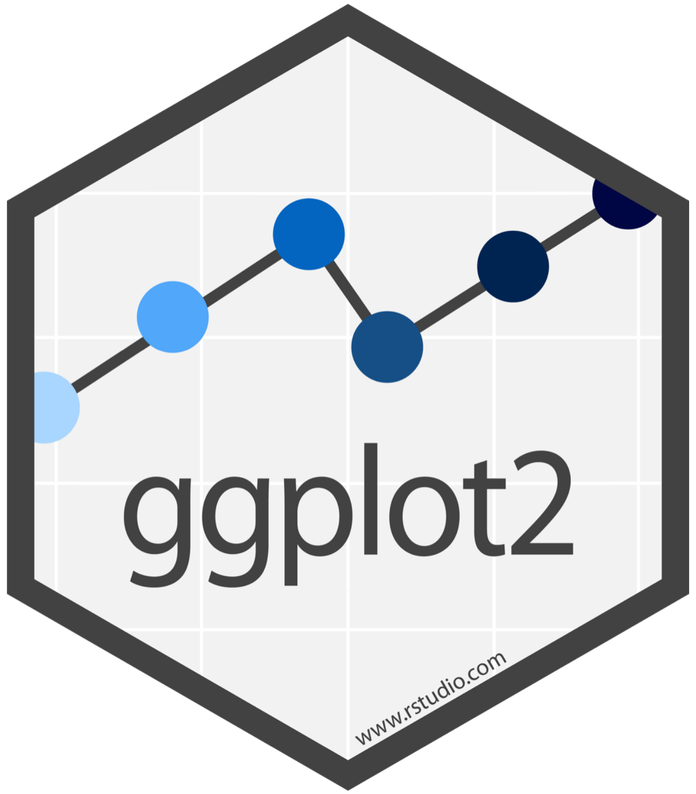
Visualize Data with

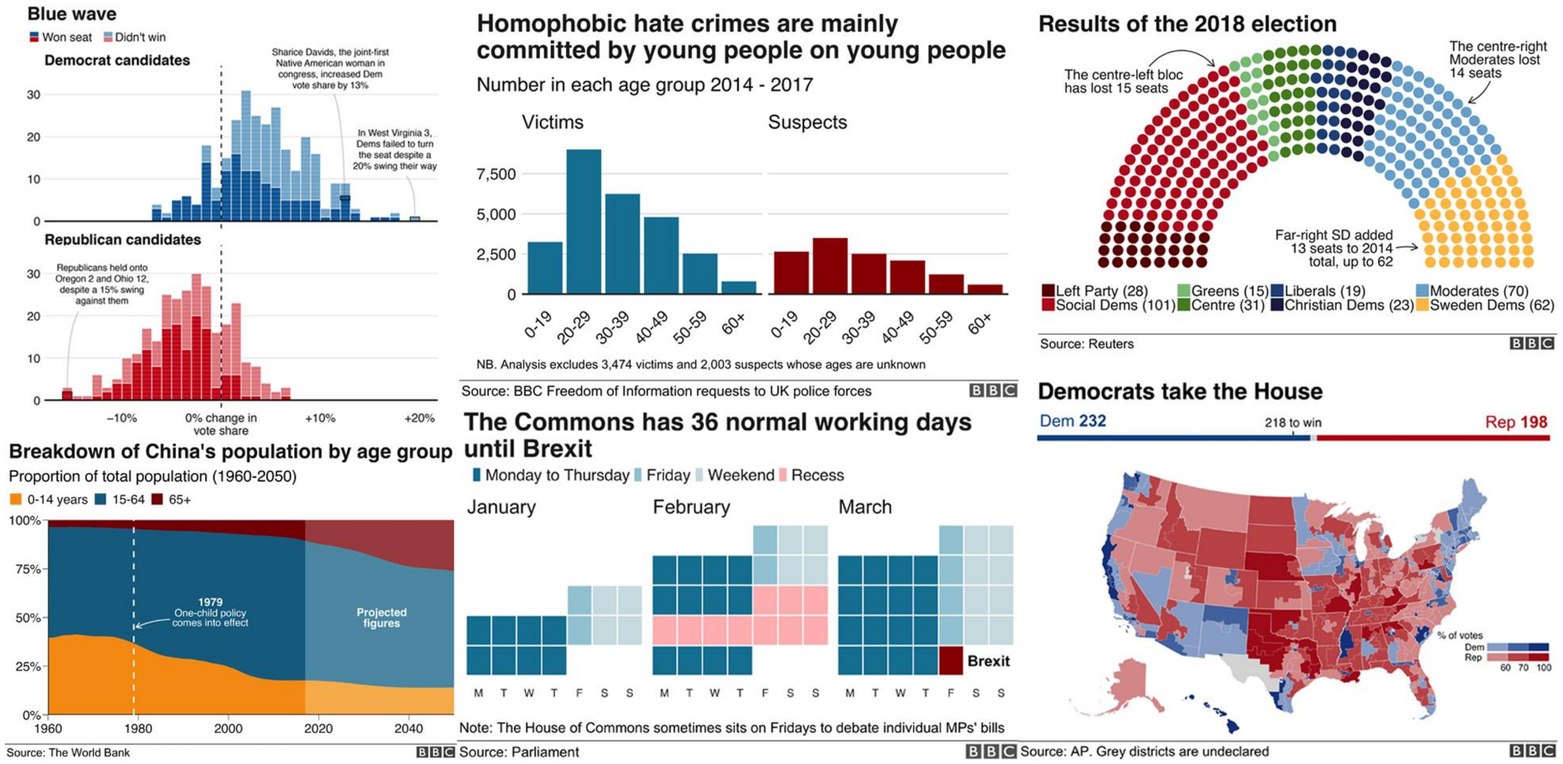


What can ggplot do?

"ggplot2 gives you far more control and creativity than a chart tool and allows you to **go beyond a limited number of graphics**. Working with scripts **saves a huge amount of time and effort**, in particular when working with data that needs **updating regularly, with reproducibility** a key requirement of our workflow."

-BBC Visual and Data Journalism

How the BBC Visual and Data Journalism team works with graphics in R



"The simple graph has brought more information to the data analyst’s mind than any other device. "

- John Tukey

Mappings

chromosome

Basic data for all human chromosomes.

chromosome

id <fctr>	length_mm <dbl>	basepairs <dbl>	variations <dbl>	protein_codinggenes <int>	pseudo_genes <int>	totallongnc_rna <int>	totalsmallnc_rna <int>
1	85	248956422	12151146	2058	1220	1200	496
2	83	242193529	12945965	1309	1023	1037	375
3	67	198295559	10638715	1078	763	711	298
4	65	190214555	10165685	752	727	657	228
5	62	181538259	9519995	876	721	844	235
6	58	170805979	9130476	1048	801	639	234
7	54	159345973	8613298	989	885	605	208
8	50	145138636	8221520	677	613	735	214
9	48	138394717	6590811	786	661	491	190
10	46	133797422	7223944	733	568	579	204

1-10 of 24 rows | 1-8 of 14 columns

Previous 1 2 3 Next

Quiz

Confer with your group.

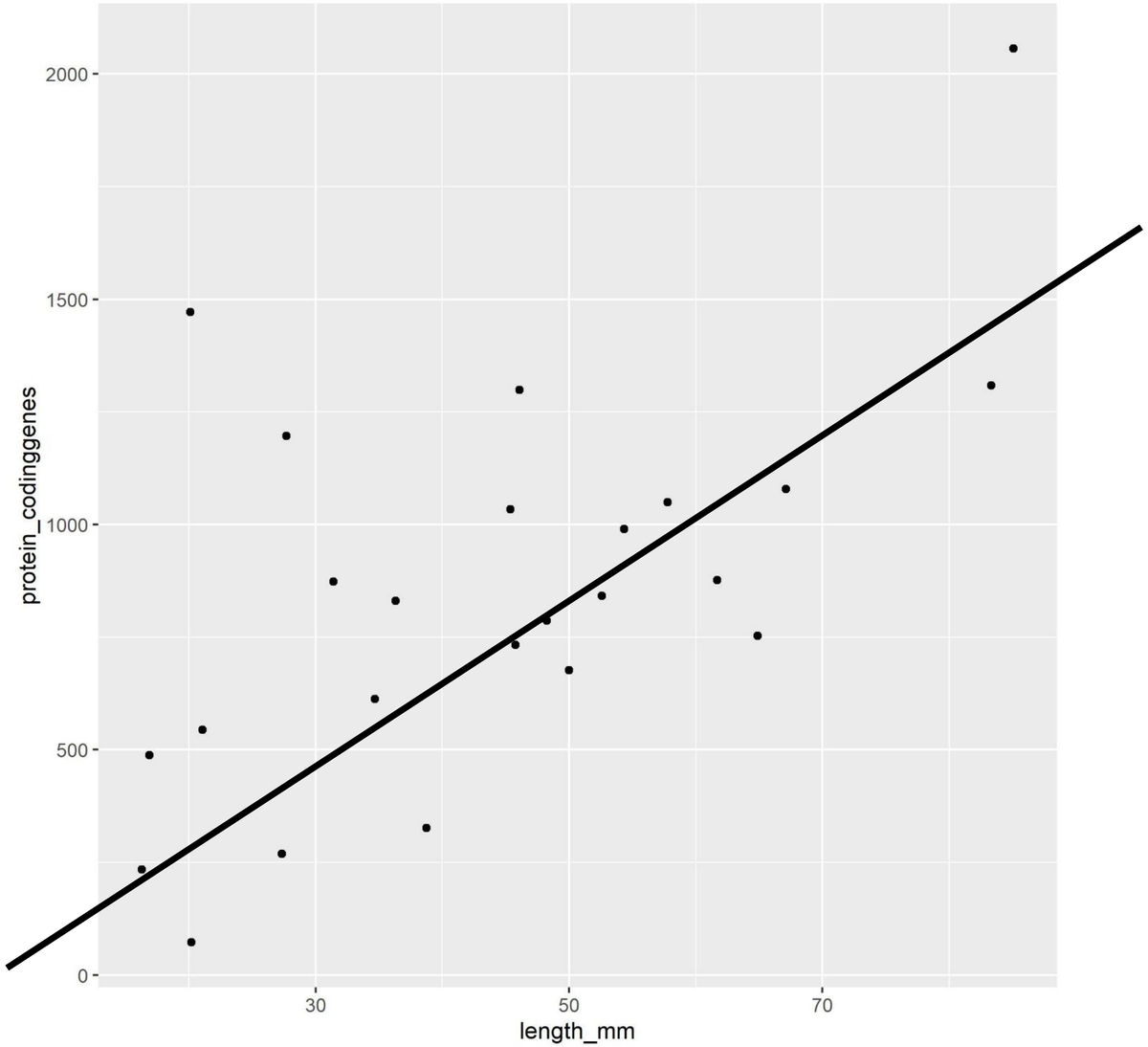
What relationship do you expect to see between chromosome size (`length_mm`) and number of genes (`protein_codinggenes`)?

No peeking ahead!

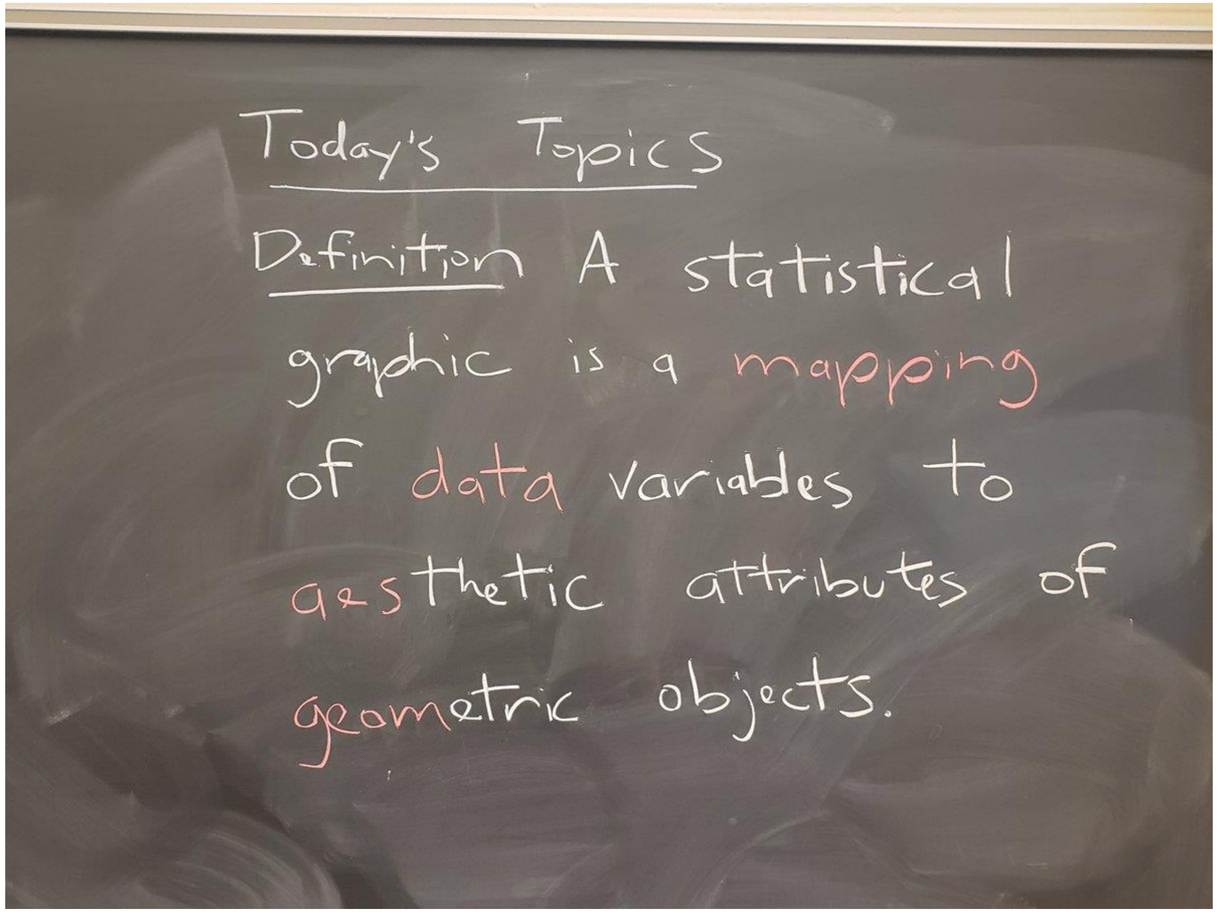
Your Turn 1

Run this code in **ggplot2-lecture.Rmd** to make a graph. Pay strict attention to spelling, capitalization, and parentheses!

```
ggplot(data = chromosome) +
  geom_point(mapping=aes(x = length_mm, y = protein_codinggenes))
```




```
ggplot(data = chromosome) +
   geom_point(mapping=aes(x = length_mm, y = protein_codinggenes))
```



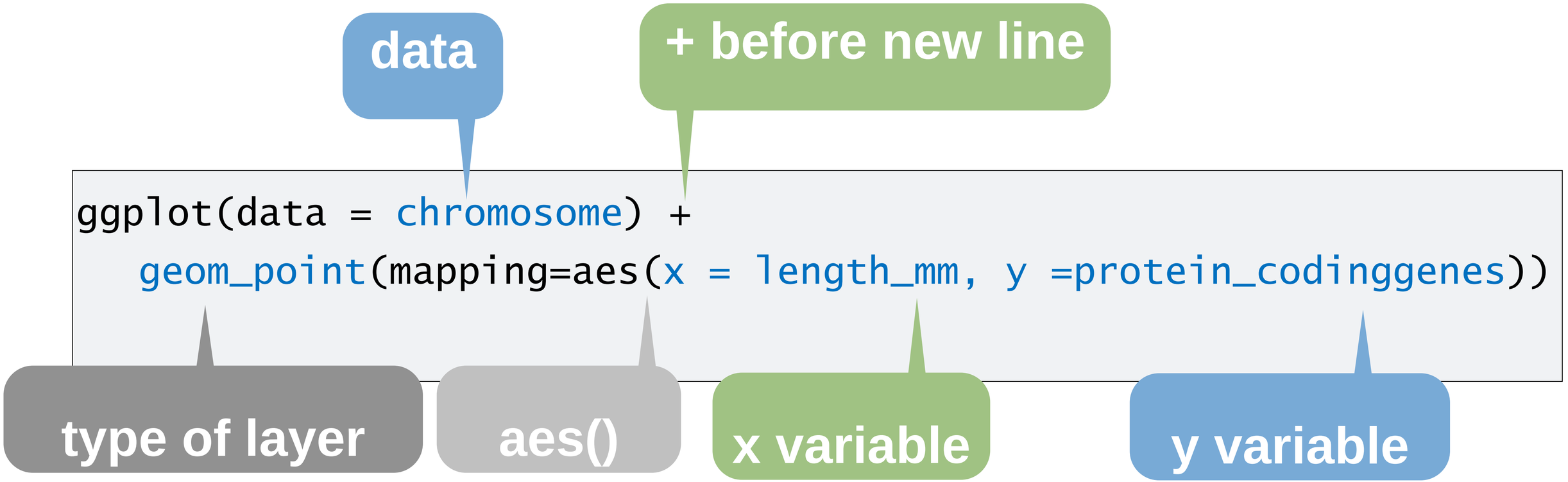

```
ggplot(data = chromosome) +
    geom_point(mapping=aes(x = length_mm, y = protein_codinggenes))
```

1. "Initialize" a plot with ggplot()
2. Add layers with geom_ functions

```
ggplot(data = chromosome) +
   geom_point(mapping=aes(x = length_mm, y =protein_codinggenes))
```

Pro tip: Always put the + at the end of a line, Never at the start

```
ggplot(data = chromosome) +
   geom_point(mapping=aes(x = length_mm, y =protein_codinggenes))
```


data
+ before new line
ggplot(data = chromosome) +
geom_point(mapping=aes(x = length_mm, y =protein_codinggenes))
type of layer
aes()
x variable
y variable

A template

```
ggplot(data = <DATA>) +
   <GEOM_FUNCTION>(mapping = aes(<MAPPINGS>))
```

```
ggplot(data = chromosome) +
   geom_point(mapping=aes(x = length_mm, y =protein_codinggenes))
```

A template

```
ggplot(data = <DATA>) +
  <GEOM_FUNCTION>(mapping = aes(<MAPPINGS>))
```

A template

```
ggplot(data = <DATA>) +
  <GEOM_FUNCTION>(mapping = aes(<MAPPINGS>))
```

A template

```
ggplot(data = <DATA>) +
  <GEOM_FUNCTION>(mapping = aes(<MAPPINGS>))
```

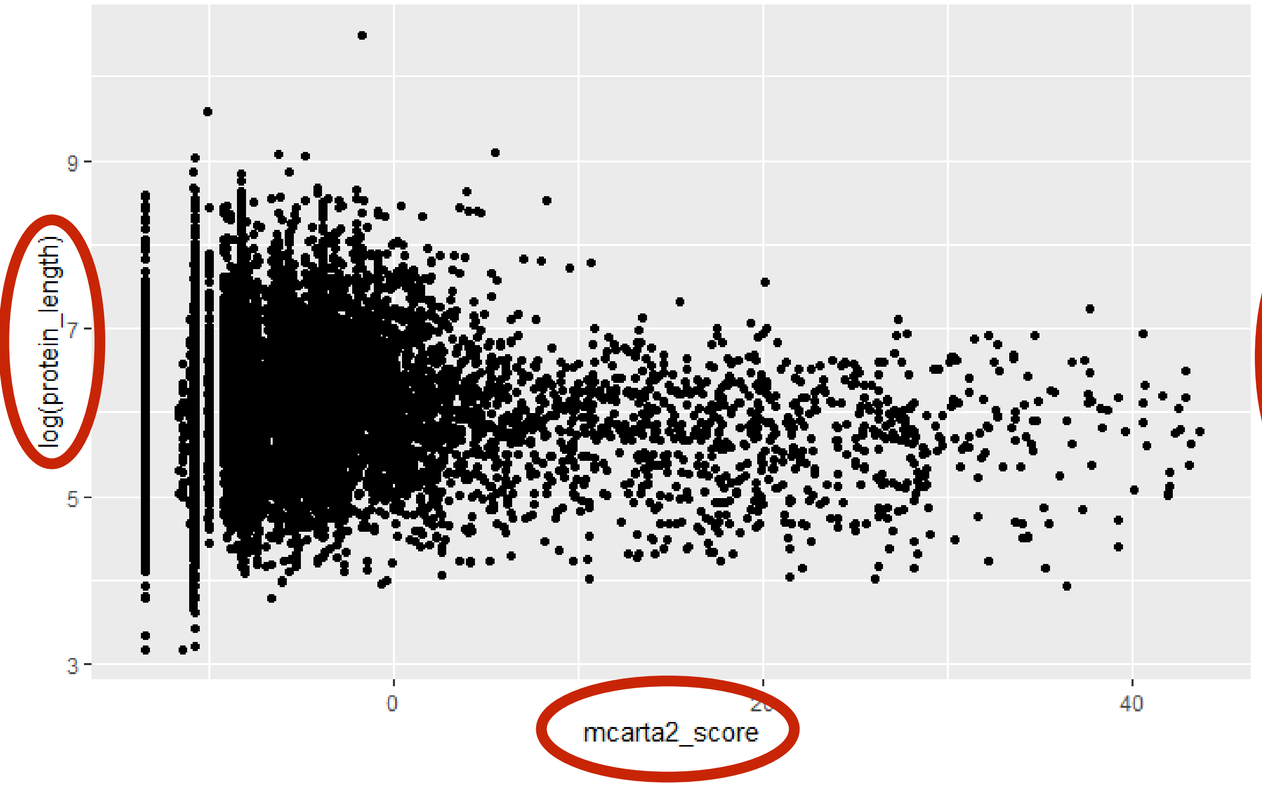
=

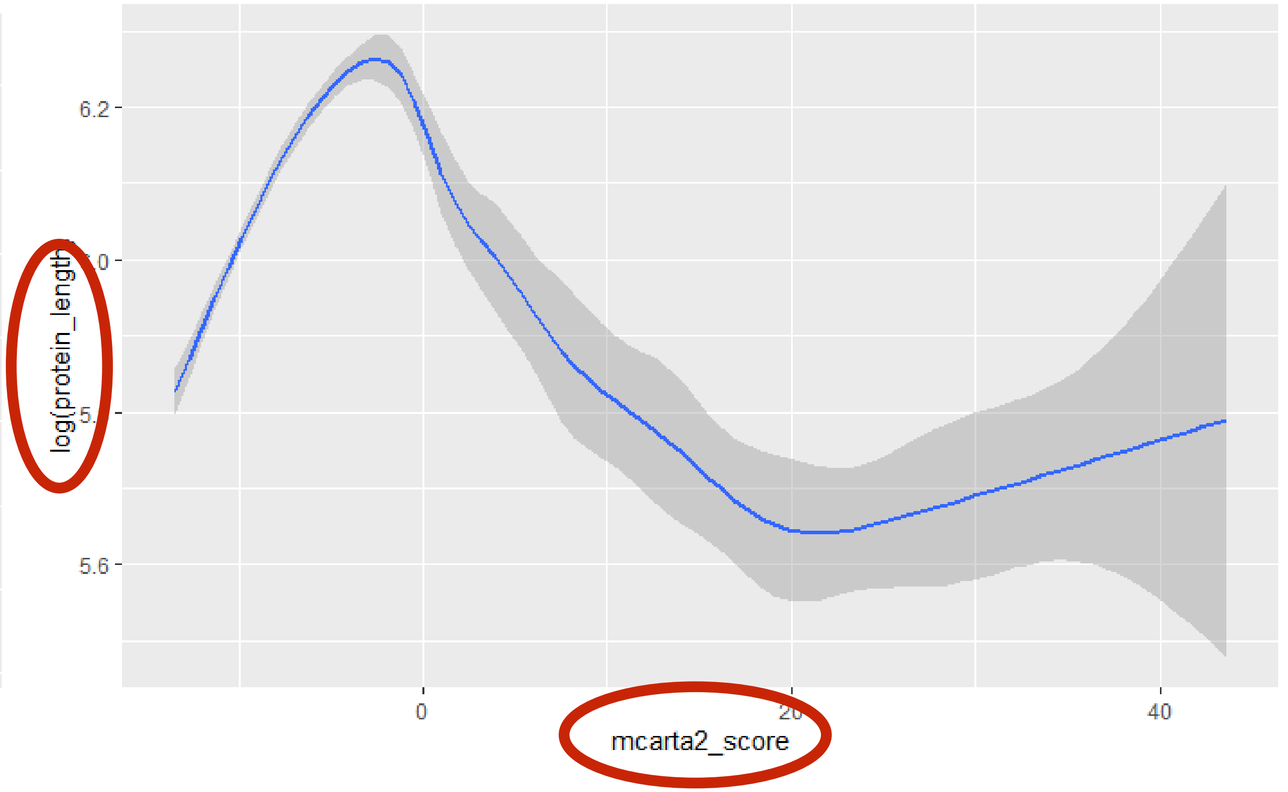
```
ggplot(<DATA>) +
  <GEOM_FUNCTION>(aes(<MAPPINGS>))
```

Geoms

How are these plots similar?

Same: x var, y var, data





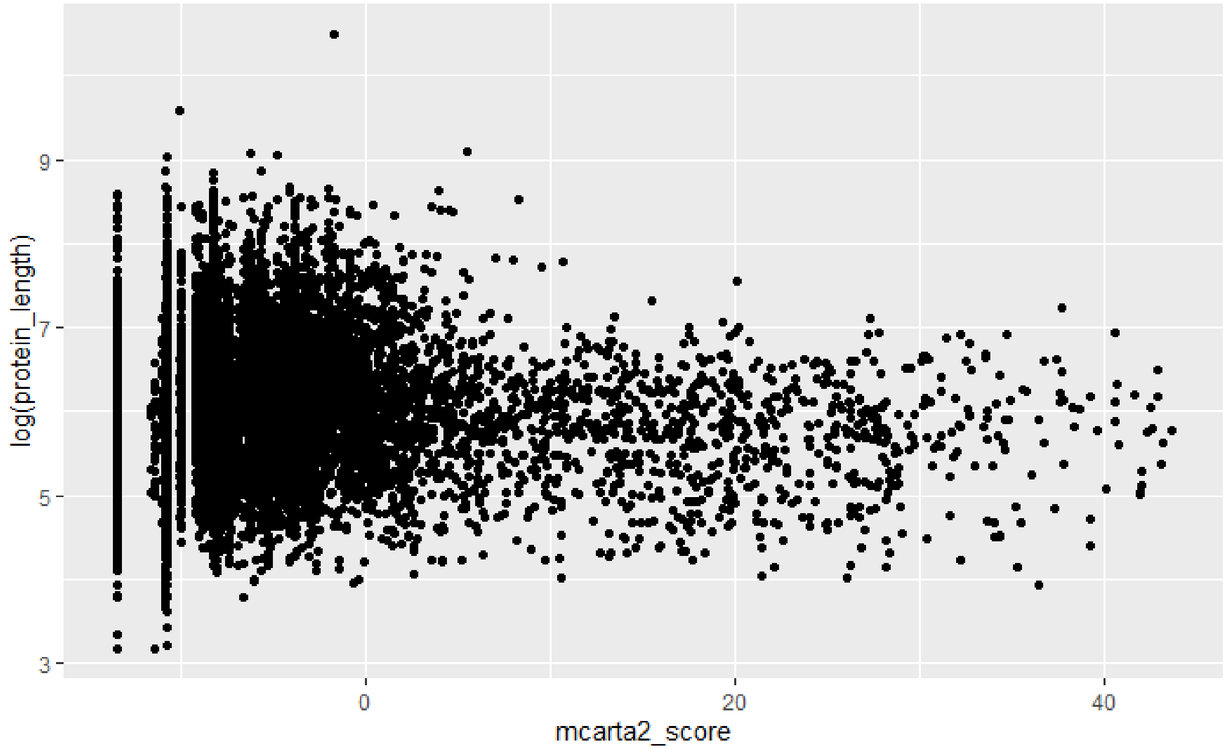

```
ggplot(mitocarta)+
  geom_point(aes(x=hg19_chromosome,
                 y=log(protein_length)))
```

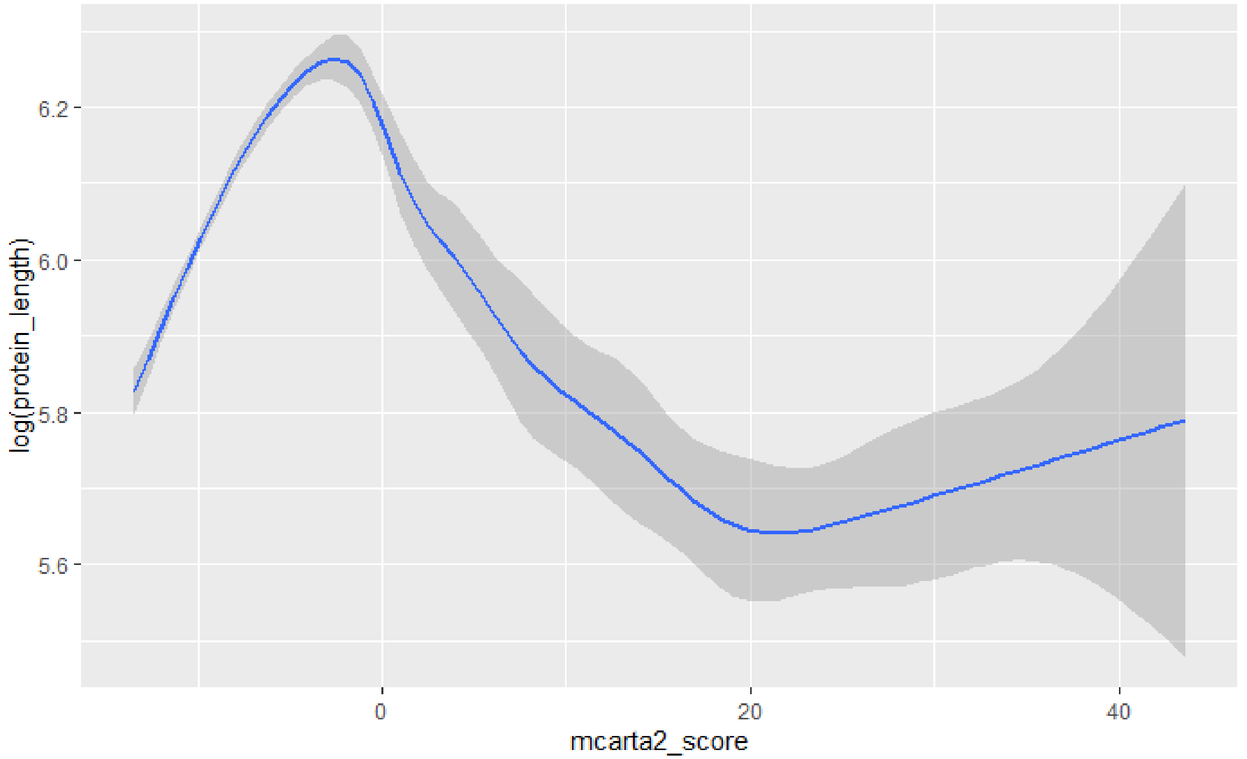
```
ggplot(mitocarta)+
  geom_smooth(aes(x=hg19_chromosome,
                  y=log(protein_length)))
```

How are these plots different?

Different: geometric object (geom),

e.g. the visual object used to represent the data






```
ggplot(mitocarta)+
  geom_point(aes(x=hg19_chromosome,
                 y=log(protein_length)))
```

```
ggplot(mitocarta)+
  geom_smooth(aes(x=hg19_chromosome,
                  y=log(protein_length)))
```

geoms

```
ggplot(<DATA>) +
  <GEOM_FUNCTION>(aes(<MAPPINGS>))
```

How do I know which geom to use?

rstudio.cloud/learn/cheat-sheets

Click CheAT Sheets in the sidebar

RStudio Cloud

rstudio.cloud/learn/cheat-sheets

Studio Cloud

Learn | Guide | What's New | Primers | Cheat Sheets | Garrett Grolemund

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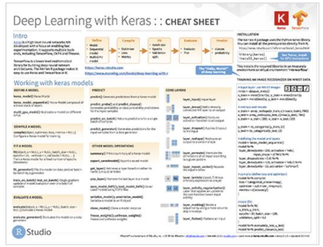
Studio Cheat Sheets

Cheat sheets make it easy to learn and use your favorite R packages and the RStudio IDE.

Deep Learning with Keras

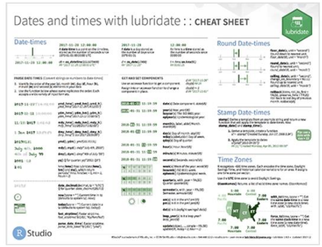


Download

Keras is a high-level neural networks API developed with a focus on enabling fast experimentation. Keras supports both convolution based networks and recurrent networks (as well as combinations of the two), runs seamlessly on both CPU and GPU devices, and is capable of running on top of multiple back-ends including TensorFlow, CNTK, and Theano.

Updated December 2017

Dates and Times

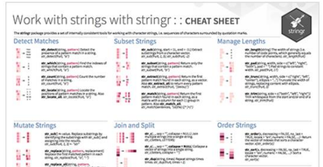


Download

Lubridate makes it easier to work with dates and times in R. This lubridate cheatsheet covers how to round dates, work with time zones, extract elements of a date or time, parse dates into R and more. The back of the cheatsheet describes lubridate's three timespan classes: periods, durations, and intervals; and explains how to do math with date-times.

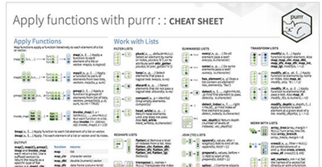
Updated December 2017

Work with Strings



The stringr package provides an easy to use toolkit for working with strings, i.e. character data, in R. This cheatsheet guides you through stringr's functions for manipulating strings. The back

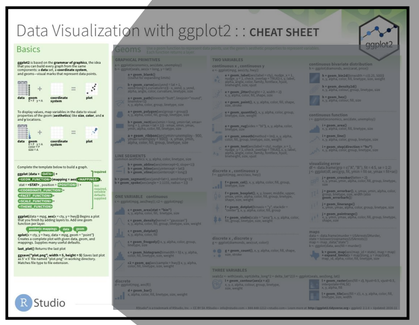
Apply Functions



The purrr package makes it easy to work with lists and functions. This cheatsheet will remind you how to manipulate lists with purrr as well as how to apply functions iteratively to each element of a list

geom_ functions

Each requires a mapping argument.



Geoms

Use a geom function to represent data points, use the geom's aesthetic properties to represent variables. Each function returns a layer.

ggplot2

GRAPHICAL PRIMITIVES

a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))

a + geom_blank()
(Useful for expanding limits)

b + geom_curve(aes(yend = lat + 1, xend=long+1,curvature=z)**)** - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend="butt", linejoin="round", linemitre=1**)**
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(group = group)**)**
x, y, alpha, color, fill, group, linetype, size

b + geom_rect(aes(xmin = long, ymin=lat, xmax= long + 1, ymax = lat + 1)**)** - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin=unemploy - 900, ymax=unemploy + 900)**)** - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept=0, slope=1)**)**
b + geom_hline(aes(yintercept = lat)**)**
b + geom_vline(aes(xintercept = long)**)**

b + geom_segment(aes(yend=lat+1, xend=long+1)**)**
b + geom_spoke(aes(angle = 1:1155, radius = 1)**)**

ONE VARIABLE continuous

c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian"**)**
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly() x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5**)** x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy)**)** x, y, alpha, color, fill, linetype, size, weight

discrete

d <- ggplot(mpg, aes(fl))

d + geom_bar()
x, alpha, color, fill, linetype, size, weight

TWO VARIABLES

continuous x , continuous y

e <- ggplot(mpg, aes(cty, hwy))

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE**)** x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_jitter(height = 2, width = 2**)**
x, y, alpha, color, fill, shape, size

e + geom_point(), x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile(), x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl"**)**, x, y, alpha, color, linetype, size

e + geom_smooth(method = lm**)**, x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE**)**, x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

discrete x , continuous y

f <- ggplot(mpg, aes(class, hwy))

f + geom_col(), x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot(), x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center"**)**, x, y, alpha, color, fill, group

f + geom_violin(scale = "area"**)**, x, y, alpha, color, fill, group, linetype, size, weight

discrete x , discrete y

g <- ggplot(diamonds, aes(cut, color))

g + geom_count(), x, y, alpha, color, fill, shape, size, stroke

continuous bivariate distribution

h <- ggplot(diamonds, aes(carat, price))

h + geom_bin2d(binwidth = c(0.25, 500)**)**
x, y, alpha, color, fill, linetype, size, weight

h + geom_density2d()
x, y, alpha, colour, group, linetype, size

h + geom_hex()
x, y, alpha, colour, fill, size

continuous function

i <- ggplot(economics, aes(date, unemploy))

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv")
x, y, alpha, color, group, linetype, size

visualizing error

df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit-se, ymax = fit+se))

j + geom_crossbar(fatten = 2**)**
x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar(), x, ymax, ymin, alpha, color, group, linetype, size, width (also **geom_errorbarh()**)

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange()
x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps

data <- data.frame(murder = USArrests$Murder, state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

k + geom_map(aes(map_id = state), map = map**)**
+ expand_limits(x = map$long, y = map$lat**)**,
map_id, alpha, color, fill, linetype, size

THREE VARIABLES

seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2))l <- ggplot(seals, aes(long, lat))

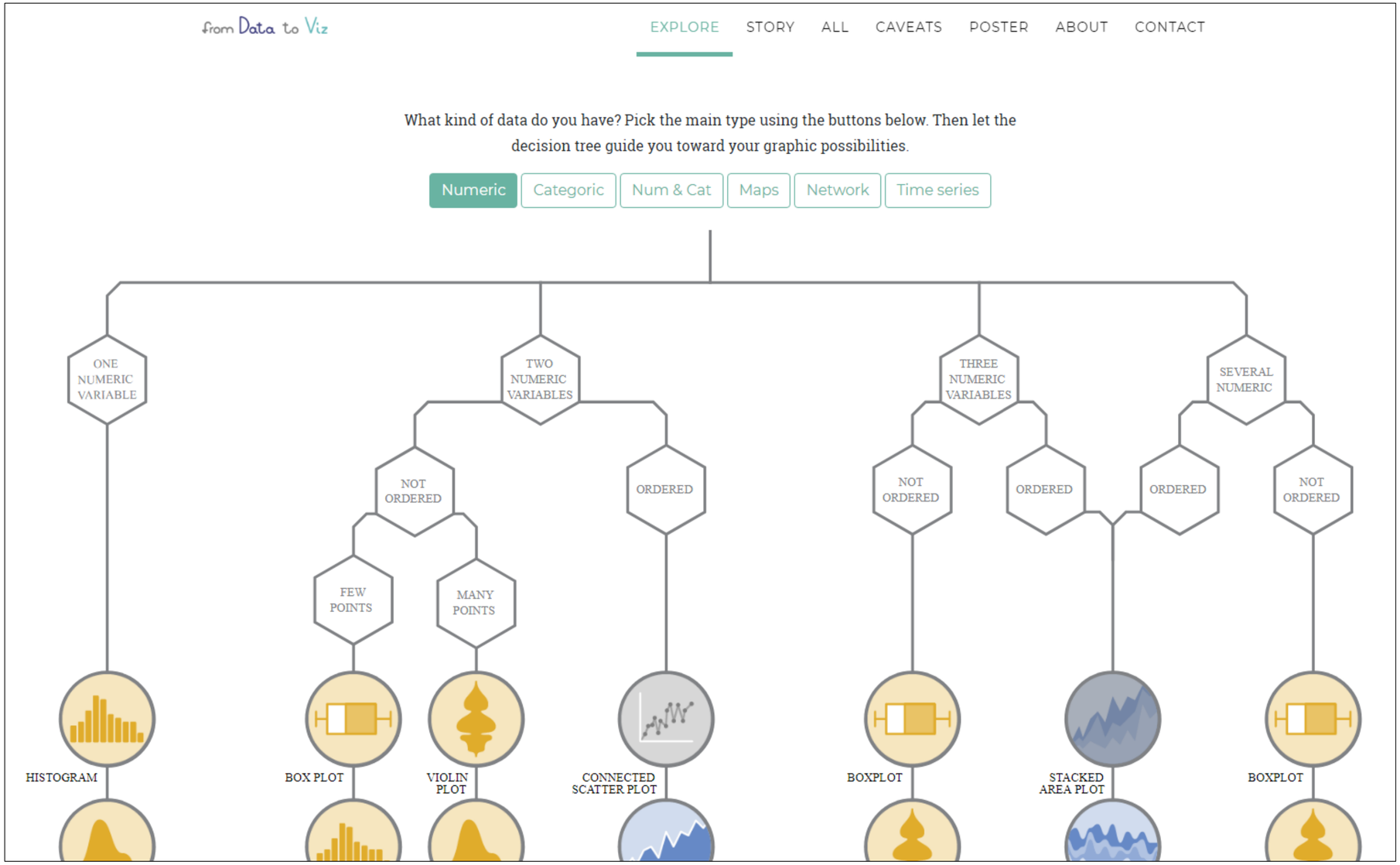
l + geom_contour(aes(z = z))
x, y, z, alpha, colour, group, linetype, size, weight

l + geom_raster(aes(fill = z), hjust=0.5, vjust=0.5, interpolate=FALSE**)**
x, y, alpha, fill

l + geom_tile(aes(fill = z)**)**, x, y, alpha, color, fill, linetype, size, width

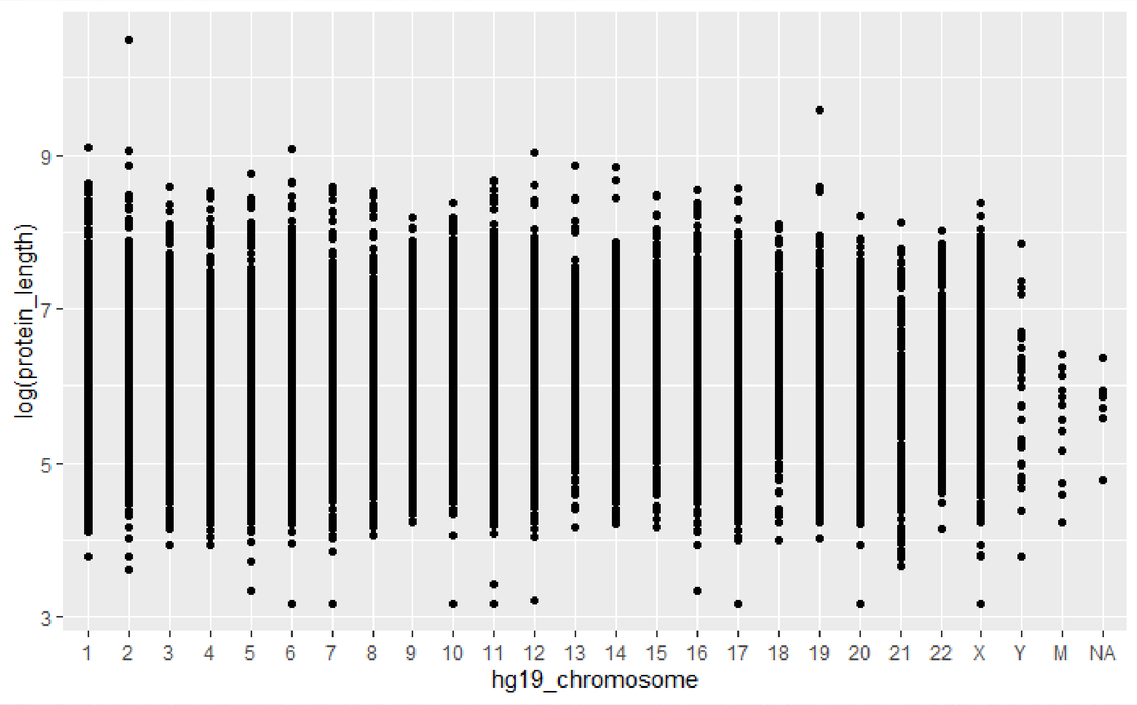
ggplot2

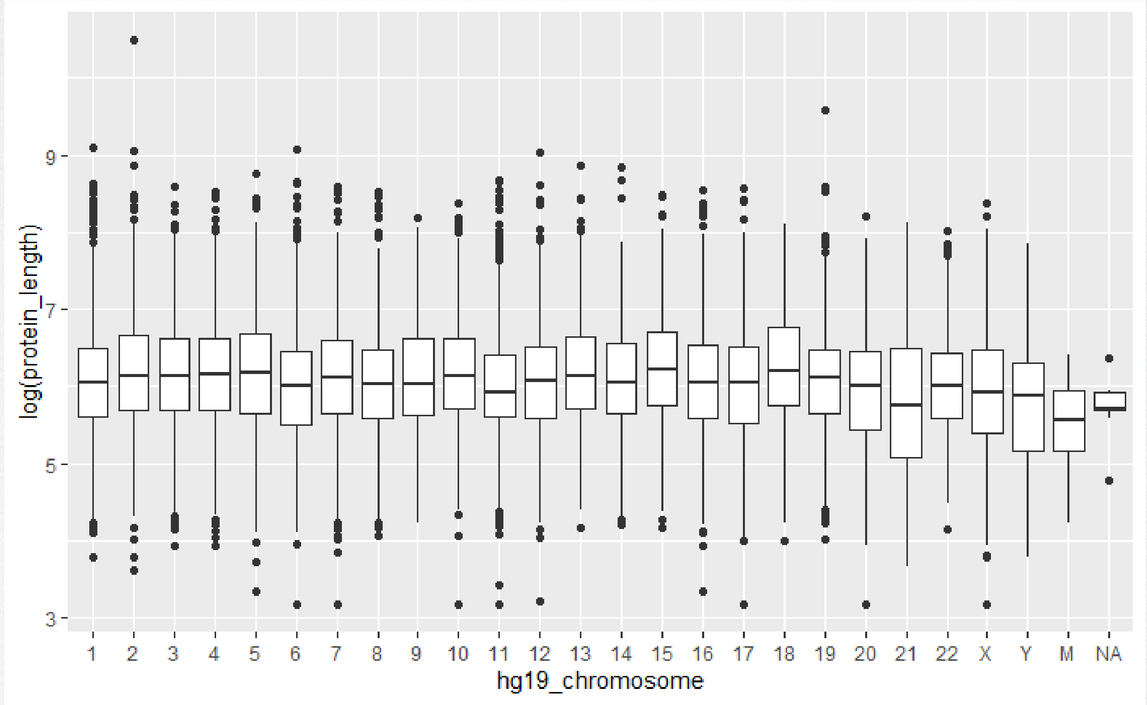
https://www.data-to-viz.com



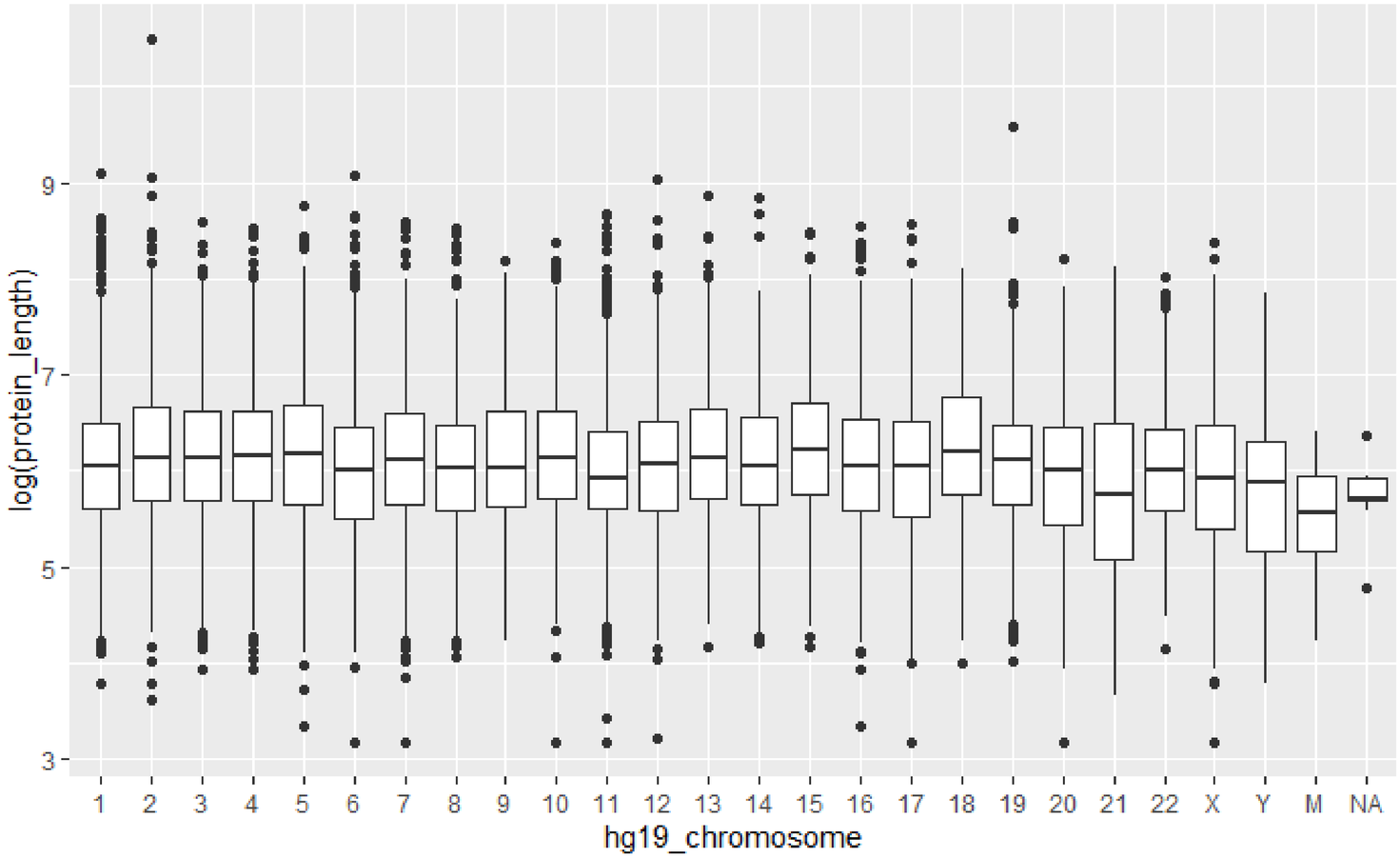
Your Turn 4

With your partner, decide how to replace this scatterplot with one that draws boxplots. Use the cheatsheet. Try your best guess.






```
ggplot(mitocarta) +
geom_point(aes(x=hg19_chromosome,y=log(protein_length)))
```




```
ggplot(mitocarta) +
geom_boxplot(aes(x=hg19_chromosome, y=log(protein_length)))
```

"Help" pages

To open the documentation for a function, type

```
?geom_histogram
```

? — **function name** (no parentheses)

geom_freqpoly {ggplot2} R Documentation

Histograms and frequency polygons

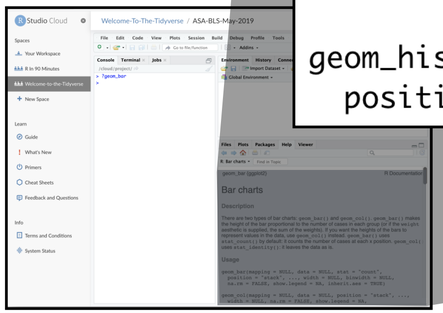
Description

Visualise the distribution of a single continuous variable by dividing the x axis into bins and counting the number of observations in each bin. Histograms (`geom_histogram()`) display the counts with bars; frequency polygons (`geom_freqpoly()`) display the counts with lines. Frequency polygons are more suitable when you want to compare the distribution across the levels of a categorical variable.

Usage

```
geom_freqpoly(mapping = NULL, data = NULL, stat = "bin",
  position = "identity", ..., na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)

geom_histogram(mapping = NULL, data = NULL, stat = "bin",
  position = "stack", ..., binwidth = NULL, bins = NULL,
```



ggplot2.tidyverse.org

Reference

Plot basics

All ggplot2 plots begin with a call to `ggplot()`, supplying default data and aesthethic mappings, specified by `aes()`. You then add layers, scales, coords and facets with `+`. To save a plot to disk, use `ggsave()`.

`ggplot()`	Create a new ggplot
`aes()`	Construct aesthetic mappings
`` `+`(<gg>) `%+%` ``	Add components to a plot
`ggsave()`	Save a ggplot (or other grid object) with sensible defaults
`qplot()` `quickplot()`	Quick plot

Layer: geoms

A layer combines data, aesthetic mapping, a geom (geometric object), a stat (statistical transformation), and a position adjustment. Typically, you will create layers using a `geom_` function, overriding the default position and stat if needed.

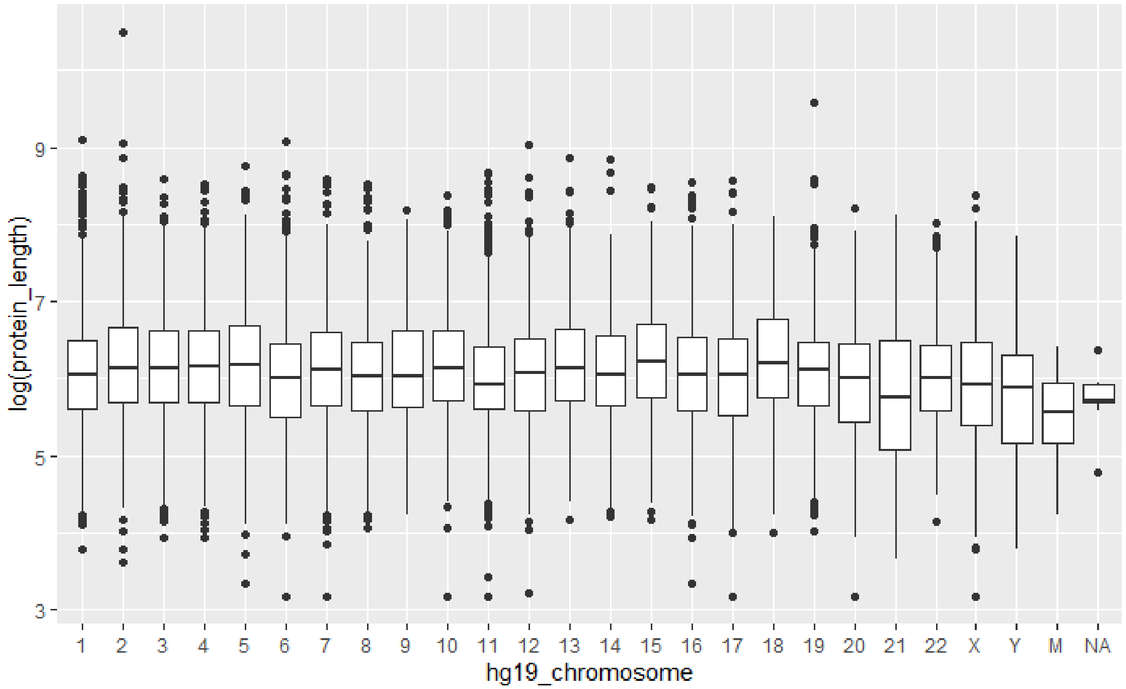
`geom_abline()` `geom_hline()` `geom_vline()`	Reference lines: horizontal, vertical, and diagonal
`geom_bar()` `geom_col()`	Bar charts

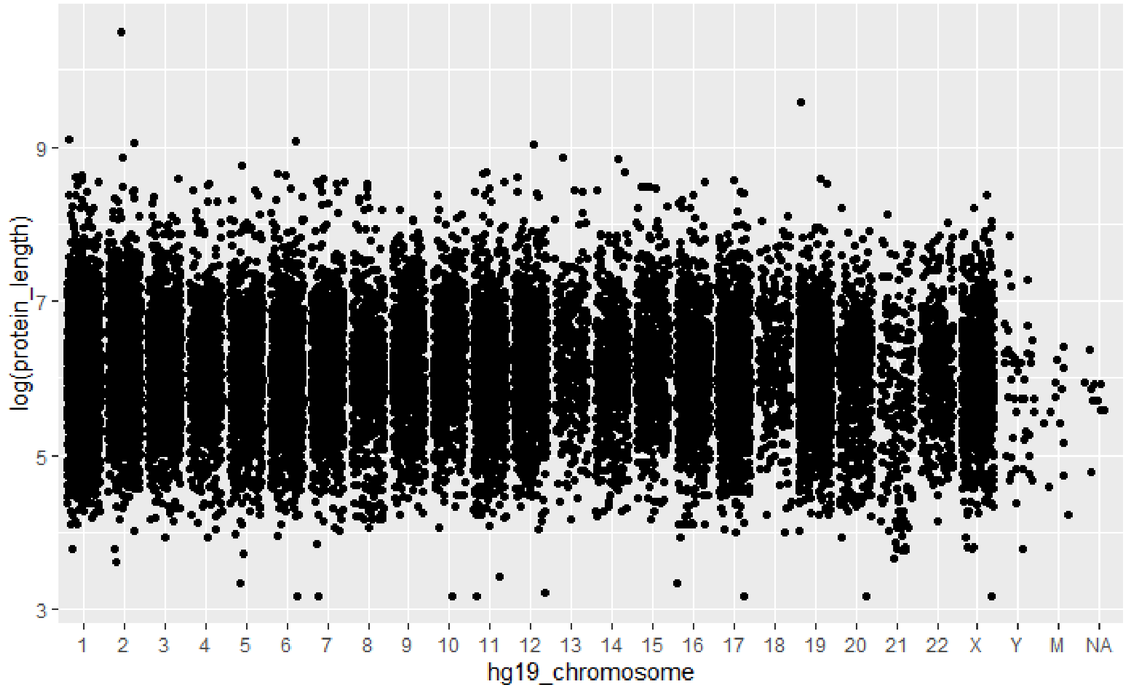
Contents

Question?

What will this code do?

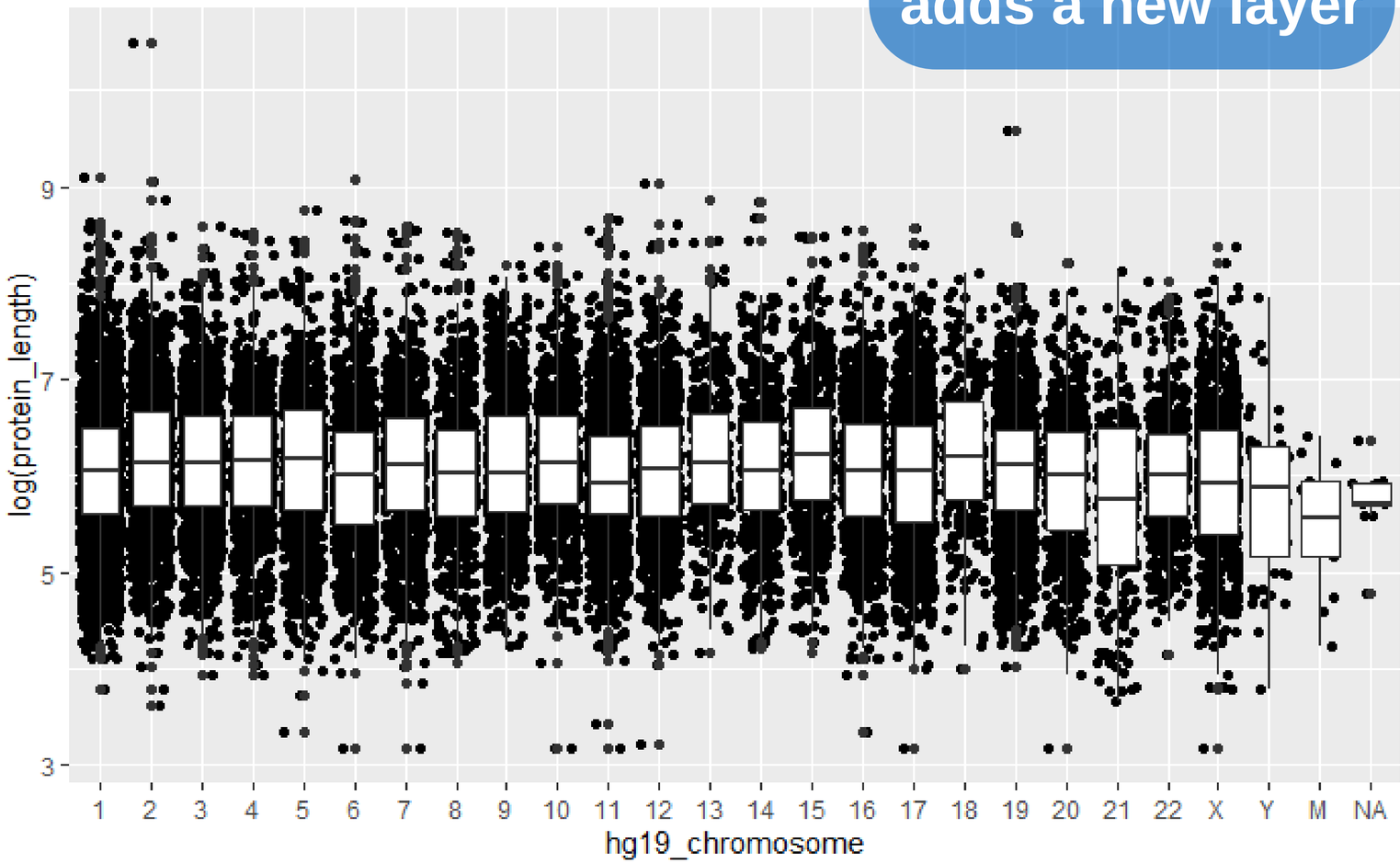
```
ggplot(mitocarta)+
  geom_jitter(aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_boxplot(aes(x=hg19_chromosome, y=log(protein_length)))
```






```
ggplot(mitocarta)+
  geom_jitter(aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_boxplot(aes(x=hg19_chromosome, y=log(protein_length)))
```

Each new geom adds a new layer



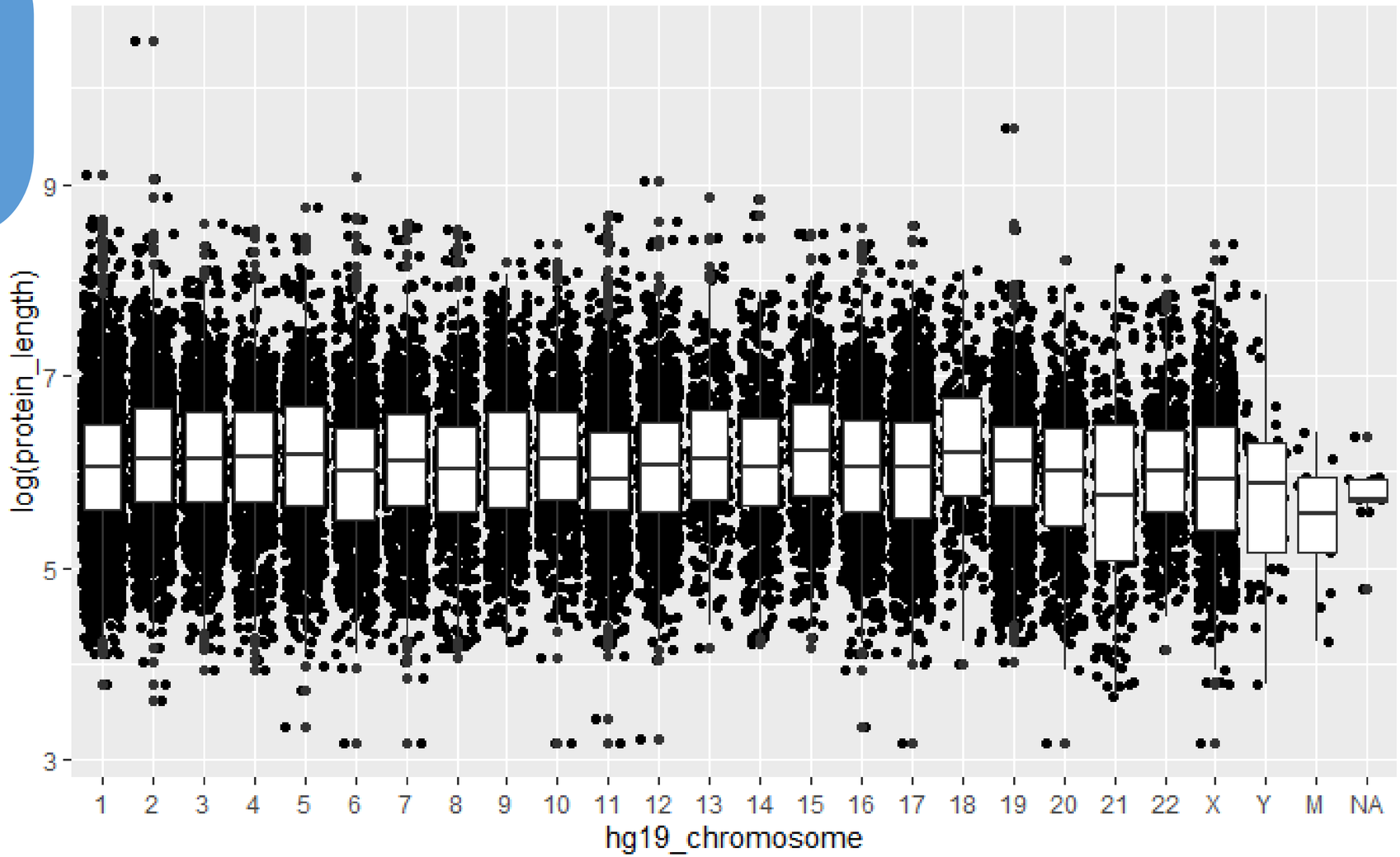

```
ggplot(mitocarta)+
  geom_jitter(aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_boxplot(aes(x=hg19_chromosome, y=log(protein_length)))
```

Aesthetics

"The greatest value of a picture is when it forces us to notice what we never expected to see."

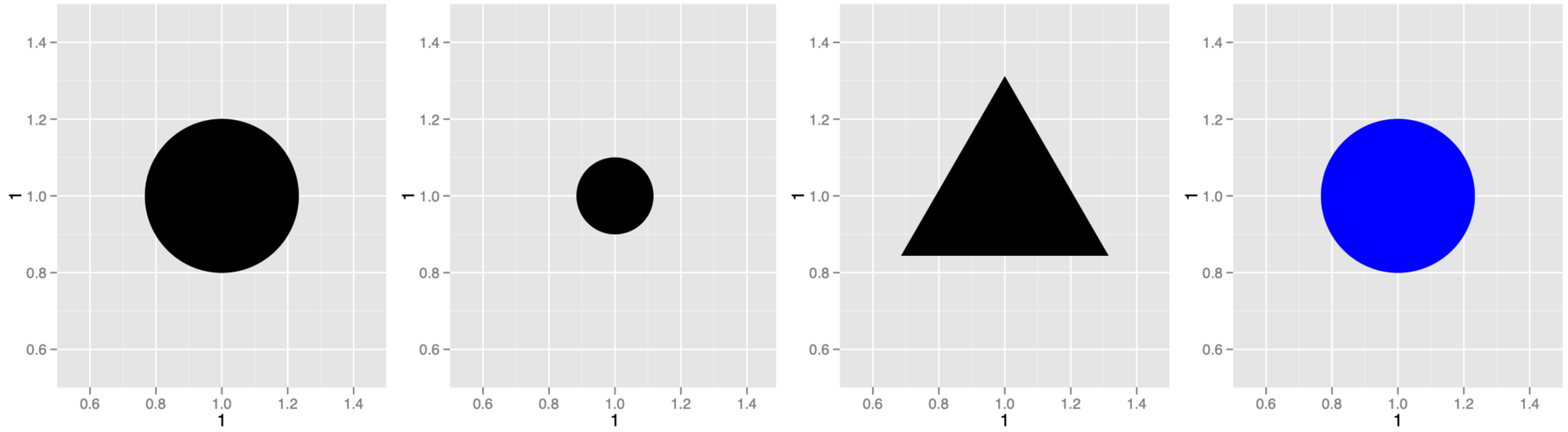
- John Tukey

What are the 5 largest proteins?




```
ggplot(mitocarta) +
  geom_point(aes(hg19_chromosome,log(protein_length)))
```

Aesthetics- Shape, Size, Color



Aesthetics

aesthetic property

Variable to map it to

```
ggplot(mitocarta) +
  geom_point(aes(x=hg19_chromosome, y=log(protein_length), color= mcarta2_score))
ggplot(mitocarta) +
  geom_point(aes(x=hg19_chromosome, y=log(protein_length), size = mcarta2_score))

ggplot(mitocarta) +
  geom_point(aes(x=hg19_chromosome, y=log(protein_length), shape = mcarta2_score))

ggplot(mitocarta) +
  geom_point(aes(x=hg19_chromosome, y=log(protein_length), alpha = mcarta2_score))

ggplot(mitocarta) +
  geom_point(aes(x=hg19_chromosome, y=log(protein_length), fill = mcarta2_score))
```

NOTE: Color vs Fill- depends on shape!

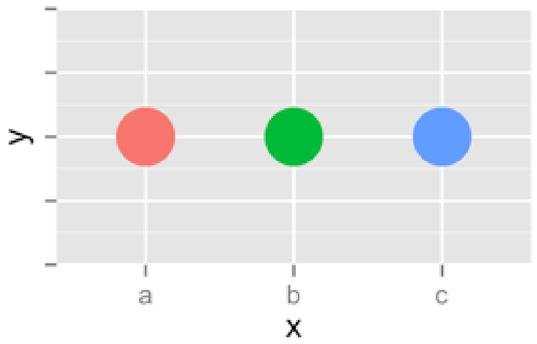
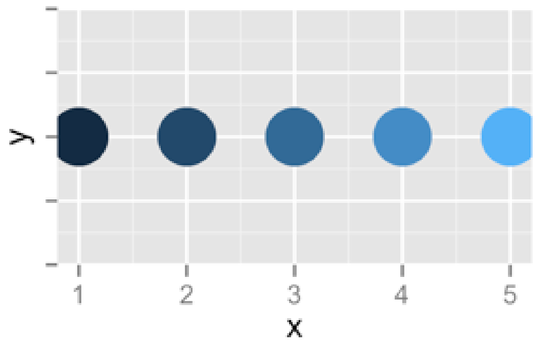
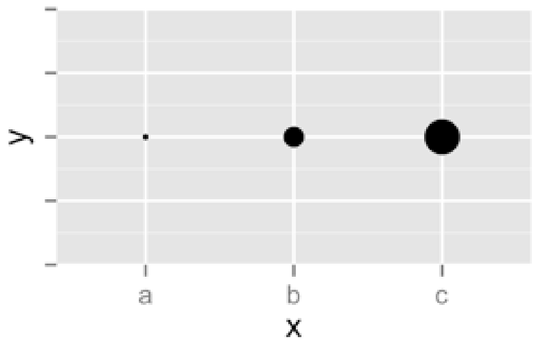
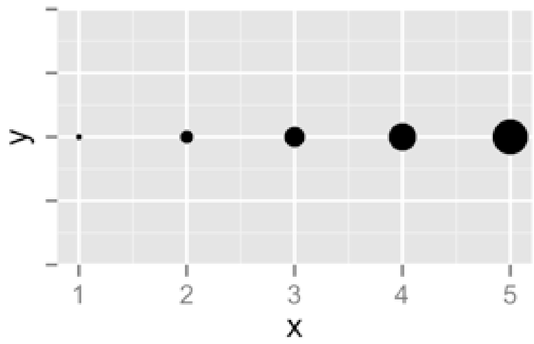
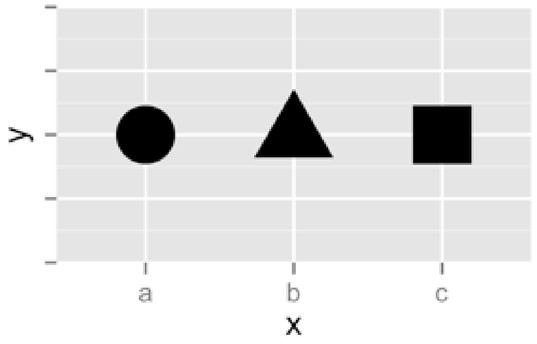
color= outline color, **fill =** fill color

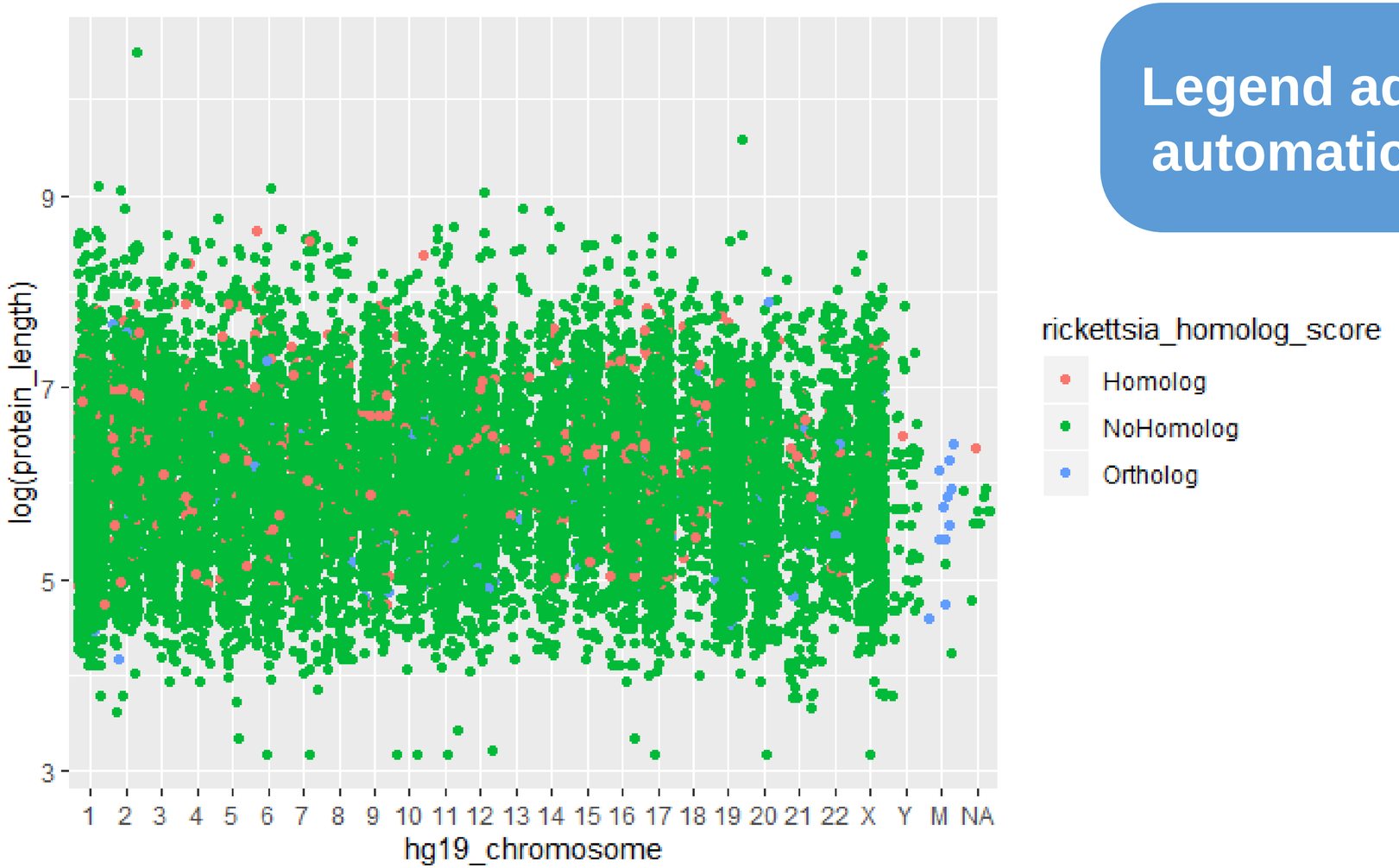
Exercise 3

In the next chunk, add color, size, alpha, and shape aesthetics to your graph. Experiment.

Do different things happen when you map aesthetics to discrete and continuous variables?

What happens when you use more than one aesthetic?

	Discrete	Continuous
Color		
Size		
Shape		



Legend added automatically

```
ggplot(mitocarta) +
  geom_jitter(aes(hg19_chromosome,log(protein_length), color=
rickettsia_homolog_score))
```

Exercise 4

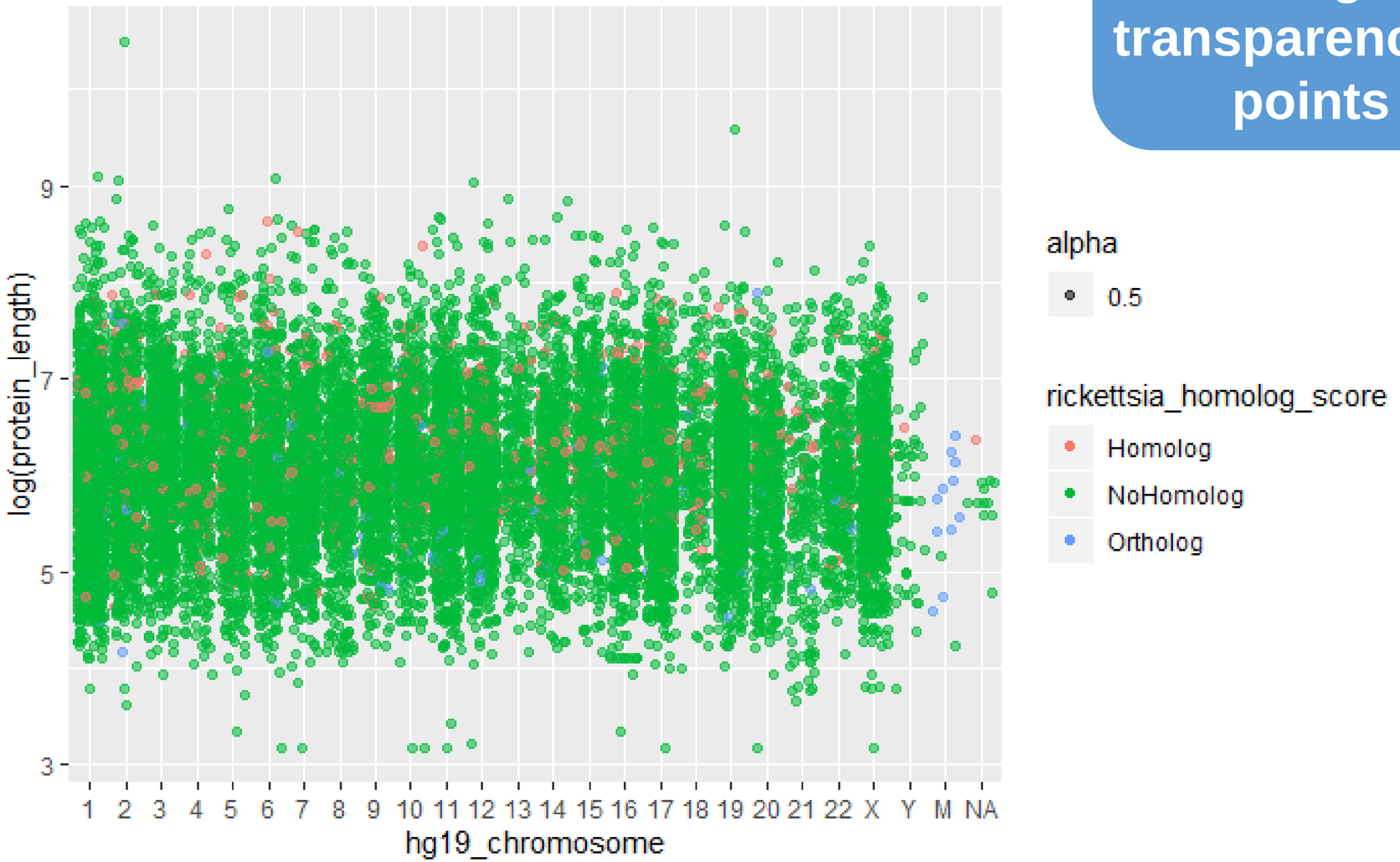
What happens when you change the alpha aes?

```
ggplot(mitocarta) +
  geom_jitter(aes(hg19_chromosome,log(protein_length), color=
rickettsia_homolog_score, alpha=0.5))
```

Error!

```
ggplot(mitocarta) +
  geom_point(aes(hg19_chromosome,log(protein_length)), fill=
rickettsia_homolog_score)
```

Changes transparency of points




```
ggplot(mitocarta) +
  geom_jitter(aes(hg19_chromosome,log(protein_length), color=
rickettsia_homolog_score, alpha=0.5))
```

A Note on Color…

Color can be a very powerful tool in dataviz, however, it can also be where many plots go wrong. Some tips:

1. less is often more.

2. remember colorblind color pairs (ex: red/green)

3. Consider installing the viridis package for colorblind friendly continuous color scales

4. When you have few colors= keep them distinct (ex: red vs blue instead of red vs orange)

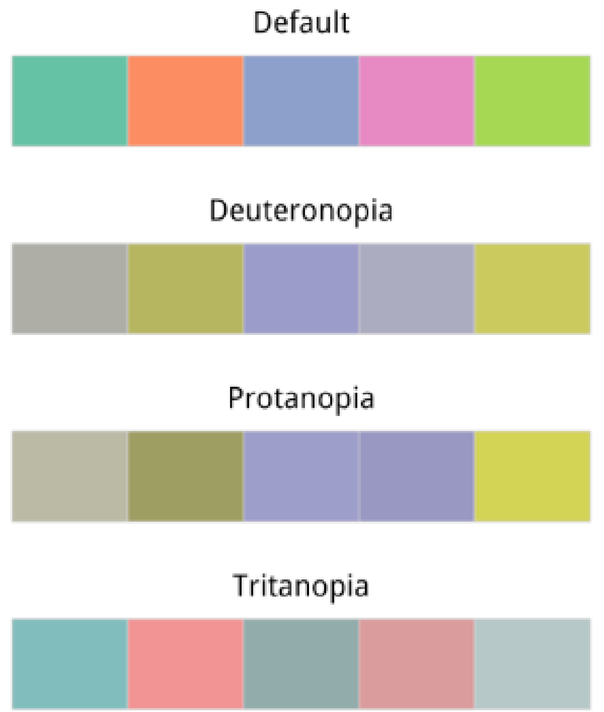
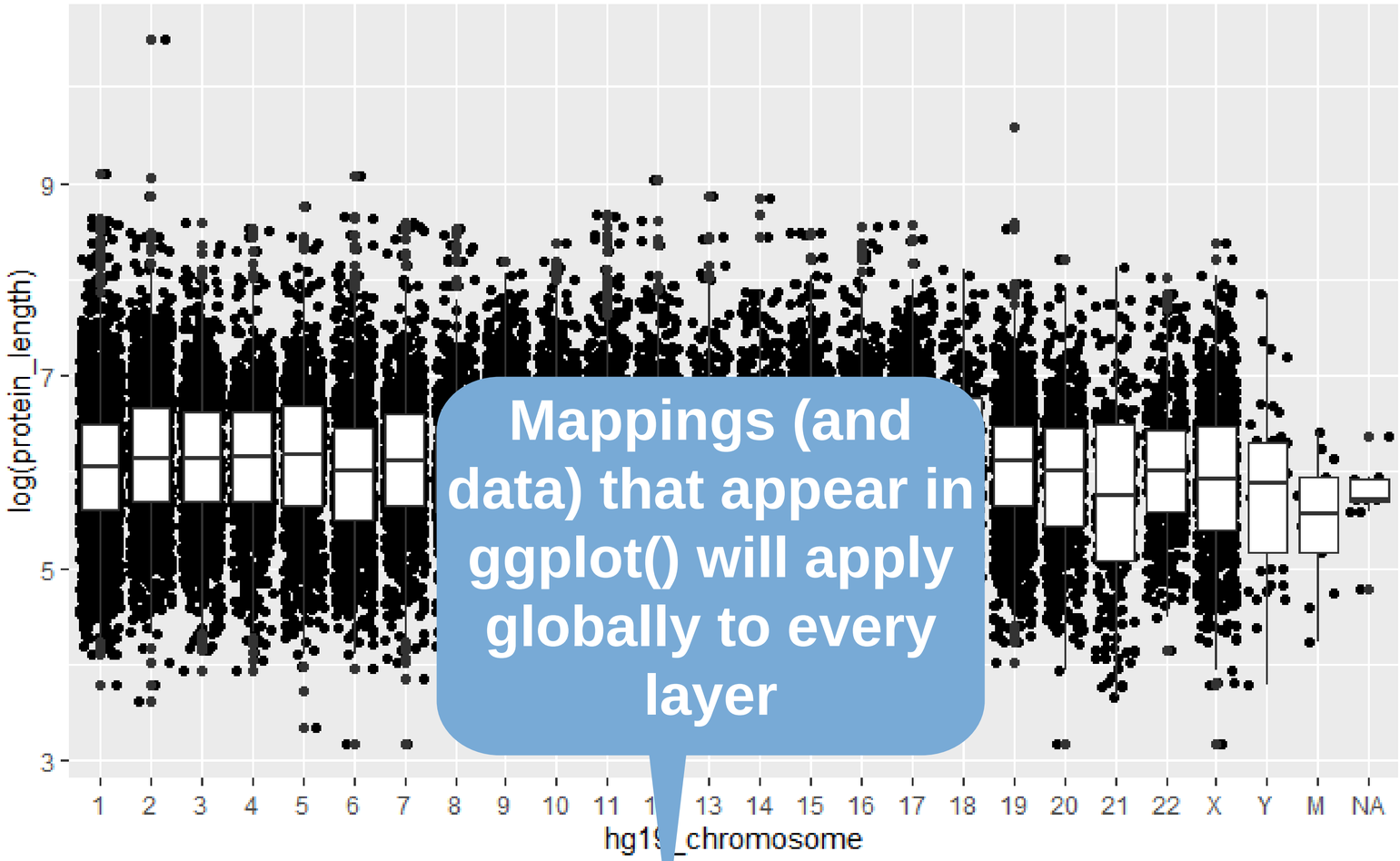


Figure 8.9: Comparing a default color palette with an approximation of how the same palette appears to people with one of three kinds of color blindness.

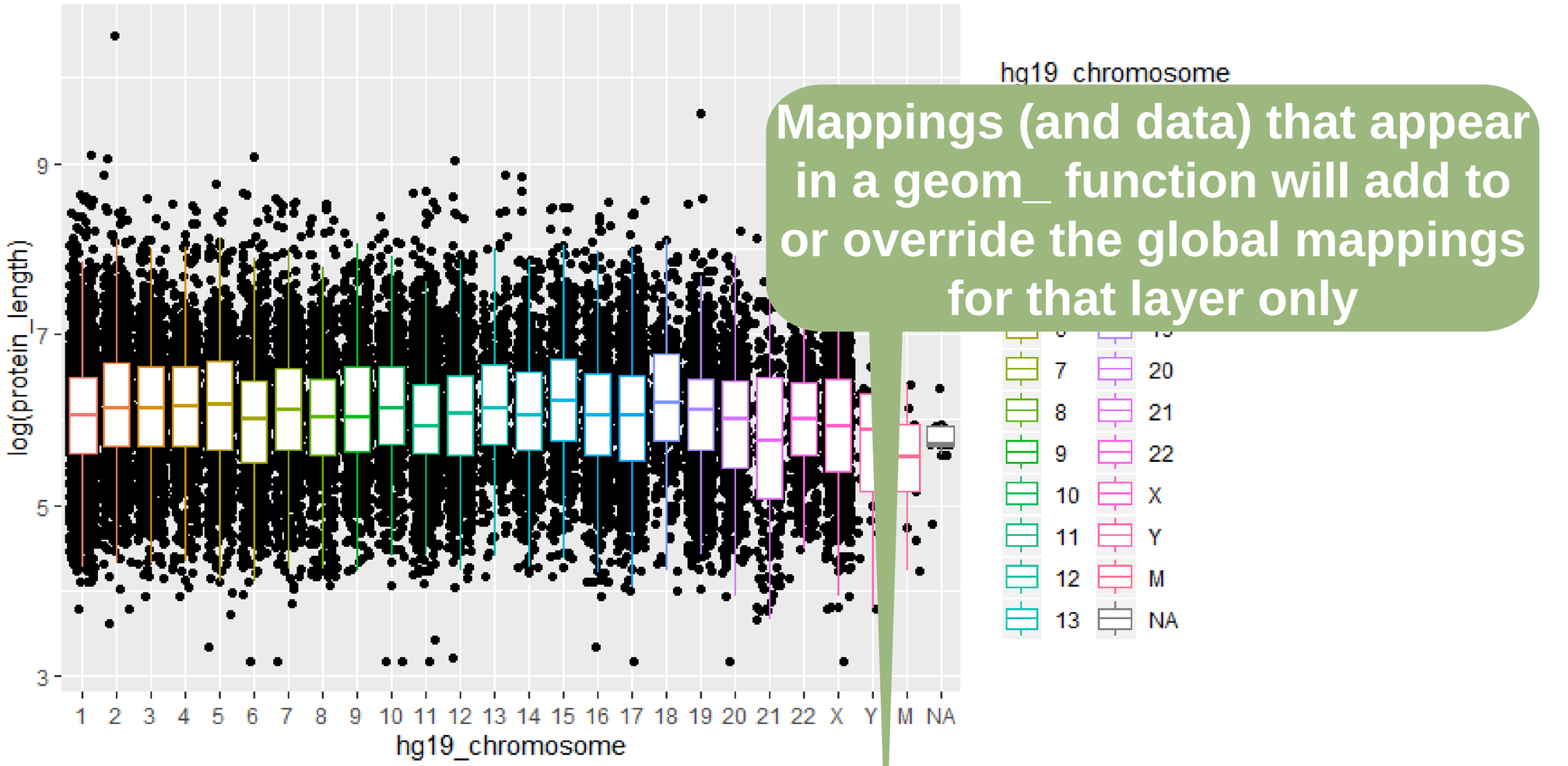
https://socviz.co/refineplots.html

global vs. local



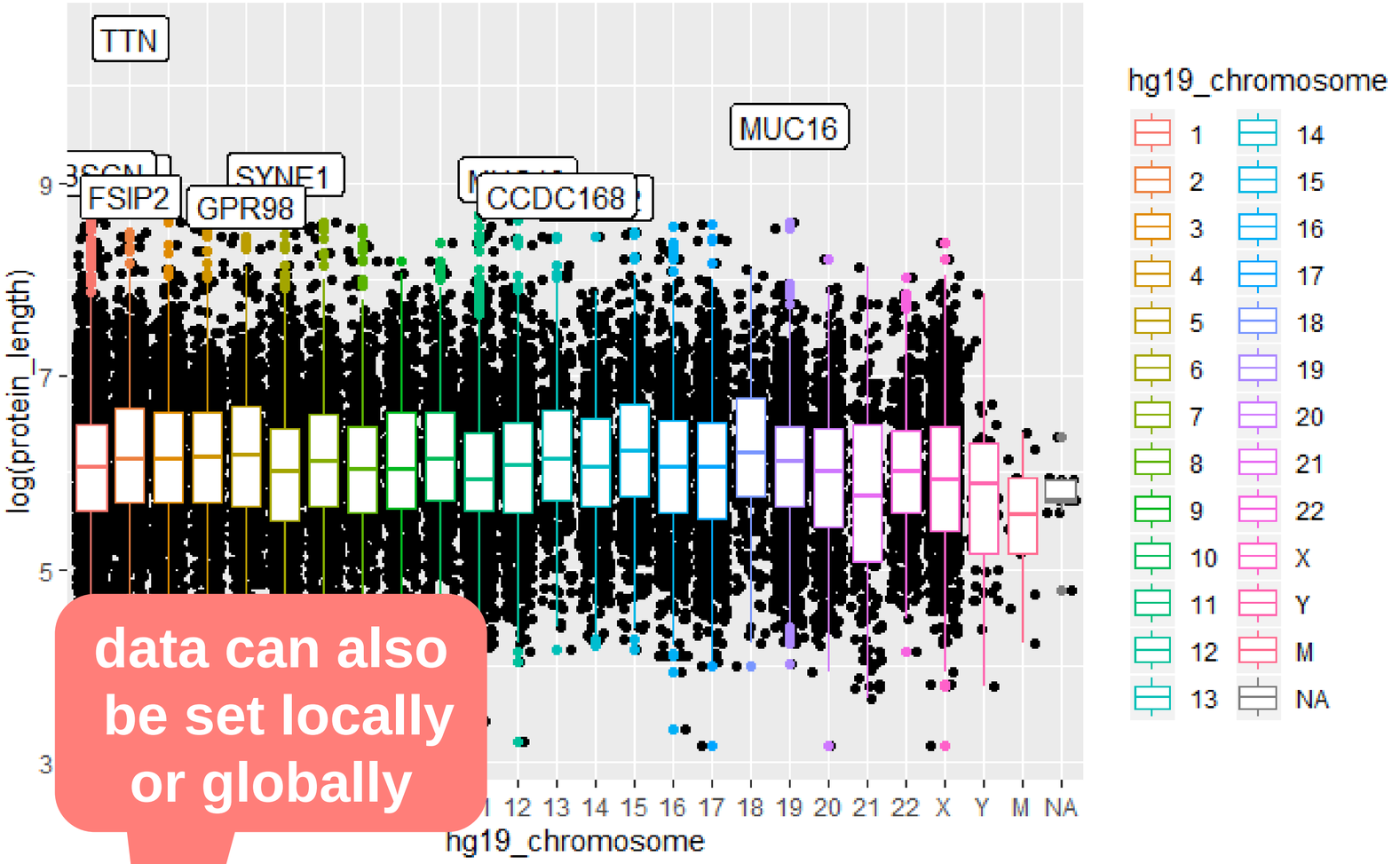

```
ggplot(mitocarta, aes(x=hg19_chromosome,
y=log(protein_length)))+
  geom_jitter()+
  geom_boxplot()
```

ggplot2



Mappings (and data) that appear in a geom_ function will add to or override the global mappings for that layer only

```
ggplot(mitocarta, aes(x=hg19_chromosome,
y=log(protein_length)))+
  geom_jitter()+
  geom_boxplot(aes(color=hg19_chromosome))
```

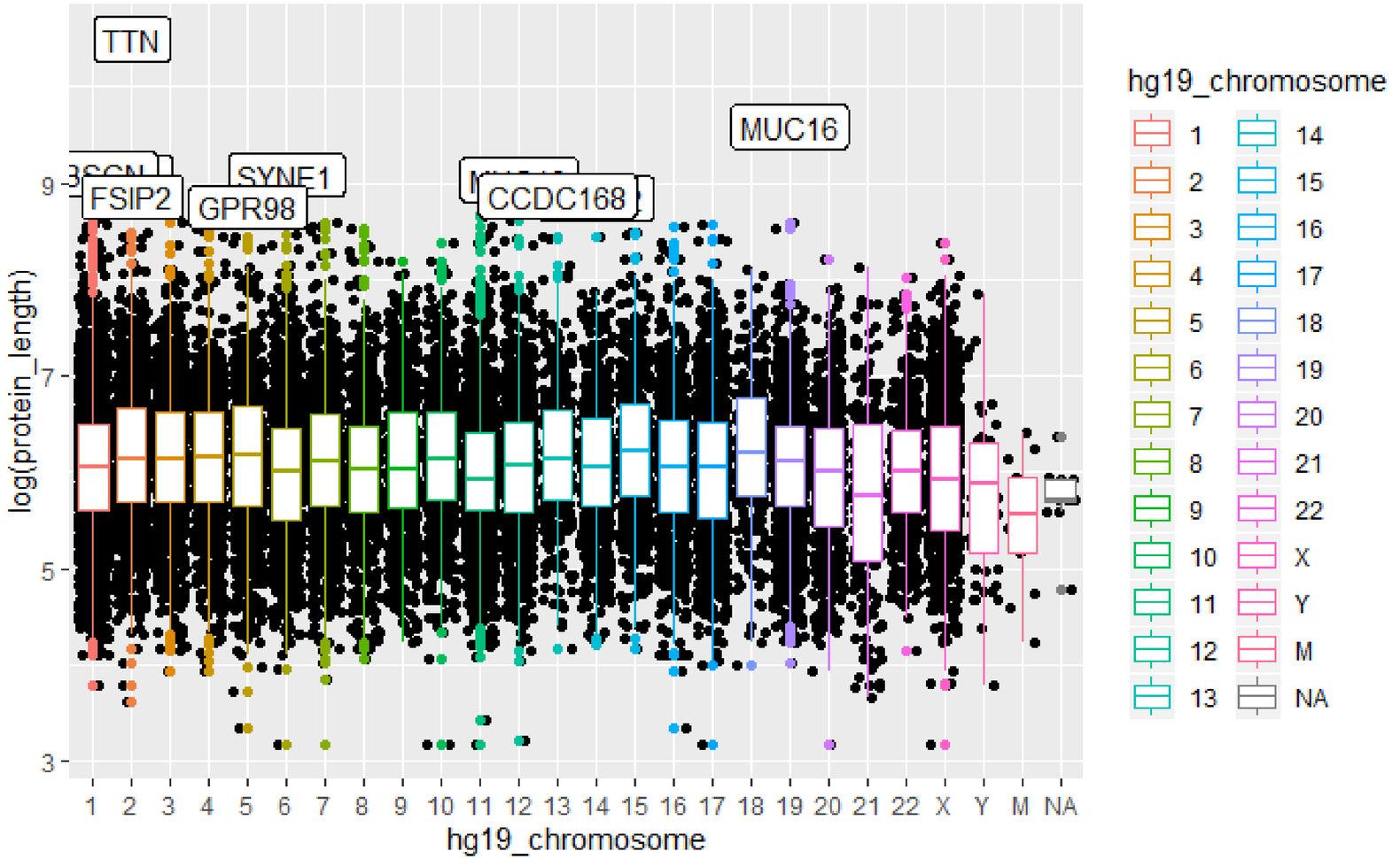


data can also be set locally or globally

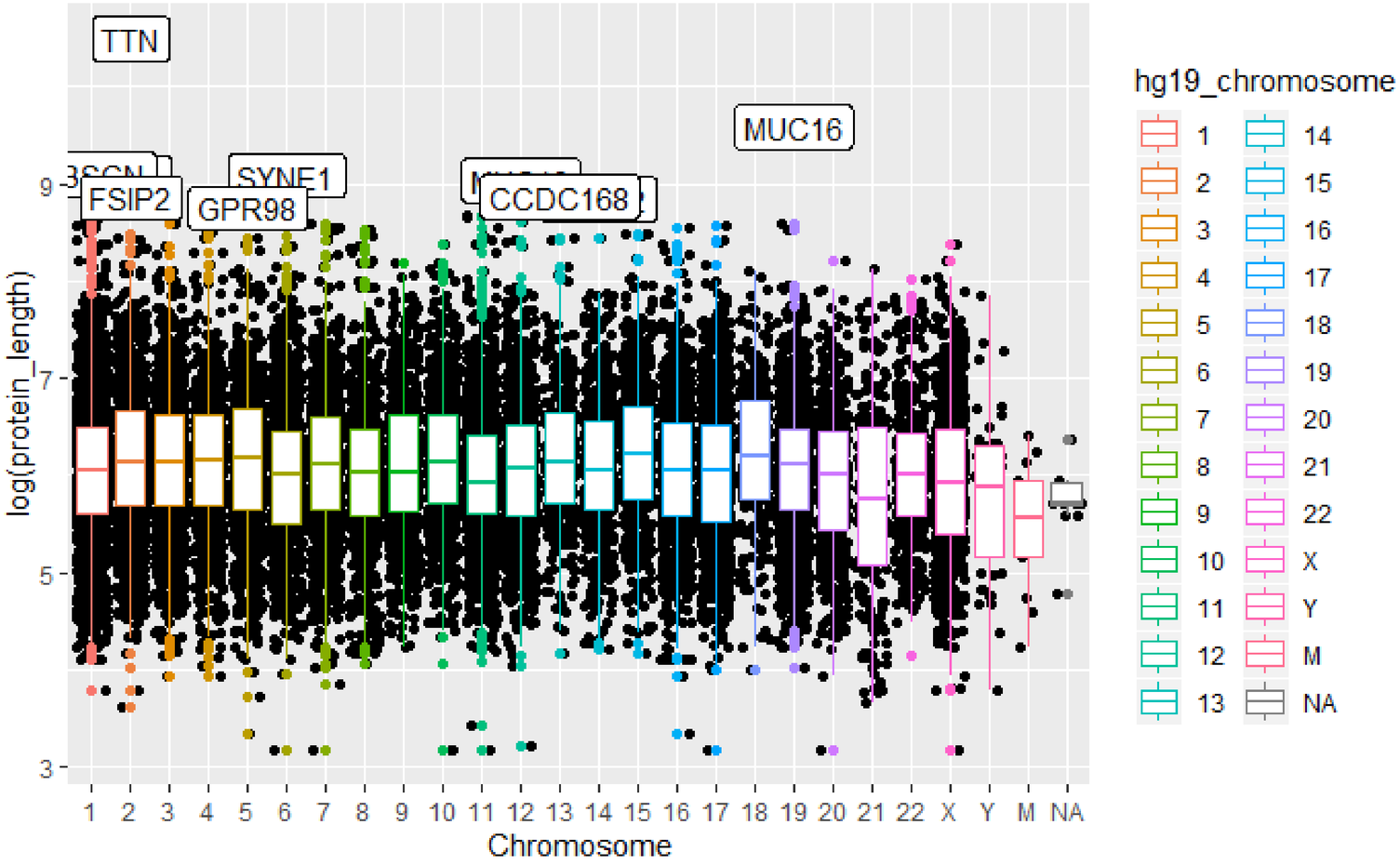
```
ggplot(mitocart     aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_jitter()
  geom_boxplot(aes(color=hg19_chromsome))+
 geom_label(data=large_prot, aes(label= symbol))
```

ggplot2

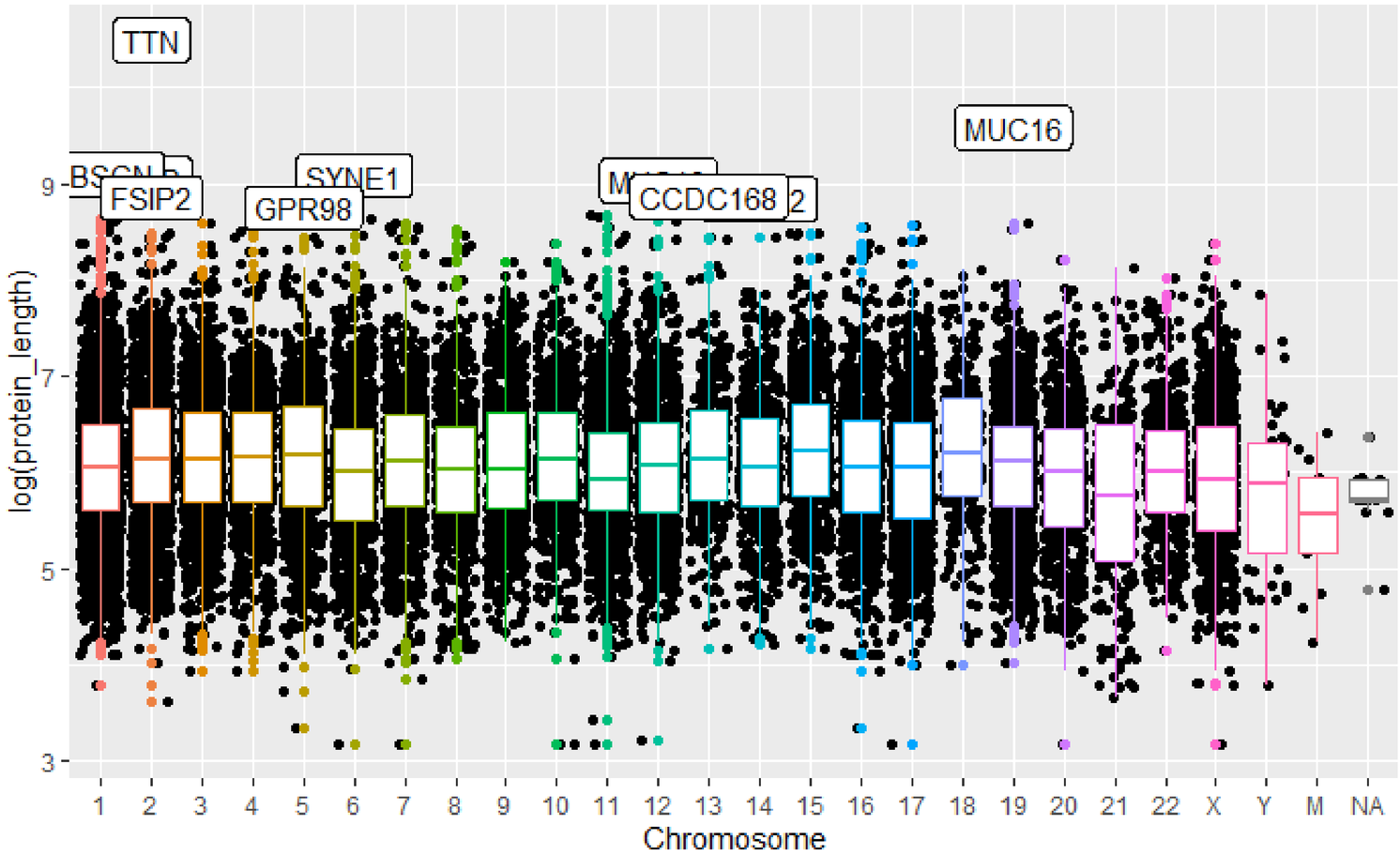
Labels and Legends




```
ggplot(mitocarta, aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_jitter()+
  geom_boxplot(aes(color=hg19_chromsome))+
  geom_label(data=large_prot, aes(label= symbol))
```




```
ggplot(mitocarta, aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_jitter()+
  geom_boxplot(aes(color=hg19_chromosome))+
  geom_label(data=large_prot, aes(label= symbol))+
  labs(x="Chromosome")
```

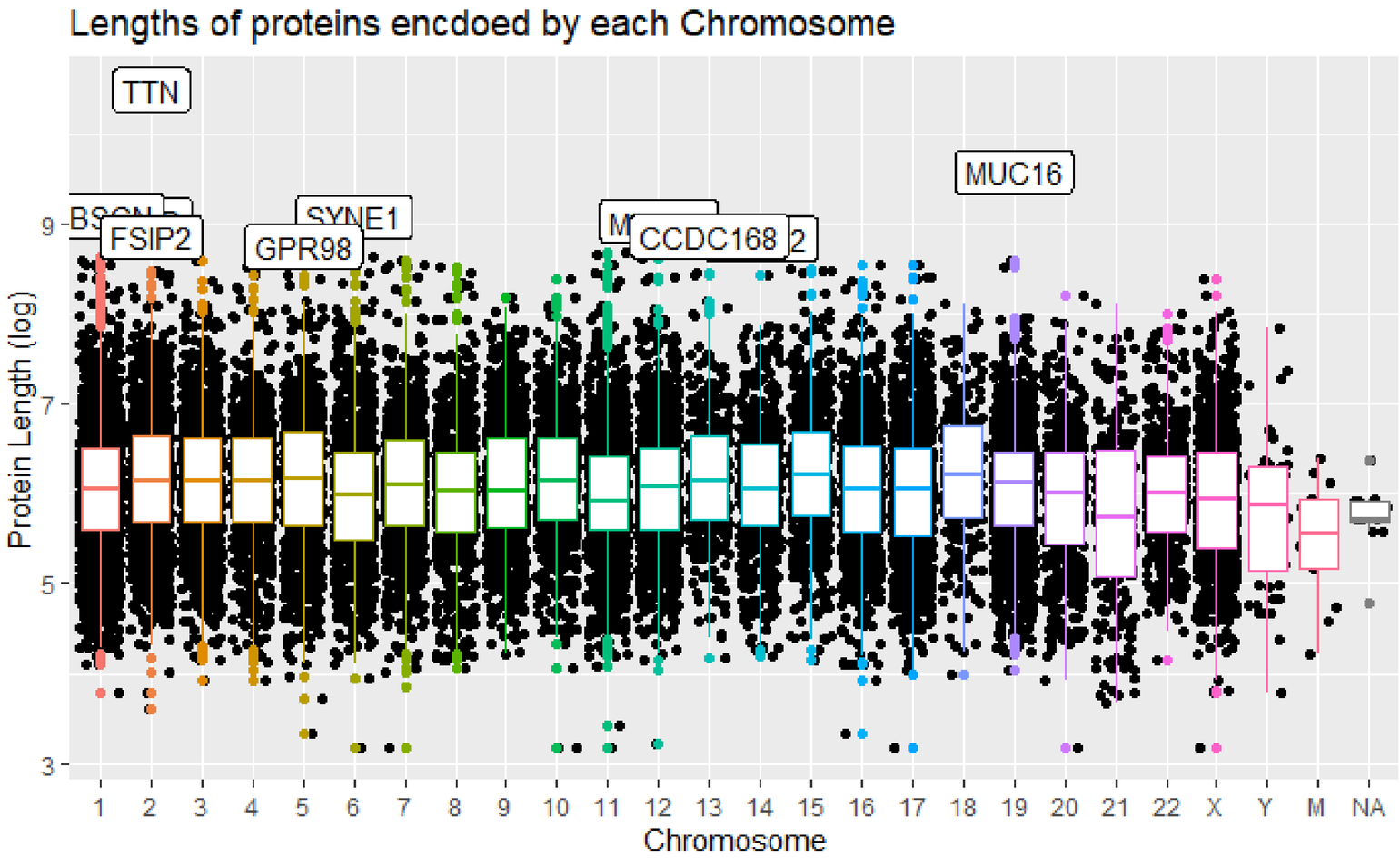



```
ggplot(mitocarta, aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_jitter()+
  geom_boxplot(aes(color=hg19_chromosome))+
   geom_label(data=large_prot, aes(label= symbol))+
   labs(x="Chromosome")+
   guides(fill="none")
```

Exercise 5

Change the x and y axis labels and add a title

```
ggplot(mitocarta, aes(x=hg19_chromosome, y=log(protein_length)))+
  geom_jitter()+
  geom_boxplot(aes(color=hg19_chromosome))+
  geom_label(data=large_prot, aes(label= symbol))
```

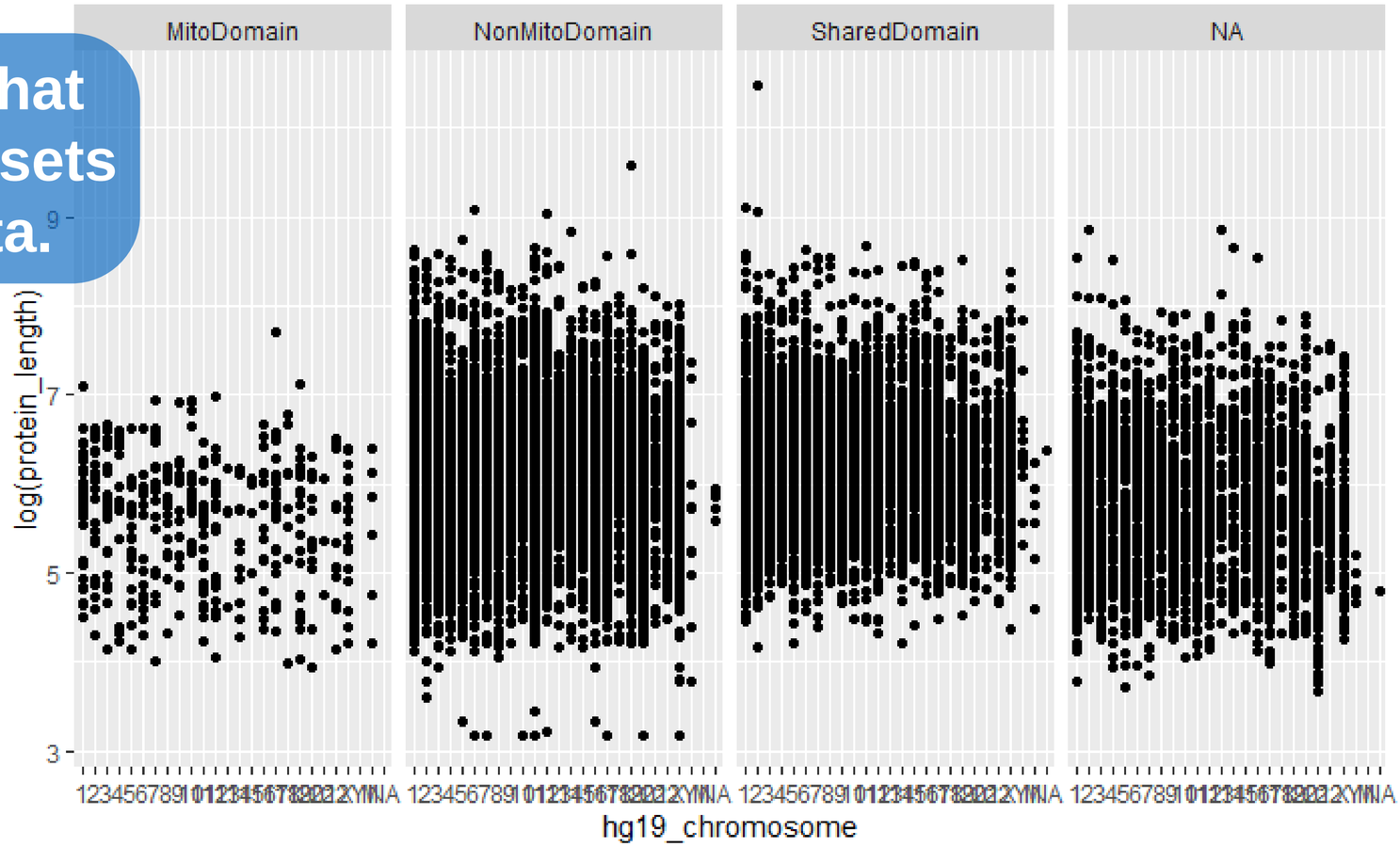



```
ggplot(mitocarta, aes(x = hg19_chromosome, y = log(protein_length))) +
  geom_jitter() +
  geom_boxplot(aes(color = hg19_chromosome)) +
   geom_label(data = large_prot, aes(label = symbol)) +
  guides(color = "none") +
  labs(x = "Chromosome", y = "Protein Length (log)", title = "Lengths of proteins encdoed by each Chromosome")
```

Facets

Facets

Subplots that display subsets of the data.



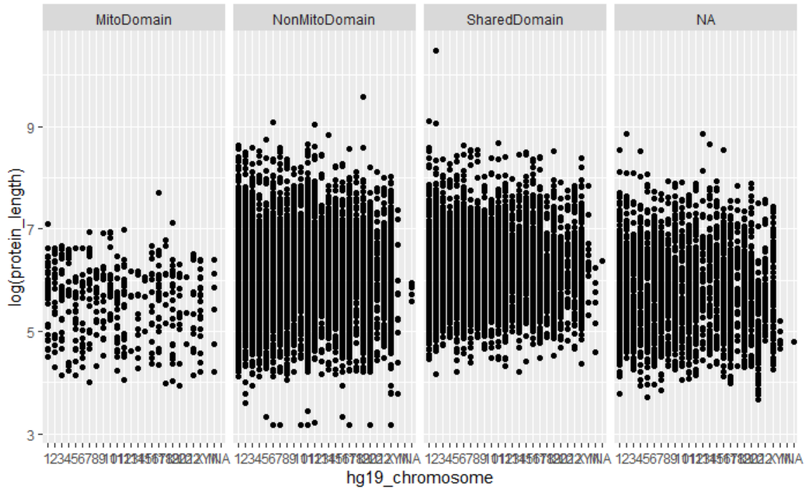

```
ggplot(mitocarta)+
  geom_point(aes(x=hg19_chromosome, y=log(protein_length)))+
  facet_grid(cols = vars(mito_domain_score))
```

Exercise 6

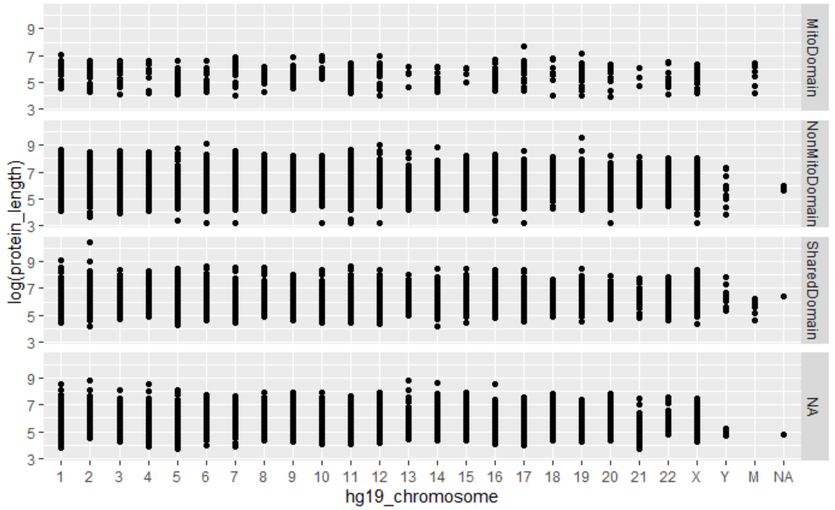
What do **facet_grid** and **facet_wrap** do?

```
q <- ggplot(mitocarta) + geom_point(aes(x =
hg19_chromosome, y = log(protein_length))
q + facet_grid(. ~ hg19_chromosome)
q + facet_grid(hg19_chromosome ~ .)
q + facet_wrap(~ hg19_chromosome)
```

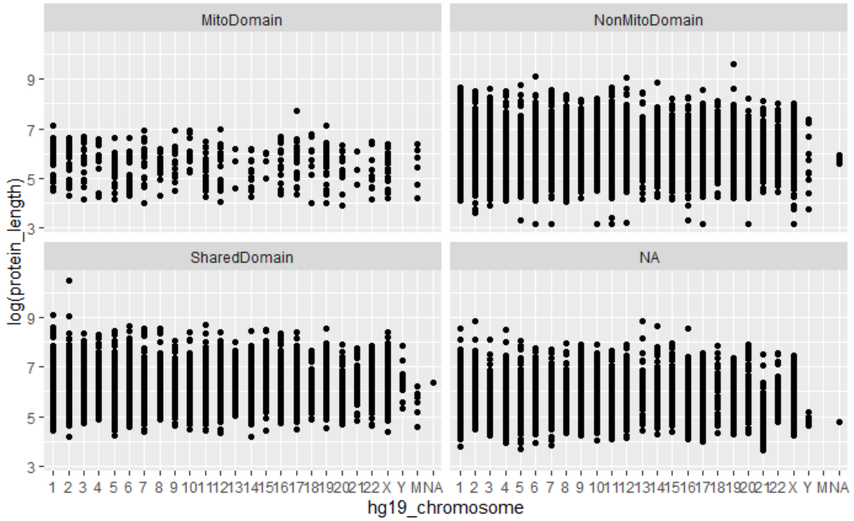
Facets




```
q + facet_grid(. ~ hg19_chromosome)
```




```
q + facet_grid(hg19_chromosome ~ .)
```

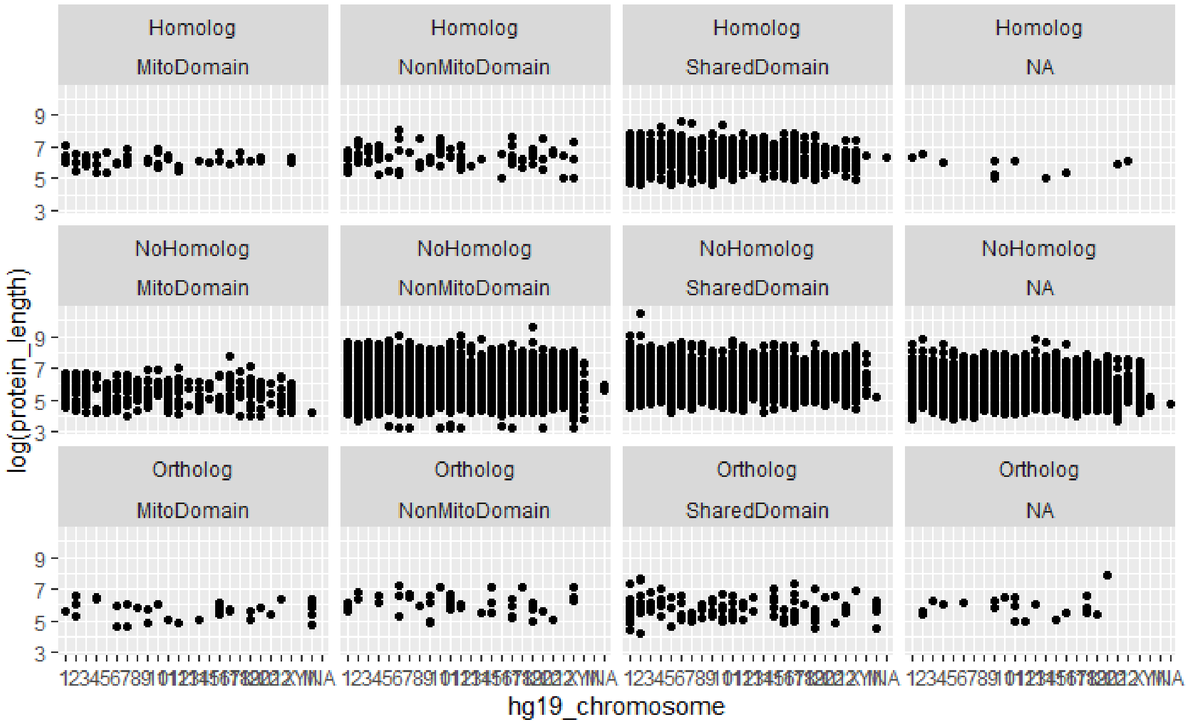



```
q + facet_wrap(~ hg19_chromosome)
```

facet_grid() - 2D grid, rows ~ cols, . for no split

facet_wrap() - 1D ribbon wrapped into 2D

Facets

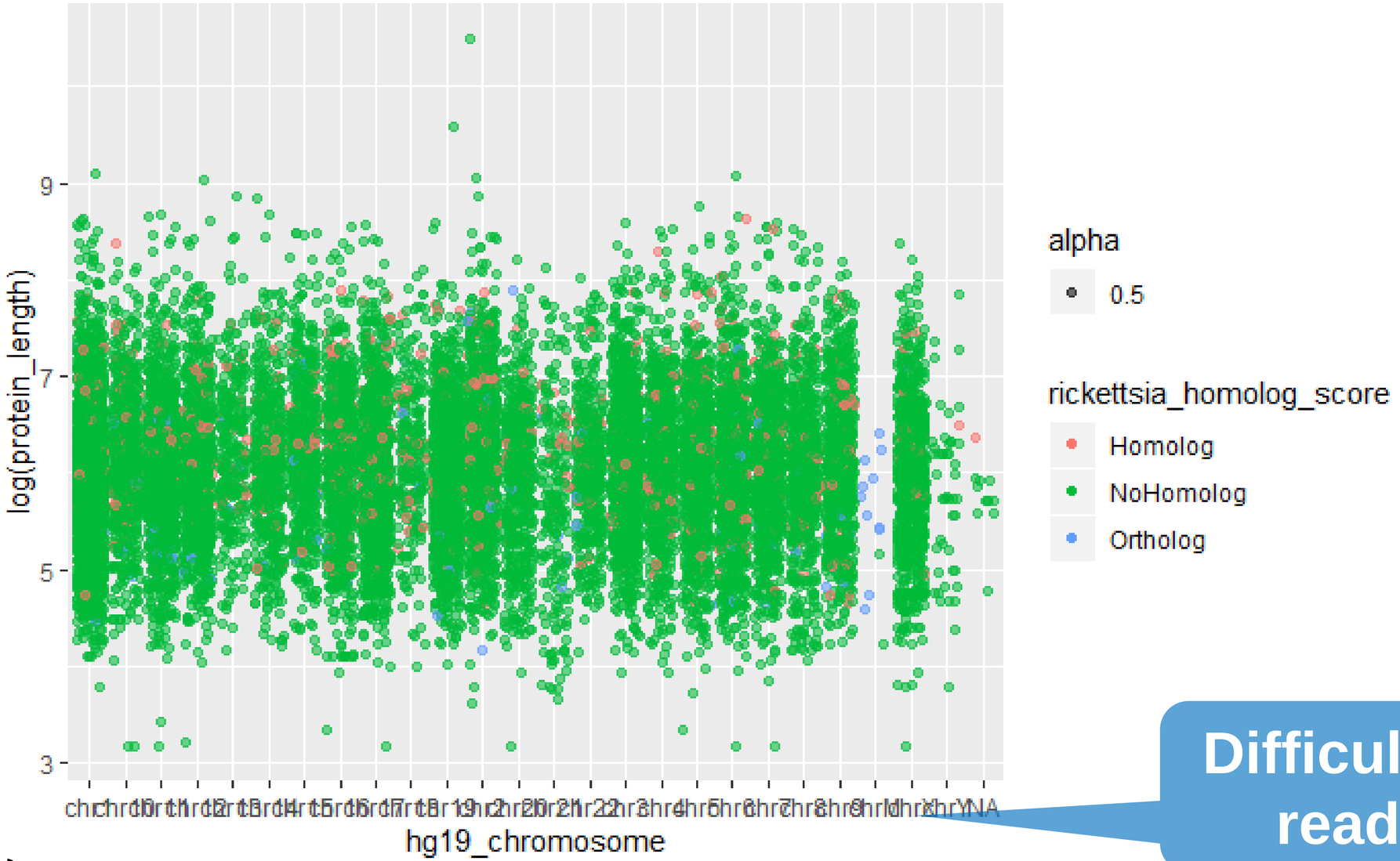



```
q + facet_wrap(rickettsia_homolog_score~ hg19_chromosome)
```

facet_grid() - 2D grid, rows ~ cols, . for no split

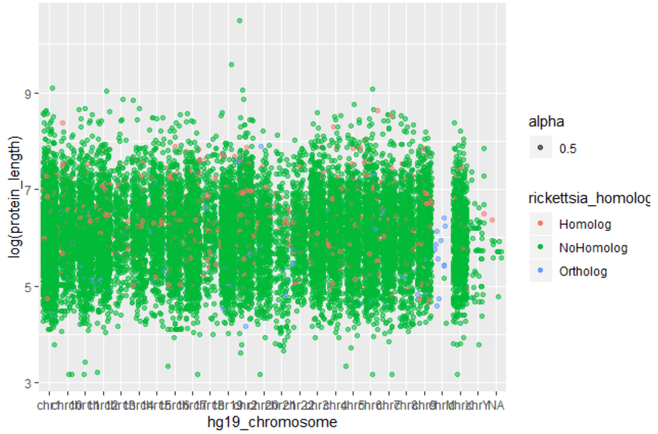
facet_wrap() - 1D ribbon wrapped into 2D

Coordinate Flipping

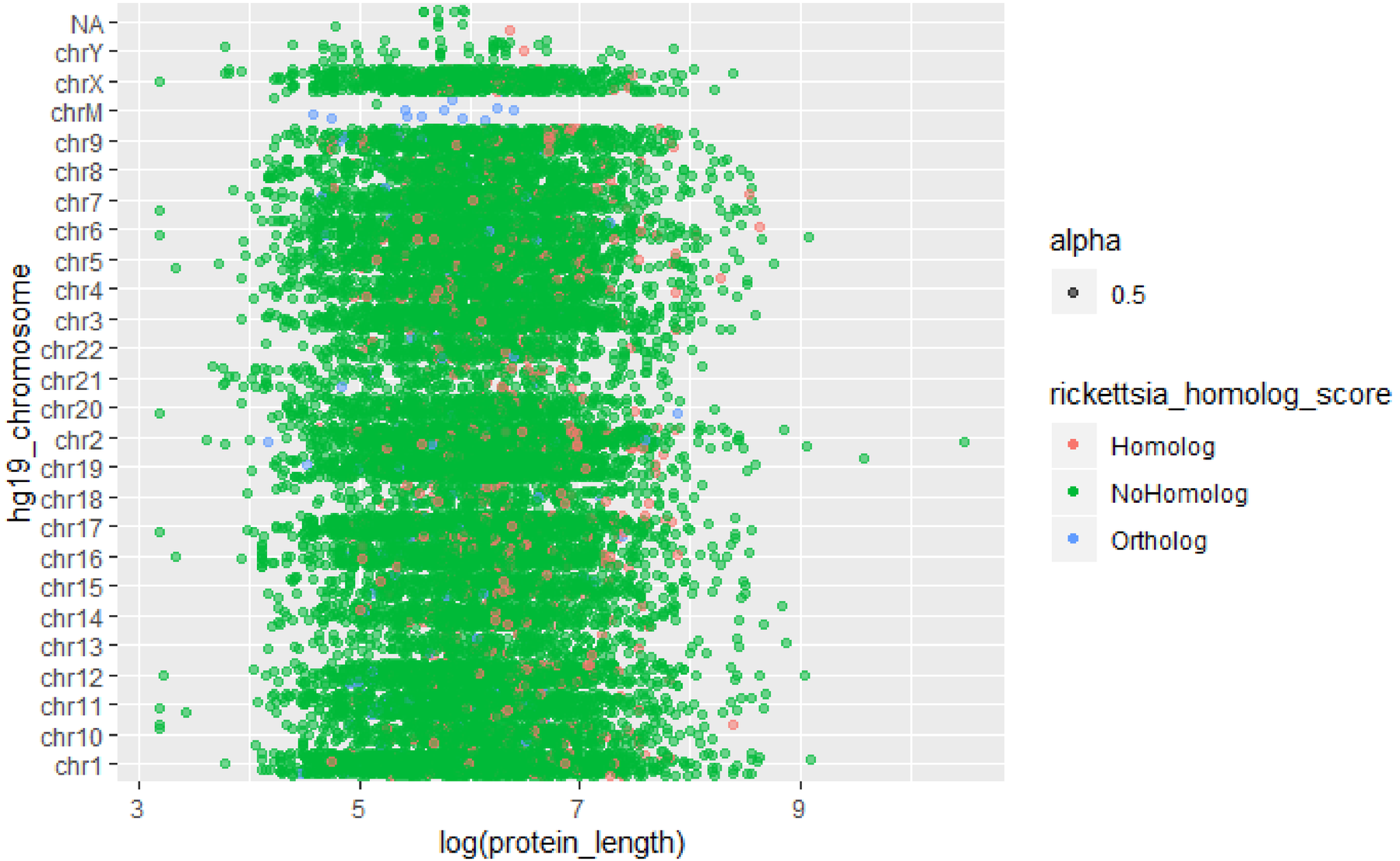


Difficult to read!

```
ggplot(mitocarta) +
  geom_point(aes(x = hg19_chromosome, y = log(protein_length), color =
rickettsia_homolog_score, alpha = 0.5))
```



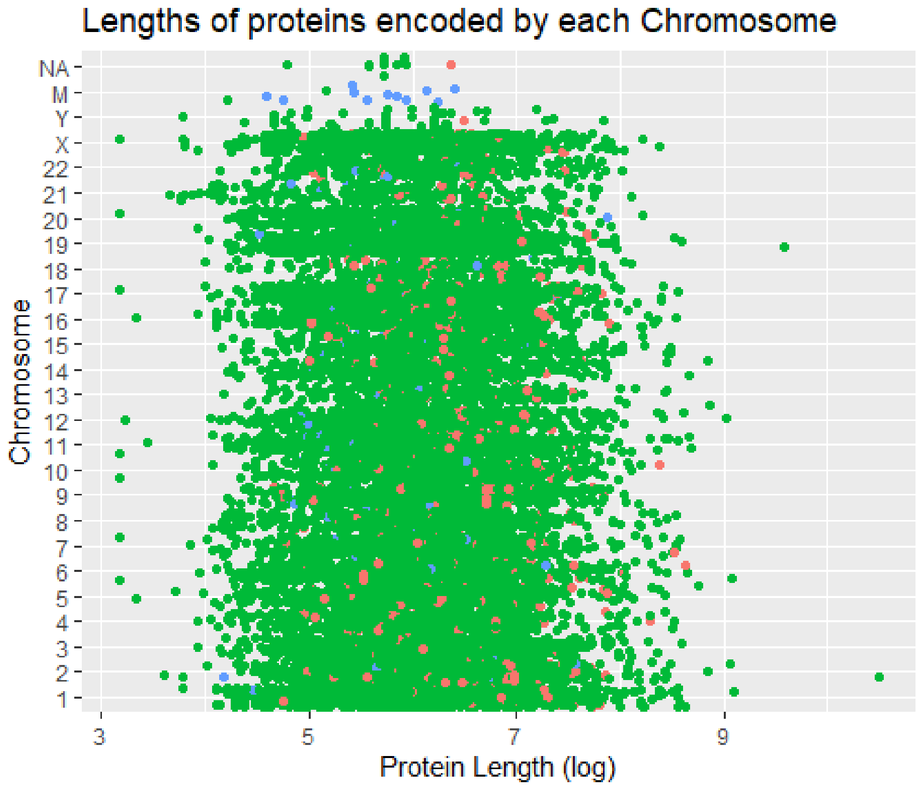
Can read the axis labels!

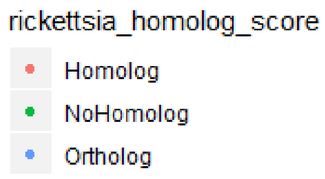


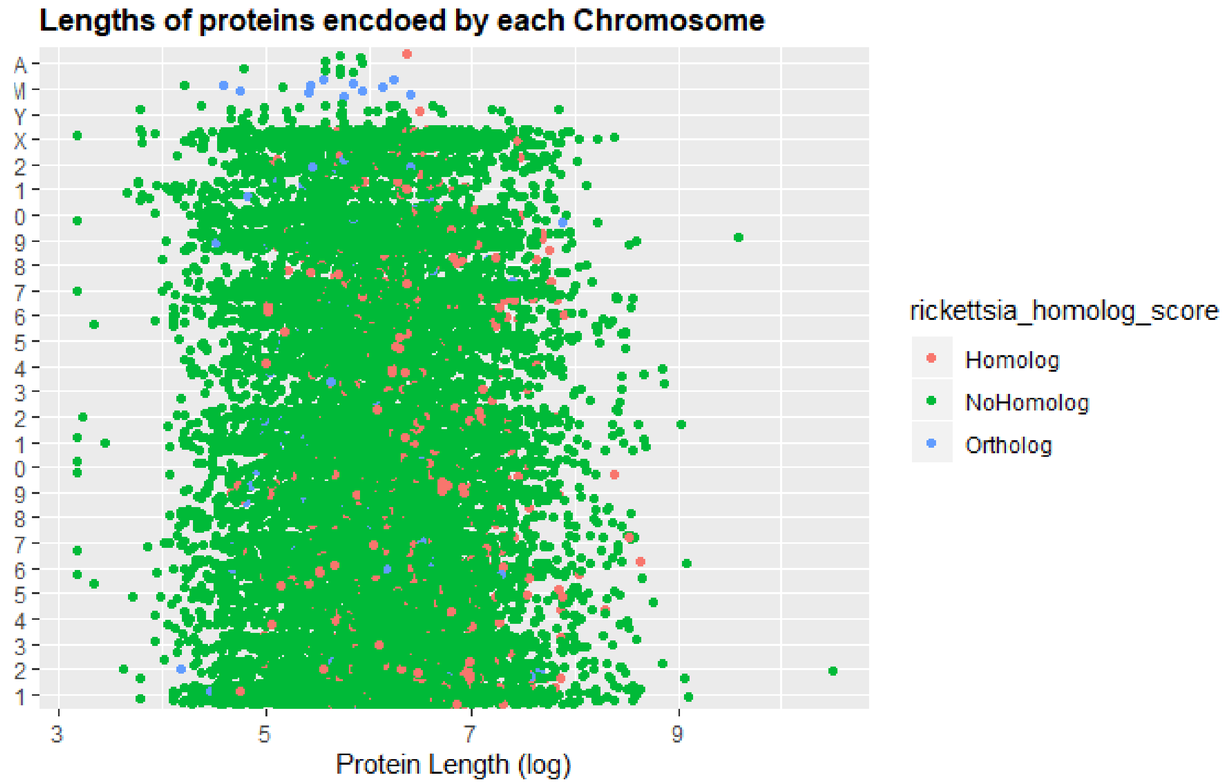

```
ggplot(mitocarta) +
  geom_point(aes(x = hg19_chromosome, y = log(protein_length), color =
rickettsia_homolog_score, alpha = 0.5)) +
coord_flip()
```

Themes

Themes

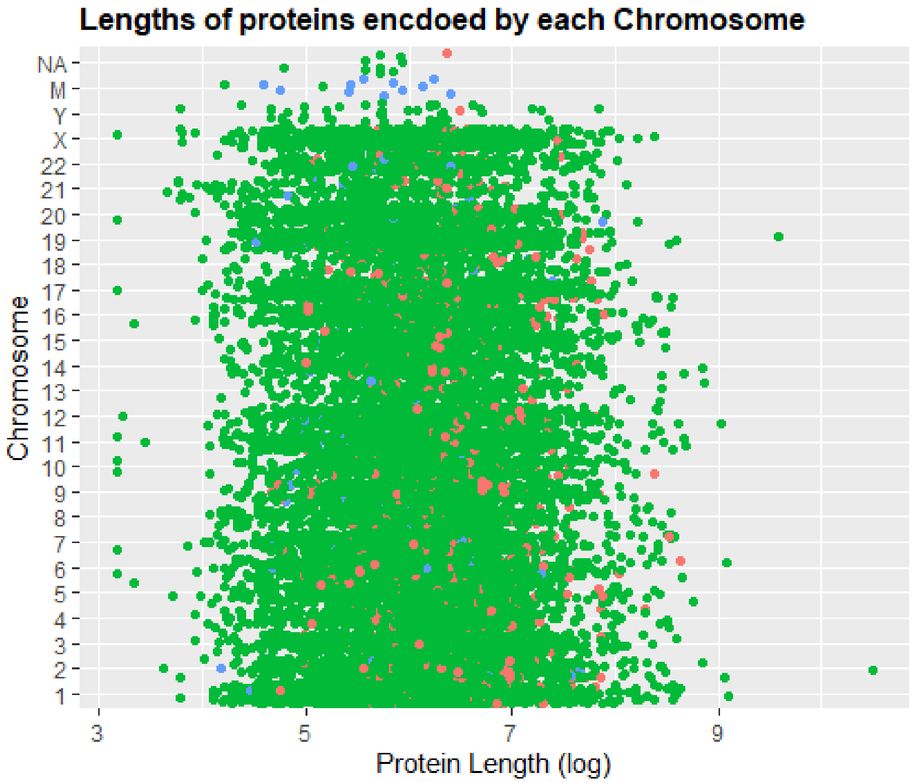


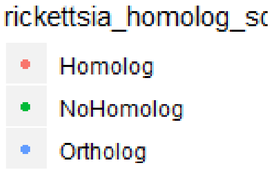


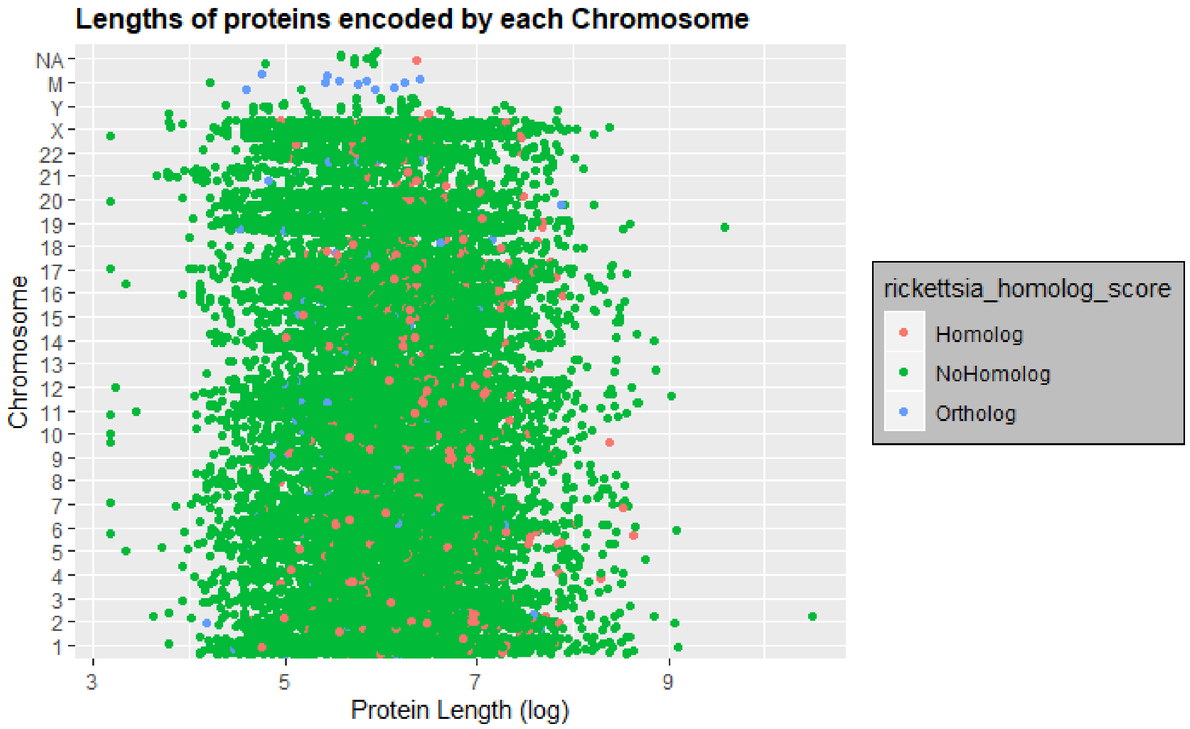



```
ggplot(mitocarta) +
  geom_jitter(aes(hg19_chromosome,log(protein_length), color=
rickettsia_homolog_score))+
  coord_flip()+
  labs(x = "Chromosome", y = "Protein Length (log)", title = "Lengths of proteins
encoded by each Chromosome")+
  theme(plot.title = element_text(face = "bold", size = 12))
```

Themes

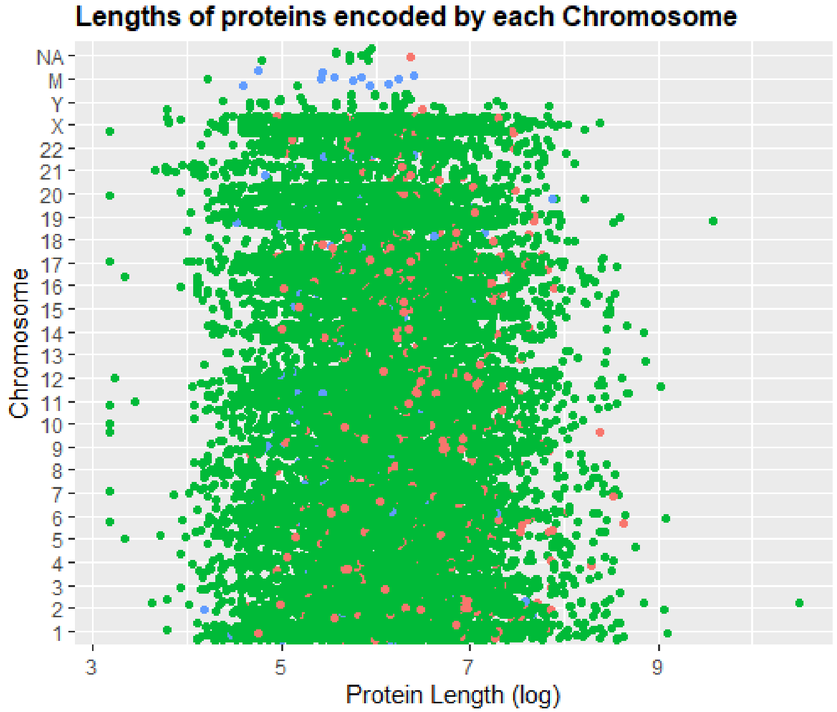


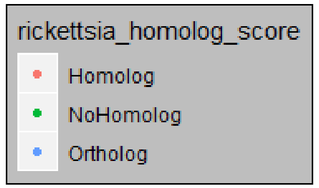


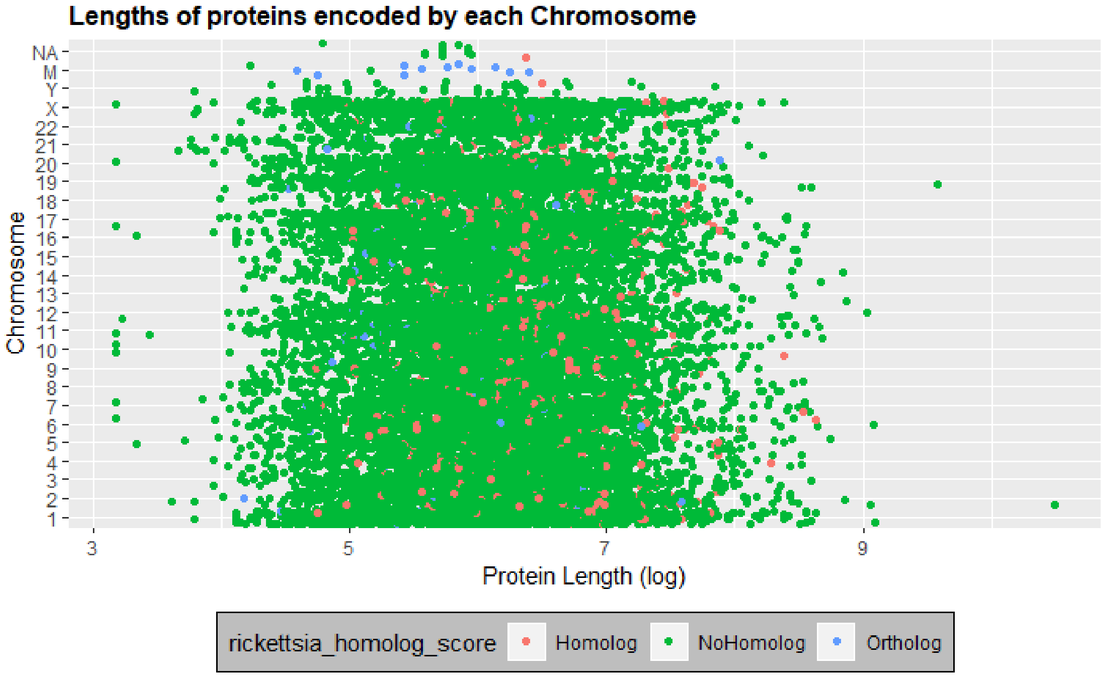



```
ggplot(mitocarta) +
  geom_jitter(aes(hg19_chromosome,log(protein_length), color= rickettsia_homolog_score))+
  coord_flip()+
  labs(x = "Chromosome", y = "Protein Length (log)", title = "Lengths of proteins encoded by each Chromosome")+
  theme(plot.title = element_text(face = "bold", size = 12),
legend.background = element_rect(fill = "gray", colour = "black"))
```

Themes

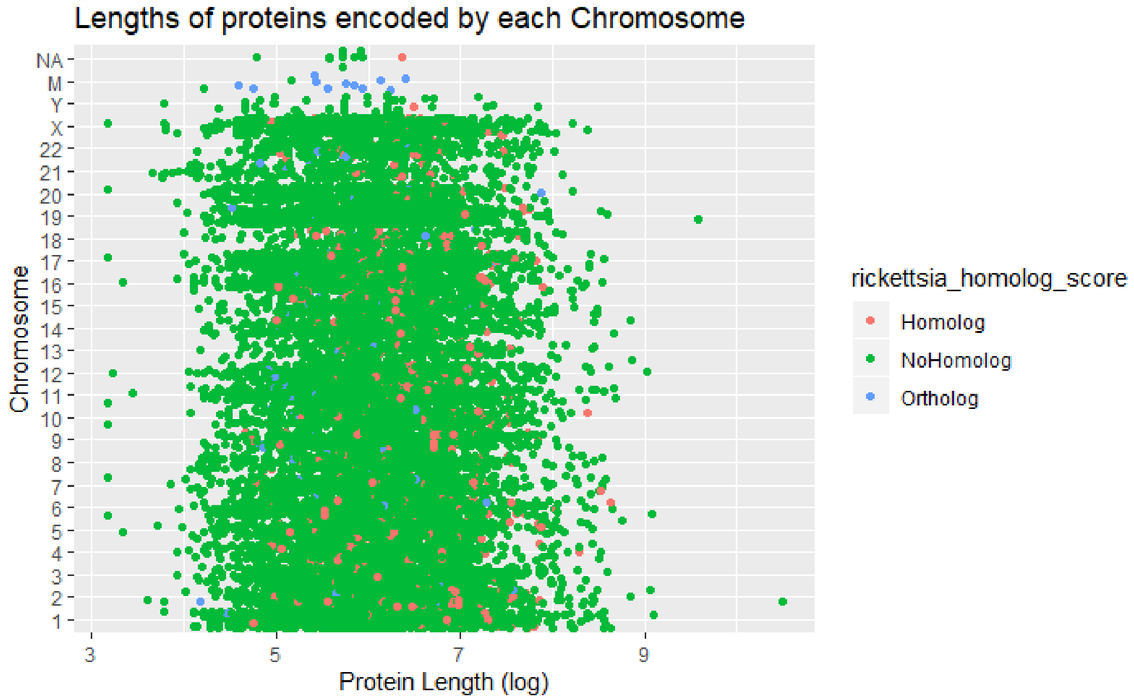


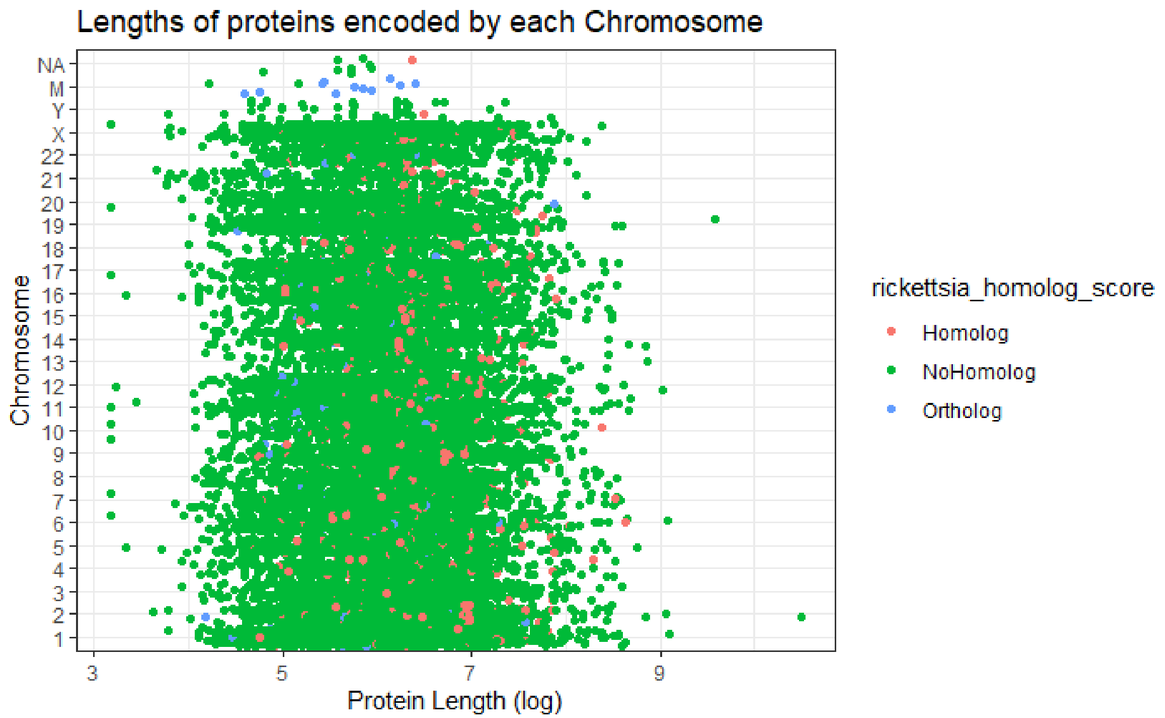





```
ggplot(mitocarta) +
  geom_jitter(aes(hg19_chromosome,log(protein_length), color= rickettsia_homolog_score))+
  coord_flip()+
  labs(x = "Chromosome", y = "Protein Length (log)", title = "Lengths of proteins encoded by each Chromosome")+
  theme(plot.title = element_text(face = "bold", size = 12),
legend.background = element_rect(fill = "gray", colour = "black"),
legend.postion= “bottom”)
```

Pre-set Themes



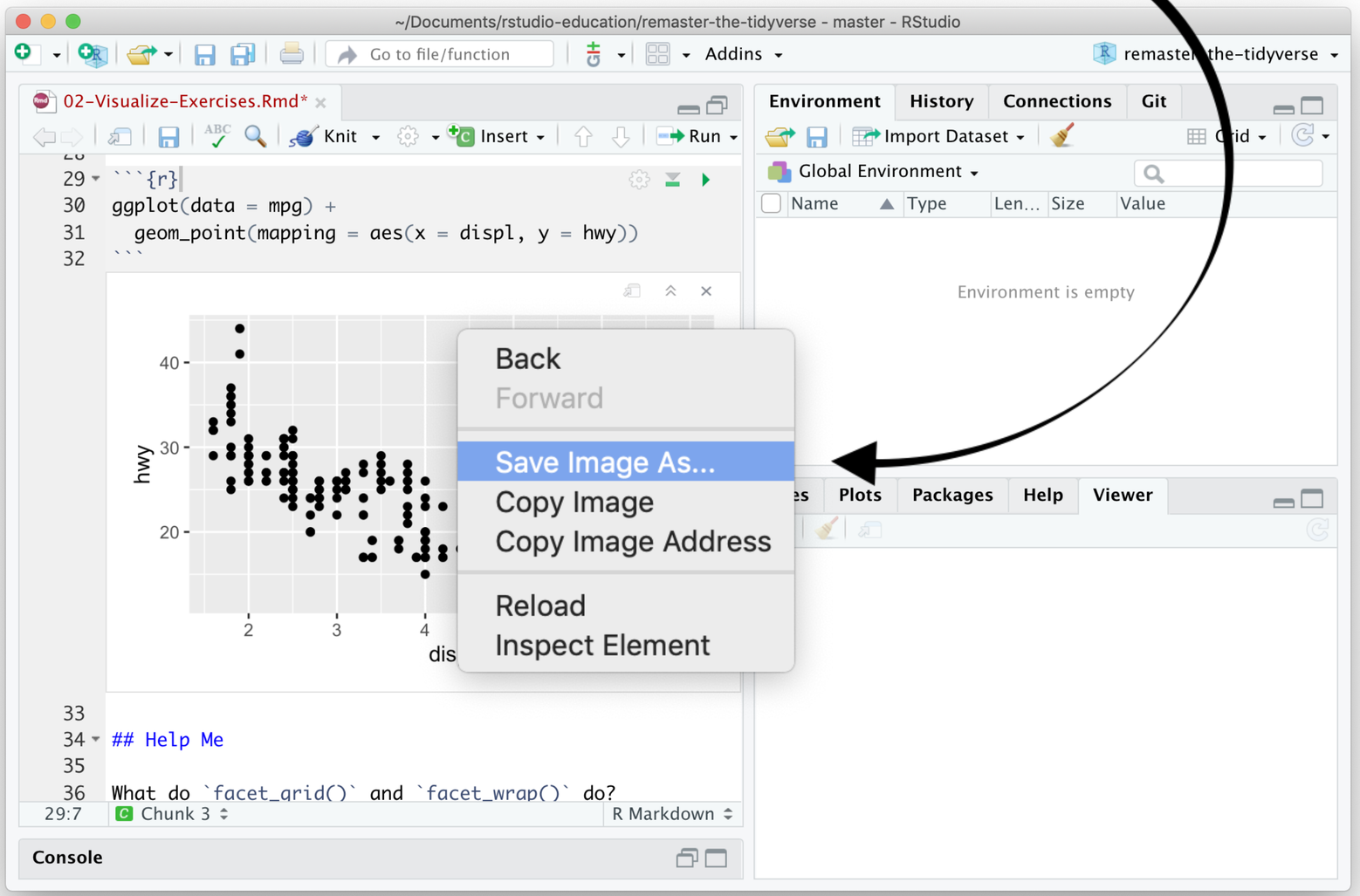



```
ggplot(mitocarta) +
  geom_jitter(aes(hg19_chromosome,log(protein_length), color= rickettsia_homolog_score))+
  coord_flip()+
  labs(x = "Chromosome", y = "Protein Length (log)", title = "Lengths of proteins encoded by each Chromosome")+
  theme_bw()
```

Saving graphs

GUI method

Right click on the plot



Code method

ggsave() saves the last plot.
Uses size on screen:

```
ggsave("my-plot.pdf")
ggsave("my-plot.png")
```

Specify size in inches

```
ggsave("my-plot.pdf", width = 6, height
```

Q: But where will it save it?

A: Alongside your .Rmd

A ggplot2 template

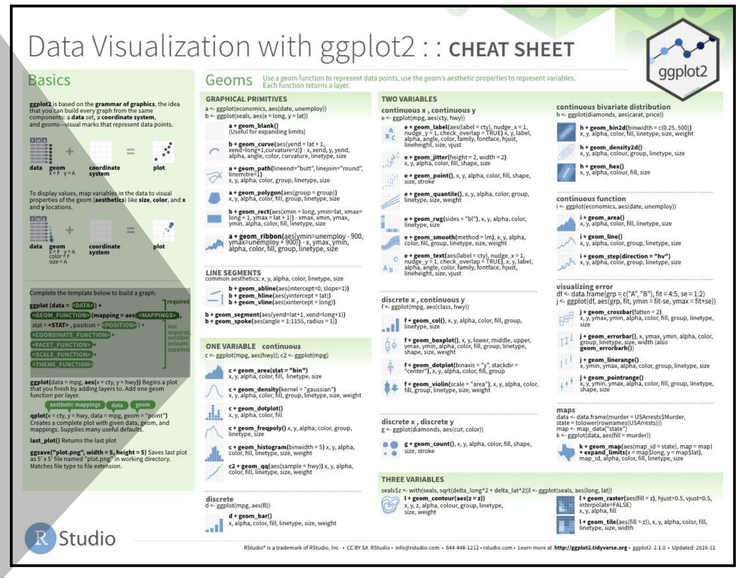
Make any plot by filling in the parameters of this template

Complete the template below to build a graph.

```
ggplot (data = <DATA>) +
<GEOM_FUNCTION> (mapping = aes(<MAPPINGS>),
 stat = <STAT>, position = <POSITION> ) +
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>
```

required

Not required, sensible defaults supplied



Your Turn

Open the **Day-3---ggplot2-hw.Rmd**