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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)
```

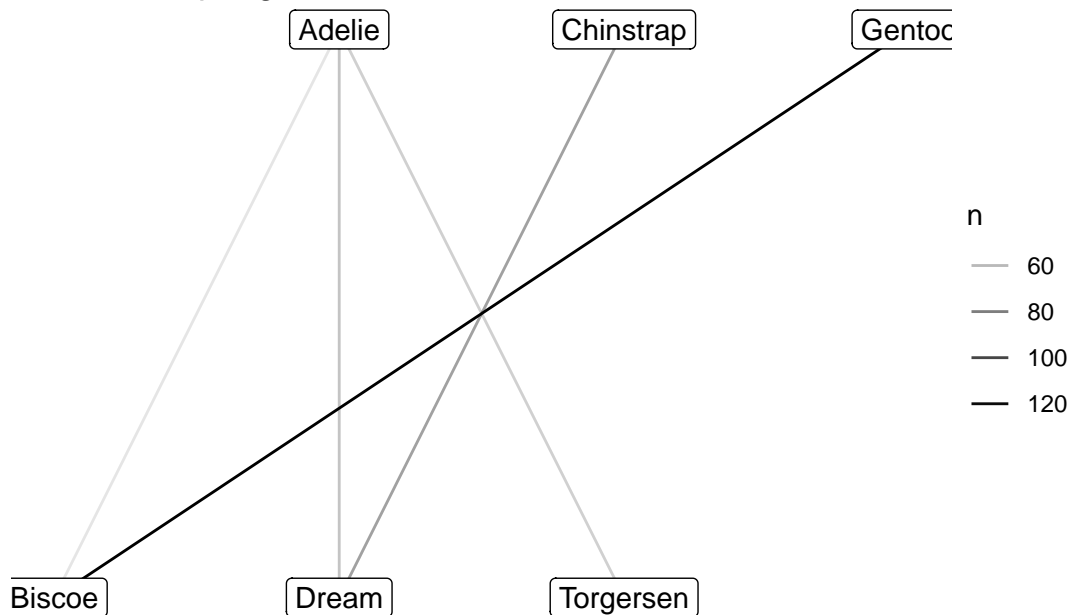
```
# A tibble: 3 x 2
  species      n
  <fct>    <int>
1 Adelie   152
2 Chinstrap 68
3 Gentoo   124
```

```
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.