNum4 <- NA
  i <- 1 #set index
  repeat {
    if ((i %% 2)) { #if statement for when "i" is odd
      a$rowNum4[i] <- 1
    }
    else #else statement for when "i" is even
      a$rowNum4[i] <- 2
    i <- i + 1 #counter for "i", increments by 1 with each loop iteration
    if (i > nrow(a)) {
      break
    }
  }
  n rowNum1 rowNum6 rowNum2 rowNum3 rowNum4
1 1
          1
                  1
                          1
                                  1
2 2
          2
                  2
                          2
                                  2
                                           2
3 3
                  1
          1
                          1
                                  1
                                           1
```

4.7 Exercise 6: using the rep function

Use the rep command to insert into the data frame a a column named rowNum5 that contains a 1 in even rows and a 2 in odd rows.

```
Expand to see the answer
  # This will only work correctly if nrow(a) is even
  a$rowNum5 <- rep(c(1,2), nrow(a)/2)
  n rowNum1 rowNum6 rowNum2 rowNum3 rowNum4 rowNum5
1 1
                  1
                           1
          2
                           2
                                            2
2 2
                  2
                                                    2
3 3
                                   1
          1
                  1
                           1
                                            1
                                                    1
4 4
          2
                           2
                   2
                                   2
                                            2
                                                    2
```

4.8 Exercise 7

List all even rows of the data frame a.

List rows 3 and 4 of the data frame a.

```
? Expand to see the answer
  # All even rows
  a[a$rowNum1==2,]
  n rowNum1 rowNum6 rowNum2 rowNum3 rowNum4 rowNum5
2 2
          2
                  2
                           2
                                   2
                                            2
          2
                  2
                           2
                                   2
                                            2
                                                    2
  # All odd rows
  a[a$rowNum1==1,]
  n rowNum1 rowNum6 rowNum2 rowNum3 rowNum4 rowNum5
```

```
    1 1
    1
    1
    1
    1
    1

    3 3
    1
    1
    1
    1
    1
```

4.9 Exercise 8

i Note

Learning objective: Learn how to alter the options of an R command to achieve your goals.

This exercise should help answer this question: "When reading a file, will missing data be automatically represented as NA values, or does that need to be coded/manually curated?"

The tab-delimited file in testdata.txt contains the following data:

```
1 1 1
2 2 2
3 NA 99
4 4 4
```

Your collaborator who gave you these data informed you that in this file 99 stands for a missing value, as does NA.

However if we use the read.table command with its default options to read this in, we fail to accomplish the desired task, as 99 is not reading as a missing value:

```
infile <- "data/testdata.txt"
# Adjust the read.table options to read the file correctly as desired.
b <- read.table(infile)
b

V1 V2 V3
1 1 1 1
2 2 2 2 2
3 3 NA 99
4 4 4 4</pre>
```

str(b)

```
'data.frame': 4 obs. of 3 variables:

$ V1: int 1 2 3 4

$ V2: int 1 2 NA 4

$ V3: int 1 2 99 4
```

Use the read.table command to read this file in while automatically setting both the 'NA" and the 99 to NA. This can be done by adjusting the various options of the read.table command.



Read the help page for the read.table command

Expand to see the answer To read this in properly, we have to let 'read.table' know that there is no header and that which values should be mapped to the missing NA value: b <- read.table(infile, header = FALSE, na.strings = c("NA","99")) b V1 V2 V3 1 1 1 1</pre>

str(b)

2 2 2 3 NA NA 4 4 4

```
'data.frame': 4 obs. of 3 variables: $ V1: int 1 2 3 4
```

\$ V2: int 1 2 NA 4 \$ V3: int 1 2 NA 4

summary(b)

	V1		V2	,	V3
Min.	:1.00	Min.	:1.000	Min.	:1.000
1st Qu	.:1.75	1st Qu	.:1.500	1st Qu	.:1.500
Median	:2.50	Median	:2.000	Median	:2.000
Mean	:2.50	Mean	:2.333	Mean	:2.333

5 R Character Exercise

5.1 Load Libraries

```
library(tidyverse)
# library(tidylog)
library(knitr)
```

5.2 Useful RStudio cheatsheet

See the "String manipulation with stringr cheatsheet" at https://www.rstudio.com/resources/cheatsheets/

5.3 Scenario 1

You are working with three different sets of collaborators: 1) the clinical group that did the field work and generated the anthropometric measurements; 2) the medical laboratory that measured blood pressure in a controlled environment; and 3) the molecular laboratory that generated the genotypes.

```
clin <- read.table(file = "data/clinical_data.txt", header=TRUE)
kable(clin)</pre>
```

ID	height
1	152
104	172
2112	180
2543	163

```
lab <- read.table(file = "data/lab_data.txt", header = TRUE)
kable(lab)</pre>
```

ID	SBP
SG0001	120
SG0104	111
SG2112	125
SG2543	119

```
geno <- read.table(file = "data/genotype_data.txt", header = TRUE)
kable(geno)</pre>
```

rs1212
G/C
G/G
C/C
C/G

5.4 Discussion Questions

5.4.1 Question 1

The clinical group, which measured height, used integer IDs, but the medical group, which measured the blood pressure, decided to prefix the integer IDs with the string 'SG' (so as to distinguish them from other studies that were also using integer IDs). So ID '1' was mapped to ID 'SG0001'.

Discuss how, using R commands, you would reform at the integer IDs to be in the format "SGXXXX". Write down your ideas in the next section, and, if you have time, try them out within an R chunk.

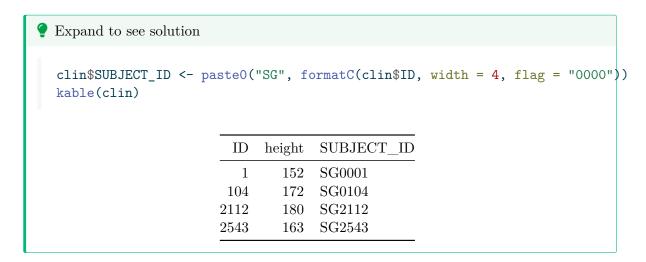
Table 5.4: The clin data frame

ID	height
1	152
104	172
2112	180

ID	height
2543	163

Hint: Use the formatC function.

5.4.2 Answer 1



5.4.3 Question 2

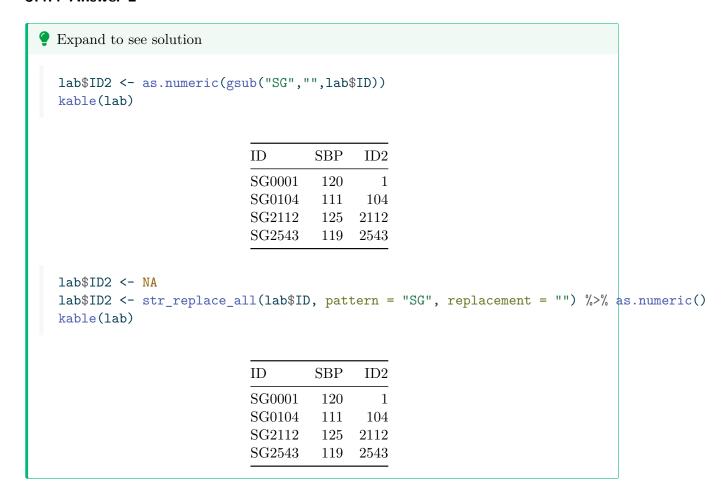
Discuss how, using R commands, you would reform at the "SGXXXX" IDs to be integer IDs. Write down your ideas in the next section, and, if you have time, try them out within an R chunk.

Table 5.6: The lab data frame

ID	SBP
SG0001	120
SG0104	111
SG2112	125
SG2543	119

Hint: Use either the gsub command or the str_replace_all command.

5.4.4 Answer 2



5.4.5 Question 3

The genotype group used IDs in the style "TaqMan-SG0001-190601", where the first string is "TaqMan" and the ending string is the date of the genotyping experiment.

Discuss how, using R commands, you would extract an "SGXXXX" style ID from the "TaqMan-SG0001-190601" style IDs. Write down your ideas in the next section, and, if you have time, try them out within an R chunk.

Note that one of the IDs has a lower case 'g' in it - how would you correct this, using R commands?

Table 5.9: The geno data frame

Sample	rs1212
TaqMan-SG0001-190601	G/C
TaqMan-SG0104-190602	G/G
TaqMan-SG2112-190603	C/C
TaqMan-Sg2543-190603	C/G

Hint: Use either the str_split_fixed function or the separate function.

5.4.6 Answer 3

```
? Expand to see solution
  a <- str_split_fixed(geno$Sample, pattern = "-",n=3)
              [,2]
     [,1]
                        [,3]
[1,] "TaqMan" "SG0001" "190601"
[2,] "TaqMan" "SG0104" "190602"
[3,] "TaqMan" "SG2112" "190603"
[4,] "TaqMan" "Sg2543" "190603"
  geno$ID <- toupper(a[,2])</pre>
  kable(geno)
                                          rs1212
                                                  ID
                   Sample
                   TaqMan-SG0001-190601
                                          G/C
                                                  SG0001
                   TaqMan-SG0104-190602
                                          G/G
                                                  SG0104
                   TaqMan-SG2112-190603
                                          C/C
                                                  SG2112
                   TaqMan-Sg2543-190603
                                          C/G
                                                  SG2543
```

The separate function from the tidyr package is also useful:

geno %>% separate(Sample, into=c("Tech","ID","Suffix"), sep="-")

Tech ID Suffix rs1212
1 TaqMan SG0001 190601 G/C
2 TaqMan SG0104 190602 G/G
3 TaqMan SG2112 190603 C/C
4 TaqMan Sg2543 190603 C/G

5.5 Scenario 2

A replication sample has been measured, and that is using IDs in the style "RP5XXX".

```
joint <- read.table(file = "data/joint_data.txt", header = TRUE)
kable(joint)</pre>
```

ID	SBP
SG0001	120
SG0104	111
SG2112	125
SG2543	119
RP5002	121
RP5012	118
RP5113	112
RP5213	142

5.5.1 Question 4

Discuss how you would use R commands to split the 'joint' data frame into an 'SG' and 'RP' specific piece? Write down your ideas in the next section, and, if you have time, try them out within an R chunk.

Table 5.12: The joint data frame

ID	SBP
SG0001	120
SG0104	111

ID	SBP
SG2112	125
SG2543	119
RP5002	121
RP5012	118
RP5113	112
RP5213	142

5.5.2 Answer 4

```
? Expand to see solution
  grep(pattern = "SG",joint$ID)
[1] 1 2 3 4
  grep(pattern = "RP", joint$ID)
[1] 5 6 7 8
  joint.SG <- joint[grep(pattern = "SG", joint$ID), ]</pre>
  joint.RP <- joint[grep(pattern = "RP", joint$ID), ]</pre>
  kable(joint.SG)
                                ID
                                         SBP
                                SG0001
                                          120
                                SG0104
                                          111
                                SG2112
                                          125
                                SG2543
                                          119
```

kable(joint.RP)

	ID	SBP
5	RP5002	121
6	RP5012	118
7	RP5113	112
8	RP5213	142

Reset row names
rownames(joint.RP) <- NULL
kable(joint.RP)</pre>

ID	SBP
RP5002	121
RP5012	118
RP5113	112
RP5213	142

6 R Functions Excercise

6.1 Load Libraries

```
library(tidyverse)
# library(tidylog)
```

6.2 Location

This file exercise1_solution.Qmd is in the "HuGen2071_book" sub-folder of the "hugen2071" folder of our Lectures repository.

```
paste0(basename(dirname(getwd())),"/",basename(getwd()))
[1] "hugen2071/HuGen2071_book"
```

6.3 Data set creation code

```
i <- 6
for (i in 1:10) {
fl <- data.frame(name=rep(paste0("name",i),26))
b <- data.frame(name = rep(NA, 26))
b$name <- paste0(fl$name,"_",letters)
b$trait <- rnorm(26)
write_tsv(b,paste0("data/dataset",i,".txt"))
}</pre>
```

6.4 Example

Here we have been sent three data sets in the files that contain the trait quantitative values for each person in the data set:

```
"dataset1.txt" "dataset2.txt" "dataset3.txt"
```

And we've been asked to make a table that gives, for each dataset, the sample size (N), the mean of the trait, the median, and the variance.

We could do this by reading in each data set, one by one, as follows:

```
results <- data.frame(dataset=rep(NA,3),N=NA, mean=NA, median=NA, var=NA)
  fl1 <- read.table("data/dataset1.txt",sep="\t",header=TRUE)</pre>
  results$dataset[1] <- "dataset1"</pre>
  results$N <- nrow(fl1)
  results$mean[1] <- mean(fl1$trait)</pre>
  results$median[1] <- median(fl1$trait)</pre>
  results$var[1] <- var(fl1$trait)</pre>
  results
   dataset N
                              median
                     mean
1 dataset1 26 0.09762111 0.2198957 0.5974116
2
      <NA> 26
                       NA
                                   NA
                                              NA
3
      <NA> 26
                       NA
                                   NA
                                              NA
  f12 <- read.table("data/dataset2.txt",sep="\t",header=TRUE)</pre>
  results$dataset[2] <- "dataset2"</pre>
  results$N <- nrow(fl2)
  results$mean[2] <- mean(fl2$trait)</pre>
  results$median[2] <- median(fl2$trait)</pre>
  results$var[2] <- var(fl2$trait)</pre>
  results
   dataset
                              median
           N
                     mean
                                             var
1 dataset1 26 0.09762111 0.2198957 0.5974116
2 dataset2 26 0.43486401 0.3558736 1.0936651
3
      <NA> 26
                       NΑ
                                  NA
                                              NA
  f13 <- read.table("data/dataset3.txt", sep="\t", header=TRUE)
  results$dataset[3] <- "dataset3"
```

```
results$N <- nrow(fl3)
results$mean[3] <- mean(fl3$trait)
results$median[3] <- median(fl3$trait)
results$var[3] <- var(fl3$trait)
results

dataset N mean median var
1 dataset1 26 0.09762111 0.2198957 0.5974116
2 dataset2 26 0.43486401 0.3558736 1.0936651
3 dataset3 26 0.07508335 0.0445614 0.7950574</pre>
```

Your colleague initially sent you the three data sets above, but now your colleague has sent you three more data sets and asked you to update the 'results' table.

As you can see, the code above is very repetitive. So let's automate this by writing a function that loops through a list of data set files named "dataset1.txt", "dataset2.txt", "dataset3.txt", etc., building up the results table as above.

6.4.1 Question: How could we construct a list of file names?

How could we construct a list of file names?

```
Expand to see solution

Hint: the list.files command provides a handy way to get a list of the input files:

fls <- list.files(path="data",pattern="dataset*")

fls

[1] "dataset1.txt" "dataset2.txt" "dataset3.txt" "dataset4.txt" "dataset5.txt"
[6] "dataset6.txt"</pre>
```

6.4.2 Question: Outline a possible algorithm

Outline a possible algorithm that loops through a list of input data set files named "dataset1.txt", "dataset2.txt", "dataset3.txt", etc., building up the results table as above.

? Expand to see solution

- Read in the input file names into a list
- Set up an empty results table
- For each file in our file name list
 - Read the file
 - Compute the statistics
 - Insert the information into the results table
 - Return the filled-in results table

6.4.3 Question: Construct a more detailed step-by-step algorithm.

Construct a more detailed step-by-step algorithm.

? Expand to see solution

- Input the path to the folder containing the data files
- Read in the input file names into a list fls
- Count the number of input files N
- Set up an empty results table with N rows
- For each file in our file name list fls
 - Read the file
 - Compute the statistics
 - Insert the information into the correct row of the results table
- Return the filled-in results table

6.4.4 Task: Write a read data file function.

Write a read_data_file function to accomplish the required steps for a single input data file.

1. Make the number in the data file name an argument.



Here we make the number in the data file name an argument

```
results <- data.frame(dataset=rep(NA,6),N=NA, mean=NA, median=NA, var=NA)
read_data_file <- function(n=1, results) {
  fl1 <- read.table(paste0("data/dataset",n,".txt"),sep="\t",header=TRUE)
  results$dataset[n] <- paste0("dataset",n,".txt")
  results$N <- nrow(fl1)
  results$mean[n] <- mean(fl1$trait)
  results$median[n] <- median(fl1$trait)
  results$var[n] <- var(fl1$trait)
  invisible(results)
}</pre>
```

2. Make the path to the input file an argument to your read_data_file function.

```
Expand to see solution

Here we make the path to the input file an argument.

read_data_file_v2 <- function(flnm, results) {
    fl1 <- read.table(paste0("data/",flnm),sep="\t",header=TRUE)
    results$dataset[n] <- flnm
    results$N <- nrow(fl1)
    results$mean[n] <- mean(fl1$trait)
    results$median[n] <- median(fl1$trait)
    results$var[n] <- var(fl1$trait)
    invisible(results)
}</pre>
```

6.4.5 Question: What does the above code assume?

What does the above code assume?

? Expand to see solution

Assumes a file naming style of 'dataset*.txt' where the asterisk represents 1, 2, 3, ... Assumes the files are in the "data" folder.

6.4.6 Question: Extend your function to process all of the files

The above function read_data_file processes one file at a time. How would you write a function to loop this over to process all of our files?

```
Expand to see solution
  fls <- list.files(path="data",pattern="dataset*")</pre>
  loop_over_dataset <- function(fls) {</pre>
    # Input: the list of file names
    # Output: the 'results table
    # Count the number of data set file names in fls
    n datasets <- length(fls)</pre>
    # Set up a results dataframe with n_datasets rows
    results <- data.frame(dataset=rep(NA, n datasets), N=NA, mean=NA, median=NA, var=NA)
    for (n in 1:n_datasets) {
      results <- read_data_file(n=n, results=results)</pre>
    return(results)
  }
  loop_over_dataset(fls = fls)
       dataset N
                                    median
                          mean
1 dataset1.txt 26  0.09762111  0.21989574  0.5974116
2 dataset2.txt 26  0.43486401  0.35587359  1.0936651
3 dataset3.txt 26  0.07508335  0.04456140  0.7950574
4 dataset4.txt 26 0.06259720 0.04813915 0.9186042
5 dataset5.txt 26 -0.09288522 -0.19155759 0.9978161
6 dataset6.txt 26 -0.20266667 -0.23845426 1.5605823
```

6.4.7 Bonus question

Can you find a subtle mistake in the read_data_file function?

```
results <- data.frame(dataset=rep(NA,6),N=NA, mean=NA, median=NA, var=NA)
read_data_file <- function(n=1, results) {
  fl1 <- read.table(paste0("data/dataset",n,".txt"),sep="\t",header=TRUE)
  results$dataset[n] <- paste0("dataset",n,".txt")</pre>
```

```
results$N <- nrow(fl1)
results$mean[n] <- mean(fl1$trait)
results$median[n] <- median(fl1$trait)
results$var[n] <- var(fl1$trait)
invisible(results)
}</pre>
```

? Expand to see solution

If ${\tt N}$ varies across the data sets, then this line will not do the right thing:

```
results$N <- nrow(fl1)

results <- data.frame(dataset=rep(NA,6),N=NA, mean=NA, median=NA, var=NA)
read_data_file <- function(n=1, results) {
   fl1 <- read.table(paste0("data/dataset",n,".txt"),sep="\t",header=TRUE)
   results$dataset[n] <- paste0("dataset",n,".txt")
   results$N[n] <- nrow(fl1)
   results$mean[n] <- mean(fl1$trait)
   results$median[n] <- median(fl1$trait)
   results$var[n] <- var(fl1$trait)
   invisible(results)
}</pre>
```

7 R Tidyverse Exercise

7.1 Load Libraries

Load the tidyverse packages

```
library(tidyverse)
# library(tidylog)
```

7.2 Untidy data

Let's use the World Health Organization TB data set from the tidyr package

```
who <- tidyr::who
dim(who)

[1] 7240 60

head(who[,1:6] %>% filter(!is.na(new_sp_m014)))
```

```
# A tibble: 6 x 6
  country
             iso2 iso3
                           year new_sp_m014 new_sp_m1524
  <chr>>
              <chr> <chr> <int>
                                       <int>
                                                     <int>
1 Afghanistan AF
                    AFG
                           1997
                                          0
                                                        10
2 Afghanistan AF
                    AFG
                           1998
                                          30
                                                       129
3 Afghanistan AF
                    AFG
                           1999
                                           8
                                                        55
                    AFG
                                          52
                                                       228
4 Afghanistan AF
                           2000
5 Afghanistan AF
                    AFG
                           2001
                                         129
                                                       379
6 Afghanistan AF
                    AFG
                                          90
                                                       476
                           2002
```

See the help page for who for more information about this data set.

In particular, note this description:

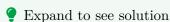
"The data uses the original codes given by the World Health Organization. The column names for columns five through 60 are made by combining new_ to a code for method of diagnosis (rel = relapse, sn = negative pulmonary smear, sp = positive pulmonary smear, ep = extrapulmonary) to a code for gender (f = female, m = male) to a code for age group (014 = 0-14 yrs of age, 1524 = 15-24 years of age, 2534 = 25 to 34 years of age, 3544 = 35 to 44 years of age, 4554 = 45 to 54 years of age, 5564 = 55 to 64 years of age, 65 = 65 years of age or older)."

So new_sp_m014 represents the counts of new TB cases detected by a positive pulmonary smear in males in the 0-14 age group.

7.3 Tidy data

Tidy data: Have each variable in a column.

Question: Are these data tidy?



No these data are not tidy because aspects of the data that should be variables are encoded in the name of the variables.

These aspects are

- 1. test type.
- 2. sex of the subjects.
- 3. age range of the subjects.

Question: How would we make these data tidy?

Consider this portion of the data:

```
head(who[,1:5] %>% filter(!is.na(new_sp_m014) & new_sp_m014>0), 1)

# A tibble: 1 x 5
```

```
country iso2 iso3 year new_sp_m014
<chr> <chr> <chr> <chr> Afghanistan AF AFG 1998 30
```

? Expand to see solution

We would replace the new_sp_m014 with the following four columns:

```
\begin{array}{ccccc} \text{type} & \text{sex} & \text{age} & \text{n} \\ \text{sp} & \text{m} & 014 & 30 \end{array}
```

This would place each variable in its own column.

7.4 Gather

```
stocks <- tibble(</pre>
    time = as.Date('2009-01-01') + 0:9,
    X = rnorm(10, 0, 1),
    Y = rnorm(10, 0, 2),
    Z = rnorm(10, 0, 4)
  )
  head(stocks)
# A tibble: 6 x 4
  time
                  Х
                          Y
  <date>
              <dbl>
                      <dbl> <dbl>
1 2009-01-01 -0.567 0.243 -5.03
2 2009-01-02 -0.542 2.62
                             1.84
3 2009-01-03 -0.332 1.37
                             1.27
4 2009-01-04 0.174 -0.0429 -4.75
5 2009-01-05 -0.231
                    0.557
                            -4.18
6 2009-01-06 0.218 2.20
                             4.24
  stocks %>% gather("stock", "price", -time) %>% head()
# A tibble: 6 x 3
             stock price
  time
             <chr> <dbl>
  <date>
1 2009-01-01 X
                   -0.567
2 2009-01-02 X
                   -0.542
3 2009-01-03 X
                   -0.332
4 2009-01-04 X
                    0.174
```

```
5 2009-01-05 X -0.231
6 2009-01-06 X 0.218
```

7.5 Pivot_longer

```
stocks %>% pivot_longer(c(X,Y,Z), names_to= "stock", values_to = "price") %>%
    head()
# A tibble: 6 x 3
             stock price
  time
  <date>
             <chr> <dbl>
1 2009-01-01 X
                   -0.567
2 2009-01-01 Y
                    0.243
3 2009-01-01 Z
                   -5.03
4 2009-01-02 X
                   -0.542
5 2009-01-02 Y
                    2.62
6 2009-01-02 Z
                    1.84
```

7.6 WHO TB data

Question: How would we convert this to tidy form?

```
head(who[,1:6] %>% filter(!is.na(new_sp_m014)))
```

```
# A tibble: 6 x 6
  country
              iso2 iso3
                            year new_sp_m014 new_sp_m1524
  <chr>
              <chr> <chr> <int>
                                       <int>
                                                     <int>
                    AFG
1 Afghanistan AF
                            1997
                                           0
                                                        10
2 Afghanistan AF
                    AFG
                                          30
                                                       129
                            1998
                    AFG
3 Afghanistan AF
                            1999
                                           8
                                                        55
4 Afghanistan AF
                    AFG
                            2000
                                          52
                                                       228
5 Afghanistan AF
                    AFG
                            2001
                                         129
                                                       379
6 Afghanistan AF
                    AFG
                            2002
                                          90
                                                       476
```

```
Expand to see solution
  who.long <- who %>% pivot_longer(starts_with("new"), names_to = "demo", values_to = "n")
  head(who.long)
# A tibble: 6 x 6
  country
              iso2
                           year demo
                    iso3
  <chr>
              <chr> <chr> <int> <chr>
                                              <int>
1 Afghanistan AF
                    AFG
                           1997 new_sp_m014
                                                  0
2 Afghanistan AF
                    AFG
                           1997 new_sp_m1524
                                                 10
3 Afghanistan AF
                           1997 new_sp_m2534
                    AFG
                                                  6
4 Afghanistan AF
                    AFG
                           1997 new_sp_m3544
                                                  3
5 Afghanistan AF
                    AFG
                            1997 new_sp_m4554
                                                  5
6 Afghanistan AF
                    AFG
                            1997 new_sp_m5564
                                                  2
```

Question: How would we split demo into variables?

```
head(who.long)
```

```
# A tibble: 6 x 6
  country
              iso2 iso3
                           year demo
  <chr>
              <chr> <chr> <int> <chr>
                                              <int>
                           1997 new_sp_m014
1 Afghanistan AF
                    AFG
                                                  0
2 Afghanistan AF
                           1997 new_sp_m1524
                    AFG
                                                 10
3 Afghanistan AF
                    AFG
                           1997 new_sp_m2534
                                                  6
4 Afghanistan AF
                    AFG
                           1997 new_sp_m3544
                                                  3
5 Afghanistan AF
                    AFG
                           1997 new_sp_m4554
                                                  5
6 Afghanistan AF
                    AFG
                                                  2
                           1997 new_sp_m5564
```

Look at the variable naming scheme:

```
names(who) %>% grep("m014",., value=TRUE)
```

```
[1] "new_sp_m014" "new_sn_m014" "new_ep_m014" "newrel_m014"
```

Question: How should we adjust the demo strings so as to be able to easily split all of them into the desired variables?

```
Expand to see solution

who.long <- who.long %>%
    mutate(demo = str_replace(demo, "newrel", "new_rel"))
    grep("m014",who.long$demo, value=TRUE) %>% unique()

[1] "new_sp_m014" "new_sn_m014" "new_ep_m014" "new_rel_m014"
```

Question: After adjusting the demo strings, how would we then separate them into the desired variables?

```
Expand to see solution
  who.long <- who.long %>%
    separate(demo, into = c("new", "type", "sexagerange"), sep="_") %>%
    separate(sexagerange, into=c("sex", "age_range"), sep=1) %>%
    select(-new)
  head(who.long)
# A tibble: 6 x 8
              iso2 iso3
  country
                            year type sex
                                              age_range
  <chr>
              <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
                                                        <int>
1 Afghanistan AF
                     AFG
                                              014
                            1997 sp
                                                            0
2 Afghanistan AF
                     AFG
                            1997 sp
                                              1524
                                                           10
                                       m
3 Afghanistan AF
                    AFG
                            1997 sp
                                              2534
                                                            6
                                       m
4 Afghanistan AF
                    AFG
                            1997 sp
                                              3544
                                                            3
                                       m
5 Afghanistan AF
                    AFG
                            1997 sp
                                              4554
                                                            5
                                       m
6 Afghanistan AF
                     AFG
                                                            2
                            1997 sp
                                              5564
```

7.7 Conclusion

Now our untidy data are tidy.

1	${\tt Afghanistan}$	AF	AFG	1997	sp	m	014	0
2	${\tt Afghanistan}$	AF	AFG	1997	sp	m	1524	10
3	${\tt Afghanistan}$	AF	AFG	1997	sp	m	2534	6
4	Afghanistan	AF	AFG	1997	sp	m	3544	3
5	Afghanistan	AF	AFG	1997	sp	m	4554	5
6	Afghanistan	AF	AFG	1997	sp	m	5564	2

7.8 Acknowledgment

This exercise was modeled, in part, on this exercise:

 $https://people.duke.edu/\sim ccc14/cfar-data-workshop-2018/CFAR_R_Workshop_2018_Exercisees.html$

8 R Recoding Reshaping Exercise

8.1 Load Libraries

```
library(tidyverse)
# library(tidylog)
```

8.2 Project 1 Data

In the ds data frame we have the synthetic yet realistic data we will be using in Project 1. In the dd data frame we have the corresponding data dictionary.

```
load("data/exercise.RData", verbose = TRUE)
Loading objects:
  ds
  dd
  DictPer
  dim(ds)
[1] 191 24
  names(ds)
 [1] "sample_id"
                                 "Sample_trimester"
 [3] "Gestationalage_sample"
                                 "subject_id"
 [5] "strata"
                                 "race"
 [7] "maternal_age_delivery"
                                 "case_control_status"
 [9] "prepregnancy_weight"
                                 "height"
```

```
[11] "prepregnancy_BMI"
                                 "gravidity"
[13] "parity"
                                 "gestationalage_delivery"
[15] "average_SBP_lt20weeks"
                                 "average_DBP_lt20weeks"
[17] "average_SBP_labor"
                                 "average_DBP_labor"
[19] "smoke_lifetime"
                                 "baby_birthweight"
[21] "baby_sex"
                                 "baby_birthweight_centile"
[23] "baby_SGA"
                                 "placental_pathology"
  dim(dd)
[1] 27 5
  names (dd)
[1] "Original.Variable.Name" "R21.Variable.Name"
                                                        "Description"
[4] "Variable.Units"
                              "Variable.Coding"
```

8.3 Exercise 1

Skill: Checking for duplicated IDs

```
ds %>%
      select(subject_id, sample_id, height) %>%
      head(n = 10)
  subject_id sample_id height
      SUBJ48
                SAMP149
                          64.6
1
2
      SUBJ46
               SAMP037
                         65.7
3
                         63.3
      SUBJ28
               SAMP120
4
      SUBJ26
               SAMP187
                         61.1
5
      SUBJ49
               SAMP082
                         67.6
6
      SUBJ48
               SAMP149
                         64.6
7
      SUBJ19
               SAMPO74
                         66.1
8
      SUBJ07
               SAMP063
                         64.4
9
      SUBJ28
                SAMP053
                         63.3
                          65.7
10
      SUBJ43
                SAMP085
```

Check if there are any duplicated sample_id's using the duplicated command.

```
Expand to see solution

sum(duplicated(ds$sample_id))

[1] 72
```

Construct a table of the number of times each sample_id is duplicated:

```
? Expand to see solution
  table(table(ds$sample_id))
67 35 13 2 1
  # But?
  sum(duplicated(ds$sample_id))
[1] 72
  35 + 13 * 2 + 2 * 3 + 1 * 4
[1] 71
  sum(duplicated(ds$sample_id, incomparables = NA))
[1] 71
  table(table(ds$sample_id, useNA = "always"))
 1 2 3
67 36 13 2 1
  36 + 13 * 2 + 2 * 3 + 1 * 4
[1] 72
```

Check if there are any duplicated subject_ids

```
Expand to see solution

sum(duplicated(ds$subject_id))

[1] 137
```

8.4 Checking for duplicates

How do we return every row that contains a duplicate?

```
f <- data.frame(ID = c(1, 1, 2), c2 = c(1, 2, 3))
f

ID c2
1    1    1
2    1    2
3    2    3

f[duplicated(f$ID), ]</pre>
ID c2
2    1    2
```

8.5 Counting the number of occurences of the ID

```
f %>%
    group_by(ID) %>%
    summarise(n = n())

# A tibble: 2 x 2
    ID     n
    <dbl> <int>
1     1     2
2     2     1
```

8.6 Count sample_id duplicates

Using Tidyverse commands, count how many times each sample_id occcurs in the ds data frame, reporting the counts in descending order, from highest to lowest.

```
? Expand to see solution
  ds %>%
      group_by(sample_id) %>%
      summarise(n = n()) \%>\%
      filter(n > 1) %>%
      arrange(desc(n)) %>%
      head()
# A tibble: 6 x 2
  sample_id
  <chr>
            <int>
1 SAMP100
2 SAMP125
                 4
3 SAMP155
                 4
4 SAMP017
                 3
                 3
5 SAMP048
6 SAMP058
                3
  ds %>%
      group_by(sample_id) %>%
      summarise(n = n()) \%>\%
      filter(n > 1) \%>\%
      arrange(desc(n)) %>%
      pull(n) %>%
      table()
    3
       4 5
36 13
       2 1
```

8.7 Checking for duplicates

Here we list all of the rows containing a duplicated 'ID' value using functions from the 'tidy-verse' package:

```
f %>%
    group_by(ID) %>%
    filter(n() > 1)

# A tibble: 2 x 2
# Groups: ID [1]
    ID    c2
    <dbl> <dbl>
1     1    1
2     1    2
```

8.7.1 How to list all duplicates

Use Tidyverse commands to list all duplicates for sample_id and for subject_id. Sort the results by the ID.

```
? Expand to see solution
8.7.2 Sample ID
  ds %>%
      group_by(sample_id) %>%
      filter(n() > 1) \%>\%
      select(sample_id, subject_id, Sample_trimester, Gestationalage_sample) %>%
      arrange(sample_id, Sample_trimester, Gestationalage_sample) %>%
      head()
# A tibble: 6 x 4
# Groups:
            sample_id [3]
  sample_id subject_id Sample_trimester Gestationalage_sample
  <chr>
            <chr>
                                   <dbl>
                                                          <dbl>
1 SAMP002
            SUBJ20
                                       2
                                                          19.3
2 SAMP002
            SUBJ20
                                       2
                                                          19.7
3 SAMP003
                                                          8.25
            SUBJ12
                                       1
4 SAMP003
            SUBJ12
                                       1
                                                          8.35
5 SAMP004
                                       2
                                                          20.4
            SUBJ35
6 SAMP004
            SUBJ35
                                       2
                                                          20.9
```

8.7.3 Subject ID ds %>% group_by(subject_id) %>% filter(n() > 1) %>% select(subject_id, sample_id, Sample_trimester, Gestationalage_sample) %>% arrange(subject_id, sample_id, Sample_trimester, Gestationalage_sample) %>% head(10) # A tibble: 10 x 4 # Groups: subject_id [2] subject_id sample_id Sample_trimester Gestationalage_sample <chr> <chr> <dbl> <dbl> 1 SUBJ01 SAMP011 9.00 1 2 SUBJ01 SAMP034 3 39.8 3 SUBJ01 SAMP034 3 42.1 2 4 SUBJ01 SAMP103 19.9 2 5 SUBJ01 SAMP103 20.0 SAMP155 6 SUBJ01 3 40.0 7 SUBJ01 3 40.5 SAMP155 8 SUBJ01 3 40.7 SAMP155 9 SUBJ01 3 41.6 SAMP155 3 10 SUBJ02 38.6 SAMP113

8.8 Exercise 2

Skill: Reshaping data

Select only three columns "sample_id", "Sample_trimester", "Gestationalage_sample", and then reshape from 'long' format to 'wide' format using pivot_wider, taking time as the "Sample_trimester".

```
Expand to see solution

b <- ds %>%
    select(sample_id, Sample_trimester, Gestationalage_sample)

b2 <- b %>%
    pivot_wider(id_cols = sample_id, names_from = Sample_trimester, values_from = Gestatent
```

```
Warning: Values from `Gestationalage_sample` are not uniquely identified; output will conta
* Use `values_fn = list` to suppress this warning.
* Use `values_fn = {summary_fun}` to summarise duplicates.
* Use the following dplyr code to identify duplicates.
  {data} %>%
    dplyr::group_by(sample_id, Sample_trimester) %>%
    dplyr::summarise(n = dplyr::n(), .groups = "drop") %>%
    dplyr::filter(n > 1L)
  head(b2)
# A tibble: 6 x 5
                                            `NA`
  sample_id `1`
                       `3`
                                 `2`
  <chr>
            st>
                       st>
                                 st>
                                            st>
1 SAMP149
            <dbl [3]> <NULL>
                                 <NULL>
                                            <NULL>
            <dbl [2]> <NULL>
2 SAMP037
                                 <NULL>
                                            <NULL>
            <dbl [3]> <NULL>
3 SAMP120
                                 <NULL>
                                            <NULL>
4 SAMP187
            <NULL>
                       <dbl [1]> <NULL>
                                            <NULL>
5 SAMP082
            <NULL>
                       <NULL>
                                 <dbl [1]> <NULL>
6 SAMP074
            <NULL>
                       <NULL>
                                 <dbl [3]> <NULL>
8.8.1 Comment
View b2 via the View(b2) command in RStudio - it nicely put all the different gestational
age observations into one list for each sample_id x Sample_trimester combination.
```

8.9 Exercise 3

Skill: Aggregating data

Make a table showing the proportion of blacks and whites that are controls and cases.

8.9.1 Comment:

The margin parameter of the prop.table command has to be specified in order to get the desired answer: "1 indicates rows, 2 indicates columns.

Construct more readable tables with labels using xtabs

Create a count cross table using Tidyverse commands

```
    Expand to see solution

ds %>%
    group_by(case_control_status, race) %>%
    summarize(n = n()) %>%
    spread(race, n)
```

```
`summarise()` has grouped output by 'case_control_status'. You can override
using the `.groups` argument.
# A tibble: 2 x 4
            case_control_status [2]
# Groups:
  case_control_status
                          В
                                W White
                <dbl> <int> <int> <int>
                    0
                         68
                               33
                                     NA
1
2
                    1
                         58
                               31
                                      1
  addmargins(xtabs(~case_control_status + race, data = ds))
                   race
case_control_status
                      В
                          W White Sum
                                0 101
                     68
                         33
                     58
                         31
                                1 90
                Sum 126 64
                                1 191
```

Create a proportion cross table using Tidyverse commands

```
? Expand to see solution
  ds %>%
      group_by(case_control_status, race) %>%
      summarize(n = n()) \%>\%
      mutate(prop = n/sum(n)) %>%
      select(-n) %>%
      spread(race, prop)
`summarise()` has grouped output by 'case_control_status'. You can override
using the `.groups` argument.
# A tibble: 2 x 4
# Groups:
            case_control_status [2]
  case_control_status
                          В
                                     White
                <dbl> <dbl> <dbl>
                                     <dbl>
                    0 0.673 0.327 NA
1
2
                    1 0.644 0.344 0.0111
```

8.10 Exercise 4

Skill: Summarizing within groups

Apply the summary command to the "Gestationalage_sample" within each "Sample_trimester" group.

```
? Expand to see solution
  f <- split(ds[, "Gestationalage_sample"], ds$Sample_trimester)</pre>
  sapply(f, summary)
                 1
                          2
Min.
         4.934325 16.53800 31.44880
         7.838825 18.45761 35.16305
1st Qu.
Median
         8.565282 19.72388 37.71093
Mean
         8.616799 19.83310 37.37827
3rd Qu.
         9.193104 20.69576 39.11360
        13.026958 24.60659 42.09340
Max.
  # Or 'tapply' can be used:
  tapply(ds$Gestationalage_sample, ds$Sample_trimester, summary)
$`1`
  Min. 1st Qu.
                 Median
                            Mean 3rd Qu.
                                             Max.
  4.934
          7.839
                   8.565
                           8.617
                                    9.193
                                          13.027
$`2`
  Min. 1st Qu.
                 Median
                            Mean 3rd Qu.
                                             Max.
                                    20.70
  16.54
          18.46
                   19.72
                           19.83
                                            24.61
$`3`
  Min. 1st Qu.
                 Median
                            Mean 3rd Qu.
                                             Max.
          35.16
                   37.71
                           37.38
                                    39.11
                                            42.09
Note: With split(x, f), any missing values in f are dropped together with the corre-
sponding values of x.
```

8.11 Exercise 5: Recoding data

Approach 1

- Implement our dictionaries using look-up tables
 - Use a named vector.

Skill:: Recoding IDs using a dictionary

Create a new subject ID column named "subjectID" where you have used the DictPer named vector to recode the original "subject_id" IDs into integer IDs.

```
head(DictPer)
```

```
SUBJ48 SUBJ46 SUBJ28 SUBJ26 SUBJ49 SUBJ19
40 2 23 38 10 27
```

```
Expand to see solution
  a5 <- ds
  a5$ID <- DictPer[a5$subject_id]
  a5 %>%
      select(subject_id, ID) %>%
      head
  subject_id ID
      SUBJ48 40
1
2
      SUBJ46 2
3
      SUBJ28 23
4
      SUBJ26 38
5
      SUBJ49 10
      SUBJ48 40
  head(DictPer)
SUBJ48 SUBJ46 SUBJ28 SUBJ26 SUBJ49 SUBJ19
    40
            2
                  23
                          38
                                 10
                                        27
```

8.12 Recoding data

Approach 2

• Implement our dictionaries using left joins

8.12.1 Comment

I usually prefer to use a merge command like left_join to merge in the new IDs into my data frame.

```
? Expand to see solution
  key <- data.frame(SubjID = names(DictPer), ID = DictPer)</pre>
  head(key)
       SubjID ID
SUBJ48 SUBJ48 40
SUBJ46 SUBJ46 2
SUBJ28 SUBJ28 23
SUBJ26 SUBJ26 38
SUBJ49 SUBJ49 10
SUBJ19 SUBJ19 27
  b5 <- left_join(ds, key, by = c(subject_id = "SubjID"))
      select(subject_id, ID) %>%
      head()
  subject_id ID
1
      SUBJ48 40
2
      SUBJ46 2
3
      SUBJ28 23
4
      SUBJ26 38
5
      SUBJ49 10
      SUBJ48 40
```

8.13 Exercise 6

Skill: Filtering rows.

Create a data frame tri1 containing the records for Trimester 1, and a second data frame tri2 containing the records for Trimester 2.

```
? Expand to see solution
  tri1 <- ds %>%
      filter(Sample_trimester == 1)
      select(subject_id, sample_id, Sample_trimester) %>%
      head()
  subject_id sample_id Sample_trimester
1
      SUBJ48
               SAMP149
2
      SUBJ46
                                        1
               SAMP037
3
      SUBJ28
               SAMP120
                                        1
4
      SUBJ48
               SAMP149
5
      SUBJ07
               SAMP063
                                        1
      SUBJ28
               SAMP053
  tri2 <- ds %>%
      filter(Sample_trimester == 2)
      select(subject_id, sample_id, Sample_trimester) %>%
      head()
  subject_id sample_id Sample_trimester
1
      SUBJ49
               SAMP082
                                        2
2
      SUBJ19
               SAMPO74
                                        2
3
      SUBJ10
                                        2
               SAMP121
4
      SUBJ22
               SAMP184
                                        2
5
                                        2
      SUBJ29
               SAMP100
                                        2
      SUBJ19
               SAMP074
```

8.14 Exercise 7

Skill: Selecting columns

Update tri1 and tri2 to only contain the three columns "sample_id", "Sample_trimester", "Gestationalage_sample"

```
Expand to see solution
  tri1 <- tri1 %>%
      select(sample_id, Sample_trimester, Gestationalage_sample)
  head(tri1)
 sample_id Sample_trimester Gestationalage_sample
   SAMP149
                                          8.094299
                           1
   SAMP037
                           1
                                          7.146034
3
   SAMP120
                           1
                                          7.122495
   SAMP149
                                          8.473876
                           1
   SAMP063
                           1
                                          7.510132
   SAMP053
                           1
                                          7.446434
  tri2 <- tri2 %>%
      select(sample_id, Sample_trimester, Gestationalage_sample)
  head(tri2)
 sample_id Sample_trimester Gestationalage_sample
   SAMP082
                                          21.89337
1
                           2
2 SAMP074
                           2
                                          21.26259
   SAMP121
                           2
3
                                          18.29106
   SAMP184
                           2
                                          18.76825
5
                           2
                                          24.48074
   SAMP100
   SAMP074
                           2
                                          21.24652
```

9 R Merging Exercise

9.1 Load Libraries

```
library(tidyverse)
library(tidylog)
```

9.2 Input data

Let's load the synthetic simulated Project 1 data and associated data dictionary:

```
load("data/project1.RData", verbose = TRUE)
Loading objects:
   ds
   dd
```

9.3 Select a subset of subject-level fields

```
Set up a data frame 'a' that has these subject-level fields: "subject_id" "mater-
nal_age_delivery" "case_control_status"
"prepregnancy_BMI"

a <- ds %>%
    select("subject_id", "maternal_age_delivery", "case_control_status", "prepregnancy_BMI
    arrange(subject_id)
```

select: dropped 20 variables (sample_id, Sample_trimester, Gestationalage_sample, strata, ra-

```
head(a, 10)
```

```
subject_id maternal_age_delivery case_control_status prepregnancy_BMI
       SUBJ01
                             20.01345
                                                                    45.29379
1
2
                                                         0
       SUBJ01
                             20.01345
                                                                    45.29379
3
       SUBJ01
                                                         0
                                                                    45.29379
                            20.01345
4
                                                         0
       SUBJ01
                            20.01345
                                                                    45.29379
5
       SUBJ01
                                                         0
                                                                    45.29379
                            20.01345
6
       SUBJ01
                            20.01345
                                                         0
                                                                    45.29379
7
       SUBJ01
                            20.01345
                                                         0
                                                                    45.29379
8
       SUBJ01
                            20.01345
                                                         0
                                                                    45.29379
9
       SUBJ01
                            20.01345
                                                         0
                                                                    45.29379
10
       SUBJ02
                            22.22541
                                                         1
                                                                    41.63679
  tail(a)
    subject_id maternal_age_delivery case_control_status prepregnancy_BMI
186
        SUBJ55
                             23.79660
                                                                     30.73757
                                                          1
187
        SUBJ56
                             20.77767
                                                                     32.30103
188
        SUBJ56
                             20.77767
                                                          1
                                                                     32.30103
189
                             20.77767
                                                          1
                                                                     32.30103
        SUBJ56
```

9.4 Unique records

SUBJ56

SUBJ56

190

191

The data were given to us in a way that repeated subject-level information, once for each sample from each individual subject.

1

1

32.30103

32.30103

From your data frame 'a' select only the unique records, creating data frame b.

20.77767

20.77767

```
Expand to see solution
  b <- unique(a)
  head(b)
   subject_id maternal_age_delivery case_control_status prepregnancy_BMI
                                                         0
1
       SUBJ01
                            20.01345
                                                                    45.29379
                                                         1
10
       SUBJ02
                            22.22541
                                                                    41.63679
13
       SUBJ03
                            20.80036
                                                         1
                                                                    32.55473
15
       SUBJ04
                            21.94422
                                                         0
                                                                    35.09978
19
       SUBJ05
                            20.18760
                                                                    41.85877
```

```
22
       SUBJ06
                            25.70581
                                                                    38.02936
  b1 <- a %>%
      distinct()
distinct: removed 137 rows (72%), 54 rows remaining
  all.equal(b, b1)
[1] "Attributes: < Component \"row.names\": Mean relative difference: 0.7157633 >"
  all.equal(b, b1, check.attributes = FALSE)
[1] TRUE
  head(rownames(b))
[1] "1" "10" "13" "15" "19" "22"
  head(rownames(b1))
[1] "1" "2" "3" "4" "5" "6"
  # Reset row names
  rownames(b) <- NULL
  rownames(b1) <- NULL
  all.equal(b, b1)
[1] TRUE
9.4.1 Comment
It is better to apply unique to the whole data frame, not just to the subject_id column,
as that ensures that you are selecting whole records that are unique across all of their
columns.
```

 $(ex1 \leftarrow data.frame(ID = c(1, 1, 1, 2), trait = c(10, 9, 9, 11)))$

```
ID trait
3 1
         9
        11
  unique(ex1)
  ID trait
        10
  1
         9
  2
        11
  ex1 %>%
      distinct()
distinct: removed one row (25%), 3 rows remaining
  ID trait
        10
2 1
        9
3
  2
        11
```

9.5 Check that the subject_id's are now not duplicated

Are the subject_id's unique?

```
Expand to see solution

sum(duplicated(b$subject_id))

[1] 0

b %>%
    group_by(subject_id) %>%
    filter(n() > 1)

group_by: one grouping variable (subject_id)
```

```
filter (grouped): removed all rows (100%)

# A tibble: 0 x 4

# Groups: subject_id [0]

# ... with 4 variables: subject_id <chr>, maternal_age_delivery <dbl>,

# case_control_status <dbl>, prepregnancy_BMI <dbl>
```

9.6 Create random integer IDs

Create a new column ID containing randomly chosen integer IDs; this is necessary to de-identify the data. To do this, use the sample command, sampling integers from 1 to the number of rows in data frame b.

```
Expand to see solution
  set.seed(10234)
  b$ID <- sample(c(1:nrow(b)), replace = FALSE)</pre>
  head(b %>%
      select(subject_id, ID))
select: dropped 3 variables (maternal_age_delivery, case_control_status, prepregnancy_BMI)
  subject_id ID
      SUBJ01 6
1
2
      SUBJ02 4
3
      SUBJ03 41
      SUBJ04 14
      SUBJ05 51
      SUBJ06 37
  sum(duplicated(b$ID))
[1] 0
```

9.7 Merge in new phenotype information

The PI has sent you new trait data for your subjects.

```
new <- read_tsv("data/newtrait.tsv")</pre>
Rows: 54 Columns: 2
-- Column specification -----
Delimiter: "\t"
chr (1): subject_id
dbl (1): trait
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(new)
# A tibble: 6 x 2
 subject_id trait
 <chr>
            <dbl>
1 SUBJ48
             130.
2 SUBJ46
             104.
3 SUBJ28
             125.
4 SUBJ26
             108.
5 SUBJ49
             129.
6 SUBJ19
             117.
  dim(new)
[1] 54 2
  dim(b)
[1] 54 5
```

Carefully merge this in using tidyverse commands.

If you notice any problems with this merge, prepare a report for the PI detailing what you noticed and what you'd like to ask the PI about.

9.8 Always be careful when merging.

- Always check for duplicated IDs before doing the merge.
- Always check that your ID columns do not contain any missing values.
- Check that the values in the ID columns (e.g., the keys) match.
 - Can use an 'anti_join' to check this.
 - Inconsistencies in the values of the keys can be hard to fix.
- Always check the dimensions to make sure the merged object has the expected number of rows and columns.
- Always explicitly name the keys you are merging on.
 - If you don't name them, then the join command will use all variables in common across x and y.

9.9 Merge in new phenotype information

Carefully merge in the new data in using tidyverse commands.

If you notice any problems with this merge, prepare a report for the PI detailing what you noticed and what you'd like to ask the PI about.

```
# Expand to see solution

# Check for duplicated IDs
sum(duplicated(b$subject_id))

[1] 0

sum(duplicated(new$subject_id))

[1] 1

# Which one is duplicated
new %>%
group_by(subject_id) %>%
mutate(n = n()) %>%
filter(n > 1)

group_by: one grouping variable (subject_id)
```

```
mutate (grouped): new variable 'n' (integer) with 2 unique values and 0% NA
filter (grouped): removed 52 rows (96%), 2 rows remaining
# A tibble: 2 x 3
           subject_id [1]
# Groups:
  subject_id trait
  <chr>
           <dbl> <int>
1 SUBJ09
              115.
2 SUBJ09
              115.
                      2
  # Check for missing IDs
  sum(is.na(b$subject_id))
Γ1 0
  sum(is.na(new$subject_id))
[1] 0
  # Check the dimensions
  dim(b)
[1] 54 5
  dim(new)
[1] 54 2
  b2 <- left_join(b, new, by = "subject_id")
left_join: added one column (trait)
           > rows only in x
                              2
           > rows only in y (1)
           > matched rows
                                   (includes duplicates)
                            53
```

```
> rows total
                              55
  head(b2)
  subject_id maternal_age_delivery case_control_status prepregnancy_BMI ID
     SUBJ01
                          20.01345
                                                                 45.29379 6
1
2
      SUBJ02
                          22.22541
                                                      1
                                                                 41.63679 4
3
     SUBJ03
                          20.80036
                                                       1
                                                                 32.55473 41
                          21.94422
                                                      0
                                                                 35.09978 14
     SUBJ04
     SUBJ05
                          20.18760
                                                                 41.85877 51
                                                                 38.02936 37
     SUBJ06
                          25.70581
     trait
1 138.1346
2 113.3822
3 116.0071
4 127.5887
5 113.8754
6 110.7376
  dim(b2)
[1] 55 6
  b3 <- full_join(b, new, by = "subject_id")
full_join: added one column (trait)
           > rows only in x
                               2
           > rows only in y
           > matched rows
                              53
                                     (includes duplicates)
           > rows total
                              56
  dim(b3)
[1] 56 6
```

```
anti_join() return all rows from x without a match in y.
  anti_join(b, new, by = "subject_id")
anti_join: added no columns
           > rows only in x
                             2
           > rows only in y (1)
           > matched rows
                            (52)
                             ====
           > rows total
                               2
  subject_id maternal_age_delivery case_control_status prepregnancy_BMI ID
      SUBJ18
                          27.54075
                                                                44.14983 18
                                                     0
      SUBJ24
                          21.93645
                                                                31.73762 9
  anti_join(new, b, by = "subject_id")
anti_join: added no columns
           > rows only in x
           > rows only in y (2)
           > matched rows
                             (53)
                             ====
           > rows total
                             1
# A tibble: 1 x 2
  subject_id trait
  <chr>
             <dbl>
1 SUBJOO
              127.
```

10 R Graphics Exercise

10.1 Load Libraries

```
library(tidyverse)
library(ggforce)
# library(tidylog) Set the default font to be a bit larger:
theme_set(theme_gray(base_size = 18))
```

10.2 Exercise 1

Read in and set up the data set b, a cleaned version of our simulated data set:

```
a <- read.csv("data/study1.csv")
a$ind <- seq_along(a$t)
b <- a[-c(1001:1004), ]
b$g.f <- factor(b$g)
b$geno <- paste(b$all1, b$all2, sep = "/")</pre>
```

Using ggplot and data set b, plot ind vs. t, coloring by case-control status (trait). What do you observe about the data?

```
Expand to see solution

ggplot(data = b, aes(x = ind, y = t, color = trait)) + geom_point()
```



10.3 Exercise 2

Using ggplot, plot ind vs. t, coloring by case-control status (trait) and faceting by geno. What do you observe about the data?

```
Expand to see solution

ggplot(data = b, aes(x = ind, y = t, color = trait)) + geom_point() + facet_grid(~geno)
```



10.4 Always plot your data

```
n1 <- rep(c("x", "y"), 13)
n2 <- c("", "", rep("_", 24))
n3 <- c("", "", c(sort(rep(c(1:12), 2))))
names(d) <- pasteO(n1, n2, n3)
names(d)

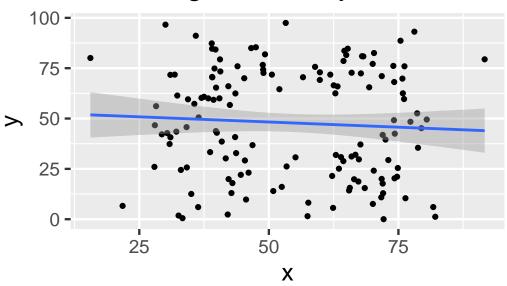
[1] "x" "y" "x_1" "y_1" "x_2" "y_2" "x_3" "y_3" "x_4" "y_4"
[11] "x_5" "y_5" "x_6" "y_6" "x_7" "y_7" "x_8" "y_8" "x_9" "y_9"
[21] "x_10" "y_10" "x_11" "y_11" "x_12" "y_12"
```

10.5 Similar regression lines

These three data sets have very similar regression lines:

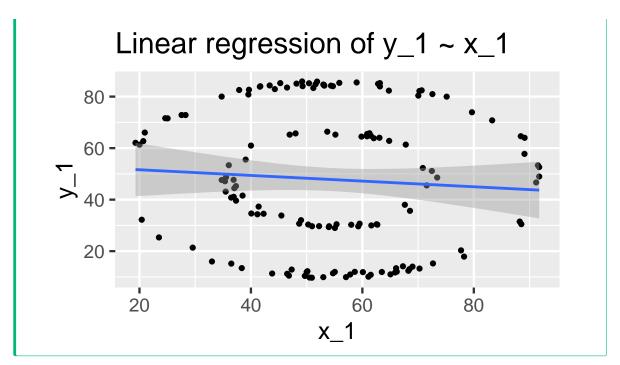
```
summary(lm(x \sim y, data = d)) \%>\%
      coef()
               Estimate Std. Error t value
(Intercept) 56.17563819 2.87986960 19.5063131 9.435087e-42
            -0.03991951 0.05250204 -0.7603419 4.483288e-01
У
  summary(lm(x_1 \sim y_1, data = d)) %>%
      coef()
               Estimate Std. Error
                                      t value
                                                  Pr(>|t|)
(Intercept) 56.31108156 2.87906158 19.5588319 7.158847e-42
            -0.04269949 0.05249244 -0.8134407 4.173467e-01
y_1
  summary(lm(x_3 \sim y_3, data = d)) \%%
      coef()
               Estimate Std. Error t value
                                                  Pr(>|t|)
(Intercept) 56.18271411 2.87924135 19.5130270 9.107718e-42
            -0.04012859 0.05249468 -0.7644316 4.458966e-01
у_3
```

Linear regression of y ~ x



Now try this:

```
ggplot(d,aes(x=x_1,y=y_1)) + geom_point() +
  geom_smooth(method="lm")
```



And now try this:

```
ggplot(d,aes(x=x_3,y=y_3)) + geom_point() +
  geom_smooth(method="lm")
```



10.6 Always plot your data

Delete the first column

f <- read_tsv("data/BoxPlots.tsv")</pre>

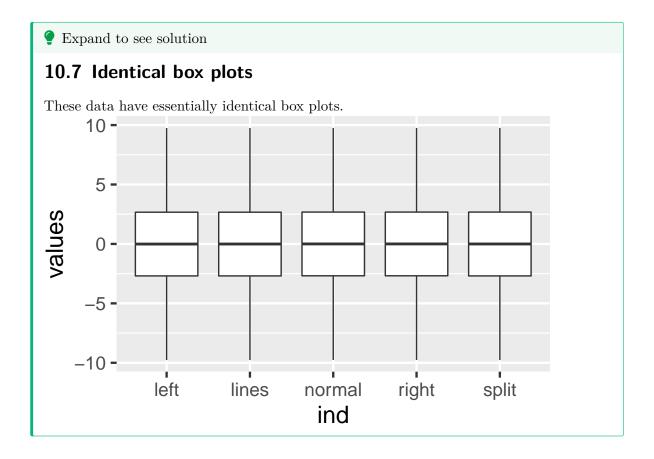
Stacking vectors concatenates multiple vectors into a single vector along with a factor indicating where each observation originated.

```
head(stack(f), 2)

values ind
1 -9.769107 left
2 -9.763145 left

Now try this:

ggplot(stack(f), aes(x = ind, y = values)) +
   geom_boxplot()
```



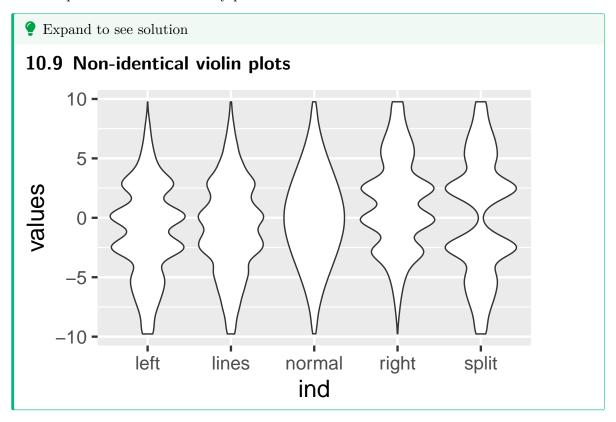
10.8 Boxplots

While the box plots are identical, box plots may not tell the whole story.

Let's try violin plots instead:

```
ggplot(stack(f), aes(x = ind, y = values)) +
  geom_violin()
```

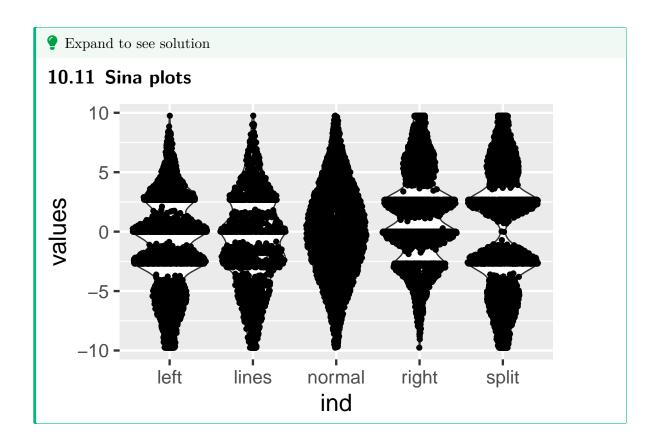
A violin plot is a mirrored density plot.



10.10 Sina plots

Sidiropoulos, N., Sohi, S.H., Rapin, N., and Bagger, F.O. (2015). SinaPlot: an enhanced chart for simple and truthful representation of single observations over multiple classes. bioRxiv 28191. https://www.biorxiv.org/content/early/2015/10/02/028191

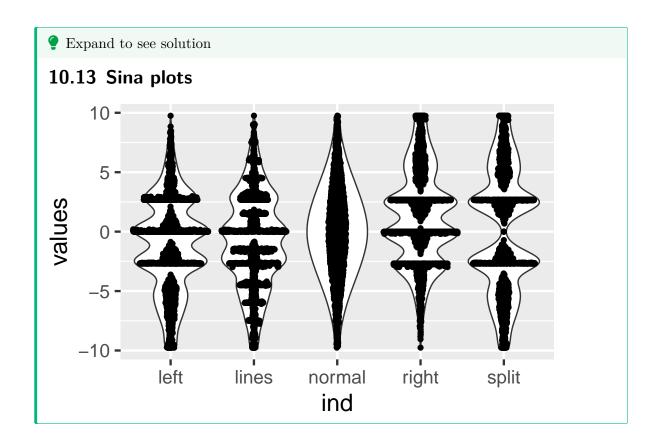
```
library(ggforce)
ggplot(stack(f), aes(x = ind, y = values)) +
    geom_violin() + geom_sina()
```



10.12 Sina plots

method == "counts": The borders are defined by the number of samples that occupy the same bin.

```
ggplot(stack(f), aes(x = ind, y = values)) +
  geom_violin() + geom_sina(method="count")
```



10.14 Writing ggplot functions

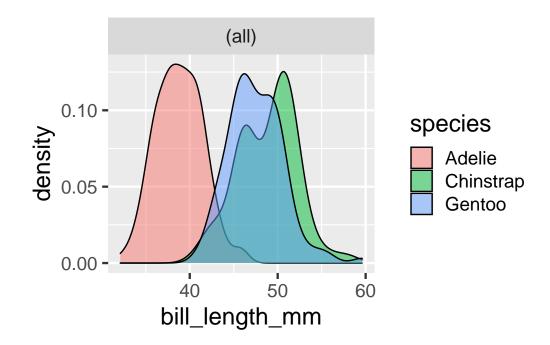
See https://r4ds.hadley.nz/functions.html#plot-functions

```
library(palmerpenguins)

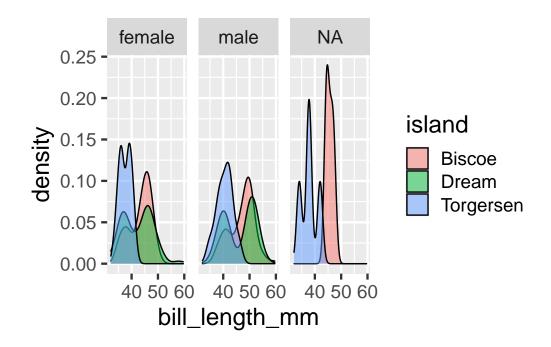
PlDensity <- function(fill, ...) {
    ggplot(penguins %>%
        filter(!is.na(bill_length_mm)), aes(bill_length_mm, fill = {
        fill
        }
    })) + geom_density(alpha = 0.5) + facet_wrap(vars(...))
}
```

 $\label{lem:example from: https://twitter.com/yutannihilat_en/status/1574387230025875457?s=20\&t=FLbwErwEKQKWtKIGufDLIQ$

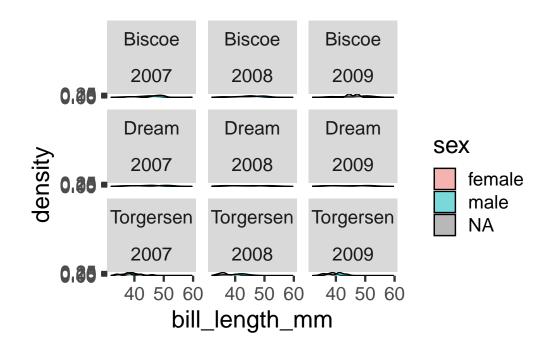
PlDensity(species)



PlDensity(island, sex) %>%
 print() %>%
 suppressWarnings()



PlDensity(sex, island, year) %>%
 print() %>%
 suppressWarnings()



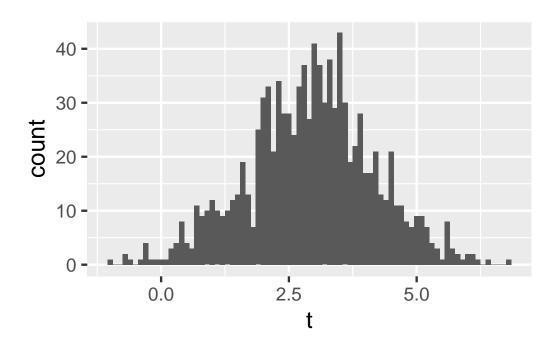
10.15 Exercise 3

Consider this example code:

 $From: \ https://twitter.com/hadleywickham/status/1574373127349575680?s = 20\&t = FLbwErwEKQKWtKIGufDLIQ$

When applied to the quantitative trait t from the data frame b, this generates this histogram:

```
histogram(b, t, 0.1)
```



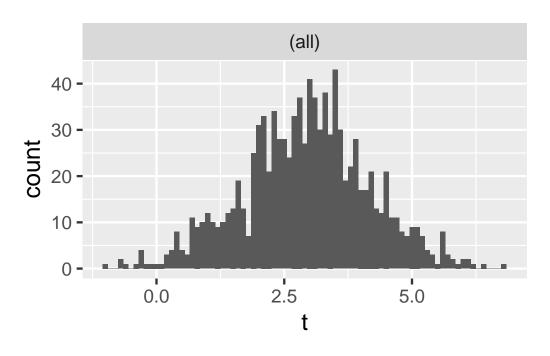
10.15.1 Exercise

After reading the example above, extend the histogram function to allow facetting and use it to draw a histogram of the quantitative trait t facetted by geno using the data set b that we set up above.

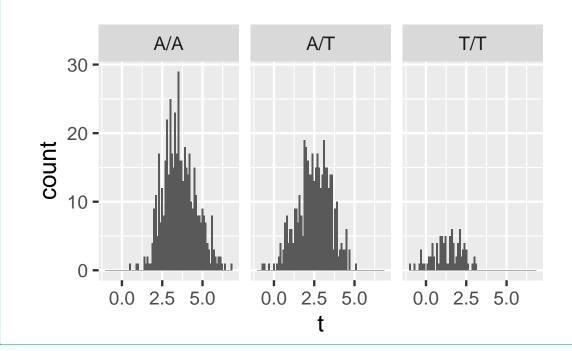


- See https://r4ds.hadley.nz/functions.html#facetting
- Use the vars() function

```
Expand to see solution
Hadley Wickham states:
You have to use the vars() syntax
foo <- function(x) {</pre>
  ggplot(mtcars) +
    aes(x = mpg, y = disp) +
    geom_point() +
    facet_wrap(vars({{ x }}))
}
\label{twister:twister} \textbf{Tweet: https://twitter.com/hadleywickham/status/1574380137524887554?s=20\&t=F}
LbwErwEKQKWtKIGufDLIQ\\
  histogram <- function(df, var, binwidth, grp) {</pre>
       df |>
            ggplot(aes({
                {
                     var
                }
            })) + geom_histogram(binwidth = binwidth) + facet_wrap(vars({
                grp
            }
       }))
  }
  histogram(b, t, 0.1)
```



histogram(b, t, 0.1, geno)



10.16 Source of data

Illustrative data sets from https://www.autodeskresearch.com/publications/samestats

11 Summary

In summary, this book is a work in progress.

References