HW 01 - Pet names

Meet the toolkit

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Contents

The goal of this assignment is to introduce you to R, RStudio, Git, and GitHub, which you'll be using throughout the course both to learn the data science concepts discussed in the course and to analyze real data and come to informed conclusions.

Figure 1: Photo by Jovana Askrabic on Unsplash

1 Getting started

1.1 Prerequisites

This assignment assumes that you have reviewed the lectures titled “Meet the toolkit: Programming” and “Meet the toolkit: version control and collaboration”. If you haven’t yet done so, please pause and complete the following before continuing.

1.2 Terminology

We’ve already thrown around a few new terms, so let’s define them before we proceed.

- **R:** Name of the programming language we will be using throughout the course.
- **RStudio:** An integrated development environment for R. In other words, a convenient interface for writing and running R code.
- **Git:** A version control system.
- **GitHub:** A web platform for hosting version controlled files and facilitating collaboration among users.
- **Repository:** A Git repository contains all of your project’s files and stores each file’s revision history. It’s common to refer to a repository as a repo.
  - In this course, each assignment you work on will be contained in a Git repo.
  - For individual assignments, only you will have access to the repo. For team assignments, all team members will have access to a single repo where they work collaboratively.
  - All repos associated with this course are housed in the course GitHub organization. The organization is set up such that students can only see repos they have access to, but the course staff can see all of them.

1.3 Starting slow

As the course progresses, you are encouraged to explore beyond what the assignments dictate; a willingness to experiment will make you a much better programmer! Before we get to that stage, however, you need to build some basic fluency in R. First, we will explore the fundamental building blocks of all of these tools.

Before you can get started with the analysis, you need to make sure you:

- have a GitHub account
- are a member of the course GitHub organization
- are a member of the course RStudio Cloud space

If you failed to confirm any of these, it means you have not yet completed the prerequisites for this assignment. Please go back to Prerequisites and complete them before continuing the assignment.

2 Workflow

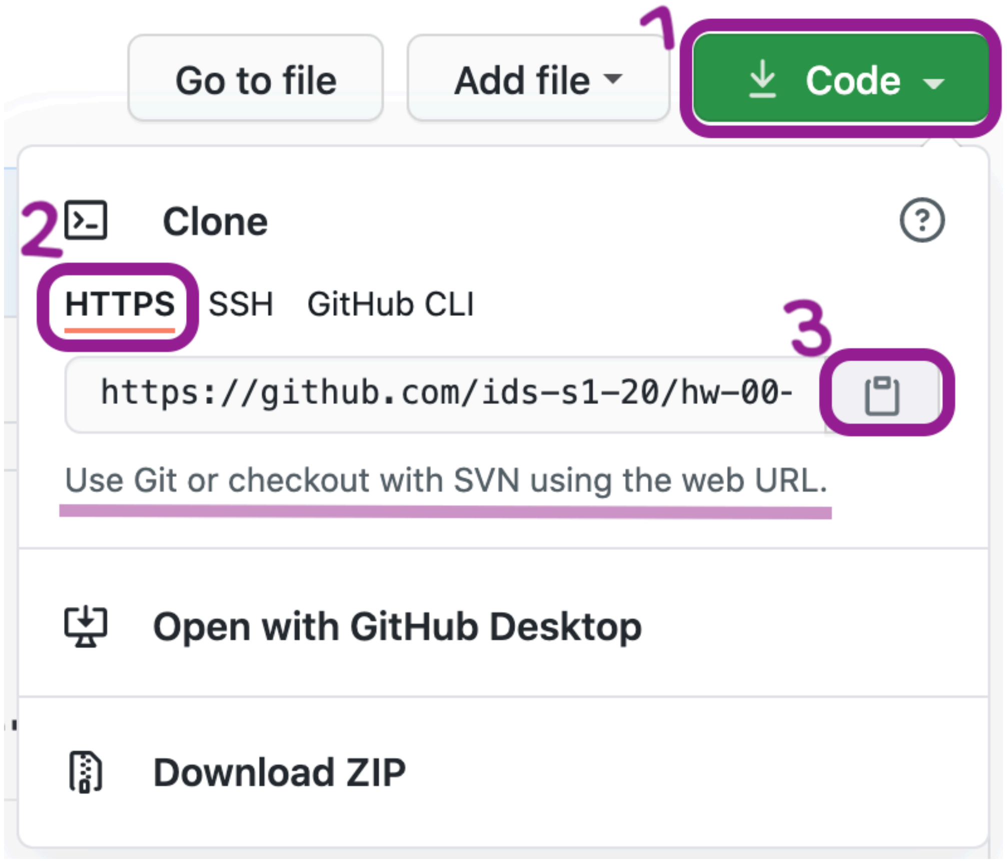
```
**IMPORTANT:** If there is no GitHub repo created for you for this assignment, it means I didn't have y
```

For each assignment in this course you will start with a GitHub repo that I created for you and that contains the starter documents you will build upon when working on your assignment. The first step is always to bring these files into RStudio so that you can edit them, run them, view your results, and interpret them. This action is called **cloning**.

Then you will work in RStudio on the data analysis, making **commits** along the way (snapshots of your changes) and finally **push** all your work back to GitHub.

The next few steps will walk you through the process of getting information of the repo to be cloned, cloning your repo in a new RStudio Cloud project, and getting started with the analysis.

2.0.1 Step 1. Get URL of repo to be cloned

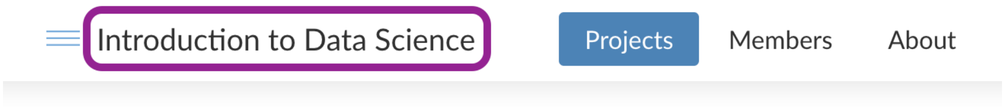


On GitHub, click on the green **Code** button, select **HTTPS** (this might already be selected by default, and if it is, you'll see the text *Use Git or checkout with SVN using the web URL* jas in the image on the right). Click on the clipboard icon to copy the repo URL.

2.0.2 Step 2. Go to RStudio Cloud

Go to posit.cloud and then **navigate to the course workspace** via the left sidebar. It's very important that you do this for two reasons:

- It's only when you're in the course workspace that you'll be able to benefit from R packages I've pre-installed for you so that your project can be configured correctly.
- It's only when you're in the course workspace that your usage of RStudio Cloud won't count towards the free usage limits.

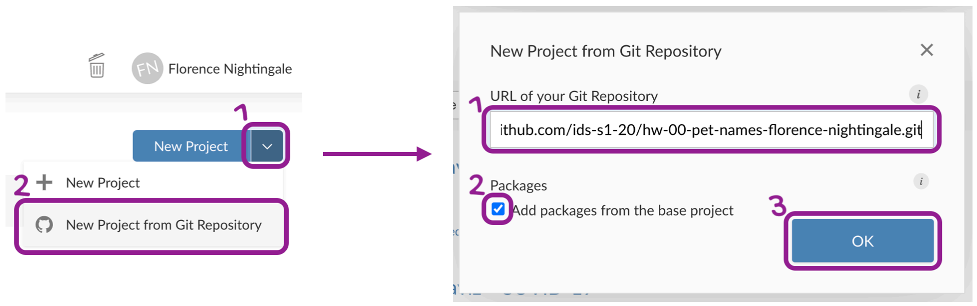


Before you proceed, confirm that you are in the course workspace by checking out what's on your top bar in RStudio Cloud.

2.0.3 Step 3. Clone the repo

In RStudio, click on the **down arrow** next to New Project and then choose **New Project from Git Repository**.

In the pop-up window, **paste the URL** you copied from GitHub, make sure the box for **Add packages from the base project** is checked (it should be, by default) and then click **OK**.

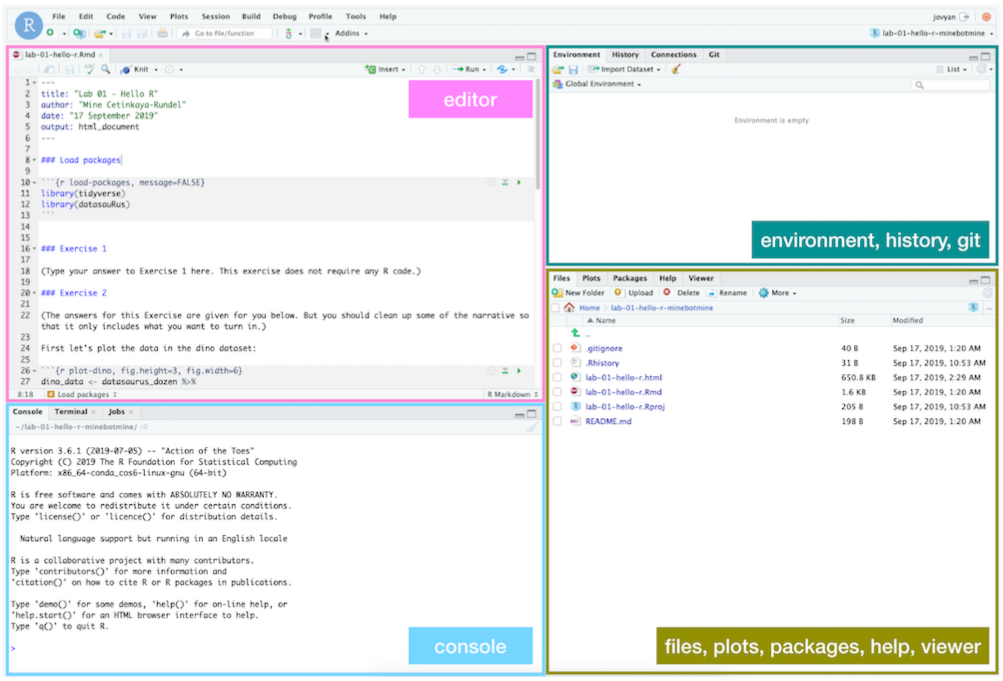

Florence Nightingale
1
New Project
2
New Project
New Project from Git Repository
New Project from Git Repository
URL of your Git Repository
1
2
Packages
3
OK

URL of your Git Repository: ithub.com/ids-s1-20/hw-00-pet-names-florence-nightingale.git

[✓] Add packages from the base project

3 Hello RStudio!

RStudio is comprised of four panes.



~~~
---
title: "Lab 01 - Hello R"
author: "Mine Cetinkaya-Rundel"
date: "17 September 2019"
output: html_document
---

### Load packages

```{r load-packages, message=FALSE}
library(tidyverse)
library(datasauRus)
~~~

Exercise 1

(Type your answer to Exercise 1 here. This exercise does not require any R code.)

Exercise 2

(The answers for this Exercise are given for you below. But you should clean up some of the narrative so
that it only includes what you want to turn in.)

First let's plot the data in the dino dataset:

```{r plot-dino, fig.height=3, fig.width=6}
dino_data <- datasaurus_dozen %>%
```

```
~/lab-01-hello-r-minebotmine/

R version 3.6.1 (2019-07-05) -- "Action of the Toes"
Copyright (C) 2019 The R Foundation for Statistical Computing
Platform: x86_64-conda_cos6-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

Home > lab-01-hello-r-minebotmine

Name	Size	Modified
.gitignore	40 B	Sep 17, 2019, 1:20 AM
.Rhistory	31 B	Sep 17, 2019, 10:53 AM
lab-01-hello-r.html	650.8 KB	Sep 17, 2019, 2:29 AM
lab-01-hello-r.Rmd	1.6 KB	Sep 17, 2019, 1:20 AM
lab-01-hello-r.Rproj	205 B	Sep 17, 2019, 10:53 AM
README.md	198 B	Sep 17, 2019, 1:20 AM

- On the bottom left is the Console, this is where you can write code that will be evaluated. Try typing `2 + 2` here and hit enter, what do you get?
- On the bottom right is the Files pane, as well as other panes that will come handy as we start our analysis.
- If you click on a file, it will open in the editor, on the top left pane.
- Finally, the top right pane shows your Environment. If you define a variable it would show up there. Try typing `x <- 2` in the Console and hit enter, what do you get in the **Environment** pane? Importantly, this pane is also where the **Git** interface lives. We will be using that regularly throughout this assignment.

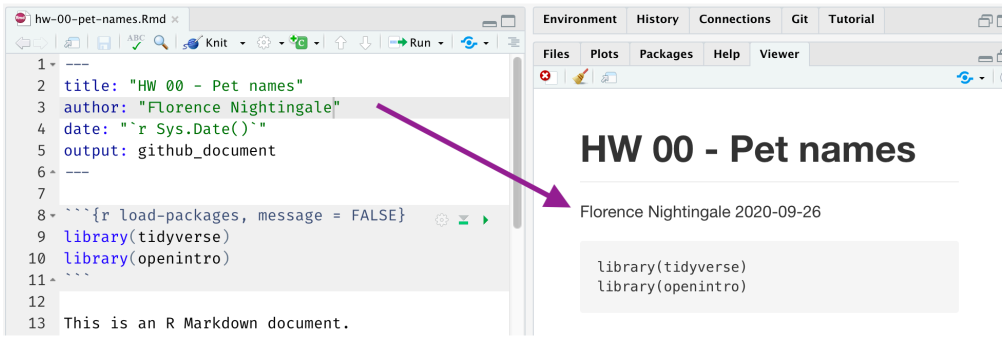
4 Warm up

Before we introduce the data, let's warm up with some simple exercises.

```
The top portion of your R Markdown file (between the three dashed lines) is called **YAML**. It stands
```

4.1 Step 1. Update the YAML

Open the R Markdown (Rmd) file in your project, change the author name to your name, and knit the document.



~~~
---
title: "HW 00 - Pet names"
author: "Florence Nightingale"
date: "`r Sys.Date()`"
output: github_document
---

```{r load-packages, message = FALSE}
library(tidyverse)
library(openintro)
```

This is an R Markdown document.
~~~

HW 00 - Pet names

Florence Nightingale 2020-09-26

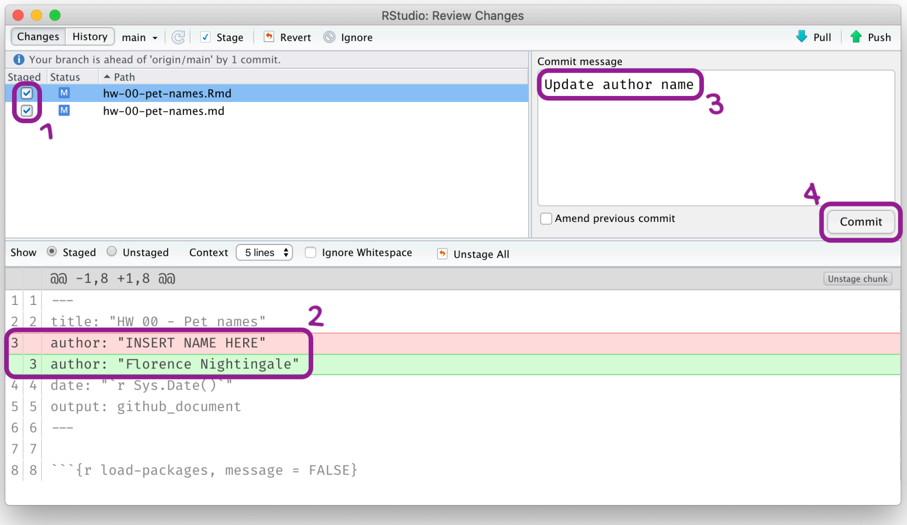
```
library(tidyverse)
library(openintro)
```

4.2 Step 2: Commit

Then Go to the **Git pane** in your RStudio.

You should see that your Rmd (R Markdown) file and its output, your md file (Markdown), are listed there as recently changed files.

Next, click on **Diff**. This will pop open a new window that shows you the **diff**erence between the last committed state of the document and its current state that includes your changes. If you're happy with these changes, click on the checkboxes of all files in the list, and type *"Update author name"* in the **Commit message** box and hit **Commit**.



```
Update author name
```

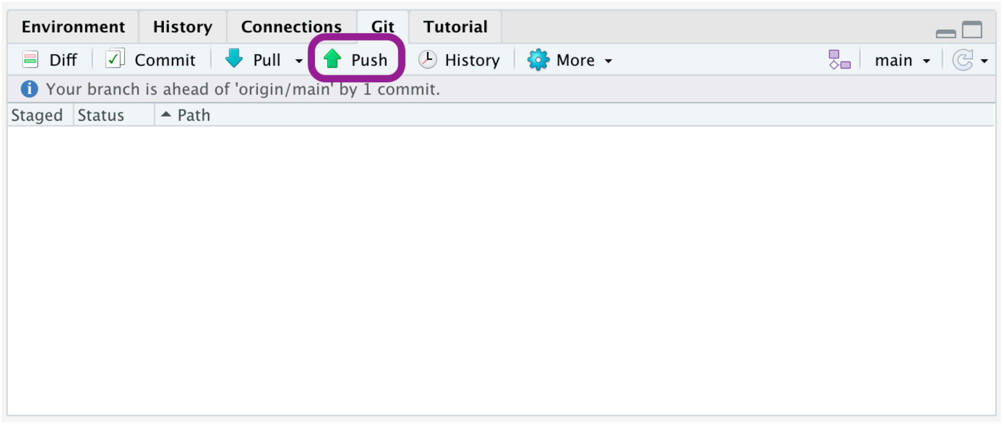
~~~
@@ -1,8 +1,8 @@
---
title: "HW 00 - Pet names"
author: "INSERT NAME HERE"
author: "Florence Nightingale"
date: "`r Sys.Date()`"
output: github_document
---

```{r load-packages, message = FALSE}
~~~

You don't have to commit after every change, this would get quite cumbersome. You should consider committing states that are *meaningful to you* for inspection, comparison, or restoration. In the first few assignments we will tell you exactly when to commit and in some cases, what commit message to use. As the semester progresses we will let you make these decisions.

4.3 Step 3. Push

Now that you have made an update and committed this change, it's time to push these changes to the web! Or more specifically, to your repo on GitHub. Why? So that others can see your changes. And by others, we mean the course teaching team (your repos in this course are private to you and us, only). In order to push your changes to GitHub, click on **Push**.



This will prompt a dialogue box where you first need to enter your user name, and then your password. This might feel cumbersome. Bear with me… I *will* teach you how to save your password so you don't have to enter it every time. But for this one assignment you'll have to manually enter each time you push in order to gain some experience with it.

Thought exercise: Which of the above steps (updating the YAML, committing, and pushing) needs to talk to GitHub?[1]

[1]Only pushing requires talking to GitHub, this is why you're asked for your password at that point.

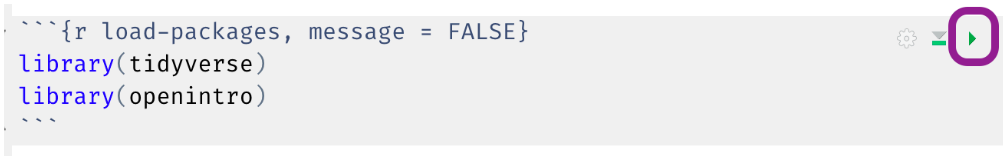
Updating the YAML is also a local operation, it doesn't require any communication with GitHub. Committing is a local operation, it doesn't require any communication with GitHub. Pushing requires communication with GitHub, as it is the step that sends your changes to GitHub.

5 Packages

R is an open-source language, and developers contribute functionality to R via packages. In this assignment we will use the following packages:

- **tidyverse**: a collection of packages for doing data analysis in a "tidy" way
- **openintro**: a package that contains the datasets from OpenIntro resources

We use the `library()` function to load packages. In your R Markdown document you should see an R chunk labelled `load-packages` which has the necessary code for loading both packages. You should also load these packages in your Console, which you can do by sending the code to your Console by clicking on the **Run Current Chunk** icon (green arrow pointing right icon).



~~~
```{r load-packages, message = FALSE}
library(tidyverse)
library(openintro)
```
~~~

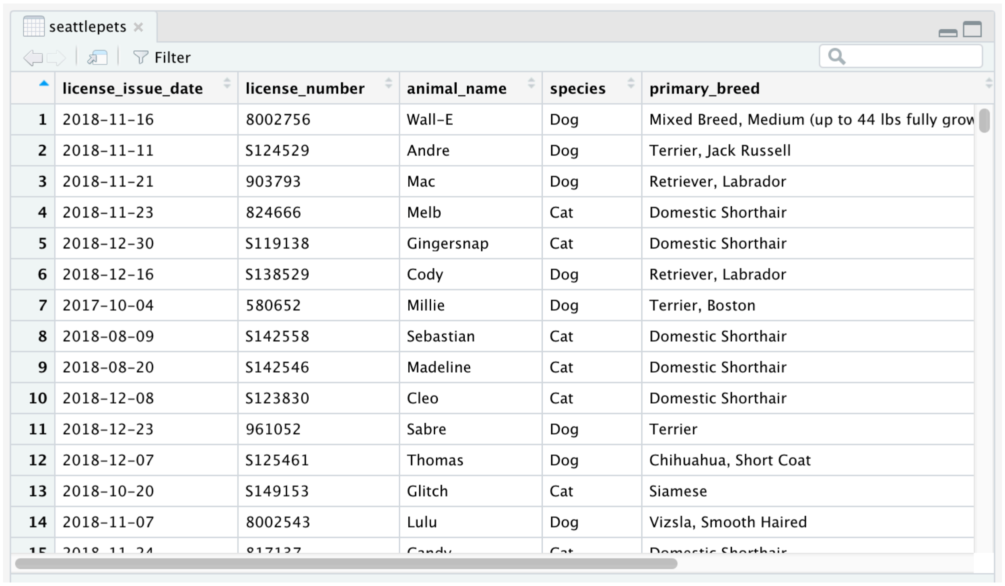
Note that these packages also get loaded in your R Markdown environment when you **Knit** your R Markdown document.

6 Data

The city of Seattle, WA has an open data portal that includes pets registered in the city. For each registered pet, we have information on the pet's name and species. The data used in this exercise can be found in the **openintro** package, and it's called `seattlepets`. Since the dataset is distributed with the package, we don't need to load it separately; it becomes available to us when we load the package.

You can view the dataset as a spreadsheet using the `View()` function. Note that you should not put this function in your R Markdown document, but instead type it directly in the Console, as it pops open a new window (and the concept of popping open a window in a static document doesn't really make sense...). When you run this in the console, you'll see the following **data viewer** window pop up.

```
View(seattlepets)
```



	license_issue_date	license_number	animal_name	species	primary_breed
1	2018-11-16	8002756	Wall-E	Dog	Mixed Breed, Medium (up to 44 lbs fully grow
2	2018-11-11	S124529	Andre	Dog	Terrier, Jack Russell
3	2018-11-21	903793	Mac	Dog	Retriever, Labrador
4	2018-11-23	824666	Melb	Cat	Domestic Shorthair
5	2018-12-30	S119138	Gingersnap	Cat	Domestic Shorthair
6	2018-12-16	S138529	Cody	Dog	Retriever, Labrador
7	2017-10-04	580652	Millie	Dog	Terrier, Boston
8	2018-08-09	S142558	Sebastian	Cat	Domestic Shorthair
9	2018-08-20	S142546	Madeline	Cat	Domestic Shorthair
10	2018-12-08	S123830	Cleo	Cat	Domestic Shorthair
11	2018-12-23	961052	Sabre	Dog	Terrier
12	2018-12-07	S125461	Thomas	Dog	Chihuahua, Short Coat
13	2018-10-20	S149153	Glitch	Cat	Siamese
14	2018-11-07	8002543	Lulu	Dog	Vizsla, Smooth Haired
15	2018-11-24	817137	Candy	Cat	Domestic Shorthair

You can find out more about the dataset by inspecting its documentation (which contains a **data dictionary**, name of each variable and its description), which you can access by running `?seattlepets` in the Console or using the Help menu in RStudio to search for `seattlepets`.

By running `?seattlepets` in the Console or using the Help menu in RStudio to search for `seattlepets`, you'll see documentation about the dataset pop up in the Help pane which contains information such as the source of the data, a brief description, and a data dictionary that describes each variable in the dataset.

7 Exercises

7.1 Exercise #1

According to the data dictionary, how many pets are included in this dataset?

There are a total of 52,519 pets in the dataset with 7 variables for each pet.

```r
# Get the number of entries (rows) and variables (columns)
nrow(seattlepets)
```

```
## [1] 52519
```

```r
ncol(seattlepets)
```

```
## [1] 7
```

Write your answer in your R Markdown document under Exercise 1, knit the document, commit your changes with a commit message that says "Completed Exercise 1", and push. Make sure to commit and push all changed files so that your Git pane is cleared up afterwards.

7.2 Exercise #2

Again, according to the data dictionary, how many variables do we have for each pet?

There are 7 variables for each pet in the dataset:

- `license_issue_date`: Date the animal was registered with Seattle
- `license_number`: Unique identifier for each pet license
- `animal_name`: Name of the pet
- `species`: Species of the pet (e.g., Dog, Cat, etc.)
- `primary_breed`: Primary breed of the pet
- `secondary_breed`: Secondary breed of the pet (if applicable)
- `zip_code`: Zip code animal is registered in

```
colnames(seattlepets)
```

```
## [1] "license_issue_date" "license_number"     "animal_name"
## [4] "species"            "primary_breed"      "secondary_breed"
## [7] "zip_code"
```

Write your answer in your R Markdown document under Exercise 2, knit the document, commit your changes with a commit message that says "Completed Exercise 2", and push. Make sure to commit and push all changed files so that your Git pane is cleared up afterwards.

7.3 Exercise #3

What are the three most common pet names in Seattle?

The most common pet names are *Lucy*, *Charlie*, and *Luna*.

To do this you will need to count the frequencies of each pet name and display the results in descending order of frequency so that you can easily see the top three most popular names. The following code does exactly that.

```
The two lines of code can be read as "Start with the seattlepets data frame, and then count the animal_
```

The code below takes the `seattlepets` dataset from the **openintro** package and produces a frequency table of pet names. It first standardizes the `animal_name` variable by converting all names to lowercase and trimming any leading or trailing spaces. It then removes missing (`NA`) or blank entries to ensure only valid names remain. Finally, it counts the occurrences of each unique name, sorts them from most to least common, and labels the frequency column as `count` for clarity.

```
popular_names <- seattlepets %>%
  mutate(animal_name = animal_name |>
    tolower() |>
    trimws()) %>% # remove leading/trailing spaces
  filter(!is.na(animal_name), animal_name != "") %>%
  count(animal_name, sort = TRUE, name = "count")
popular_names
```

```
## # A tibble: 13,775 x 2
##    animal_name count
##    <chr>       <int>
##  1 lucy          440
##  2 charlie       387
##  3 luna          357
##  4 bella         331
##  5 max           273
##  6 daisy         261
##  7 molly         240
##  8 jack          232
##  9 lily          232
## 10 stella        227
## # i 13,765 more rows
```

```
head(popular_names, 3)
```

```
## # A tibble: 3 x 2
##   animal_name count
##   <chr>       <int>
## 1 lucy          440
## 2 charlie       387
## 3 luna          357
```

Write your answer in your R Markdown document under Exercise 3. In this exercise you will not only provide a written answer but also include some code and output. You should insert the code in the code chunk provided for you, knit the document to see the output, and then write your narrative for the answer based on the output of this function, and knit again to see your narrative, code, and output in the resulting document. Then, commit your changes with a commit message that says "Completed Exercise 3", and push. Make sure to commit and push all changed files so that your Git pane is cleared up afterwards.

Let's also look to see what the most common pet names are for various species. For this we need to first `group_by()` the `species`, and then do the same counting we did before.

```
Looks like many of those NAs were cats. Poor unnamed kitties…
```

```
seattlepets %>%
  group_by(species) %>%
  count(animal_name, sort = TRUE)
```

```
## # A tibble: 16,823 x 3
## # Groups:   species [4]
##    species animal_name     n
##    <chr>   <chr>       <int>
##  1 Cat     <NA>          406
##  2 Dog     Lucy          337
##  3 Dog     Charlie       306
##  4 Dog     Bella         249
##  5 Dog     Luna          244
##  6 Dog     Daisy         221
##  7 Dog     Cooper        189
##  8 Dog     Lola          187
##  9 Dog     Max           186
## 10 Dog     Molly         186
## # i 16,813 more rows
```

But this output isn't exactly what we wanted. We wanted to know the most common cat and dog names, but there are barely any cats present in this output! This is because there are more dogs than cats in the dataset overall. We can confirm this by counting the various species in the data.

```
6 pigs in the city? Ok… But we'll continue with cats and dogs.
```

```
seattlepets %>%
  count(species, sort = TRUE)
```

```
## # A tibble: 4 x 2
##   species     n
##   <chr>   <int>
## 1 Dog     35181
## 2 Cat     17294
## 3 Goat       38
## 4 Pig         6
```

Let's search for the top 5 cat and dog names. To do this, we can use the `slice_max()` function. The first argument in the function is the variable we want to select the highest values of, which is `n`. The second argument is the number of rows to select, which is `n = 5` for the top 5. It may be a bit confusing that both of these are `n`, but this is because we already have a variable called `n` in the data frame.

```
seattlepets %>%
  group_by(species) %>%
  count(animal_name, sort = TRUE) %>%
  slice_max(n, n = 5)
```

```
## # A tibble: 53 x 3
## # Groups:   species [4]
##    species animal_name     n
##    <chr>   <chr>       <int>
##  1 Cat     <NA>          406
##  2 Cat     Luna          111
##  3 Cat     Lucy          102
##  4 Cat     Lily           86
##  5 Cat     Max            83
##  6 Dog     Lucy          337
##  7 Dog     Charlie       306
##  8 Dog     Bella         249
##  9 Dog     Luna          244
## 10 Dog     Daisy         221
## # i 43 more rows
```

This output provides the top 5 names for each species along with their respective counts. However, the results are sorted by count across all species, which means that the top names for one species may appear before those of another species.

7.4 Exercise #4

Based on the previous output we can easily identify the most common cat and dog names in Seattle, but the output is sorted by `n` (the frequencies) as opposed to being organized by the `species`. Build on the pipeline to arrange the results so that they're arranged by `species` first, and then `n`. This means you will need to add one more step to the pipeline, and you have two options: `arrange(species, n)` or `arrange(n, species)`. You should try both and decide which one organizes the output by species and then ranks the names in order of frequency for each species.

```
popular_names <- seattlepets %>%
  mutate(animal_name = animal_name |>
    tolower() |>
    trimws()) %>%
  filter(!is.na(animal_name), animal_name != "") %>%
  count(species, animal_name, sort = TRUE, name = "count")

popular_names
```

```
## # A tibble: 16,669 x 3
##    species animal_name count
##    <chr>   <chr>       <int>
##  1 Dog     lucy          338
##  2 Dog     charlie       306
##  3 Dog     bella         249
##  4 Dog     luna          246
##  5 Dog     daisy         221
##  6 Dog     cooper        189
##  7 Dog     max           189
##  8 Dog     lola          188
##  9 Dog     molly         186
## 10 Dog     stella        185
## # i 16,659 more rows
```

```
popular_names <- popular_names %>%
  group_by(species) %>%
  arrange(species, desc(count), animal_name)
popular_names
```

```
## # A tibble: 16,669 x 3
## # Groups:   species [4]
##    species animal_name count
##    <chr>   <chr>       <int>
##  1 Cat     luna          111
##  2 Cat     lucy          102
##  3 Cat     lily           86
##  4 Cat     max            83
##  5 Cat     bella          82
##  6 Cat     charlie        81
##  7 Cat     oliver         73
##  8 Cat     jack           65
##  9 Cat     sophie         59
## 10 Cat     leo            54
## # i 16,659 more rows
```

```r
# Select the top 10 most common pet names for each species and display their counts
top_species_names <- popular_names %>%
  group_by(species) %>%
  slice_max(order_by = count, n = 10, with_ties = FALSE)
top_species_names
```

```
## # A tibble: 35 x 3
## # Groups:   species [4]
##    species animal_name count
##    <chr>   <chr>       <int>
##  1 Cat     luna          111
##  2 Cat     lucy          102
##  3 Cat     lily           86
##  4 Cat     max            83
##  5 Cat     bella          82
##  6 Cat     charlie        81
##  7 Cat     oliver         73
##  8 Cat     jack           65
##  9 Cat     sophie         59
## 10 Cat     leo            54
## # i 25 more rows
```

Here, we can see the top 10 names for each species along with their counts, organized by species and then by frequency within each species.

Looking at the data more closely:

1. **Dogs**: The most popular dog names are “lucy” (338), “charlie” (306), and “bella” (249). These three names significantly outrank other dog names, with counts over 200. There’s a gradual decline in popularity after the top three names.
2. **Cats**: The most popular cat names are “luna” (111), “lucy” (102), and “lily” (86). Cat names show a more even distribution in popularity compared to dog names, with a more gradual decrease in frequency from top to bottom.
3. **Goats**: All goat names appear just once in the dataset, suggesting there are few registered goats in Seattle, and their names are quite diverse with no clear pattern of popularity.
4. **Pigs**: Similar to goats, all pig names appear only once, indicating a small population of registered pigs with unique names.

It’s interesting to note that “lucy” appears in the top names for both cats and dogs, showing some cross-species name preferences. The data also reveals that dogs are much more commonly registered pets in Seattle than cats, as evidenced by the higher counts for dog names compared to cat names.

Now that we have the top 10 names for each species, we can create a contingency table that displays the counts of these names across different species.

```r
# Start from popular_names (species, animal_name, count)
contingency_tbl <- top_species_names %>%
  pivot_wider(
    names_from = species, # columns become species
    values_from = count, # values are counts
    values_fill = NA # fill missing combos with 0
  )
contingency_tbl
```

```
## # A tibble: 30 x 5
##    animal_name   Cat   Dog  Goat   Pig
##    <chr>       <int> <int> <int> <int>
##  1 luna          111   246    NA    NA
##  2 lucy          102   338    NA    NA
##  3 lily           86    NA    NA    NA
##  4 max            83   189    NA    NA
##  5 bella          82   249    NA    NA
##  6 charlie        81   306    NA    NA
##  7 oliver         73    NA    NA    NA
##  8 jack           65    NA    NA    NA
##  9 sophie         59    NA    NA    NA
## 10 leo            54    NA    NA    NA
## # i 20 more rows
```

```r
# sort by Dog first, then Cat, then name
contingency_tbl <- contingency_tbl %>%
  arrange(desc(Dog), desc(Cat), desc(Goat), desc(Pig), animal_name)
contingency_tbl
```

```
## # A tibble: 30 x 5
##    animal_name   Cat   Dog  Goat   Pig
##    <chr>       <int> <int> <int> <int>
##  1 lucy          102   338    NA    NA
##  2 charlie        81   306    NA    NA
##  3 bella          82   249    NA    NA
##  4 luna          111   246    NA    NA
##  5 daisy          NA   221    NA    NA
##  6 max            83   189    NA    NA
##  7 cooper         NA   189    NA    NA
##  8 lola           NA   188    NA    NA
##  9 molly          NA   186    NA    NA
## 10 stella         NA   185    NA    NA
## # i 20 more rows
```

When organizing the data by `species` first and then by `n`, we can clearly see the most common names for each species:

1. For **Dogs**:
   - "lucy" is the most popular dog name (338 dogs)
   - "charlie" is the second most popular (306 dogs)
   - "bella" is third (249 dogs)
   - Other popular names include "luna" (246), "daisy" (221), "max" (189), and "cooper" (189)
2. For **Cats**:
   - "luna" is the most popular cat name (111 cats)
   - "lucy" is the second most popular (102 cats)
   - "bella" ranks third (82 cats)
   - Other popular names include "max" (83 cats) and "lily" (86 cats) arrange(desc(Dog), desc(Cat), desc(Goat), desc(Pig), animal_name) contingency_tbl

Write your answer in your R Markdown document under Exercise 4. In this exercise you're asked to complete the code provided for you. You should insert the code in the code chunk provided for you, knit *the document to see the output, and then write your narrative for the answer based on the output of this function, and knit again to see your narrative, code, and output in the resulting document. Then, commit your changes with a commit message that says "Completed Exercise 4", and push. Make sure to commit and push all changed files so that your Git pane is cleared up afterwards.*

The following visualization plots the proportion of dogs with a given name versus the proportion of cats with the same name. The 20 most common cat and dog names are displayed. The diagonal line on the plot is the $x = y$ line; if a name appeared on this line, the name's popularity would be exactly the same for dogs and cats.

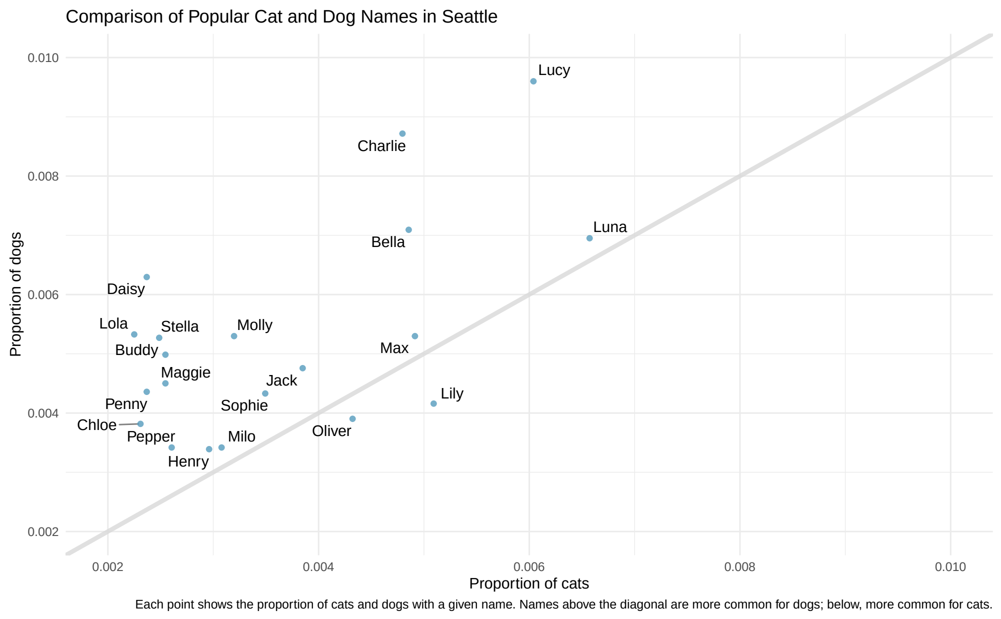
```r
# data prep
name_props <- seattlepets %>%
  filter(
    !is.na(animal_name),
    species %in% c("Dog", "Cat")
  ) %>%
  group_by(species) %>%
  count(animal_name, sort = TRUE) %>%
  mutate(prop = n / sum(n))

cat_name_props <- name_props %>%
  filter(species == "Cat") %>%
  rename(cat_prop = prop) %>%
  slice(1:30)

dog_name_props <- name_props %>%
  filter(species == "Dog") %>%
  rename(dog_prop = prop) %>%
  slice(1:30)

comb_name_props <- inner_join(cat_name_props, dog_name_props,
  by = "animal_name"
) %>%
  ungroup() %>%
  select(animal_name, cat_prop, dog_prop)

# create viz
ggplot(comb_name_props, aes(x = cat_prop, y = dog_prop)) +
  geom_abline(
    intercept = 0,
    color = COL["lgray", "full"],
    alpha = 0.8,
    linewidth = 1.5
  ) +
  geom_text_repel(aes(label = animal_name),
    segment.color = COL["gray", "full"],
    seed = 291252, max.iter = 10000
  ) +
  geom_point(color = COL["blue", "full"], alpha = 0.8) +
  theme_minimal() +
  labs(
    title = "Comparison of Popular Cat and Dog Names in Seattle",
    caption = "Each point shows the proportion of cats and dogs with a given name. Names above the diag
    x = "Proportion of cats",
    y = "Proportion of dogs"
  ) +
  xlim(0.002, 0.01) +
  ylim(0.002, 0.01)
```



1. What names are more common for cats than dogs? The ones above the line or the ones below the line?
   - **Above the line** → proportion of dogs > proportion of cats (more common among dogs). **Names below the line** (e.g., *lily*) are **more common for cats**. They have a higher proportion of cats with that name compared to dogs.
   - **Below the line** → proportion of cats > proportion of dogs (more common among cats). **Names above the line** (e.g., *daisy*) are **more common for dogs**. They have a higher proportion of dogs with that name compared to cats.
   - The name **luna** is the most popular for both cats and dogs, with a proportion of approximately 0.055 for cats and 0.007 for dogs.
2. Is the relationship between the two variables (proportion of cats with a given name and proportion of dogs with a given name) positive or negative? What does this mean in context of the data?
   - The relationship is **positive**: names that are common among cats tend also to be common among dogs. Names that are rare among cats tend also to be rare among dogs.
   - In context, this means **popular names tend to be popular across both species**. For example, *luna* and *lucy* rank highly for both cats and dogs, while less popular names remain less common in both groups.
3. Which name is the most popular for both cats and dogs?
   - The name **luna** is the most popular for both cats and dogs, with a proportion of approximately 0.055 for cats and 0.007 for dogs.
   - The name **lucy** is also very popular for both species, with a proportion of approximately 0.006 for cats and 0.0097 for dogs.

The scatter plot above visualizes the relationship between the popularity of names among cats and dogs in Seattle. Each point represents a specific pet name, with its position determined by the proportion of cats (x-axis) and dogs (y-axis) that bear that name. The diagonal reference line indicates equal popularity between the two species.

Overall Name Distribution

1. **Diagonal Reference Line**: The diagonal line represents equal popularity between cats and dogs. Names falling exactly on this line would have the same proportional representation in both populations.

2. **Clustering Pattern**: Most names cluster in the lower left portion of the plot (between 0.002-0.006 on both axes), indicating that pet name distributions have a "long tail" - a few very popular names and many less common ones.

Species Preferences

1. **Dog-Preferred Names**: Names appearing above the diagonal line are proportionally more common for dogs:
   - "Lucy" shows the strongest dog preference (around 0.01 for dogs vs. 0.006 for cats)
   - "Charlie" and "Bella" are also significantly more popular for dogs
   - "Daisy" appears almost exclusively as a dog name
2. **Cat-Preferred Names**: Names below the diagonal line are proportionally more common for cats:
   - "Lily" shows strong cat preference
   - "Oliver", "Sophie", and "Chloe" are notably more popular among cats
   - "Pepper" and "Henry" appear primarily as cat names
3. **Similar Popularity Names**: Names near the diagonal have similar proportional popularity:
   - "Luna" is popular for both species but slightly more common for cats
   - "Max" sits almost directly on the diagonal, indicating equal proportional popularity

Statistical Insights

1. **Correlation Analysis**: The plot shows a positive correlation between cat and dog name preferences, suggesting that human naming tendencies transcend pet species. However, the correlation is moderate, not strong, indicating distinct species-specific preferences.

2. **Outliers**: "Lucy" and "Charlie" appear as statistical outliers in dog naming popularity, while "Luna" is an outlier for cats.

3. **Proportion Range**: Dog name proportions extend higher (up to 0.01) than cat names (maximum around 0.008), suggesting slightly more naming concentration in dogs.

Cultural Implications

This visualization reveals how pet naming conventions reflect human cultural preferences while also showing species-specific patterns. The differences may reflect perceptions of personality traits associated with each species or gender associations with certain names. Names like "Lucy" may be perceived as fitting dog personalities, while "Lily" may be seen as more suitable for cat temperaments.

1. **Shared Naming Trends**: The overlap in popular names indicates shared cultural influences in pet naming, with certain names being trendy across both species.
2. **Species-Specific Trends**: The distinct preferences for certain names reflect cultural perceptions of cats and dogs, with some names evoking traits associated with each species (e.g., "Daisy" for dogs, "Lily" for cats).
3. **Humanization of Pets**: The use of human names for pets reflects a broader cultural trend of anthropomorphizing animals, indicating the deep emotional bonds people form with their pets.

Now is a good time to commit and push your changes to GitHub with an appropriate commit message. Commit and push all changed files so that your Git pane is cleared up afterwards. Make sure that your last push to the repo comes before the deadline. You should confirm that what you committed and pushed are indeed in your repo that we will see by visiting your repo on GitHub.