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Everything within the section above, demarcated by three dashes (—) is called a YAML header. We provide code for each lab containing a pre-formatted header, which will specify settings for the output format of your labs to look consistent and professional. We only ask that you update the document author to your name.

Before we start

If you have zero to no experience with R, please take a look at this tutorial: [SICSS Boot Camp \(Beta\)](#)

At least do

1. Installing R and R Studio (14 minutes)
2. R Basics (17 minutes)

If you are comfortable navigating R and are familiar with quarto, then feel free to skip lab 0.

If you have never coded in your life, take a deep breath and don't worry! We will provide all the necessary resources for you to succeed - with just one expectation: **read the code**.

Intro to lab format and all other stuff

What is [qmd](#), and how to use it.

Please run the following line in your *Terminal* (not the console!)

```
quarto install tinytex
```

Formatting text: pretty things and code chunks

This is a 3 level heading

This is a 1 level heading, a.k.a. title

this is text

```
1 + 1
```

```
[1] 2
```

i This is the title of the callout note

This is a callout note. If you decide to resubmit a lab, please indicate any changes using this callout format.

```
## this is a comment
```

```
print("I like networks ")
```

```
[1] "I like networks "
```

Lets save some characters into variables

```
my_name <- "Megan"  
# my_name <- "Seva"  
  
print(my_name)
```

```
[1] "Megan"
```

how about some libraries (packages)

```
#those comments will hide system messages from the console  
  
# install.packages("tidyverse")  
# install.packages("palmerpenguins")  
  
library(tidyverse)  
library(palmerpenguins)
```

a bit of data science

```
data(package = 'palmerpenguins')
head(penguins)
```

```
# A tibble: 6 x 8
  species   island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>     <fct>      <dbl>        <dbl>          <int>       <int>
1 Adelie    Torgersen      39.1         18.7           181        3750
2 Adelie    Torgersen      39.5         17.4           186        3800
3 Adelie    Torgersen      40.3         18             195        3250
4 Adelie    Torgersen       NA            NA             NA          NA
5 Adelie    Torgersen      36.7         19.3           193        3450
6 Adelie    Torgersen      39.3         20.6           190        3650
# i 2 more variables: sex <fct>, year <int>
```

```
penguins |>
  count(species)
```

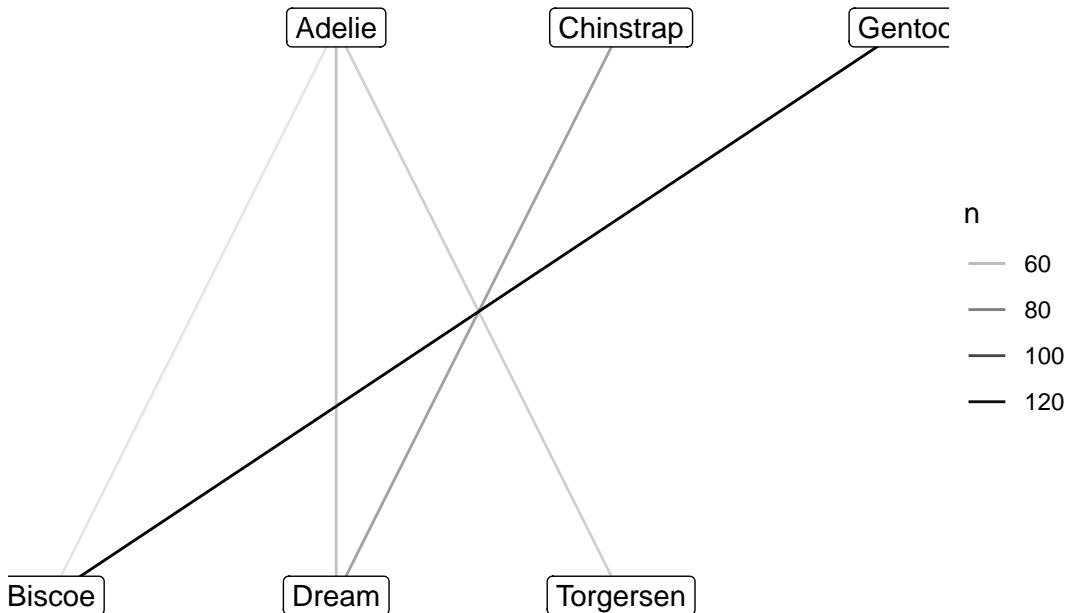
```
# A tibble: 3 x 2
  species      n
  <fct>    <int>
1 Adelie     152
2 Chinstrap   68
3 Gentoo     124
```

```
library(tidygraph)
library(igraph)
library(ggraph)
```

```
peng_island <- penguins |>
  count(species, island)

peng_island |>
  graph_from_data_frame() |>
  as_tbl_graph() |>
  ggraph(layout = "tree")+
  geom_edge_link(aes(alpha = n))+
  geom_node_label(aes(label = name))+
  theme_void()+
  ggtitle("Islands and penguins")
```

Islands and penguins



let's save our data

```
penguins |>
  head(20) |>
  write_csv("penguins20.csv")
```

```
penguins_20 <- read_csv("penguins20.csv")
```

```
Rows: 20 Columns: 8
-- Column specification ----
Delimiter: ","
chr (3): species, island, sex
dbl (5): bill_length_mm, bill_depth_mm, flipper_length_mm, body_mass_g, year

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.
```

```
penguins_20
```

```
# A tibble: 20 x 8
  species   island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <chr>     <chr>        <dbl>          <dbl>            <dbl>        <dbl>
1 Adelie   Torgersen      39.1         18.7             181       3750
2 Adelie   Torgersen      39.5         17.4             186       3800
3 Adelie   Torgersen      40.3          18              195       3250
```

```
4 Adelie Torgersen      NA          NA          NA          NA
5 Adelie Torgersen      36.7        19.3        193        3450
6 Adelie Torgersen      39.3        20.6        190        3650
7 Adelie Torgersen      38.9        17.8        181        3625
8 Adelie Torgersen      39.2        19.6        195        4675
9 Adelie Torgersen      34.1        18.1        193        3475
10 Adelie Torgersen     42           20.2        190        4250
11 Adelie Torgersen     37.8        17.1        186        3300
12 Adelie Torgersen     37.8        17.3        180        3700
13 Adelie Torgersen     41.1        17.6        182        3200
14 Adelie Torgersen     38.6        21.2        191        3800
15 Adelie Torgersen     34.6        21.1        198        4400
16 Adelie Torgersen     36.6        17.8        185        3700
17 Adelie Torgersen     38.7        19          195        3450
18 Adelie Torgersen     42.5        20.7        197        4500
19 Adelie Torgersen     34.4        18.4        184        3325
20 Adelie Torgersen     46           21.5        194        4200
# i 2 more variables: sex <chr>, year <dbl>
```

AI use disclosure

(In a few sentences describe how you used AI in this lab.)

In this lab I used Github Copilot to help me to write this AI use disclosure.