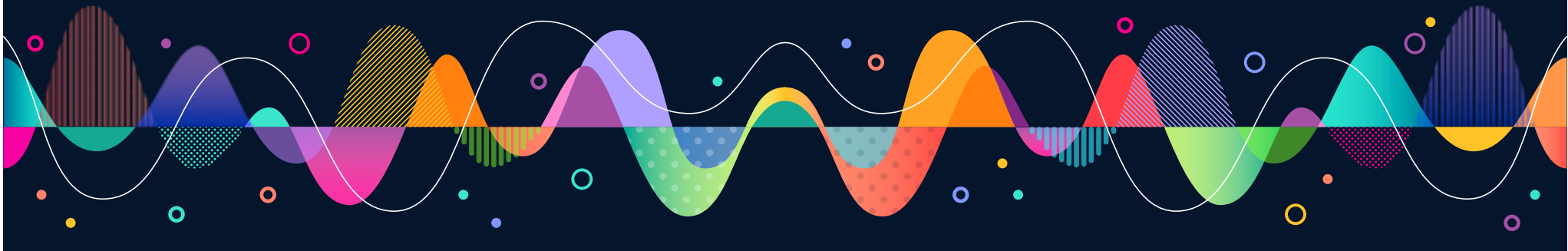


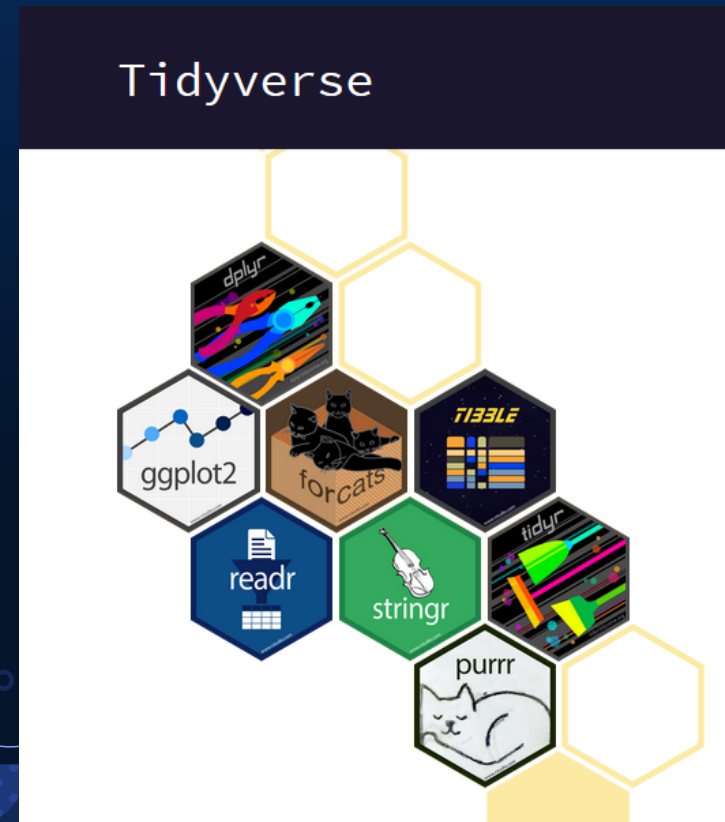
# An Introduction to Tidyverse

Roy Roberts



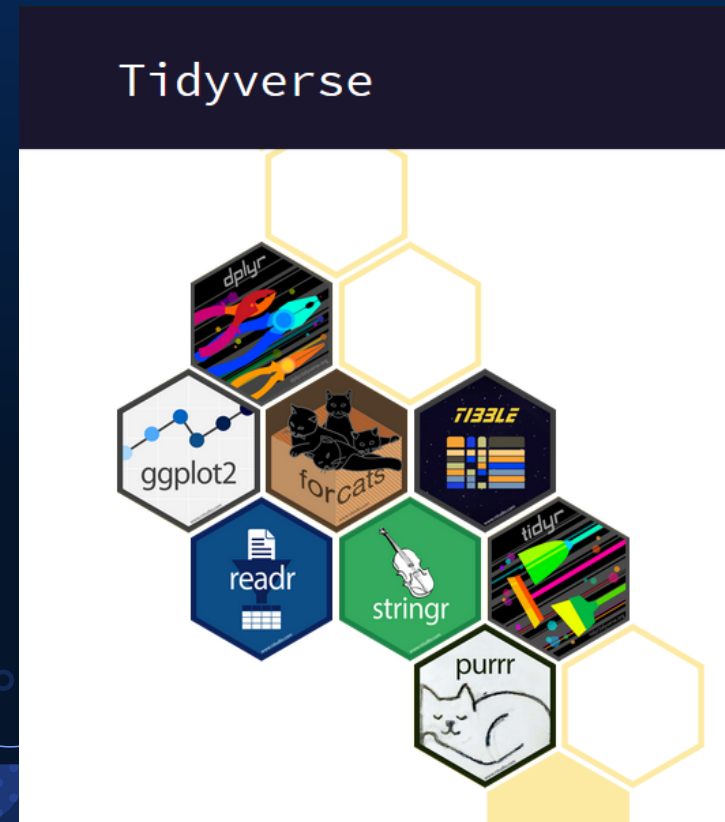
# The Tidyverse

- ▷ “The tidyverse is an opinionated collection of R packages designed for data science. All packages share an underlying design philosophy, grammar, and data structures.”



# The Tidyverse

- ▷ What is tidy data?
  - ▶ Every column is a variable
  - ▶ Every row is an observation
  - ▶ Every cell is a single value



# Packages in Tidyverse

## Core Tidyverse contains:

- ▶ tibble
- ▶ ggplot2
- ▶ dplyr
- ▶ tidyr
- ▶ readr
- ▶ purrr
- ▶ stringr
- ▶ forcats

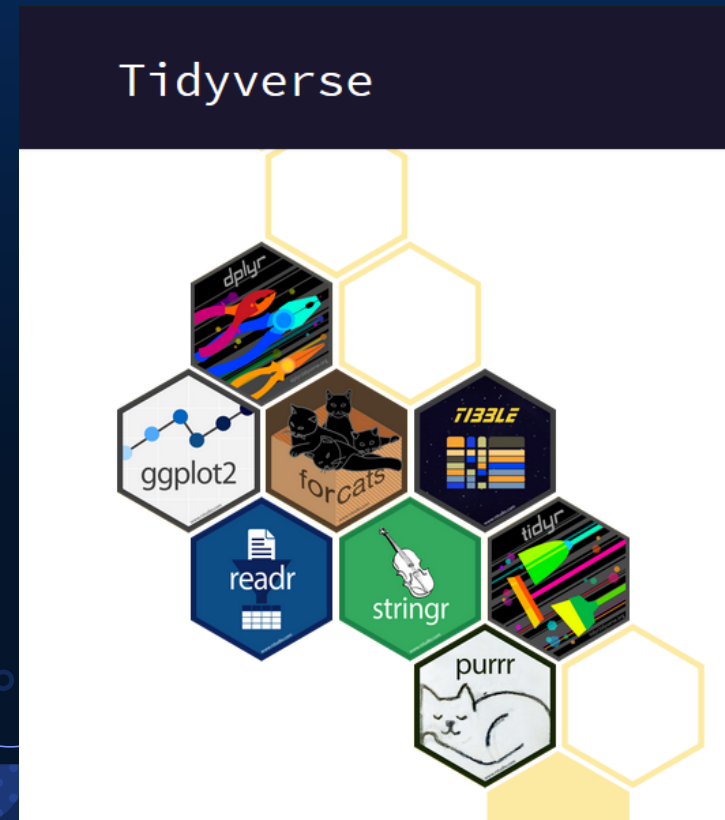


# How to Install and Load Tidyverse

- ▶ Installing and loading Tidyverse

```
install.packages("tidyverse")
```

```
library(tidyverse)
```



# Miscellaneous Information Before Starting Tidyverse



```
setwd(dirname(rstudioapi::getActiveDocumentContext()$path))
```

%>% view() function(.)

source("path/to/file")

tibble\$column\_name

# Reading in Data With readr

## ▷ Package 'readr'

- ▶ `read_tsv()`
- ▶ `read_csv()`
- ▶ `read_delim()`
- ▶ `read_table()`

## ▷ Package 'readxl'

- ▶ `read_excel()`

```
#### Reading in data ####
read_tsv("fastqc_data.tsv")
read_delim("fastqc_data.tsv",
  delim = "\t")
fastqc_tbl <- read_tsv(file = "fastqc_data.tsv",
  skip = 1,
  col_names = c("id",
    "total_sequences",
    "percent_failed",
    "percent_gc_content",
    "percent_duplication"),
  col_types = cols(id = col_character(),
    total_sequences = col_double(),
    percent_failed = col_double(),
    percent_gc_content = col_double(),
    percent_duplication = col_double()))
```

# Reading in Data With readr



Helpful options:

```
fastqc_tbl <- read_tsv(file = "fastqc_data.tsv",  
  skip = 1,  
  col_names = c("id",  
    "total_sequences",  
    "percent_failed",  
    "percent_gc_content",  
    "percent_duplication"),  
  col_types = cols(id = col_character(),  
    total_sequences = col_double(),  
    percent_failed = col_double(),  
    percent_gc_content = col_double(),  
    percent_duplication = col_double()))
```





# Tidyverse Activity 1

- ▷ Read in altered “Davis” from car dataset located in the current working directory.
- ▷ Save as a variable.
- ▷ Try and use some of the other options when saving as a variable.
- ▷ Pipe in `drop_na()` and compare with and without the new command.
- ▷ Save the above tibble as a variable to use for later activities.

# Subsetting Data in R

## ▷ `select()`

- ▶ Subsets columns of a tibble

## ▷ `filter()`

- ▶ Subsets rows of a tibble

```
#### Subsetting Your Data ####
```

```
fastqc_tbl %>%  
  select(id,  
         total_sequences)
```

```
fastqc_tbl %>%  
  select(-starts_with("percent"))
```

```
fastqc_tbl %>%  
  filter(total_sequences >= 50000000)
```

```
fastqc_tbl %>%  
  filter(percent_gc_content == 44 | percent_gc_content == 45,  
         total_sequences <= 50000000 & total_sequences >= 30000000)
```

```
fastqc_tbl %>%  
  filter(total_sequences >= 50000000) %>%  
  select(id,  
         percent_duplication)
```

# Transforming Data in R



## ▷ mutate()

- ▶ Create, modify, and delete columns
- ▶ `data %>% mutate(New_Column = Column_1 * Number)`
- ▶ `data %>% mutate(Column_1 = Column_1 * Number)`

## ▷ case\_when()

- ▶ A general vectorized conditional (if) statement that can be used with mutate
- ▶ `data %>% mutate(New_Column = case_when(Column1 == Value ~ Value,  
Column1 == Value ~ Value))`

#### #### Changing and Creating Columns ####

```
fastqc_tbl %>%  
  mutate(log_total_sequences = log10(total_sequences))  
  
fastqc_tbl %>%  
  mutate(percent_duplication = percent_duplication/100)  
  
fastqc_tbl %>%  
  mutate(percent_duplication_as_decimal = percent_duplication/100,  
         number_of_nonduplicate_sequences = percent_duplication_as_decimal * total_sequences,  
         number_of_duplicated_sequences = (1 - percent_duplication_as_decimal) * total_sequences) %>%  
  select(id,  
         total_sequences,  
         number_of_nonduplicate_sequences,  
         number_of_duplicated_sequences)  
  
fastqc_tbl %>%  
  mutate(gc_interpretation = case_when(percent_gc_content < 45 ~ "Less than 40% GC Content",  
                                       percent_gc_content > 50 ~ "Greater than 50% GC Content",  
                                       TRUE ~ "Inbetween 40 and 50% GC Content")) %>%  
  select(id,  
         gc_interpretation)
```



# Tidyverse Activity 2

- ▷ Using the previously read in davis tibble, remove both heights from the data set using select.
- ▷ Filter your data by Male or Female and also by 1 or 2 different hair colors.
- ▷ Create 2 new columns
  - ▶ The mean of weight 1 and 2
  - ▶ The difference of weight 1 and 2
- ▷ Create a new column that's value is either negative if the difference of weight 1 and 2 is negative, positive if positive, and no change if 0

# Transforming Data in R



- ▷ **relocate()**
  - ▶ Change column order
- ▷ **unite()**
  - ▶ Unite multiple columns into one by pasting strings together
- ▷ **separate()**
  - ▶ Separate a character column into multiple columns with a regular expression or numeric locations

# Transforming Data in R

## ▷ unite()

- ▶ `data %>% unite("New_Column",  
columns_to_select,  
sep = "delimiter",  
remove = FALSE)`

## ▷ separate()

- ▶ `data %>% separate(Column_1,  
into = c("New_Col1", "New_Col2", "New_Col3"),  
sep = "delimiter",  
remove = FALSE)`

```

thesis_plots.R x Untitled3* x fastqc_tbl_unite x fastqc_tbl_separate x >>
143
144
145 (fastqc_tbl_separate <- fastqc_tbl %>%
146   separate(id,
147     into = c("wga",
148       "species",
149       "repair",
150       "ng_dna"),
151     sep = "_"))
152
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155
144:1 # Changing and Creating Columns - R Script -
Console Terminal Jobs x
R 4.1.2 · C:/Users/Roy_R/Texas A&M University - Corpus Christi/Bird, Chris - Thesis_Roy_Roberts/repos/
> (fastqc_tbl_separate <- fastqc_tbl %>%
+   separate(id,
+     into = c("wga",
+       "species",
+       "repair",
+       "ng_dna"),
+     sep = "_"))
# A tibble: 101 x 8
  wga species repair ng_dna total_sequences
<chr> <chr> <chr> <chr> <dbl>
1 NoWGA Adu-AMat NR 10 22626345
2 NoWGA Adu-AMat NR 3.2 18538669
3 NoWGA Adu-AMat R 10 32061574
4 NoWGA Adu-AMat R 3.2 20795529
5 NoWGA Adu-CHam NR 10 37212563
6 NoWGA Adu-CHam NR 1 56793298
7 NoWGA Adu-CHam NR 3.2 55032990
8 NoWGA Adu-CHam R 10 56331948
9 NoWGA Adu-CHam R 1 52844376
10 NoWGA Adu-CHam R 3.2 50799485
# ... with 91 more rows, and 3 more variables:
#   percent_failed <dbl>,
#   percent_gc_content <dbl>,
#   percent_duplication <dbl>
>

```

```

thesis_plots.R x Untitled3* x fastqc_tbl_unite x fastqc_tbl_separate x >>
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155
156 (fastqc_tbl_unite <- fastqc_tbl_separate %>%
157   relocate(species,
158     ng_dna,
159     repair,
160     wga) %>%
161   unite("id",
162     species:wga,
163     sep = "-"))
164
165
165:1 # Changing and Creating Columns - R Script -
Console Terminal Jobs x
R 4.1.2 · C:/Users/Roy_R/Texas A&M University - Corpus Christi/Bird, Chris - Thesis_Roy_Roberts/repos/roberts.t
> (fastqc_tbl_unite <- fastqc_tbl_separate %>%
+   relocate(species,
+     ng_dna,
+     repair,
+     wga) %>%
+   unite("id",
+     species:wga,
+     sep = "-"))
# A tibble: 101 x 5
  id total_sequences percent_failed
<chr> <dbl> <dbl>
1 Adu-AMat-10-NR-NoWGA 22626345 36.4
2 Adu-AMat-3.2-NR-NoWGA 18538669 45.5
3 Adu-AMat-10-R-NoWGA 32061574 36.4
4 Adu-AMat-3.2-R-NoWGA 20795529 36.4
5 Adu-CHam-10-NR-NoWGA 37212563 36.4
6 Adu-CHam-1-NR-NoWGA 56793298 27.3
7 Adu-CHam-3.2-NR-NoWGA 55032990 36.4
8 Adu-CHam-10-R-NoWGA 56331948 18.2
9 Adu-CHam-1-R-NoWGA 52844376 18.2
10 Adu-CHam-3.2-R-NoWGA 50799485 18.2
# ... with 91 more rows, and 2 more variables:
#   percent_gc_content <dbl>,
#   percent_duplication <dbl>
>

```





# Tidyverse “Activity 3

- ▷ Separate name into surname and given\_name
- ▷ Combine haircolor and sex into haircolor\_sex
- ▷ Move the columns around for fun!

# Pivoting Data in R

## ▷ `pivot_longer()`

- ▶ Pivots wide data to long data
  - Wide data sets do not contain repeating values in the ID
  - Long data sets do contain repeating values in the ID

- ▶ `pivot_longer(cols = ColumnX:ColumnY, names_to = "Column_Name1", values_to = "Column_Name2")`

```
thesis_plots.R x workshop_examples_part2.R x read_data_ssl.R x
Source on Save Run Source
84
85 ##### Pivoting Data in R #####
86
87 (fastqc_tbl_long <- fastqc_tbl %>%
88   pivot_longer(cols = c(total_sequences,
89                         percent_failed,
90                         percent_gc_content,
91                         percent_duplication),
92               names_to = "metrics",
93               values_to = "values"))
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```
R 4.1.2 · C:/Users/Roy_R/Texas A&M University - Corpus Christi/Bird, Chris - Thesis_Roy_Roberts/rep
> (fastqc_tbl_long <- fastqc_tbl %>%
+   pivot_longer(cols = c(total_sequences,
+                         percent_failed,
+                         percent_gc_content,
+                         percent_duplication),
+               names_to = "metrics",
+               values_to = "values"))
# A tibble: 384 x 3
   id                metrics      values
  <chr>             <chr>      <dbl>
1 NowGA_Adu-AMat_NR_10 total_sequences 2.26e7
2 NowGA_Adu-AMat_NR_10 percent_failed 3.64e1
3 NowGA_Adu-AMat_NR_10 percent_gc_con~ 4.2 e1
4 NowGA_Adu-AMat_NR_10 percent_duplic~ 2.29e1
5 NowGA_Adu-AMat_NR_3.2 total_sequences 1.85e7
6 NowGA_Adu-AMat_NR_3.2 percent_failed 4.55e1
7 NowGA_Adu-AMat_NR_3.2 percent_gc_con~ 4.4 e1
8 NowGA_Adu-AMat_NR_3.2 percent_duplic~ 2.66e1
9 NowGA_Adu-AMat_R_10 total_sequences 3.21e7
10 NowGA_Adu-AMat_R_10 percent_failed 3.64e1
# ... with 374 more rows
>
```

# Pivoting Data in R

- ▶ `pivot_wider()`
  - ▶ Pivots long data to wide data
    - Wide data sets do not contain repeating values in the ID
    - Long data sets do contain repeating values in the ID

▶ `pivot_longer(id_cols = ColumnX,  
names_from = Column_Name1  
values_from = Column_Name2)`

```
thesis_plots.R x workshop_examples_part2.R x read_data_ssl.R x wrangle...
Source on Save Run Source
85 ##### Pivoting Data in R #####
86
87 (fastqc_tbl_long <- fastqc_tbl %>%
88   pivot_longer(cols = c(total_sequences,
89                         percent_failed,
90                         percent_gc_content,
91                         percent_duplication),
92               names_to = "metrics",
93               values_to = "values"))
94
95 (fastqc_tbl_wide <- fastqc_tbl_long %>%
96   pivot_wider(id_cols = id,
97               names_from = metrics,
98               values_from = values))
99

99:1 # Pivoting Data in R R Script

Console Terminal Jobs
R 4.1.2 · C:/Users/Roy.R/Texas A&M University - Corpus Christi/Bird, Chris - Thesis_Roy_Roberts/repos/202
# percent_duplication <dbl>
> (fastqc_tbl_wide <- fastqc_tbl_long %>%
+   pivot_wider(id_cols = id,
+               names_from = metrics,
+               values_from = values))
# A tibble: 96 x 5
   id                total_sequences percent_failed
  <chr>                <dbl>          <dbl>
1 NowGA_Adu-AMat_NR_10      22626345         36.4
2 NowGA_Adu-AMat_NR_3.2     18538669         45.5
3 NowGA_Adu-AMat_R_10      32061574         36.4
4 NowGA_Adu-AMat_R_3.2     20795529         36.4
5 NowGA_Adu-CHam_NR_1       56793298         27.3
6 NowGA_Adu-CHam_NR_10     37212563         36.4
7 NowGA_Adu-CHam_NR_3.2     55032990         36.4
8 NowGA_Adu-CHam_R_1       52844376         18.2
9 NowGA_Adu-CHam_R_10      56331948         18.2
10 NowGA_Adu-CHam_R_3.2     50799485         18.2
# ... with 86 more rows, and 2 more variables:
#   percent_gc_content <dbl>,
#   percent_duplication <dbl>
> |
```



# Tidyverse Activity 4

- ▷ Pivot longer all davis numeric davis values longer and save the new tibble as a variable.
- ▷ Pivot wider the previous tibble back to its original state.

# Summarising a Tibble in R

## ▷ summarise()

- ▶ To use summarise() a tibble must be grouped by one or more variables using group\_by()

- group\_by(ColumnX, ColumnY)

- ▶ summarise(NewColumn1 = function(Column),  
NewColumn2 = function(Column),  
...)

- ▶ Keeping a tibble grouped can cause problems with other functions so ungroup() should be used after grouping is no longer needed

```
thesis_plots.R x workshop_examples_part2.R* x Untitled1 x read_d...
Source on Save Run Source
100 ##### Summarising a Tibble #####
101
102 fastqc_tbl_separate %>%
103   group_by(species) %>%
104   summarise(number_of_observations = n()) %>%
105   ungroup()
106
107
108
109
110
111
112
113
```

113:1 # Summarising a Tibble R Script

Console Terminal Jobs

R 4.1.2 - C:/Users/Roy\_R/Texas A&M University - Corpus Christi/Bird, Chris - Thesis\_Roy\_Roberts/repc

```
> fastqc_tbl_separate %>%
+   group_by(species) %>%
+   summarise(number_of_observations = n()) %>%
+   ungroup()
# A tibble: 14 x 2
  species      number_of_observations
  <chr>                <int>
1 Adu-AMat                4
2 Adu-ATaw                2
3 Adu-CHam               12
4 Aur-APnb                6
5 Aur-CRag                6
6 Aur-CRag22              6
7 Aur-CRag39              6
8 Hte-CTic                6
9 Lle-AMnt                7
10 Lle-CNas              12
11 Sob-ABil                8
12 Ssp-AAtu                3
13 Ssp-CGub              12
14 Tbi-CJos                6
>
```

```
thesis_plots.R workshop_examples_part2.R* read_data_ssl.R wrangle_data.R wrangle_data_update_in_progress.R socialDistancing6.R test Untitled1
Source on Save Run

100 ##### Summarising a Tibble #####
101
102 fastqc_tbl_separate %>%
103   group_by(species) %>%
104   summarise(number_of_observations = n()) %>%
105   ungroup()
106
107 fastqc_tbl_separate %>%
108   group_by(wga, ng_dna) %>%
109   summarise(number_of_observations = n(),
110             mean_failed_percent = mean(percent_failed),
111             median_failed_percent = median(percent_failed),
112             mean_duplicate_percent = mean(total_sequences),
113             median_duplicate_percent = median(total_sequences),
114             mean_number_of_nonduplicate_sequences = mean((1-(percent_duplication/100)) * total_sequences)) %>%
115   ungroup()
116

116:1 Summarising a Tibble R Script

Console Terminal Jobs
R 4.1.2 C:/Users/Roy_R/Texas A&M University - Corpus Christi/Bird, Chris - Thesis_Roy_Roberts/repos/2022_PIRE_omics_workshop/R_workshop/
> fastqc_tbl_separate %>%
+   group_by(wga, ng_dna) %>%
+   summarise(number_of_observations = n(),
+             mean_failed_percent = mean(percent_failed),
+             median_failed_percent = median(percent_failed),
+             mean_duplicate_percent = mean(total_sequences),
+             median_duplicate_percent = median(total_sequences),
+             mean_number_of_nonduplicate_sequences = mean((1-(percent_duplication/100)) * total_sequences)) %>%
+   ungroup()
`summarise()` has grouped output by 'wga'. You can override using the `.groups` argument.
# A tibble: 6 x 8
  wga   ng_dna number_of_observations mean_failed_percent median_failed_percent mean_duplicate_p~ median_duplicate~ mean_number_of_no~
  <chr> <chr>          <int>          <dbl>          <dbl>          <dbl>          <dbl>          <dbl>
1 NowGA 1             16             27.3           27.3           41158135.       47215947       23223565.
2 NowGA 10            20             30.0           31.8           40486239.       44599912.       27615043.
3 NowGA 3.2           22             28.5           31.8           37670124.       44573735       24570108.
4 WGA    0.32          12             15.2           18.2           43117634.       42104900.       30987209.
5 WGA    1             13             18.2           18.2           47664618.       52688931       30218688.
6 WGA    3.2           12             16.7           18.2           42977095.       46882569       32863658.
>
```



# Tidyverse Activity 5

- ▷ Create `mean_weight` and summarise `mean_weight` by grouping by `haircolor` and `sex`, calculating the following:
  - ▶ Count, `n()`
  - ▶ Mean, `mean()`
  - ▶ Standard Deviation, `sd()`
  - ▶ Median, `median()`
  - ▶ Interquartile Range, `IQR()`