Designing data visualizations in R

making clear figures that communicate

2022-01-13

"We need to do everything we can to help our readers understand the meaning of our visualizations and see the same patterns in the data that we see. This usually means less is more. **Simplify your figures** as much as possible. **Remove all features that are tangential to your story**"

— Claus O. Wilke

act one: focus and declutter

act one: focus and declutter

act two: narrate and put in context

The cast of characters

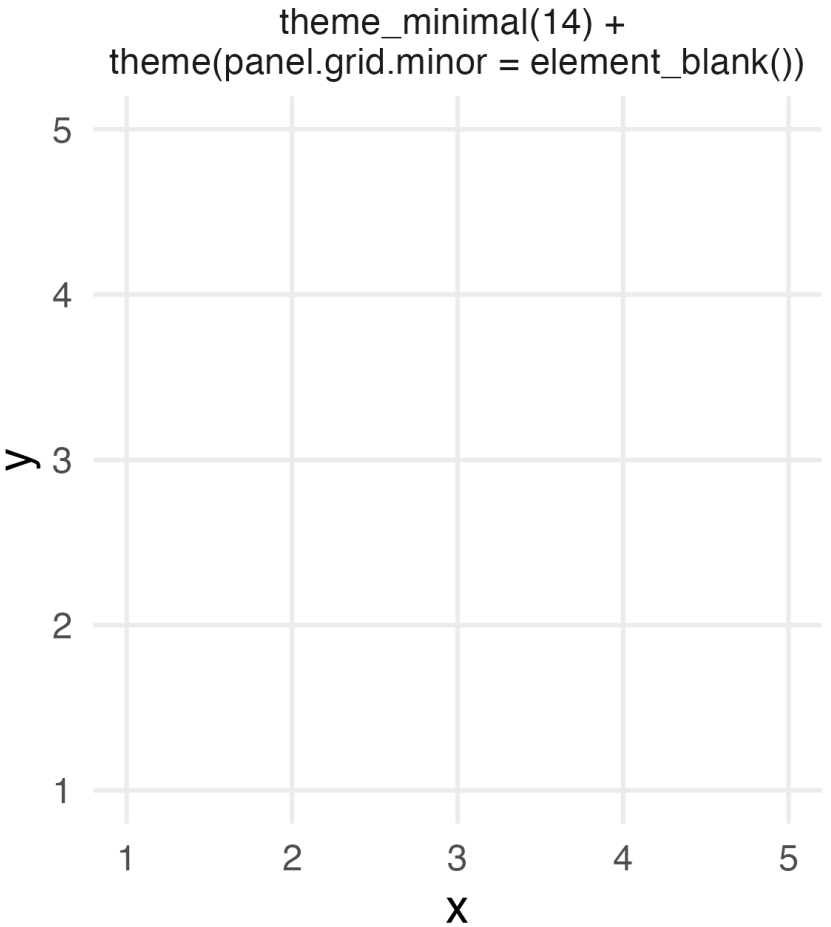
Packages

1. ggplot2
2. gghighlight
3. cowplot
4. ggtext
5. prismatic
6. patchwork

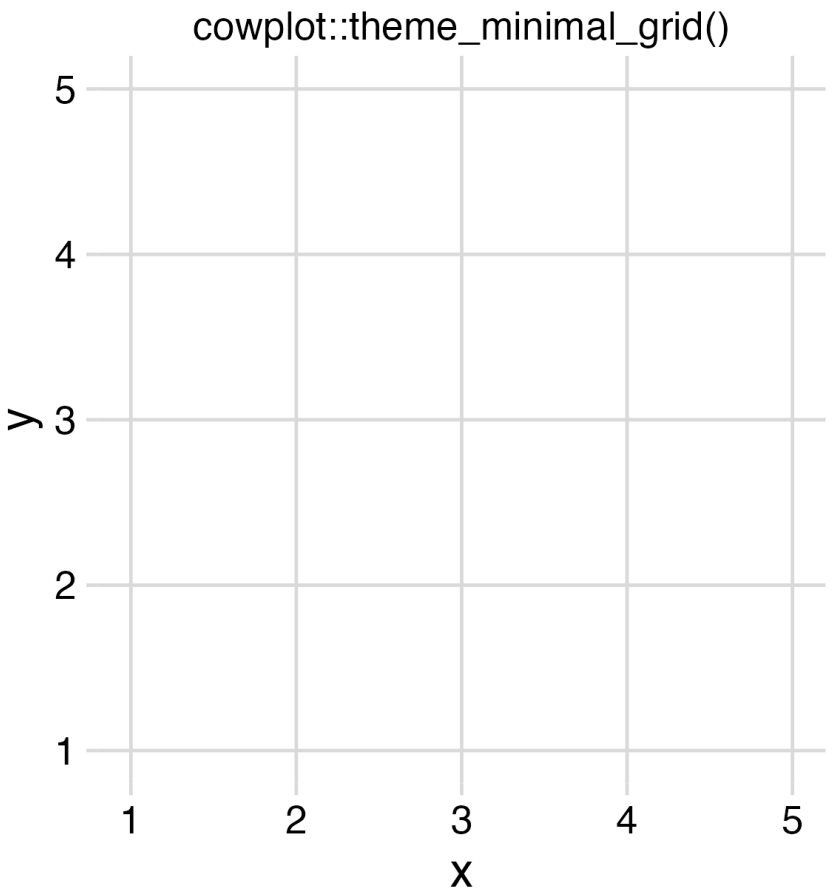
data

1. emperors (data/emperors.csv)
2. gapminder (library(gapminder))
3. nyc_squirrels (data/nyc_squirrels.csv + data/central_park/)
4. diabetes (data/diabetes.csv)
5. la_heat_income (data/los-angeles.geojson)

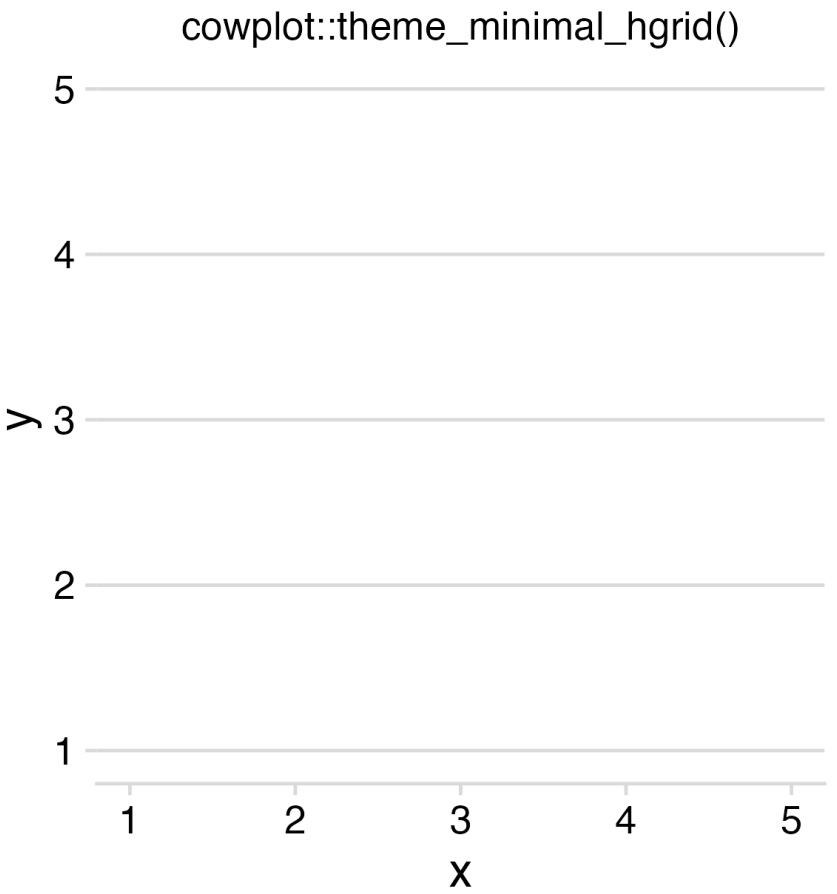
Themes


theme_minimal(14) +
theme(panel.grid.minor = element_blank())
5
4
3
2
1
y
1
2
3
4
5
x

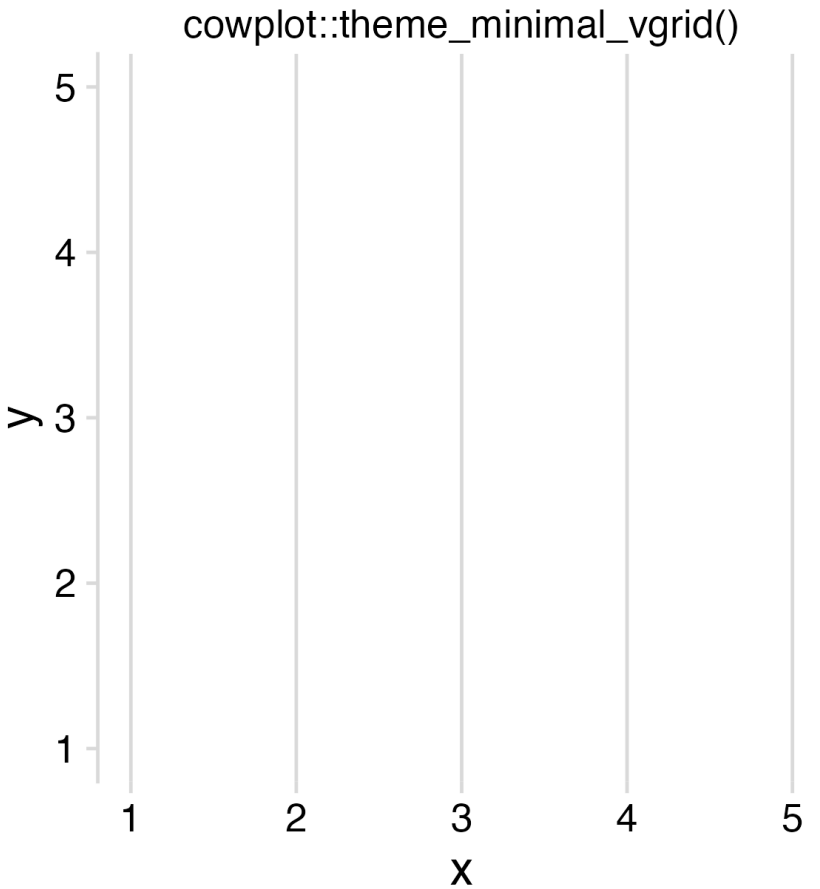
Themes: cowplot



Themes: cowplot



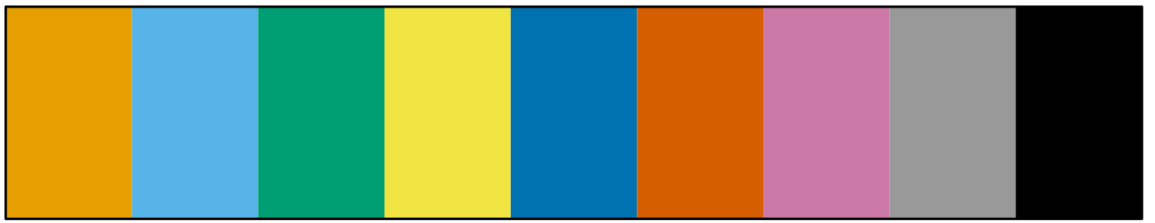
Themes: cowplot



Themes: cowplot

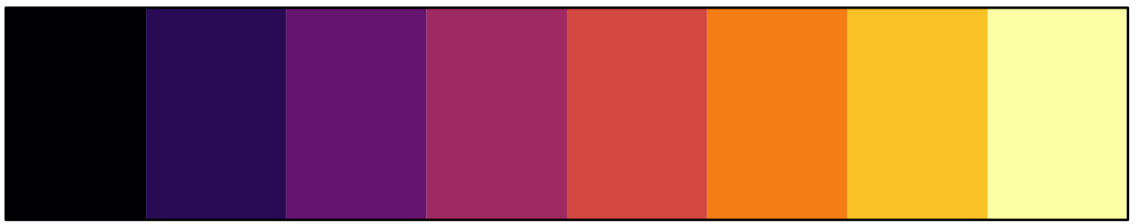
cowplot::theme_map()

Palettes



Okabe-Ito
(ggokabeito::palette_okabe_ito())

Palettes



viridis inferno (viridis::inferno())

Palettes

greys ("grey**", grey(.**))

act one: focus and declutter

or: reducing mental burden in figures

How do we reduce mental burden in our plots?

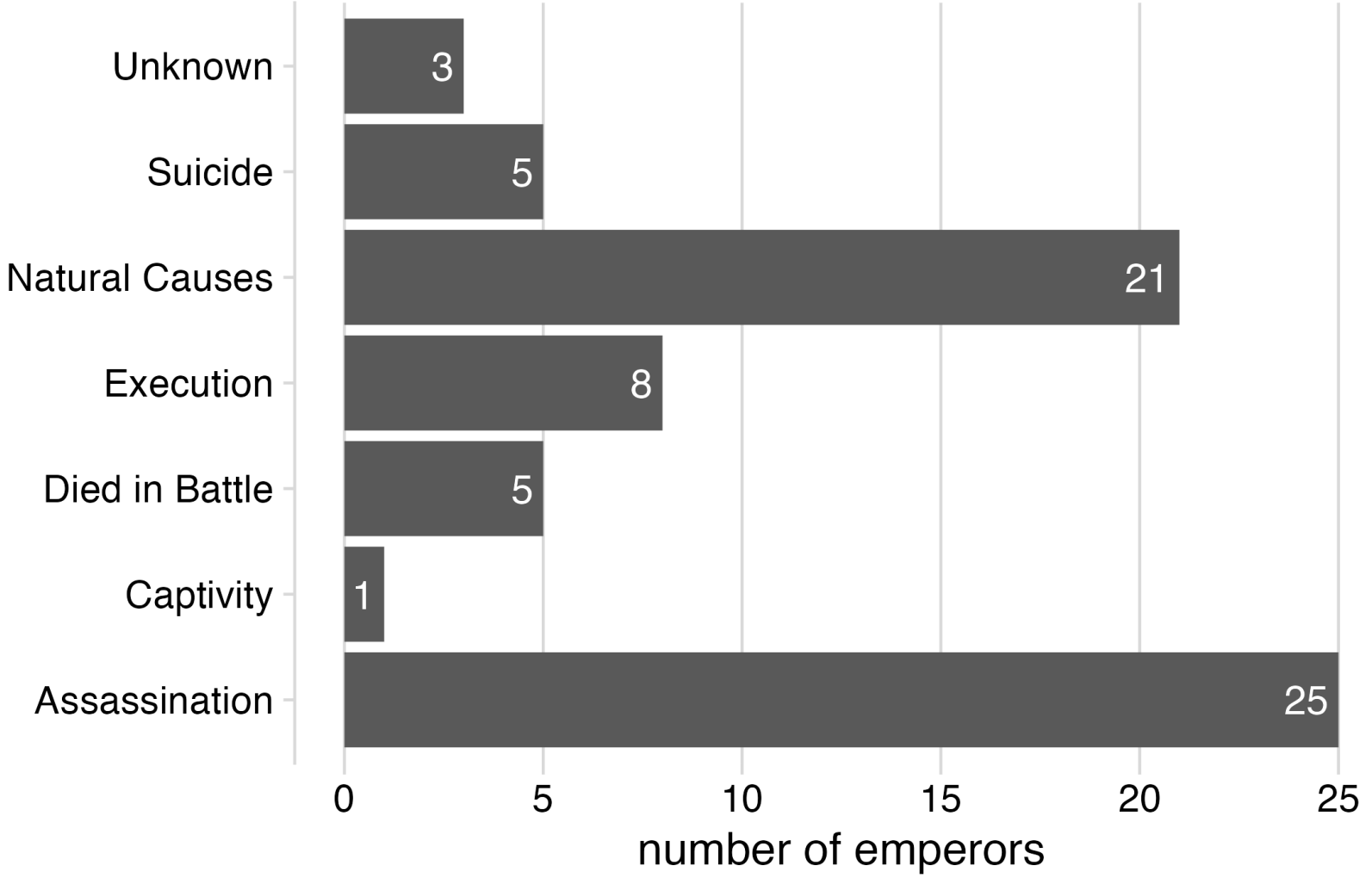
How do we reduce mental burden in our plots?

simplify aesthetics and highlight

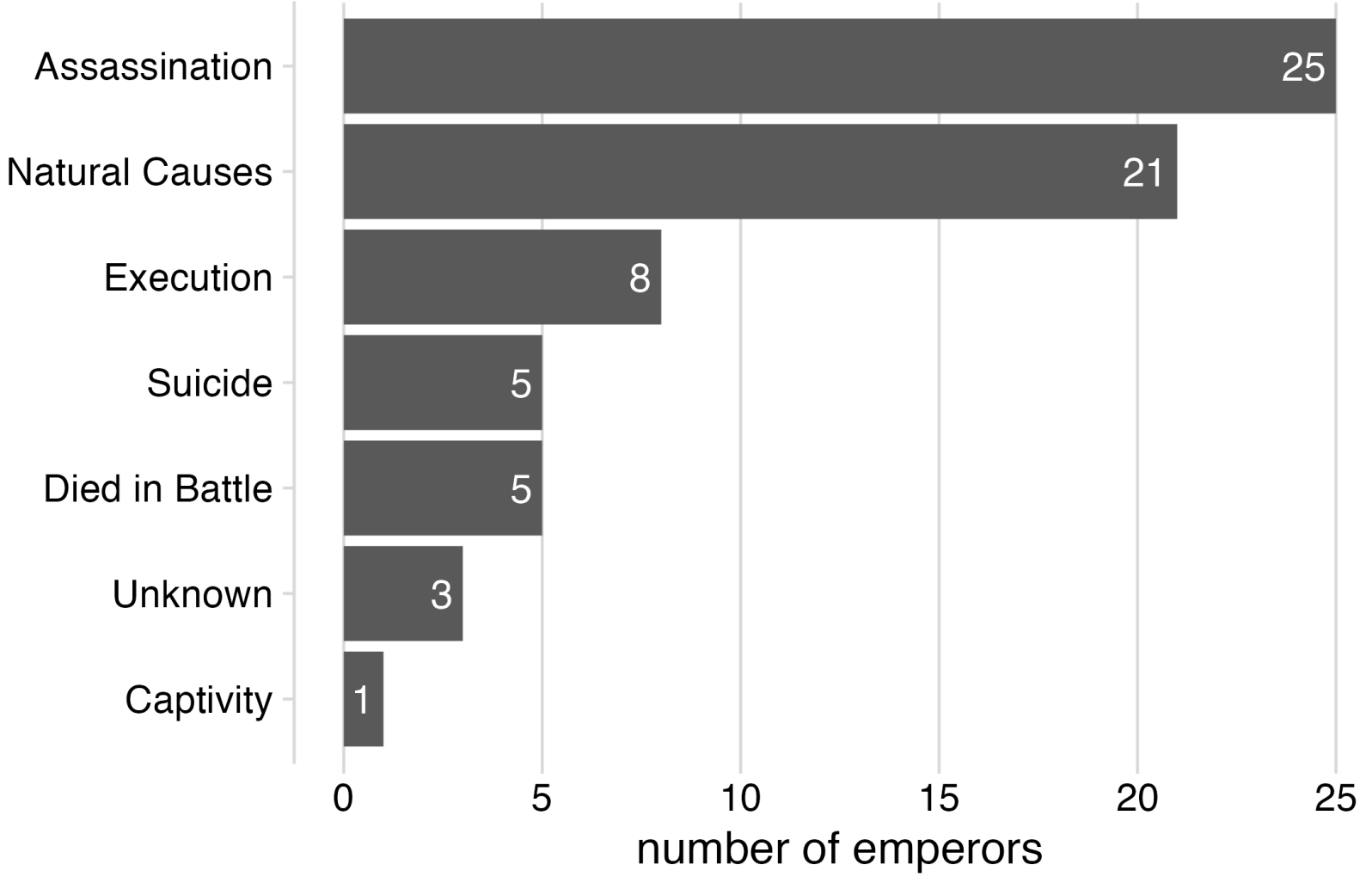
```
emperors <- read_csv(file.path("data", "emperors.csv"))

emperors
```

```
## # A tibble: 68 × 16
##    index name      name_full birth      death      birth_cty
##    <dbl> <chr>     <chr>     <date>     <date>     <chr>
##  1     1 Augustus  IMPERATO… 0062-09-23 0014-08-19 Rome
##  2     2 Tiberius  TIBERIVS… 0041-11-16 0037-03-16 Rome
##  3     3 Caligula  GAIVS IV… 0012-08-31 0041-01-24 Antitum
##  4     4 Claudius  TIBERIVS… 0009-08-01 0054-10-13 Lugdunum
##  5     5 Nero      NERO CLA… 0037-12-15 0068-06-09 Antitum
##  6     6 Galba     SERVIVS … 0002-12-24 0069-01-15 Terracina
##  7     7 Otho      MARCVS S… 0032-04-28 0069-04-16 Terentin…
##  8     8 Vitellius AVLVS VI… 0015-09-24 0069-12-20 Rome
##  9     9 Vespasian TITVS FL… 0009-11-17 0079-06-24 Falacrine
## 10    10 Titus     TITVS FL… 0039-12-30 0081-09-13 Rome
## # … with 58 more rows, and 10 more variables:
## #   birth_prv <chr>, rise <chr>, reign_start <date>,
## #   reign_end <date>, cause <chr>, killer <chr>, …
```

```r
emperors %>%
  count(cause) %>%
  ggplot(aes(x = n, y = cause)) +
  geom_col() +
  geom_text(
    aes(label = n, x = n - .25),
    color = "white",
    size = 5,
    hjust = 1
  ) +
  cowplot::theme_minimal_vgrid(16) +
  theme(
    axis.title.y = element_blank(),
    legend.position = "none"
  ) +
  xlab("number of emperors")
```

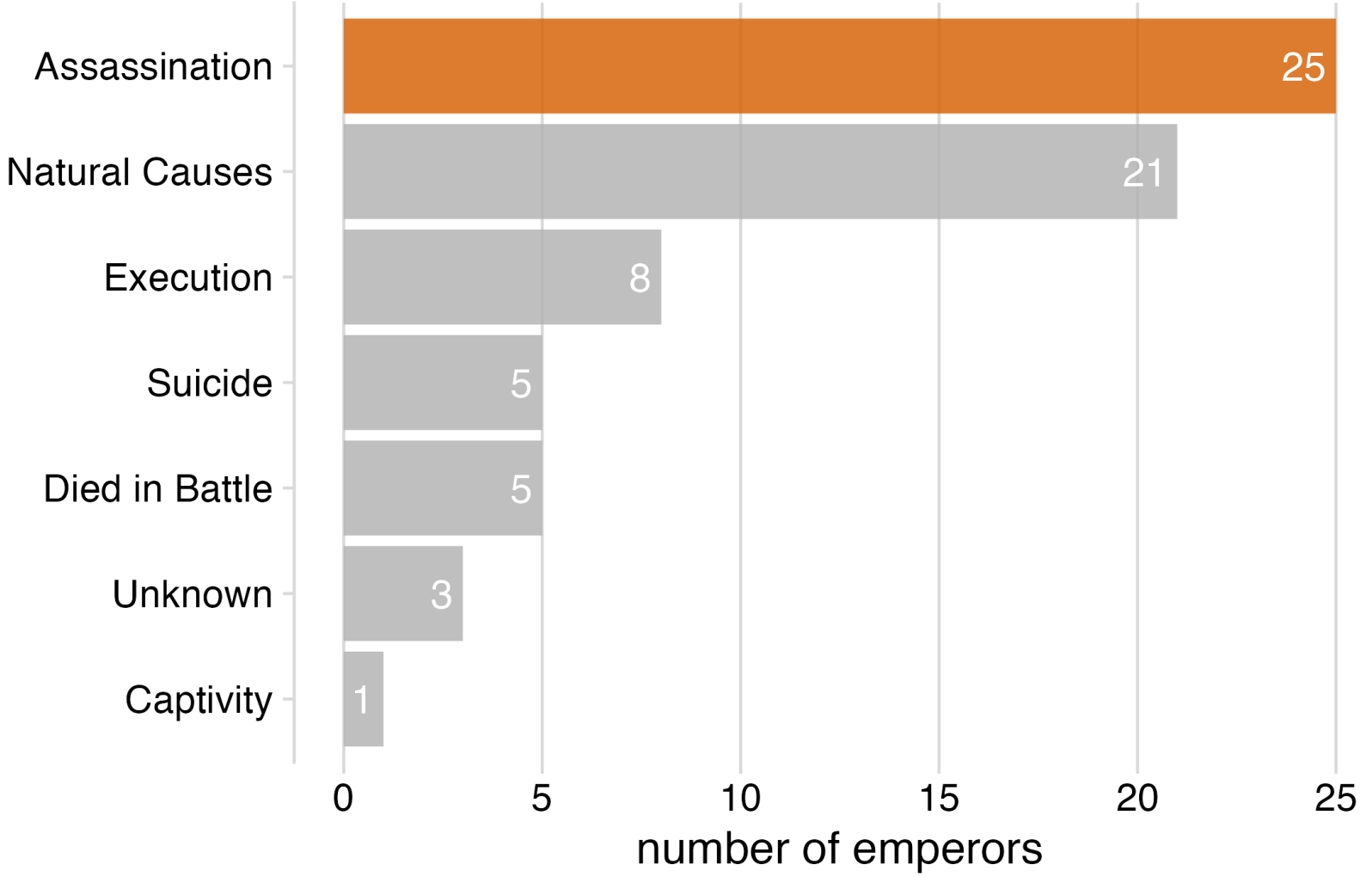

Unknown
Suicide
Natural Causes
Execution
Died in Battle
Captivity
Assassination
3
5
21
8
5
1
25
0
5
10
15
20
25
number of emperors

```r
emperors %>%
  count(cause) %>%
  arrange(n) %>%
  mutate(cause = fct_inorder(cause)) %>%
  ggplot(aes(x = n, y = cause)) +
  geom_col() +
  geom_text(
    aes(label = n, x = n - .25),
    color = "white",
    size = 5,
    hjust = 1
  ) +
  cowplot::theme_minimal_vgrid(16) +
  theme(
    axis.title.y = element_blank(),
    legend.position = "none"
  ) +
  xlab("number of emperors")
```

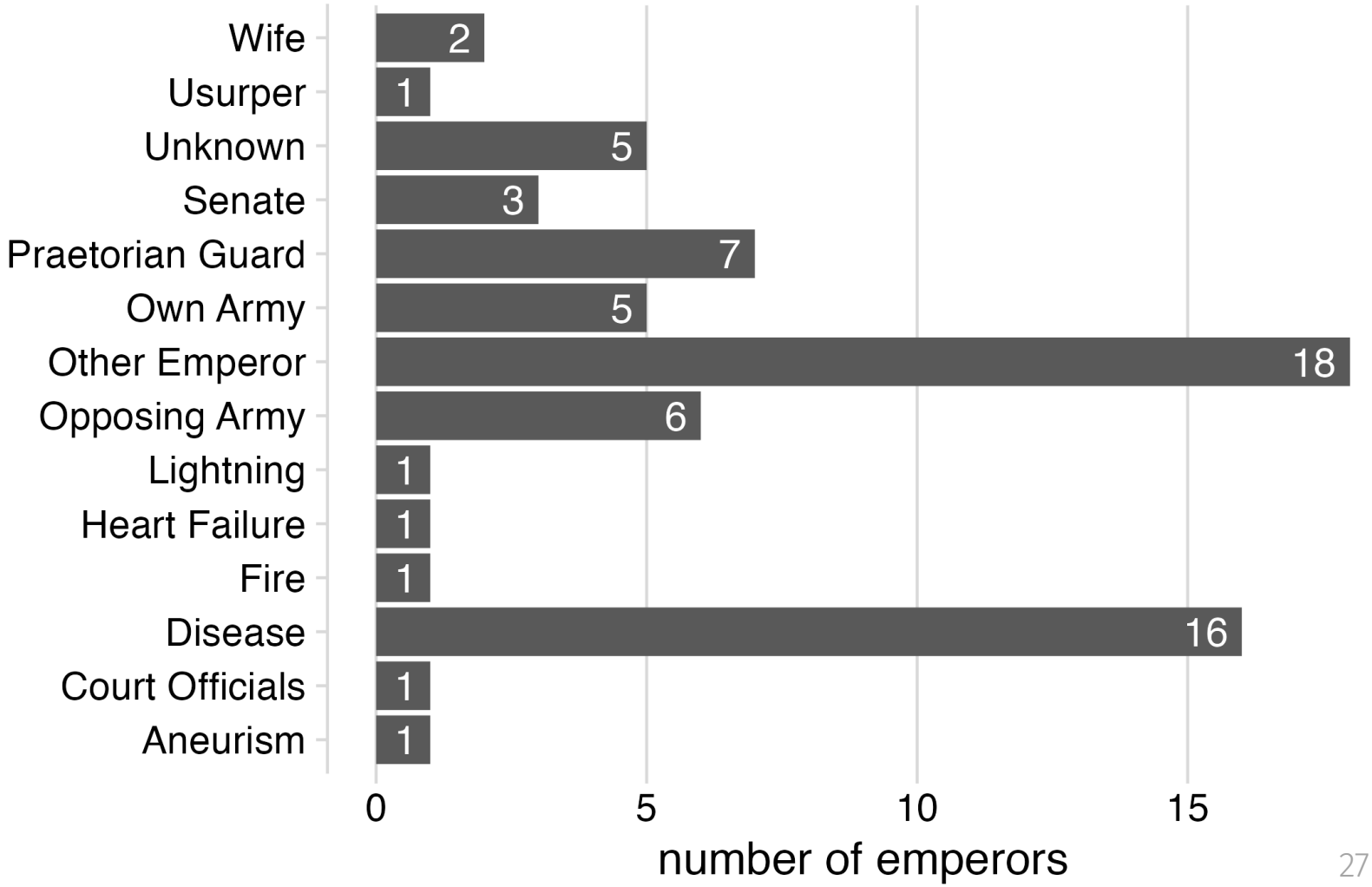

Assassination
Natural Causes
Execution
Suicide
Died in Battle
Unknown
Captivity
25
21
8
5
5
3
1
0
5
10
15
20
25
number of emperors

```r
emperors_assassinated <- emperors %>%
  count(cause) %>%
  arrange(n) %>%
  mutate(
    assassinated = ifelse(cause == "Assassination", TRUE, FALSE),
    cause = fct_inorder(cause)
  )
```

```r
emperors_assassinated %>%
  ggplot(aes(x = n, y = cause, fill = assassinated)) +
  geom_col() +
  geom_text(
    aes(label = n, x = n - .25),
    color = "white",
    size = 5,
    hjust = 1
  ) +
  cowplot::theme_minimal_vgrid(16) +
  theme(
    axis.title.y = element_blank(),
    legend.position = "none"
  ) +
  scale_fill_manual(
    name = NULL,
    values = c("#B0B0B0D0", "#D55E00D0")
  ) +
  xlab("number of emperors")
```


Assassination
Natural Causes
Execution
Suicide
Died in Battle
Unknown
Captivity
25
21
8
5
5
3
1
0
5
10
15
20
25
number of emperors

Your Turn 1


Wife
Usurper
Unknown
Senate
Praetorian Guard
Own Army
Other Emperor
Opposing Army
Lightning
Heart Failure
Fire
Disease
Court Officials
Aneurism
2
1
5
3
7
5
18
6
1
1
1
16
1
1
0
5
10
15
number of emperors

Your Turn 1

Read in the emperors data (no need to change this part of the code)

Sort the data using arrange() **by the number of each type of killer**

Take a look at the data up until this point. Pick something you find interesting that you want to highlight. Then, in mutate()**, create a new variable that is** TRUE **if** killer **matches the category you want to highlight and** FALSE **otherwise**

Use the variable you just created in the fill **aesthetic of the ggplot call**

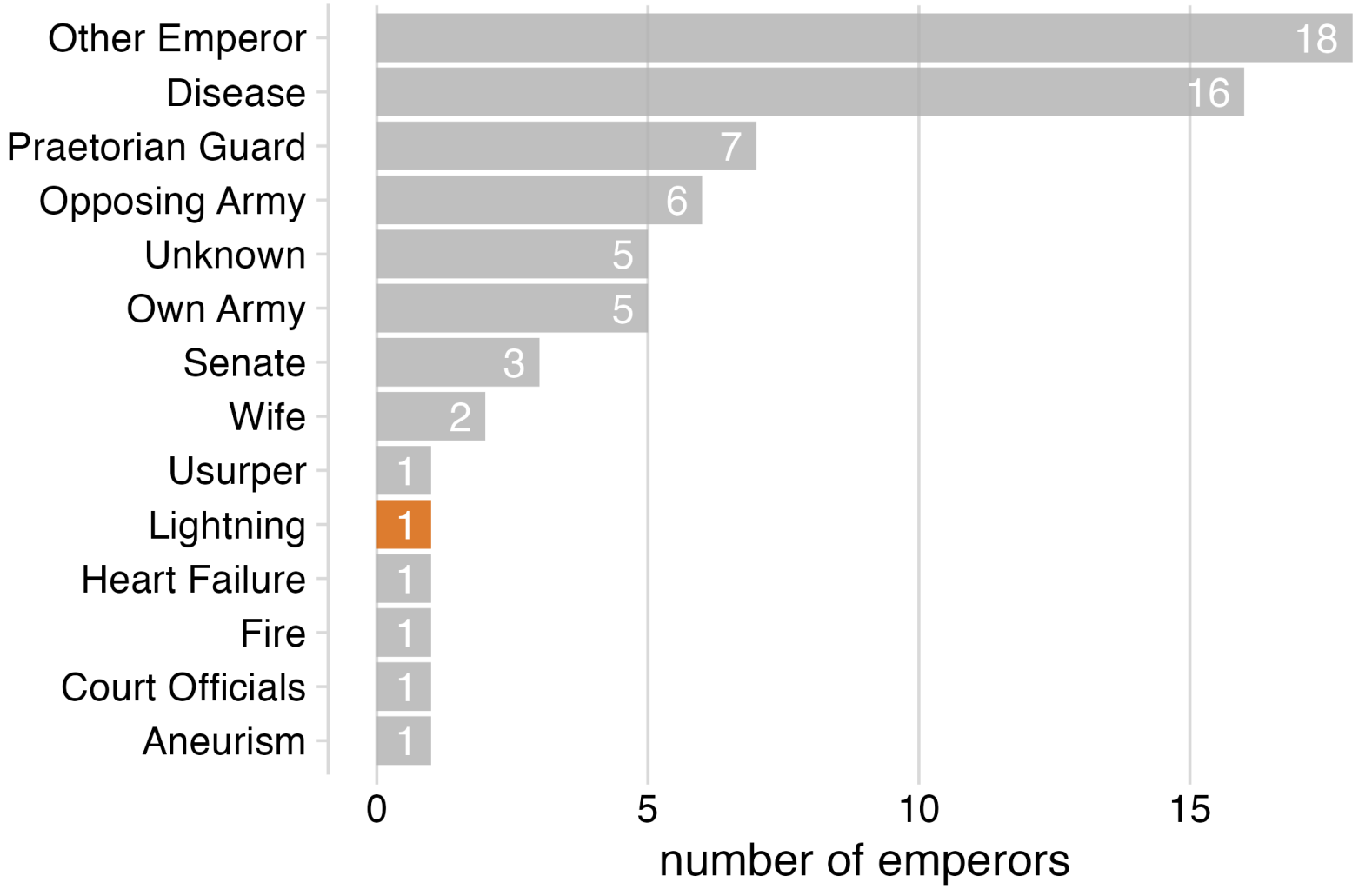
Finally, use scale_fill_manual() **to add the fill colors. Set** values **to** c("#B0B0B0D0", "#D55E00D0")**.**

```r
emperor_killers <- emperors %>%
  # group the least common killers to "other"
  mutate(killer = fct_lump(killer, 10)) %>%
  count(killer) %>%
  arrange(n)
```

```
emperor_killers
```

```
## # A tibble: 14 × 2
##    killer               n
##    <fct>            <int>
##  1 Aneurism             1
##  2 Court Officials      1
##  3 Fire                 1
##  4 Heart Failure        1
##  5 Lightning            1
##  6 Usurper              1
##  7 Wife                 2
##  8 Senate               3
##  9 Own Army             5
## 10 Unknown              5
## 11 Opposing Army        6
## 12 Praetorian Guard     7
## 13 Disease             16
## 14 Other Emperor       18
```

```r
lightning_plot <- emperor_killers %>%
  mutate(
    lightning = ifelse(killer == "Lightning", TRUE, FALSE),
    # use `fct_inorder()` to maintain the way we sorted the data
    killer = fct_inorder(killer)
  ) %>%
  ggplot(aes(x = n, y = killer, fill = lightning)) +
  geom_col() +
  geom_text(
    aes(label = n, x = n - .25),
    color = "white",
    size = 5,
    hjust = 1
  ) +
  cowplot::theme_minimal_vgrid(16) +
  theme(
    axis.title.y = element_blank(),
    legend.position = "none"
  ) +
  scale_fill_manual(values = c("#B0B0B0D0", "#D55E00D0")) +
  xlab("number of emperors")

lightning_plot
```


Other Emperor
Disease
Praetorian Guard
Opposing Army
Unknown
Own Army
Senate
Wife
Usurper
Lightning
Heart Failure
Fire
Court Officials
Aneurism
18
16
7
6
5
5
3
2
1
1
1
1
1
1
0
5
10
15
number of emperors

Use color to focus attention

1 2 3 4 5 6 7 8 9

Use color to focus attention

1 2 3 4 5 6 7 8 9

1 2 3 4 5 6 7 8 9

ggtext: Improved text rendering in ggplot2

```
library(ggtext)
```

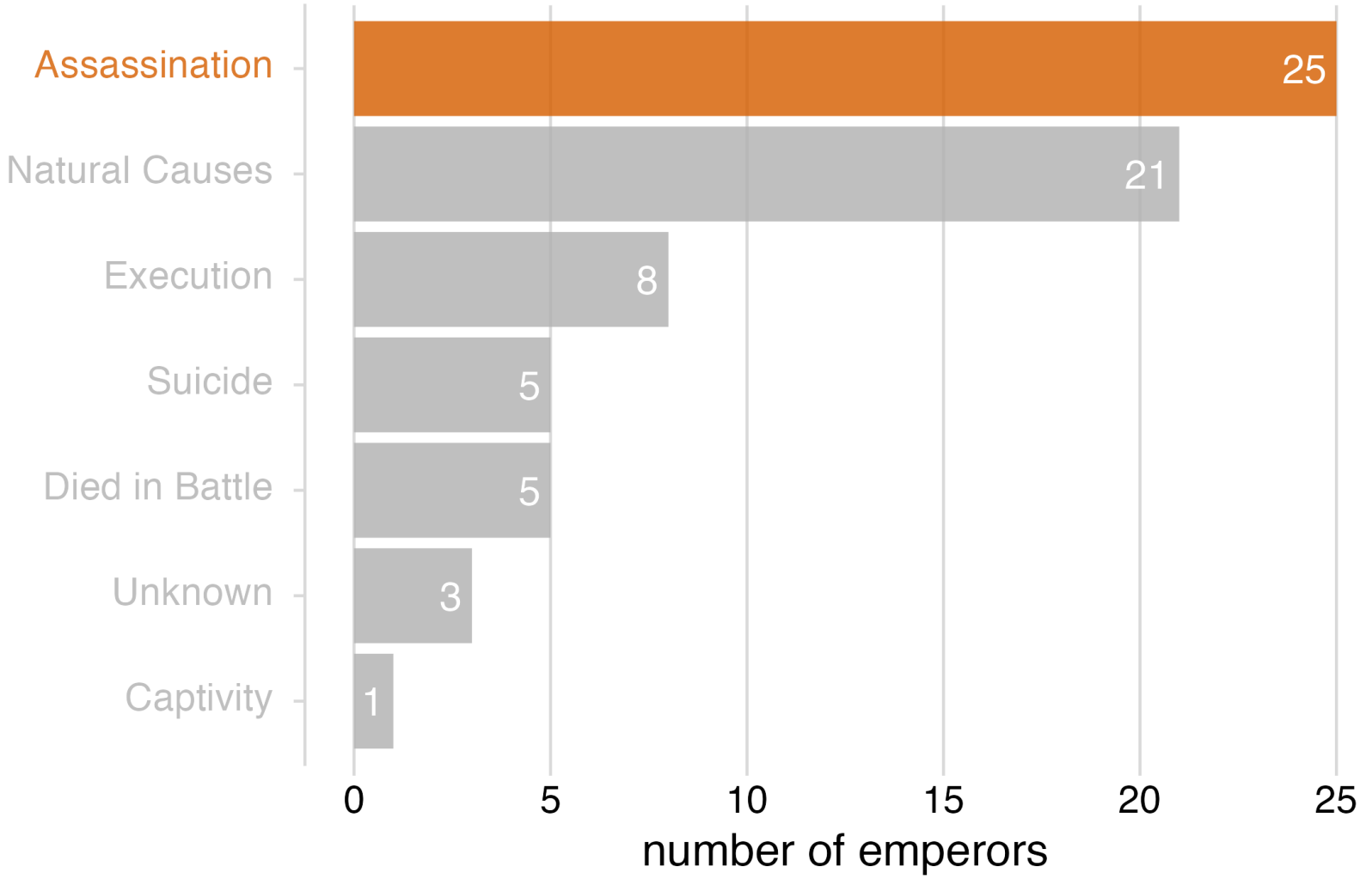
Use markdown in ggplot2 with element_markdown()

Allows styled text anywhere!

Can also insert images

```r
library(glue)
library(ggtext)

emperors_assassinated <- emperors_assassinated %>%
  mutate(
    cause = glue(
      "<span style='color:{ifelse( \\
      cause == 'Assassination', \\
      '#D55E00D0', \\
      '#B0B0B0D0')}'> \\
      {cause} \\
      </span>"
    ),
    cause = fct_inorder(cause)
  )
```

```r
emperors_assassinated %>%
  ggplot(aes(x = n, y = cause, fill = assassinated)) +
  geom_col() +
  geom_text(
    aes(label = n, x = n - .25),
    color = "white",
    size = 5,
    hjust = 1
  ) +
  cowplot::theme_minimal_vgrid(16) +
  theme(
    axis.text.y = element_markdown(),
    axis.title.y = element_blank(),
    legend.position = "none",
  ) +
  scale_fill_manual(
    name = NULL,
    values = c("#B0B0B0D0", "#D55E00D0")
  ) +
  xlab("number of emperors")
```


Assassination
Natural Causes
Execution
Suicide
Died in Battle
Unknown
Captivity
25
21
8
5
5
3
1
0
5
10
15
20
25
number of emperors

How do we reduce mental burden in our plots?

simplify aesthetics and highlight

design figures without legends

```
library(gapminder)
gapminder
```

```
## # A tibble: 1,704 × 6
##    country     continent  year lifeExp      pop gdpPercap
##    <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
##  1 Afghanistan Asia       1952    28.8  8425333      779.
##  2 Afghanistan Asia       1957    30.3  9240934      821.
##  3 Afghanistan Asia       1962    32.0 10267083      853.
##  4 Afghanistan Asia       1967    34.0 11537966      836.
##  5 Afghanistan Asia       1972    36.1 13079460      740.
##  6 Afghanistan Asia       1977    38.4 14880372      786.
##  7 Afghanistan Asia       1982    39.9 12881816      978.
##  8 Afghanistan Asia       1987    40.8 13867957      852.
##  9 Afghanistan Asia       1992    41.7 16317921      649.
## 10 Afghanistan Asia       1997    41.8 22227415      635.
## # … with 1,694 more rows
```

```r
gapminder %>%
  filter(year == 2007) %>%
  ggplot(aes(log(gdpPercap), lifeExp)) +
  geom_point(
    aes(color = country),
    size = 3.5,
    alpha = .9
  ) +
  theme_minimal(14) +
  theme(panel.grid.minor = element_blank()) +
  labs(
    x = "log(GDP per capita)",
    y = "life expectancy"
  )
```


an Republic
n. Rep.
.
e
ublic
Dominican Republic
Ecuador
Egypt
El Salvador
Equatorial Guinea
Eritrea
Ethiopia
Finland
France
Gabon
Gambia
Germany
Ghana
Greece
Guatemala
Guinea
Guinea-Bissau
Haiti
Honduras
Hong Kong, China
Hungary
Iceland
India
Indonesia
Iran
Iraq
Ireland
Israel
Italy
Jamaica
Japan
Jordan
Kenya
Korea, Dem. Rep.
Korea, Rep.
Kuwait
Lebanon
Lesotho
Liberia
Libya
Madagascar
Malawi
Malaysia
Mali
Mauritania
Mauritius
Mexico
Mongolia
Montenegro
Morocco
Mozambique
Myanmar
Namibia
Nepal
Netherlands
New Zealanc
Nicaragua
Niger
Nigeria
Norway
Oman
Pakistan
Panama
Paraguay
Peru
Philippines
Poland
Portugal
Puerto Rico
Reunion
Romania
Rwanda

Direct labeling

1. Label data directly (maybe a subset)
2. Remove the legend
3. Use proximity and similarity (e.g. same color)

```
ggplot(<data>, <mappings>) +
  <other geoms> +
  geom_text(
    data = <function or data>,
    aes(label = <label>)
  ) +
  theme(legend.position = "none")
```

```
ggplot(<data>, <mappings>) +
  <other geoms> +
  geom_text(
    data = <function or data>,
    aes(label = <label>)
  ) +
  theme(legend.position = "none")
```

label with a text geom or ggrepel

remove the legend

option 1:
pre-process data

```
ggplot(<data>, <mappings>) +
  <other geoms> +
  geom_text(
    data = <function or data>,
    aes(label = <label>)
  ) +
  theme(legend.position = "none")
```

option 2:
subset data

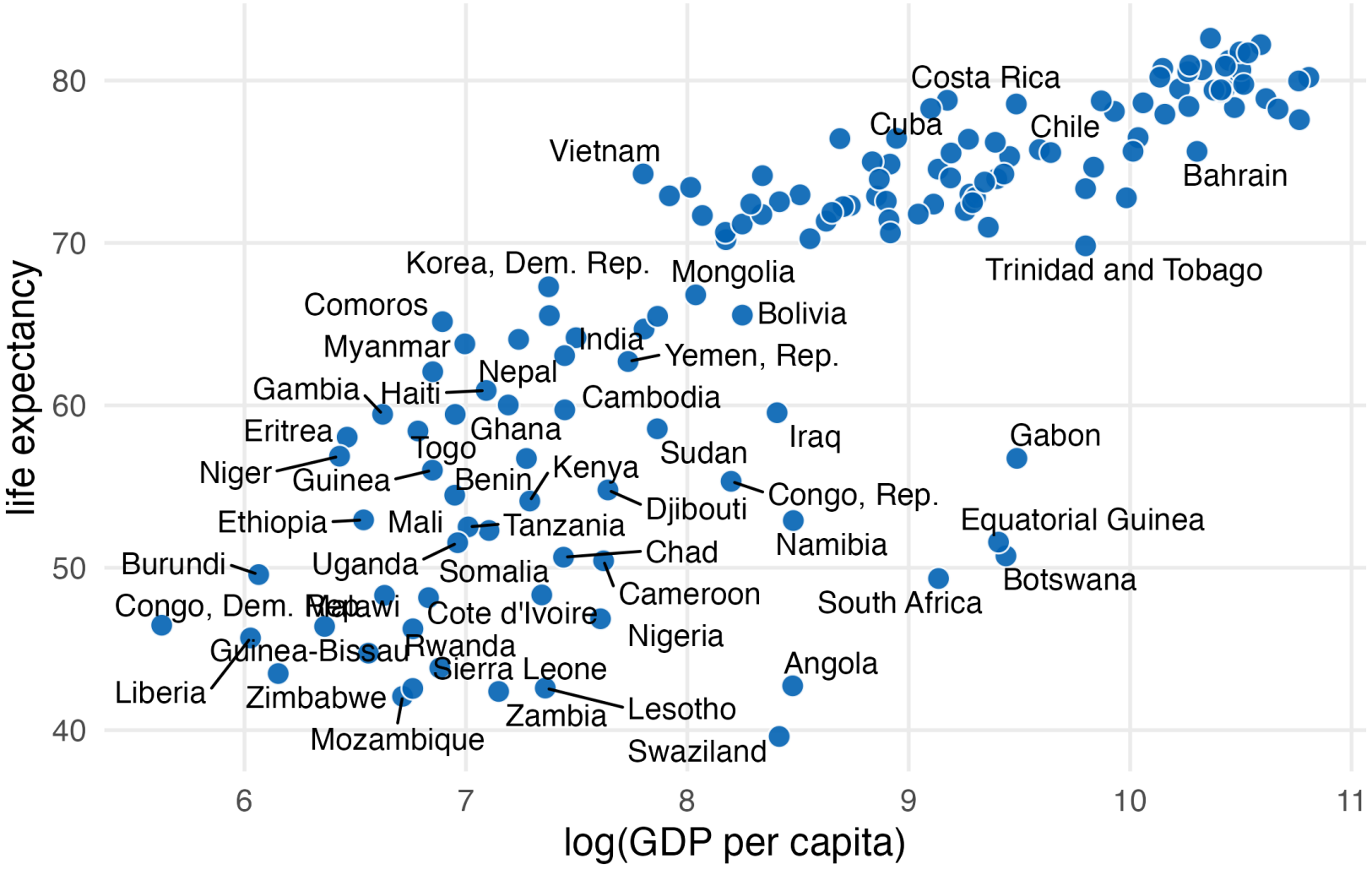
ggrepel: Repel overlapping text

```
library(ggrepel)
```

geom_text_repel()

geom_label_repel()

```r
gapminder %>%
  filter(year == 2007) %>%
  ggplot(aes(log(gdpPercap), lifeExp)) +
  geom_point(
    size = 3.5,
    alpha = .9,
    shape = 21,
    col = "white",
    fill = "#0162B2"
  ) +
  geom_text_repel(aes(label = country)) +
  theme_minimal(14) +
  theme(panel.grid.minor = element_blank()) +
  labs(
    x = "log(GDP per capita)",
    y = "life expectancy"
  )
```


life expectancy
log(GDP per capita)
80
70
60
50
40
6
7
8
9
10
11
Costa Rica
Cuba
Chile
Vietnam
Bahrain
Trinidad and Tobago
Korea, Dem. Rep.
Mongolia
Comoros
Bolivia
India
Myanmar
Yemen, Rep.
Nepal
Gambia
Haiti
Cambodia
Eritrea
Ghana
Iraq
Gabon
Togo
Sudan
Niger
Guinea
Benin
Kenya
Congo, Rep.
Djibouti
Ethiopia
Mali
Tanzania
Equatorial Guinea
Namibia
Burundi
Uganda
Somalia
Chad
Botswana
Cameroon
South Africa
Congo, Dem. Rep.
Malawi
Cote d'Ivoire
Nigeria
Guinea-Bissau
Rwanda
Angola
Sierra Leone
Liberia
Zimbabwe
Lesotho
Zambia
Mozambique
Swaziland

Your Turn 2

Use sample() **to select 10 random countries to plot (run the** set.seed() **line first if you want the same results)**

In the mutate() **call, check if** country **is one of the countries in** ten_countries**. If it's not, make the label an empty string ("""),**

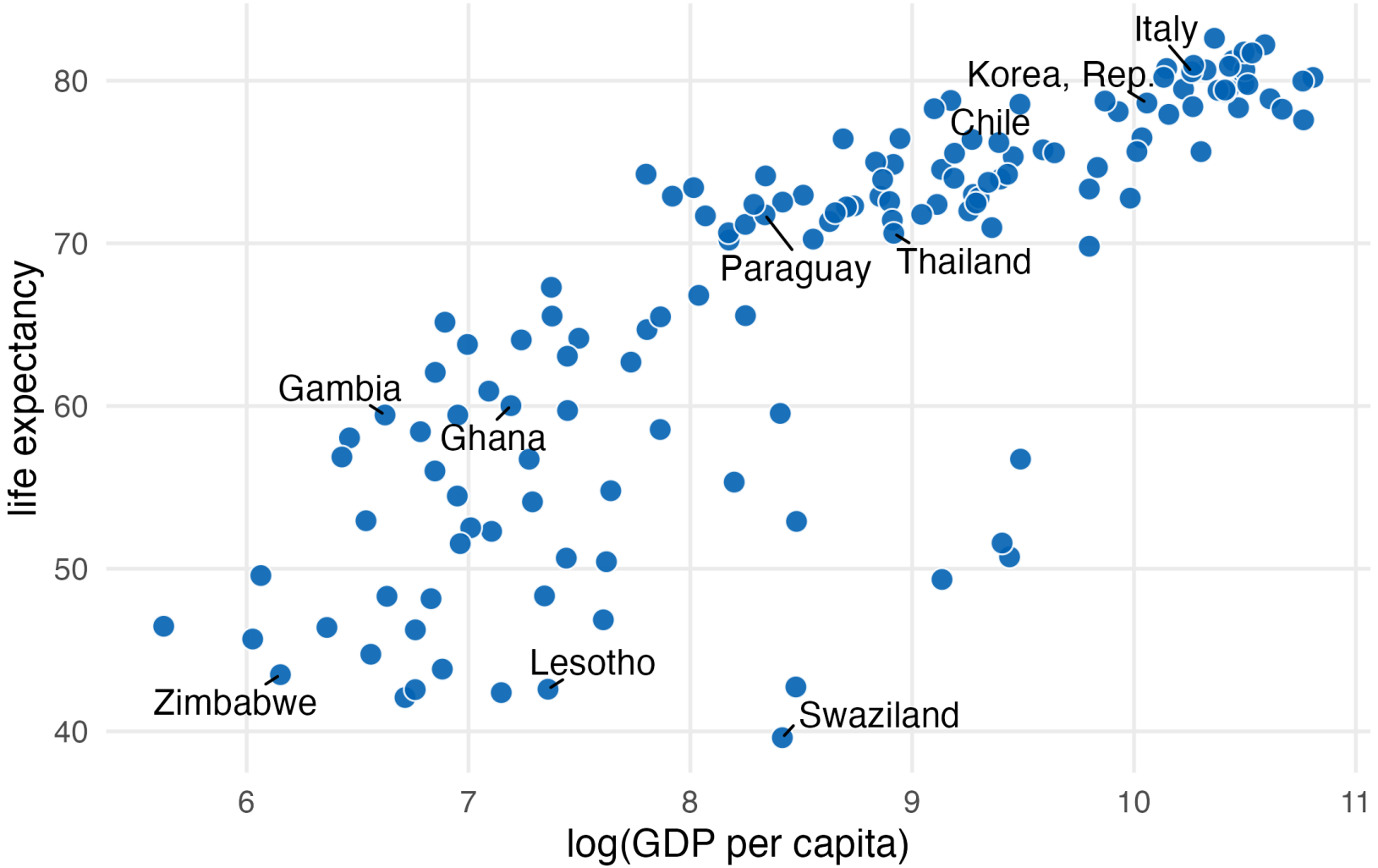
Add the text repel geom from ggrepel. Set the label **aesthetic using the variable just created in** mutate()

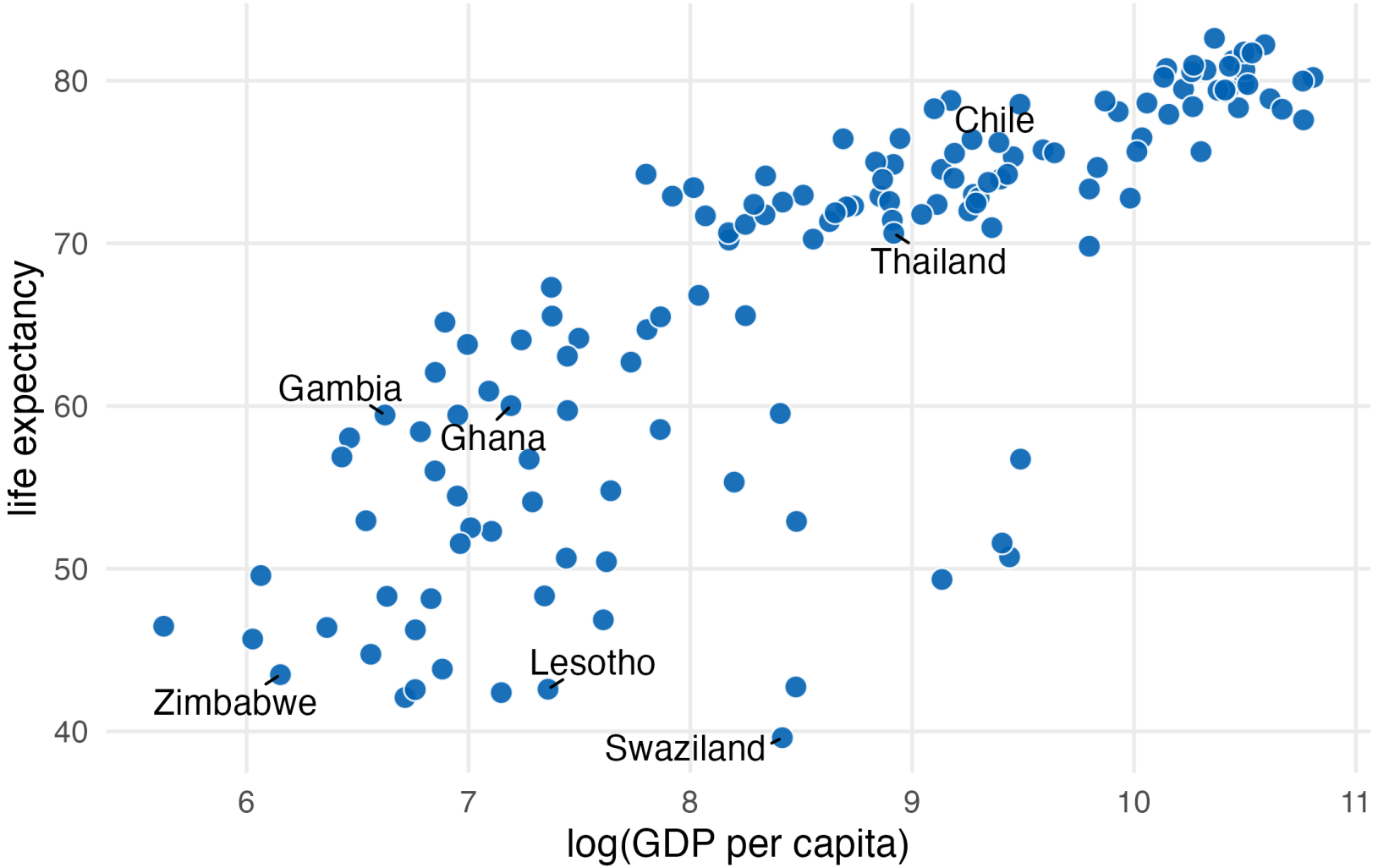
```r
library(gapminder)
library(ggrepel)

set.seed(42)

ten_countries <- gapminder$country %>%
  levels() %>%
  sample(10)

ten_countries
```

```
##  [1] "Ghana"       "Italy"       "Lesotho"     "Swaziland"   "Zimbabwe
##  [7] "Gambia"      "Chile"       "Korea, Rep." "Paraguay"
```

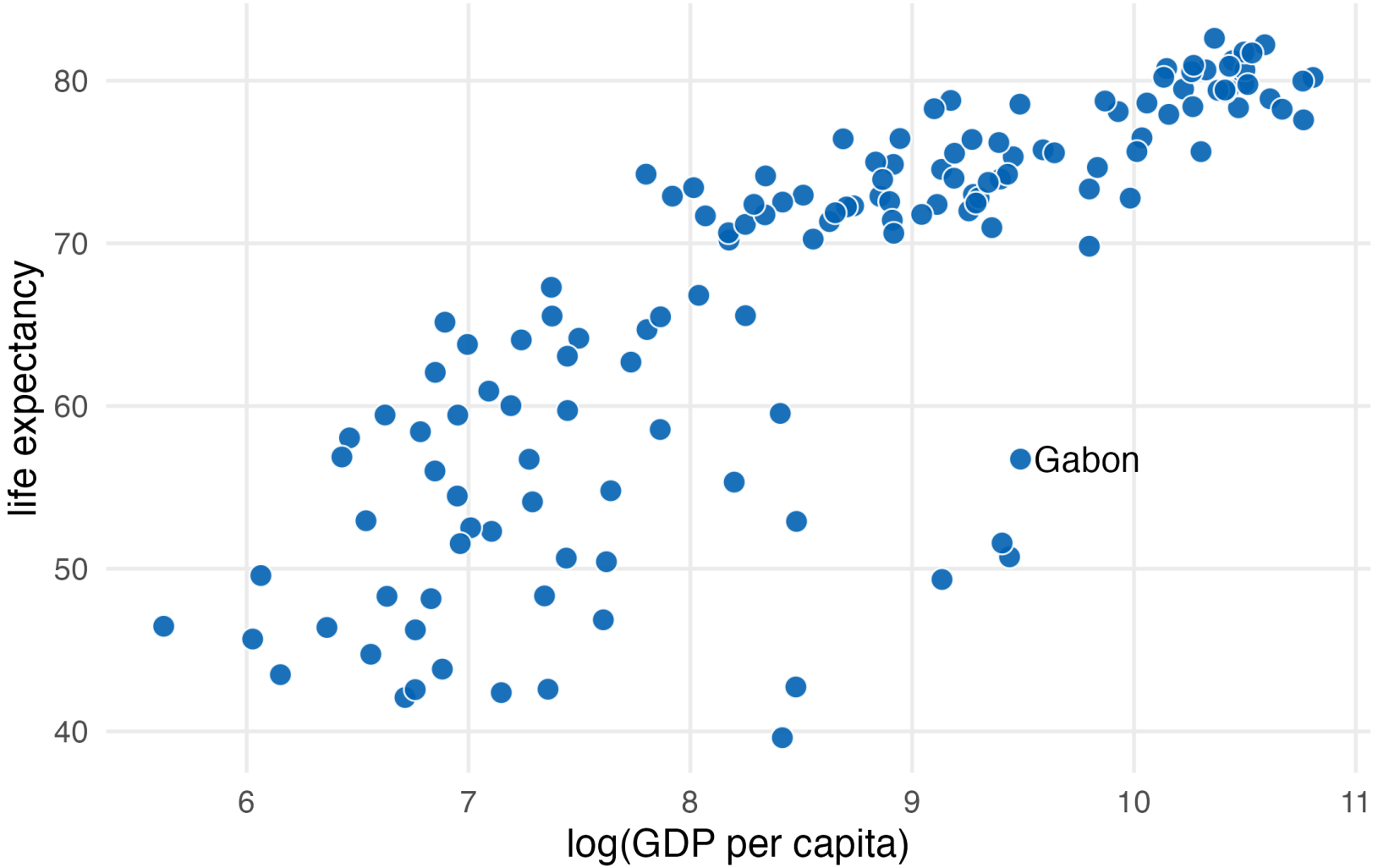
```
p1 <- gapminder %>%
  filter(year == 2007) %>%
  mutate(
    label = ifelse(
      country %in% ten_countries,
      as.character(country),
      ""
    )
  ) %>%
  ggplot(aes(log(gdpPercap), lifeExp)) +
  geom_point(
    size = 3.5,
    alpha = .9,
    shape = 21,
    col = "white",
    fill = "#0162B2"
  )
```

```r
scatter_plot <- p1 +
  geom_text_repel(
    aes(label = label),
    size = 4.5,
    max.overlaps = Inf,
    box.padding = .3,
    force = 1,
    min.segment.length = 0
  ) +
  theme_minimal(14) +
  theme(
    legend.position = "none",
    panel.grid.minor = element_blank()
  ) +
  labs(
    x = "log(GDP per capita)",
    y = "life expectancy"
  )

scatter_plot
```


Italy
Korea, Rep.
Chile
Paraguay
Thailand
Gambia
Ghana
Lesotho
Zimbabwe
Swaziland
life expectancy
80
70
60
50
40
6
7
8
9
10
11
log(GDP per capita)


80
70
60
50
40
life expectancy
Chile
Thailand
Gambia
Ghana
Lesotho
Zimbabwe
Swaziland
6
7
8
9
10
11
log(GDP per capita)

```
p1 +
  geom_text(
    data = function(x) filter(x, country == "Gabon"),
    aes(label = country),
    size = 4.5,
    hjust = 0,
    nudge_x = .06
  ) +
  theme_minimal(14) +
  theme(
    legend.position = "none",
    panel.grid.minor = element_blank()
  ) +
  labs(
    x = "log(GDP per capita)",
    y = "life expectancy"
  )
```


80
70
60
50
40
life expectancy
6
7
8
9
10
11
log(GDP per capita)
Gabon

How do we reduce mental burden in our plots?

simplify aesthetics and highlight

design figures without legends

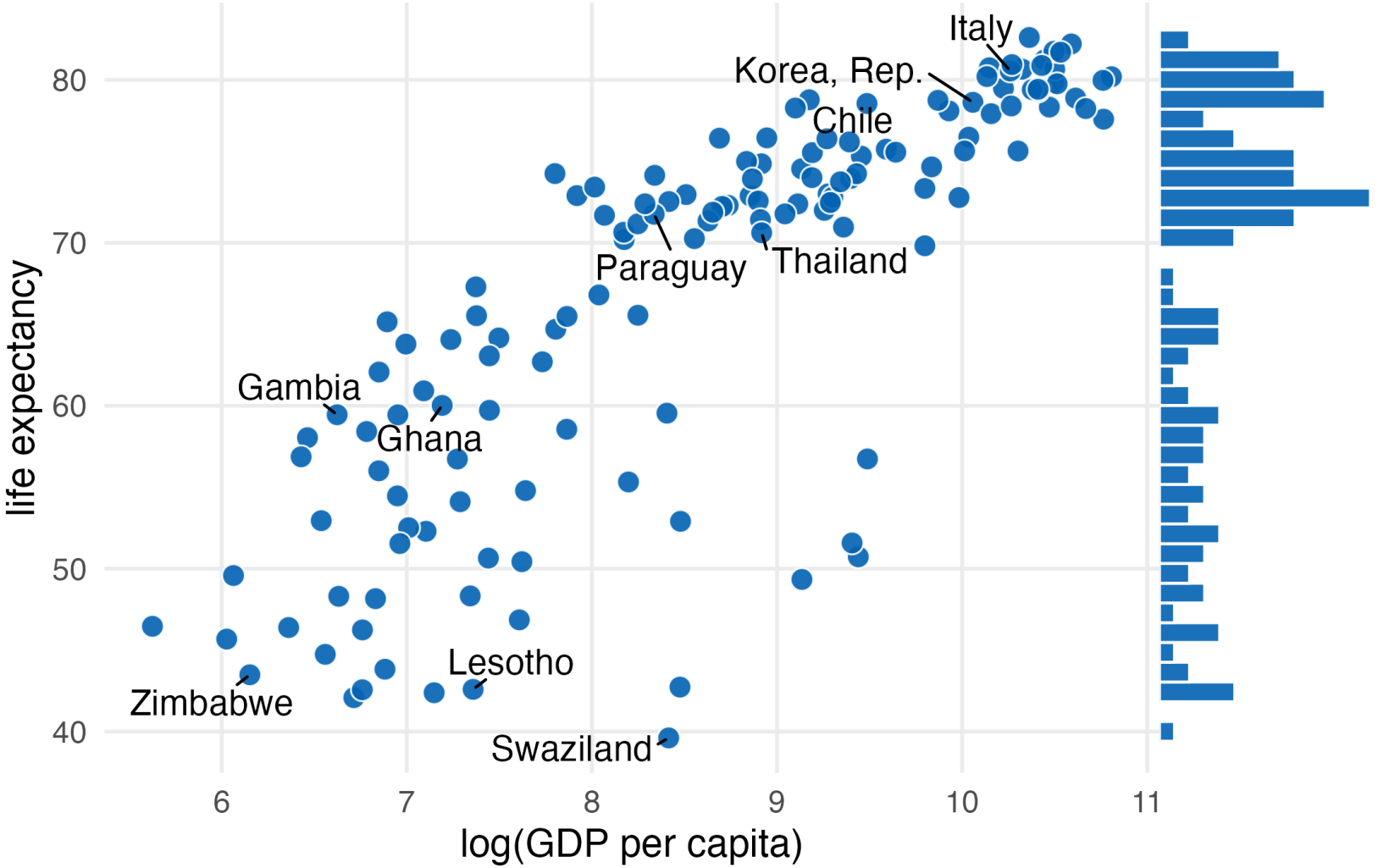
hack geoms and legends and even the plot itself

Inserting plot objects into the axis

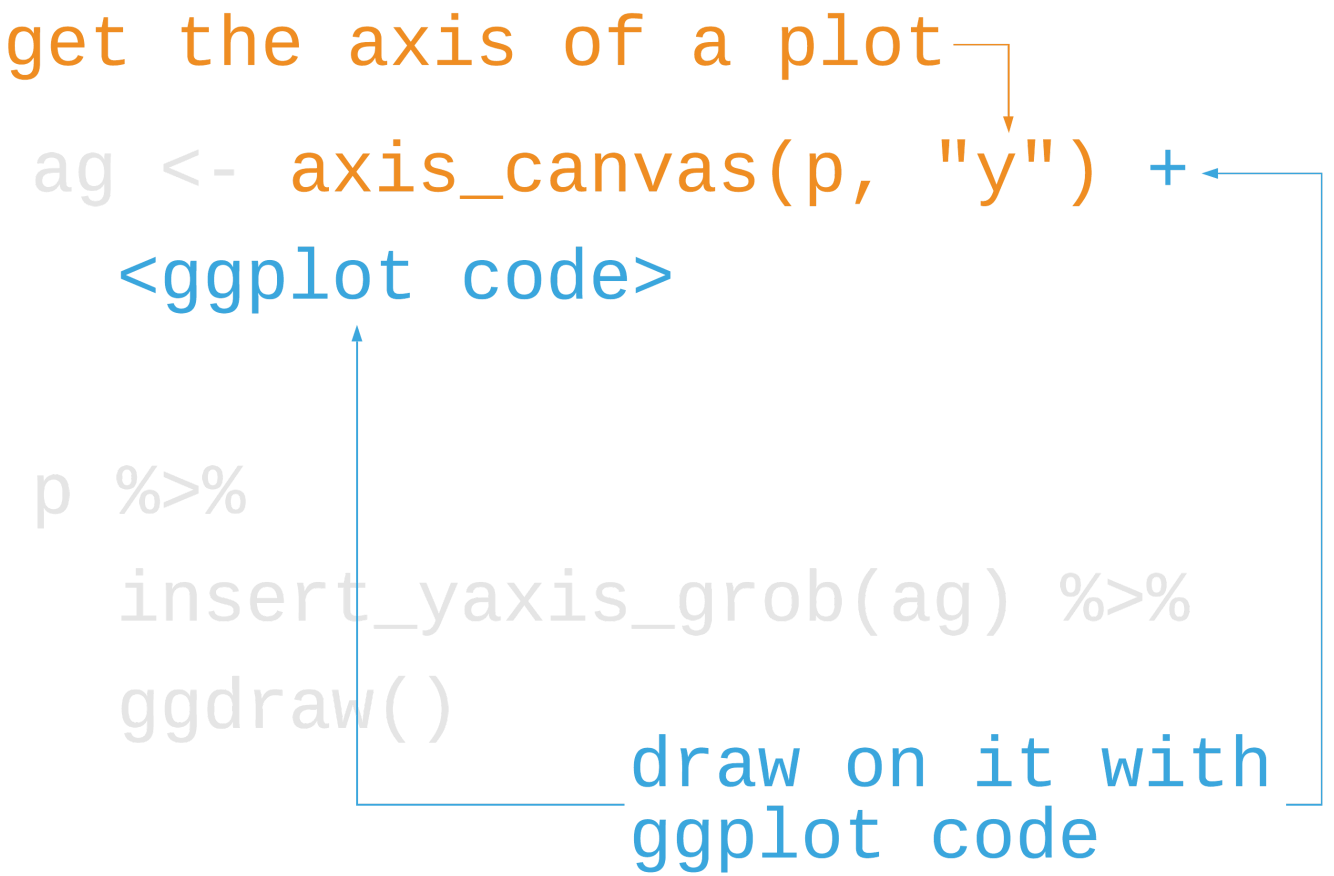
```
library(cowplot)
```

Inserting plot objects into the axis

```
library(cowplot)
marginal_histogram <- axis_canvas(scatter_plot, "y") +
  geom_histogram(
    data = gapminder %>% filter(year == 2007),
    bins = 40,
    aes(y = lifeExp),
    fill = "#0162B2E6",
    color = "white"
  )

scatter_plot %>%
  insert_yaxis_grob(marginal_histogram) %>%
  ggdraw()
```


Italy
Korea, Rep.
Chile
Paraguay
Thailand
Gambia
Ghana
Lesotho
Zimbabwe
Swaziland
life expectancy
80
70
60
50
40
6
7
8
9
10
11
log(GDP per capita)

```
ag <- axis_canvas(p, "y") +
  <ggplot code>

p %>%
  insert_yaxis_grob(ag) %>%
  ggdraw()
```


get the axis of a plot
ag <- axis_canvas(p, "y") +
<ggplot code>
p %>%
insert_yaxis_grob(ag) %>%
ggdraw()
draw on it with
ggplot code

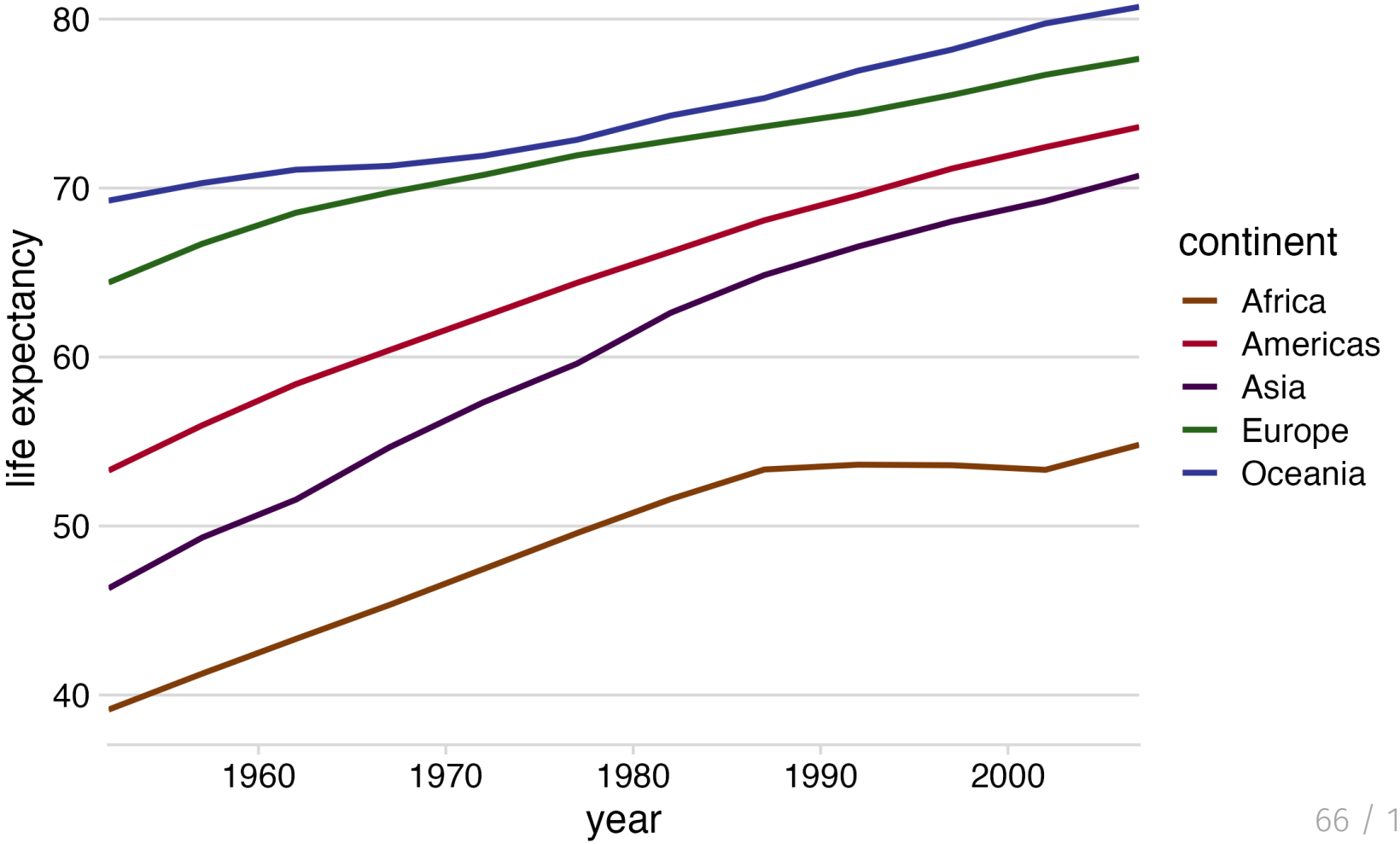
```
ag <- axis_canvas(p, "y") +
  <ggplot code>
p %>%
  insert_yaxis_grob(ag) %>%
  ggdraw()
```

put the axis drawing into the axis of the original plot

```
ag <- axis_canvas(p, "y") +
  <ggplot code>

p %>%
  insert_yaxis_grob(ag) %>%
  ggdraw()
```

draw the custom plot

Your Turn 3


80
70
60
50
40
life expectancy
1960
1970
1980
1990
2000
year
continent
Africa
Americas
Asia
Europe
Oceania

Your Turn 3

Calculate the placement of the labels: in the summarize() **call, create a variable called** y **that is the maximum** lifeExp **value for every continent For the labels, we'll use the continent names, which will be retained automatically.**

Remove the legend from the line plot. There are several ways to do so in ggplot2. I like setting legend.position = "none" **in** theme()**.**

axis_canvas(line_plot, axis = "y") **creates a new ggplot2 canvas based on the y axis from** line_plot**. Add a text geom (using + as you normally would). In the text geom: set data to** direct_labels**; in** aes()**, set** y = y**,** label = continent**; Outside of** aes() **set** x **to** 0.05 **(to add a little buffer); Make the size of the text** 4.5**; Set the horizontal justification to** 0

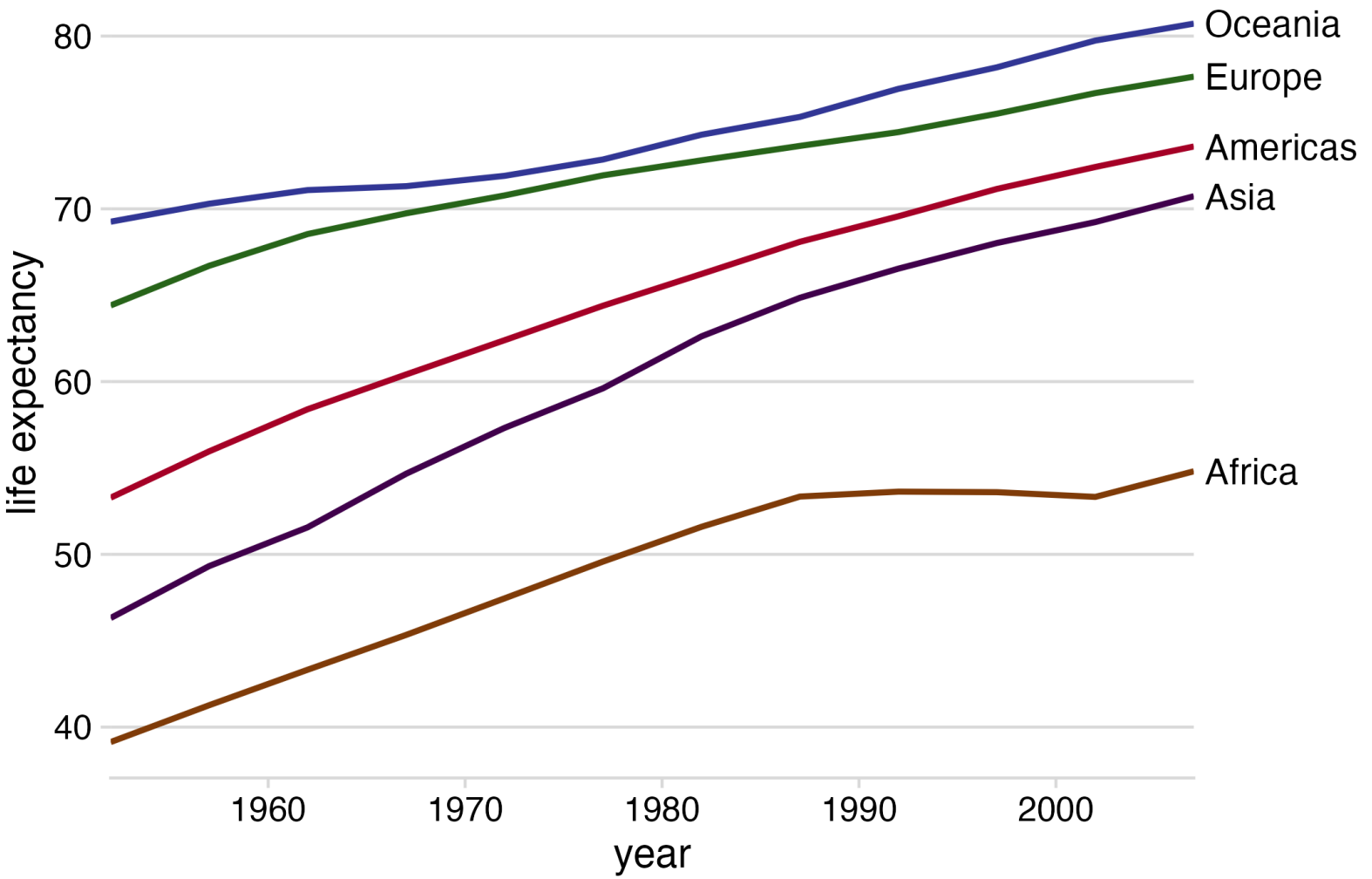
Use insert_yaxis_grob() **to take** lineplot **and insert** direct_labels_axis**.**

Draw the new plot with ggdraw()

```r
library(cowplot)

# get the mean life expectancy by continent and year
continent_data <- gapminder %>%
  group_by(continent, year) %>%
  summarise(lifeExp = mean(lifeExp))

direct_labels <- continent_data %>%
  group_by(continent) %>%
  summarize(y = max(lifeExp))
```

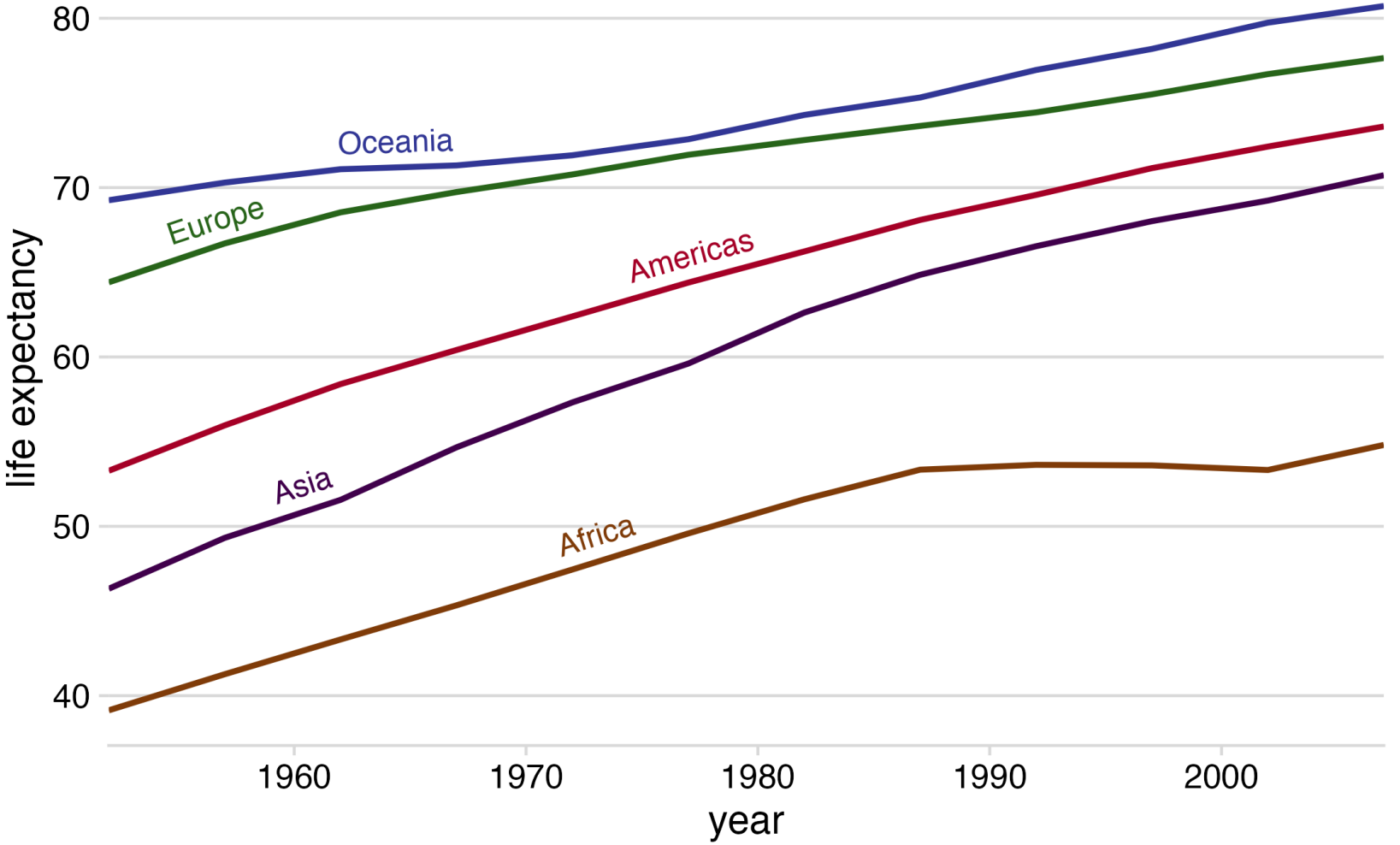
```r
line_plot <- continent_data %>%
  ggplot(aes(year, lifeExp, col = continent)) +
  geom_line(size = 1) +
  theme_minimal_hgrid() +
  theme(legend.position = "none") +
  scale_color_manual(values = continent_colors) +
  scale_x_continuous(expand = expansion()) +
  labs(y = "life expectancy")
```

```
direct_labels_axis <- axis_canvas(line_plot, axis = "y") +
  geom_text(
    data = direct_labels,
    aes(y = y, label = continent),
    x = .05,
    size = 4.5,
    hjust = 0
  )

p_direct_labels <- insert_yaxis_grob(line_plot, direct_labels_axis)

ggdraw(p_direct_labels)
```


80
70
60
50
40
life expectancy
1960
1970
1980
1990
2000
year
Oceania
Europe
Americas
Asia
Africa

geomtextpath

```
library(geomtextpath)
set.seed(787)
continent_data %>%
  ggplot(aes(year, lifeExp, col = continent)) +
  geom_textline(
    aes(label = continent),
    hjust = rnorm(60, .5, .3),
    vjust = -0.6,
    linewidth = 1
  ) +
  theme_minimal_hgrid() +
  scale_color_manual(values = continent_colors) +
  scale_x_continuous(expand = expansion()) +
  labs(y = "life expectancy") +
  theme(legend.position = "none")
```


80
70
60
50
40
life expectancy
Oceania
Europe
Americas
Asia
Africa
1960
1970
1980
1990
2000
year

How do we reduce mental burden in our plots?

simplify aesthetics and highlight

design figures without legends

hack geoms and legends and even the plot itself

use facets and data shadows to plot overlapping data

Using facets to declutter data

1. **Facets (or small multiples) are direct labeling for subsets**
2. **Put them into context with data shadows**

```
nyc_squirrels <- read_csv(file.path("data", "nyc_squirrels.csv"))
central_park <- sf::read_sf(file.path("data", "central_park"))
```

```
nyc_squirrels %>%
  drop_na(primary_fur_color) %>%
  ggplot() +
  geom_sf(data = central_park, color = "grey85") +
  geom_point(
    aes(x = long, y = lat, color = primary_fur_color),
    size = .8
  ) +
  cowplot::theme_map(16) +
  ggokabeito::scale_color_okabe_ito(name = "primary fur color")
```

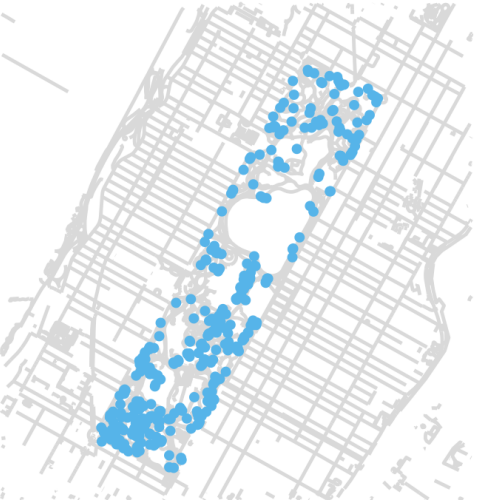
primary fur color

- Black
- Cinnamon
- Gray

```
nyc_squirrels %>%
  drop_na(primary_fur_color) %>%
  ggplot() +
  geom_sf(data = central_park, color = "grey85") +
  geom_point(
    aes(x = long, y = lat, color = primary_fur_color),
    size = .8
  ) +
  facet_wrap(vars(primary_fur_color)) +
  cowplot::theme_map(16) +
  theme(legend.position = "none") +
  ggokabeito::scale_color_okabe_ito()
```

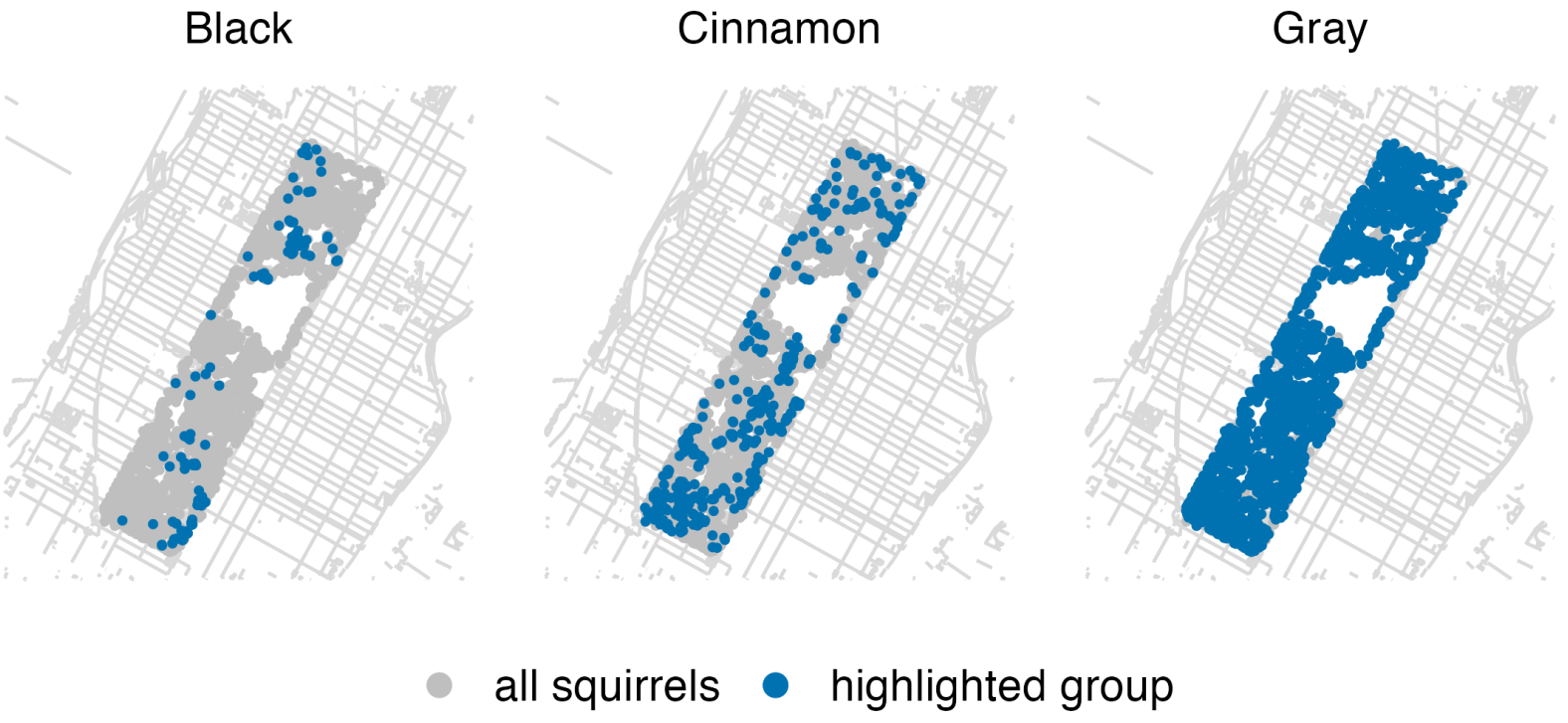
Black

Cinnamon



Gray

```r
label_colors <-
  c("all squirrels" = "grey75", "highlighted group" = "#0072B2")

nyc_squirrels %>%
  drop_na(primary_fur_color) %>%
  ggplot() +
  geom_sf(data = central_park, color = "grey85") +
  geom_point(
    data = function(x) select(x, -primary_fur_color),
    aes(x = long, y = lat, color = "all squirrels"),
    size = .8
  ) +
  geom_point(
    aes(x = long, y = lat, color = "highlighted group"),
    size = .8
  ) +
  cowplot::theme_map(16) +
  theme(
    legend.position = "bottom",
    legend.justification = "center"
  ) +
  facet_wrap(vars(primary_fur_color)) +
  scale_color_manual(name = NULL, values = label_colors) +
  guides(color = guide_legend(override.aes = list(size = 3)))
```


Black
Cinnamon
Gray
all squirrels
highlighted group

```
drop_facet <-
  function(x) select(x, -facet_var)

  ggplot(data) +
  geom_point(
    data = drop_facet,
    aes(color = "all data")
  ) +
  geom_point(aes(color = facet_var)) +
  facet_wrap(vars(facet_var))
```

```
drop_facet <-
  function(x) select(x, -facet_var)

  ggplot(data) +
  geom_point(
    data = drop_facet,
    aes(color = "all data")
  ) +
  geom_point(aes(color = facet_var)) +
  facet_wrap(vars(facet_var))
```

data shadow

highlighted geom

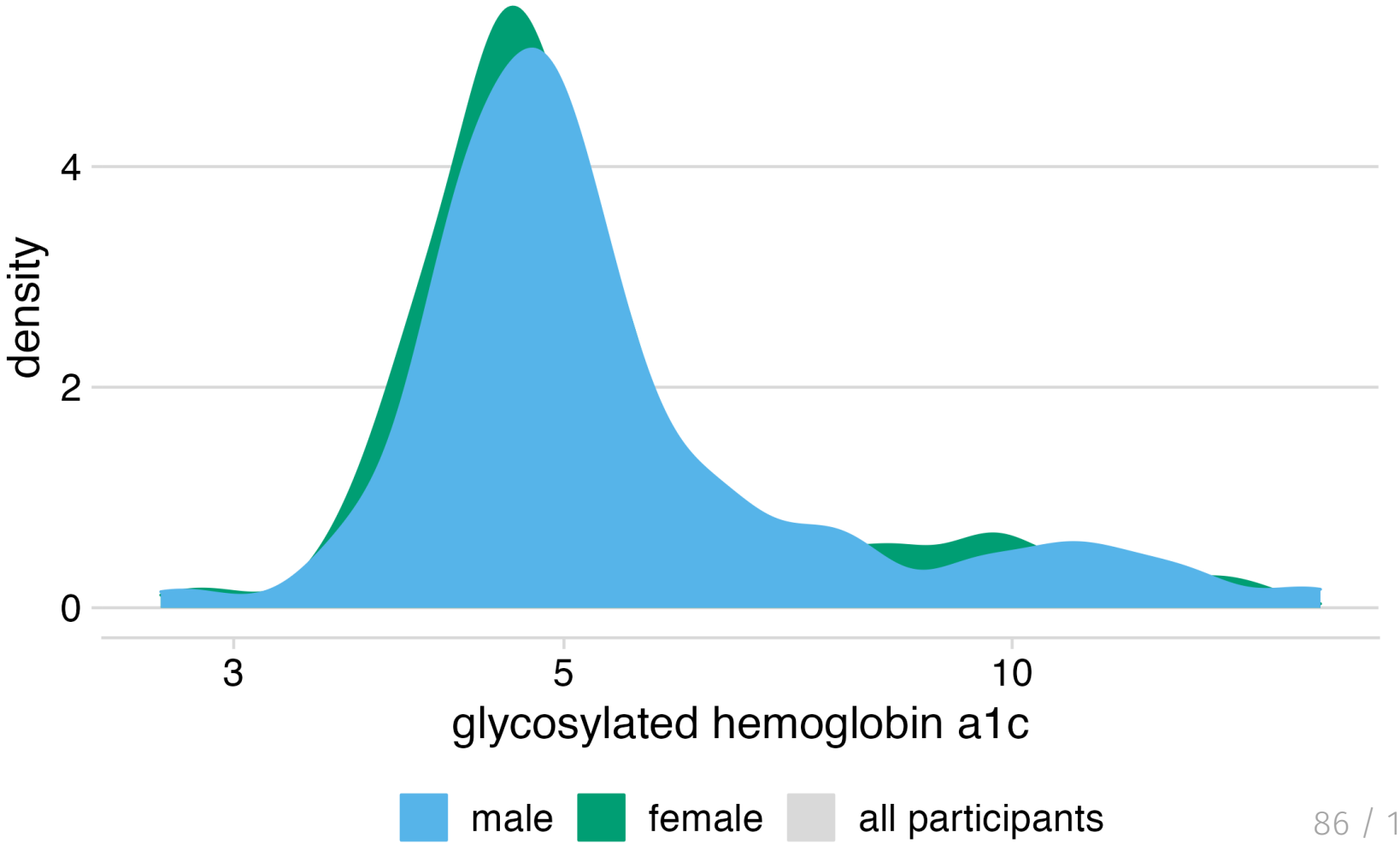
```
drop_facet <-
  function(x) select(x, -facet_var)

ggplot(data) +
geom_point(
  data = drop_facet,
  aes(color = "all data")
) +
geom_point(aes(color = facet_var)) +
facet_wrap(vars(facet_var))
```

remove the facet variable from the data shadow layer

```
drop_facet <-
  function(x) select(x, -facet_var)

  ggplot(data) +
  geom_point(
    data = drop_facet,
    aes(color = "all data")
  ) +
  geom_point(aes(color = facet_var)) +
  facet_wrap(vars(facet_var))
```

create a legend for the data shadow

Your Turn 4


density
4
2
0
3
5
10
glycosylated hemoglobin a1c
male
female
all participants

Your Turn 4

Run the code below and take a look at the resulting plot.

In the ggplot() **function, add** y = after_stat(count) **to** aes()

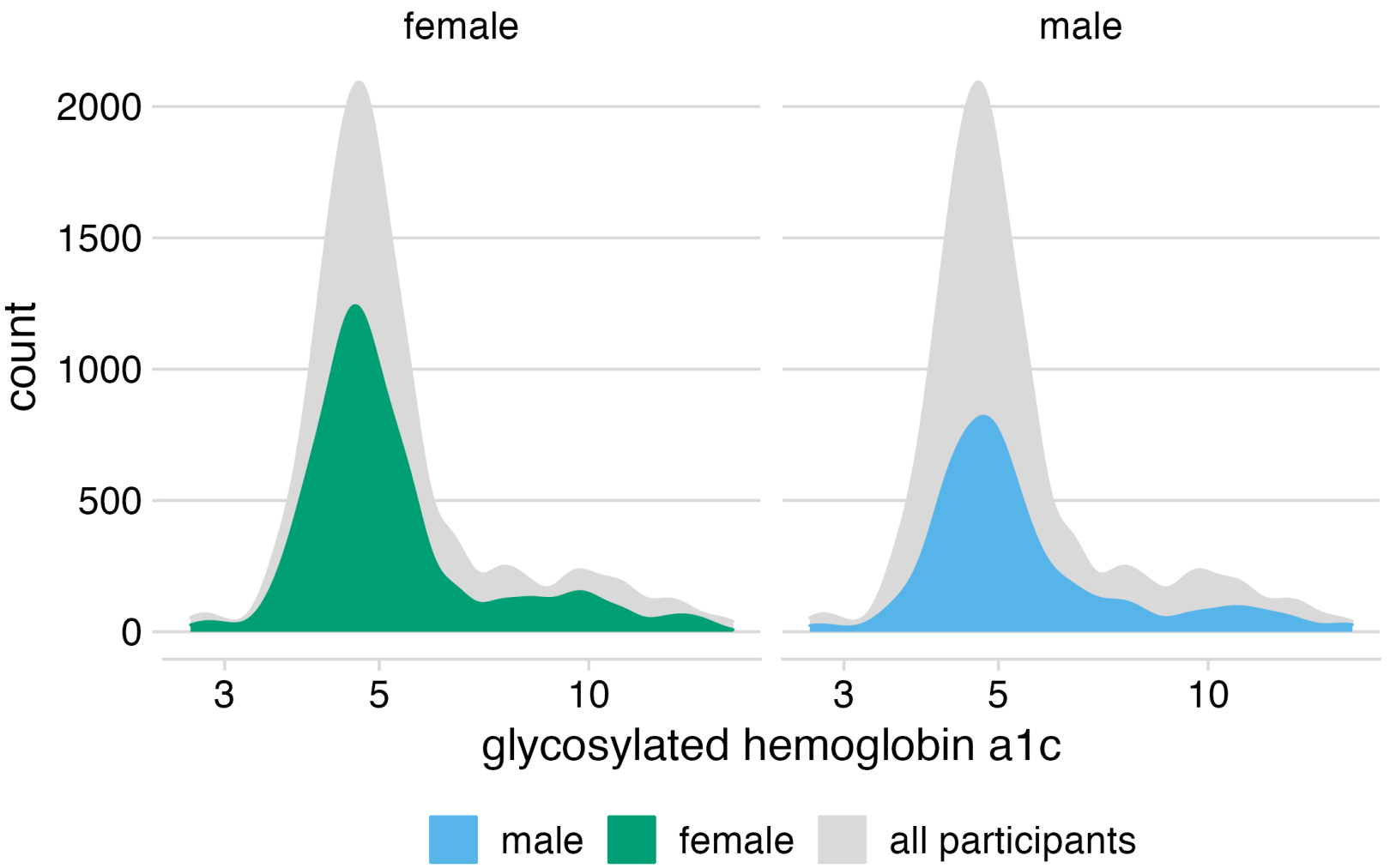
Add an additional geom_density() **to the plot. This should go before the existing** geom_density() **so that it shows up in the background.**

In the new geom_density()**, set the** data **argument to be a function. This function should take a data frame and remove gender (which we're about to facet on).**

Use aes() **to set** color **and** fill**. Both should equal "all participants", not** gender**.**

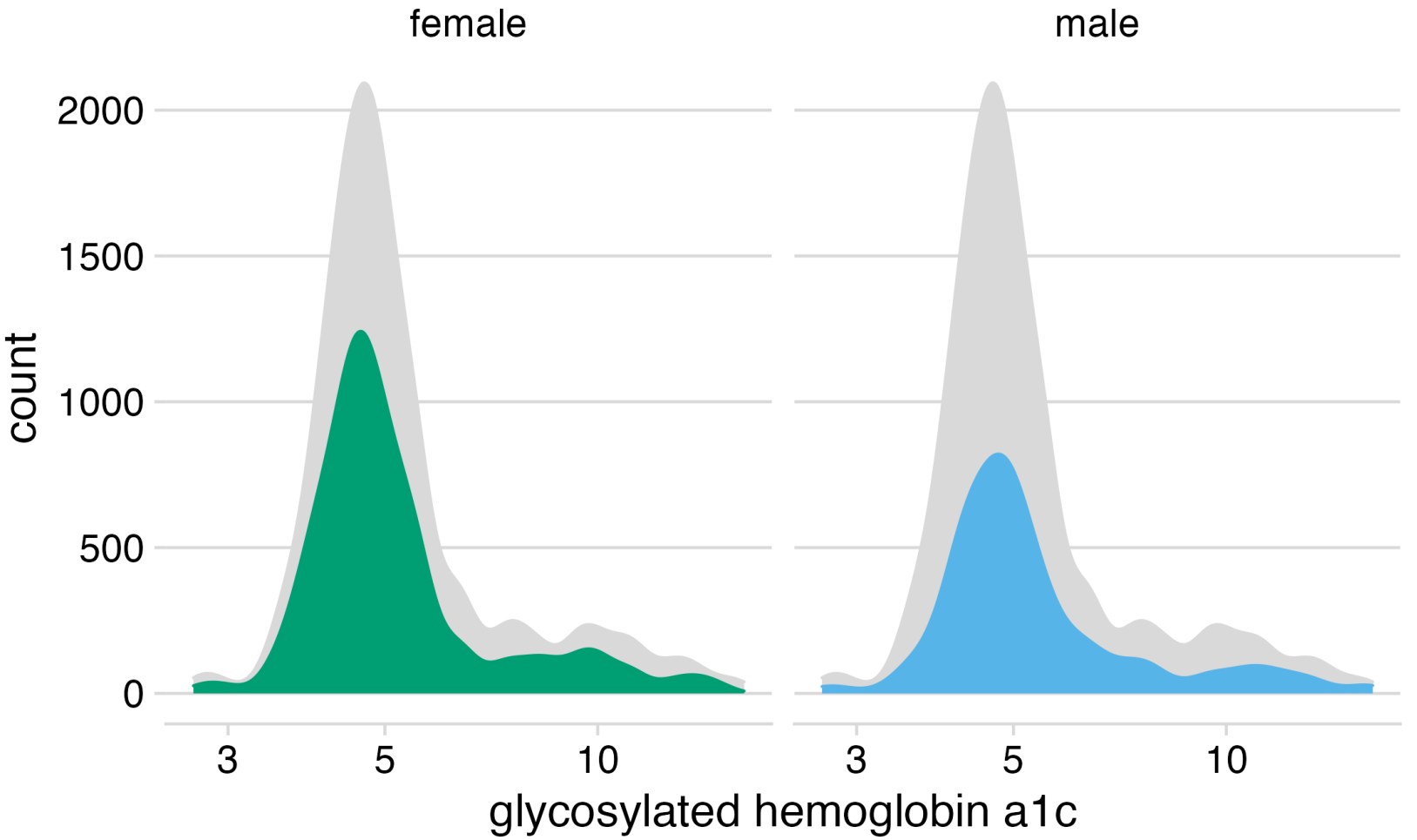
Use facet_wrap() **to facet the plot by** gender**.**

```
diabetes %>%
  drop_na(glyhb, gender) %>%
  ggplot(aes(glyhb, y = after_stat(count))) +
  geom_density(
    data = function(x) select(x, -gender),
    aes(fill = "all participants", color = "all participants")
  ) +
  geom_density(aes(fill = gender, color = gender)) +
  facet_wrap(vars(gender)) +
  scale_x_log10(name = "glycosylated hemoglobin a1c") +
  scale_color_manual(name = NULL, values = density_colors) +
  scale_fill_manual(name = NULL, values = density_colors) +
  theme_minimal_hgrid(16) +
  theme(legend.position = "bottom", legend.justification = "center")
```


female
male
2000
1500
1000
500
0
count
3
5
10
3
5
10
glycosylated hemoglobin a1c
male
female
all participants

```
title <- glue(
  "Among <b style='color:{density_colors[3]}'>\\
 all participants</b>, there were more \\
 <b style='color:{density_colors[2]}'>females</b>\\
 than <b style='color:{density_colors[1]}'>\\
 males</b>"
)

previous_plot +
  theme(
    legend.position = "none",
    plot.title.position = "plot",
    plot.title = element_textbox_simple(size = 14)
  ) +
  ggtitle(title)
```

Among all participants, there were more females than males



gghighlight: Highlight geoms

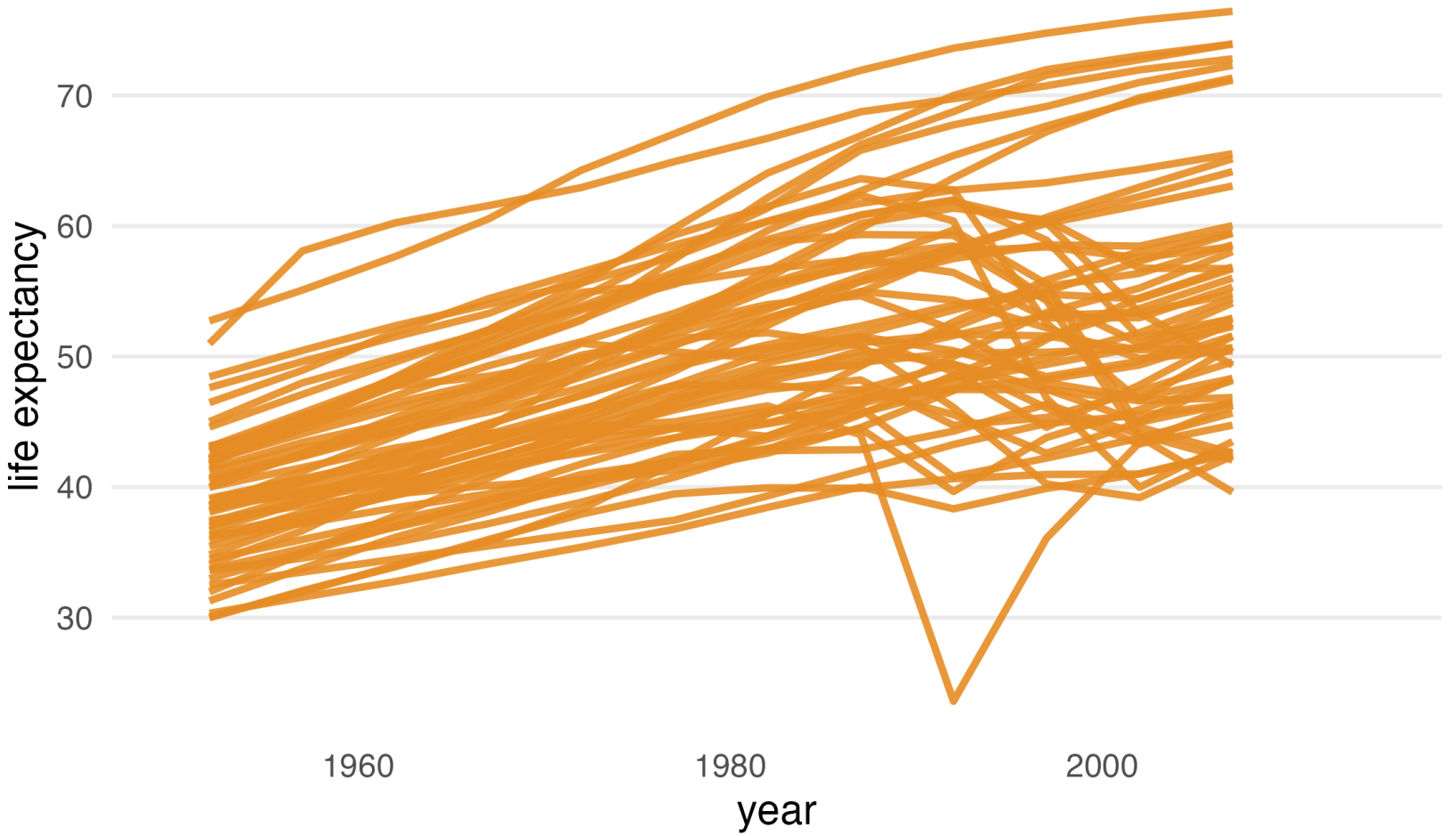
```
library(gghighlight)
```

gghighlight(predicate)

Works with points, lines, and histograms

Facets well

Your Turn 5



sorted by life expectancy in 1952

Your Turn 5

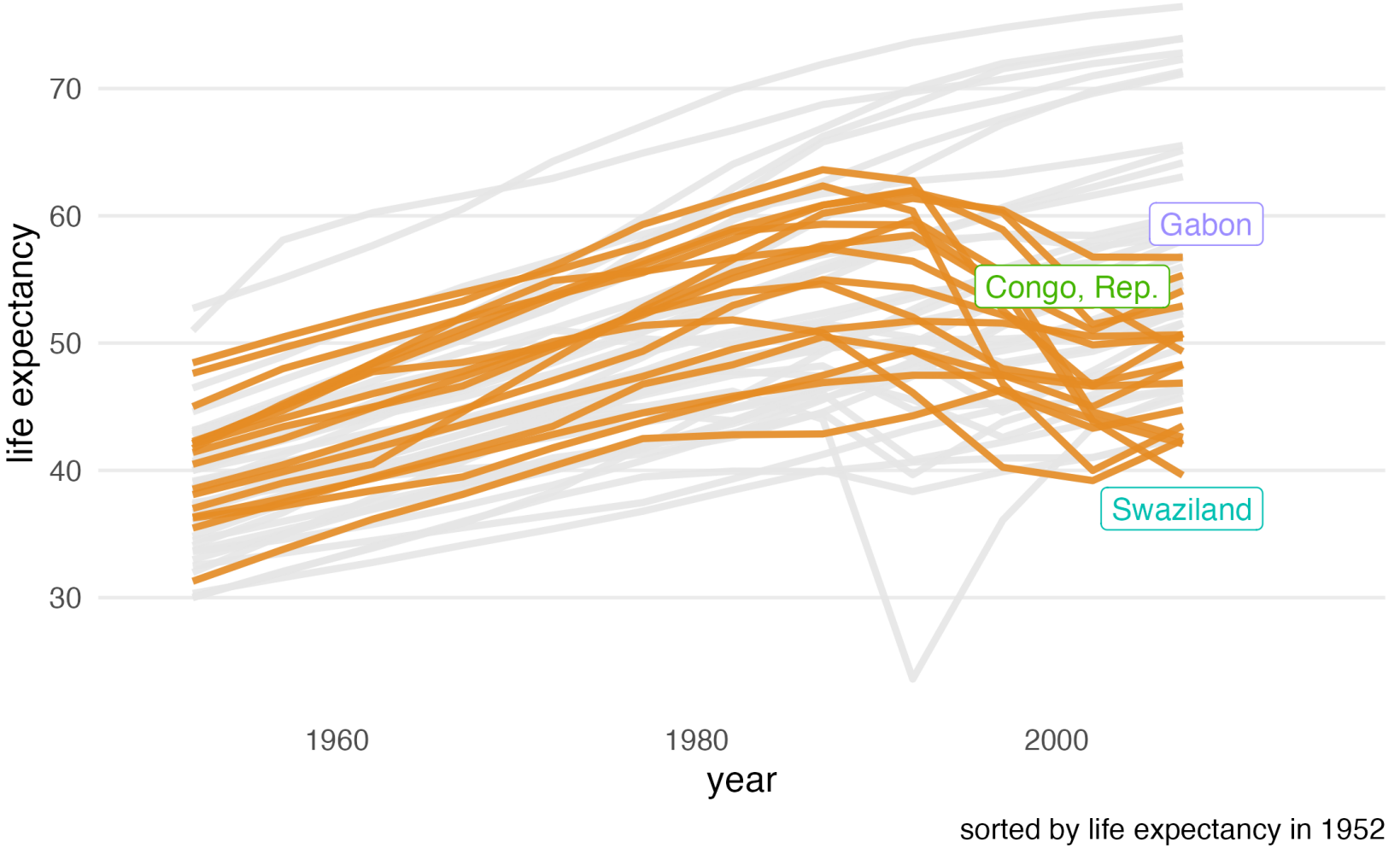
Take a look at the first few paragraphs of code. First, we're subsetting only African countries and sorting them by their life expectancy in 1952. Then, we're pivoting the data to be able to compare life expectancy in 1992 to 2007, creating a new variable, le_dropped**, that is** TRUE **if life expectancy was higher in 1992. Then, we join** le_dropped **back to the data so we can use it in** gghighlight()**. Run the code at each step.**

Remove the legend from the plot using the legend.position **argument in** theme()**. Take a look at the base plot.**

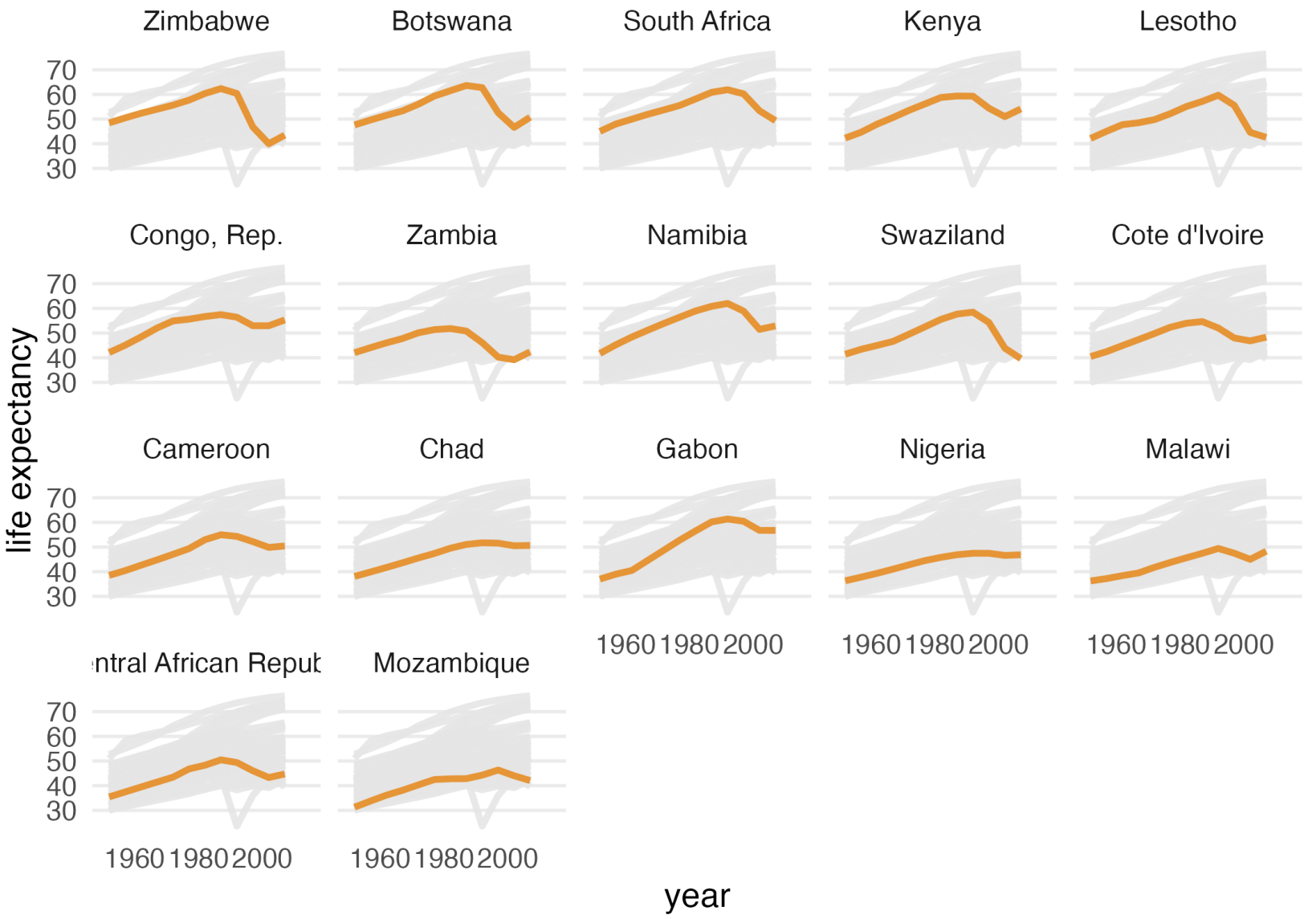
Use gghighlight() **to add direct labels to the plot. For the first argument, tell it which lines to highlight using** le_dropped**. Also add the arguments** use_group_by = FALSE **and** unhighlighted_params = list(color = "grey90")**.**

Add use_direct_label = FALSE **to** gghighlight() **and then facet the plot (using** facet_wrap()**) by country**

```
le_line_plot +
  gghighlight(
    le_dropped,
    use_group_by = FALSE,
    unhighlighted_params = list(color = "grey90")
  )
```


70
60
50
40
30
life expectancy
Gabon
Congo, Rep.
Swaziland
1960
1980
2000
year
sorted by life expectancy in 1952

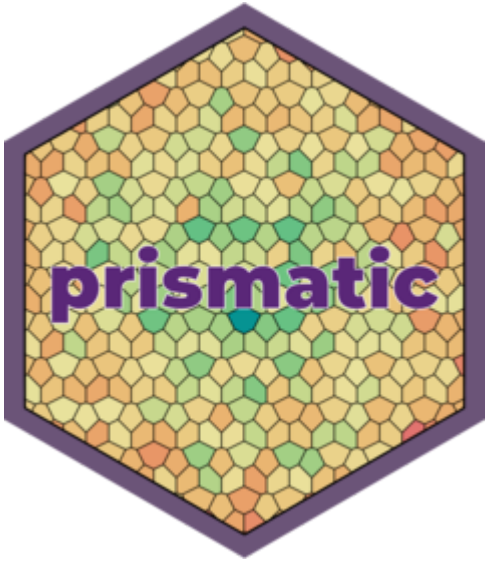
```
le_line_plot +
  gghighlight(
    le_dropped,
    use_group_by = FALSE,
    use_direct_label = FALSE,
    unhighlighted_params = list(color = "grey90")
  ) +
  facet_wrap(vars(country))
```


Zimbabwe
Botswana
South Africa
Kenya
Lesotho
Congo, Rep.
Zambia
Namibia
Swaziland
Cote d'Ivoire
Cameroon
Chad
Gabon
Nigeria
Malawi
ntral African Reput
Mozambique
life expectancy
70
60
50
40
30
1960 1980 2000
year
sorted by life expectancy in 1952

intermission: working with colors

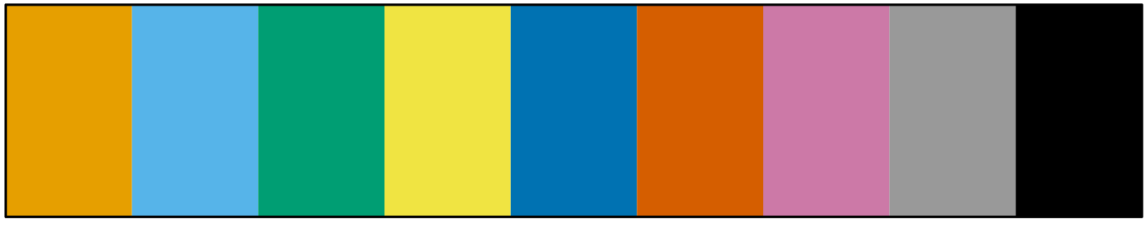
prismatic: manipulate colors in R

```
library(prismatic)
```



Visualize palettes

```
library(ggokabeito)
library(prismatic)
palette_okabe_ito() %>%
  color() %>%
  plot()
```

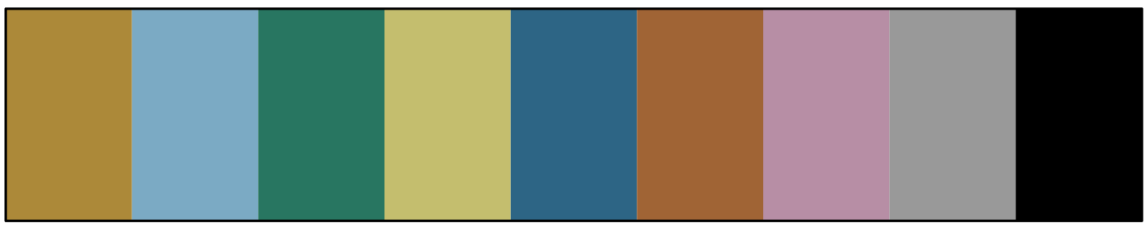


Darken and lighten colors

```
palette_okabe_ito() %>%
  clr_darken() %>%
  plot()
```

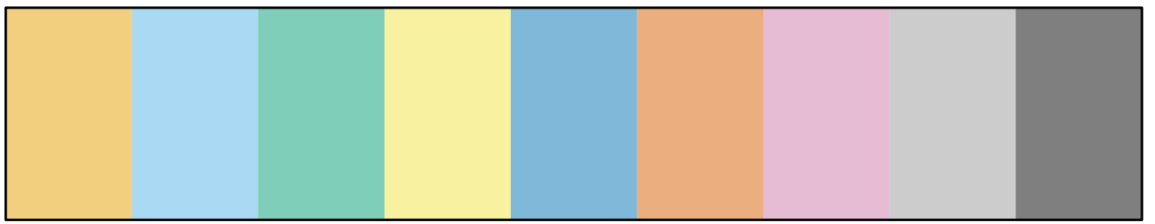
Saturate and desaturate colors

```
palette_okabe_ito() %>%
  clr_desaturate() %>%
  plot()
```



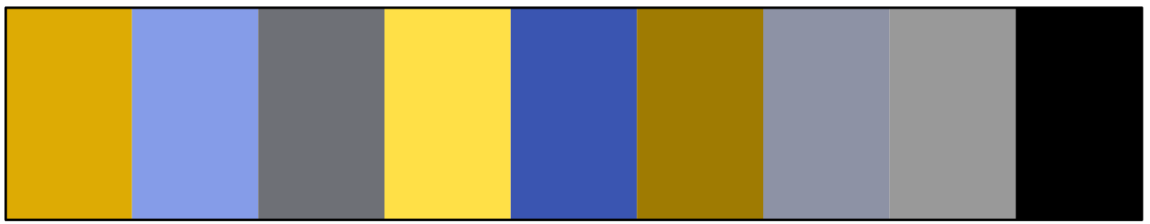
Set transparency

```
palette_okabe_ito() %>%
  clr_alpha(.5) %>%
  plot()
```



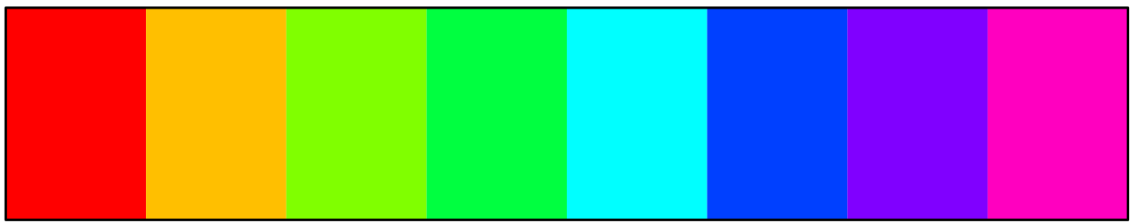
Simulate colorblindness

```
palette_okabe_ito() %>%
  clr_deutan() %>%
  plot()
```



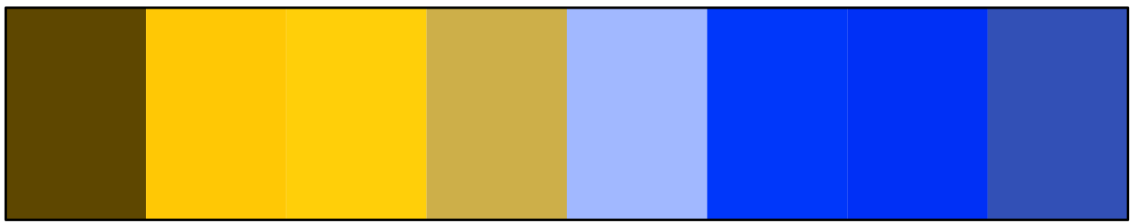
Simulate colorblindness

```
rainbow(8) %>%
  color() %>%
  plot()
```



Simulate colorblindness

```
rainbow(8) %>%
  clr_deutan() %>%
  plot()
```



act two: narrate and put in context

or: storytelling with data visualization

How do we augment plots to explain?

How do we augment plots to explain?

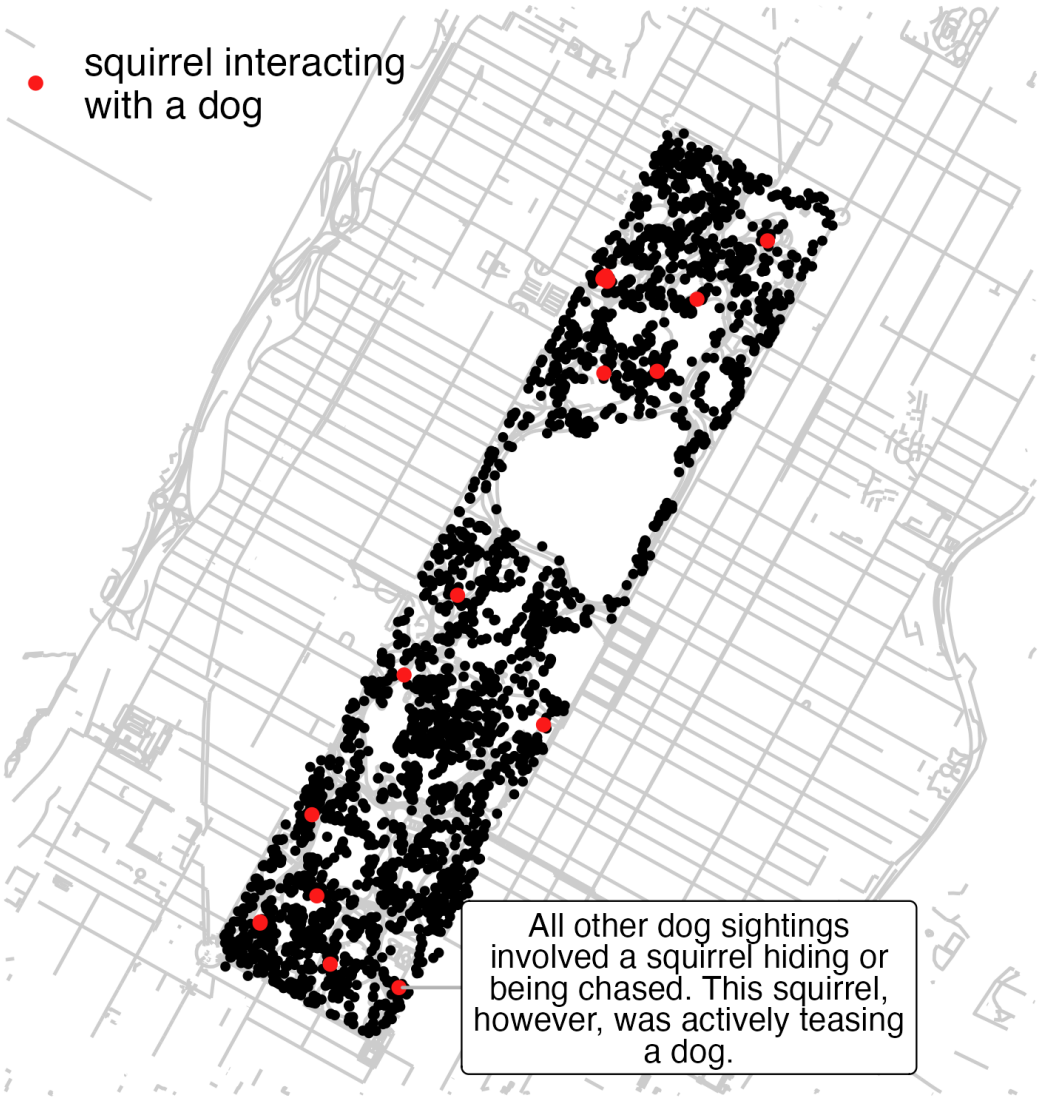
Annotate plots using text geoms and arrows

Squirrels and dogs

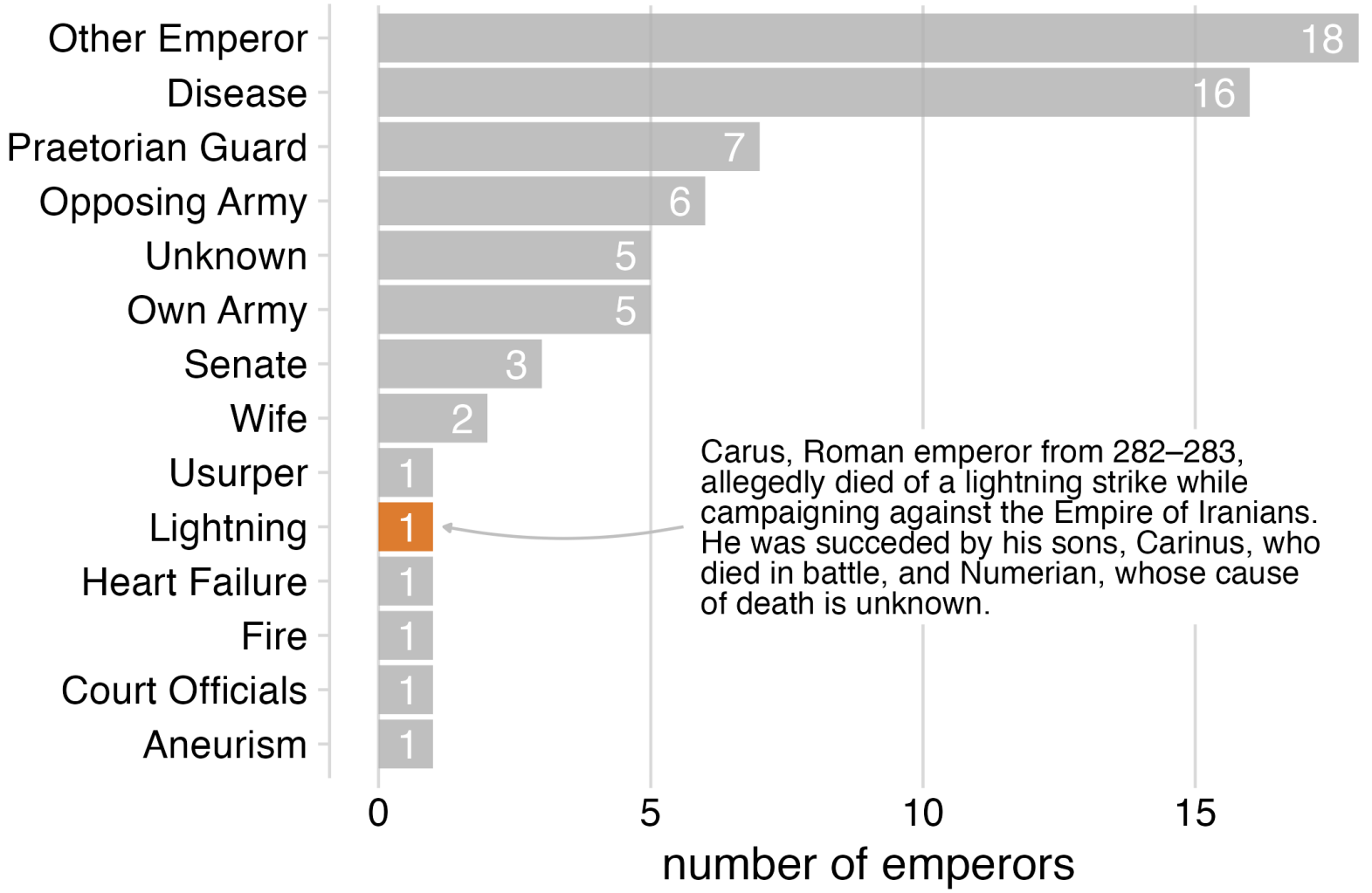
```
dog_sighting <- nyc_squirrels %>%
  mutate(dog = str_detect(other_activities, "dog")) %>%
  filter(dog)
```

```
lbl <- "All other dog sightings
involved a squirrel hiding or
being chased. This squirrel,
however, was actively teasing
a dog."

dog_plot <- nyc_squirrels %>%
  ggplot() +
  geom_sf(data = central_park, color = "grey80") +
  geom_point(aes(x = long, y = lat), size = .8) +
  geom_point(
    data = dog_sighting,
    aes(
      x = long,
      y = lat,
      color = "squirrel interacting\nwith a dog"
    ),
    size = 1.5
  )
```

```
dog_plot +
  ggrepel::geom_label_repel(
    data = filter(
      dog_sighting,
      str_detect(other_activities, "teasing")
    ),
    aes(x = long, y = lat, label = lbl),
    nudge_x = .015,
    size = 3.5,
    lineheight = .8,
    segment.color = "grey70"
  ) +
  cowplot::theme_map() +
  theme(legend.position = c(.05, .9)) +
  scale_color_manual(name = NULL, values = "#FB1919")
```

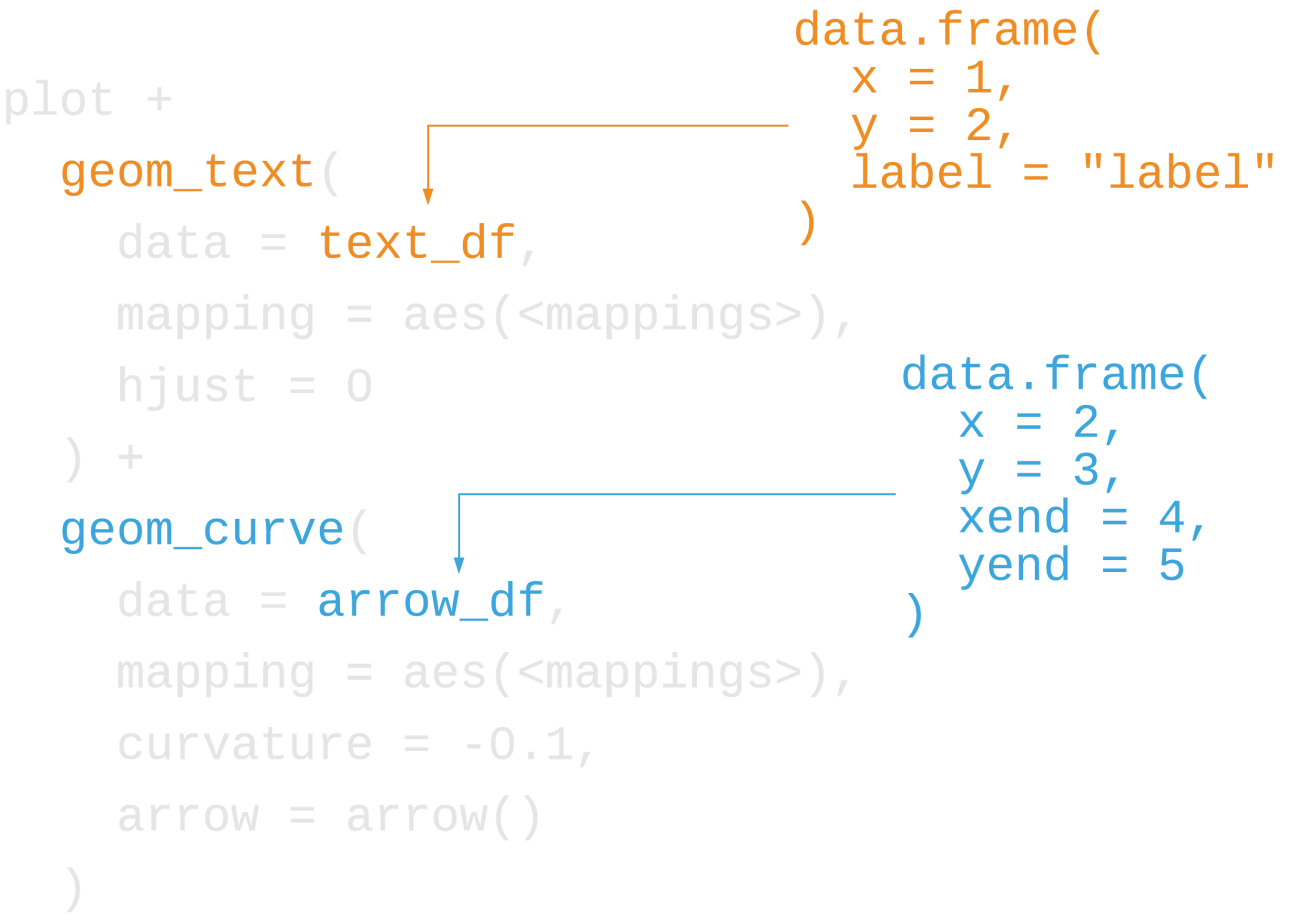

squirrel interacting with a dog
All other dog sightings involved a squirrel hiding or being chased. This squirrel, however, was actively teasing a dog.

```
label <- "Carus, Roman emperor from 282–283,
allegedly died of a lightning strike while
campaigning against the Empire of Iranians.
He was succeded by his sons, Carinus, who
died in battle, and Numerian, whose cause
of death is unknown."

lightning_plot +
  geom_label(
    data = data.frame(x = 5.8, y = 5, label = label),
    aes(x = x, y = y, label = label),
    hjust = 0,
    lineheight = .8,
    inherit.aes = FALSE,
    label.size = NA
  ) +
  geom_curve(
    data = data.frame(x = 5.6, y = 5, xend = 1.2, yend = 5),
    mapping = aes(x = x, y = y, xend = xend, yend = yend),
    colour = "grey75",
    size = 0.5,
    curvature = -0.1,
    arrow = arrow(length = unit(0.01, "npc"), type = "closed"),
    inherit.aes = FALSE
  )
```

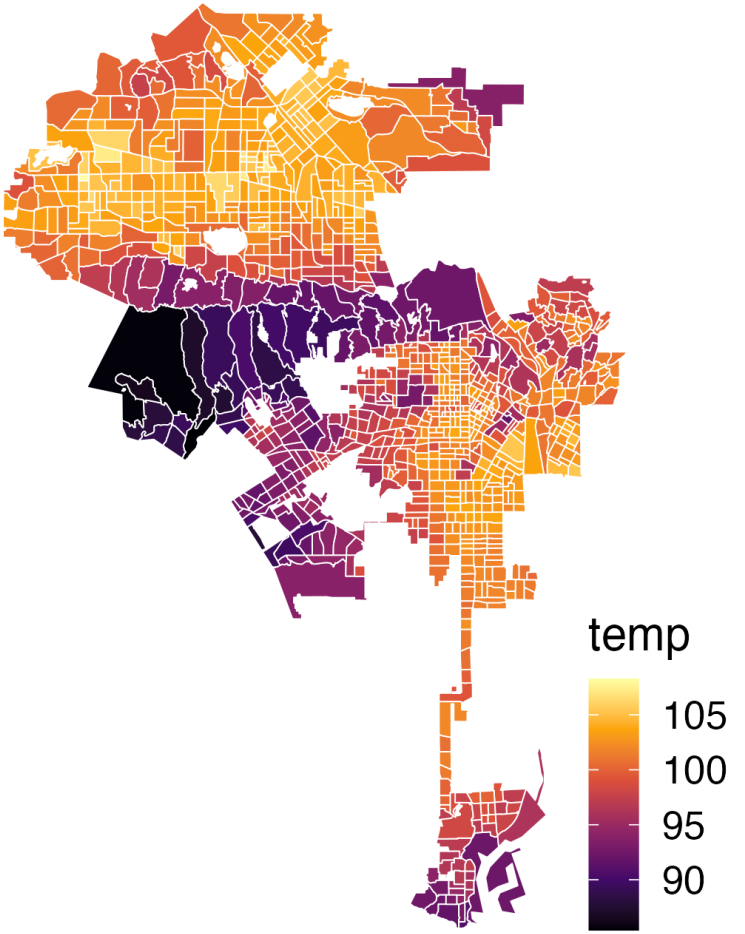

Other Emperor
Disease
Praetorian Guard
Opposing Army
Unknown
Own Army
Senate
Wife
Usurper
Lightning
Heart Failure
Fire
Court Officials
Aneurism
18
16
7
6
5
5
3
2
1
1
1
1
1
1
0
5
10
15
number of emperors
Carus, Roman emperor from 282–283, allegedly died of a lightning strike while campaigning against the Empire of Iranians. He was succeded by his sons, Carinus, who died in battle, and Numerian, whose cause of death is unknown.

We won't use it today, but the **ggannotate** package has an add-in to help place annotations with less trial and error

```
plot +
  geom_text(
    data = text_df,
    mapping = aes(<mappings>),
    hjust = 0
  ) +
  geom_curve(
    data = arrow_df,
    mapping = aes(<mappings>),
    curvature = -0.1,
    arrow = arrow()
  )
```


plot +
geom_text(
data = text_df,
mapping = aes(<mappings>),
hjust = 0
) +
geom_curve(
data = arrow_df,
mapping = aes(<mappings>),
curvature = -0.1,
arrow = arrow()
)
data.frame(
x = 1,
y = 2,
label = "label"
)
data.frame(
x = 2,
y = 3,
xend = 4,
yend = 5
)

Your Turn 6



Your Turn 6

Run the first code chunk and take a look at the map of surface heat in Los Angeles.

In the second code chunk, we need to create two new data frames to draw the annotations and arrows. Pick a name for each.

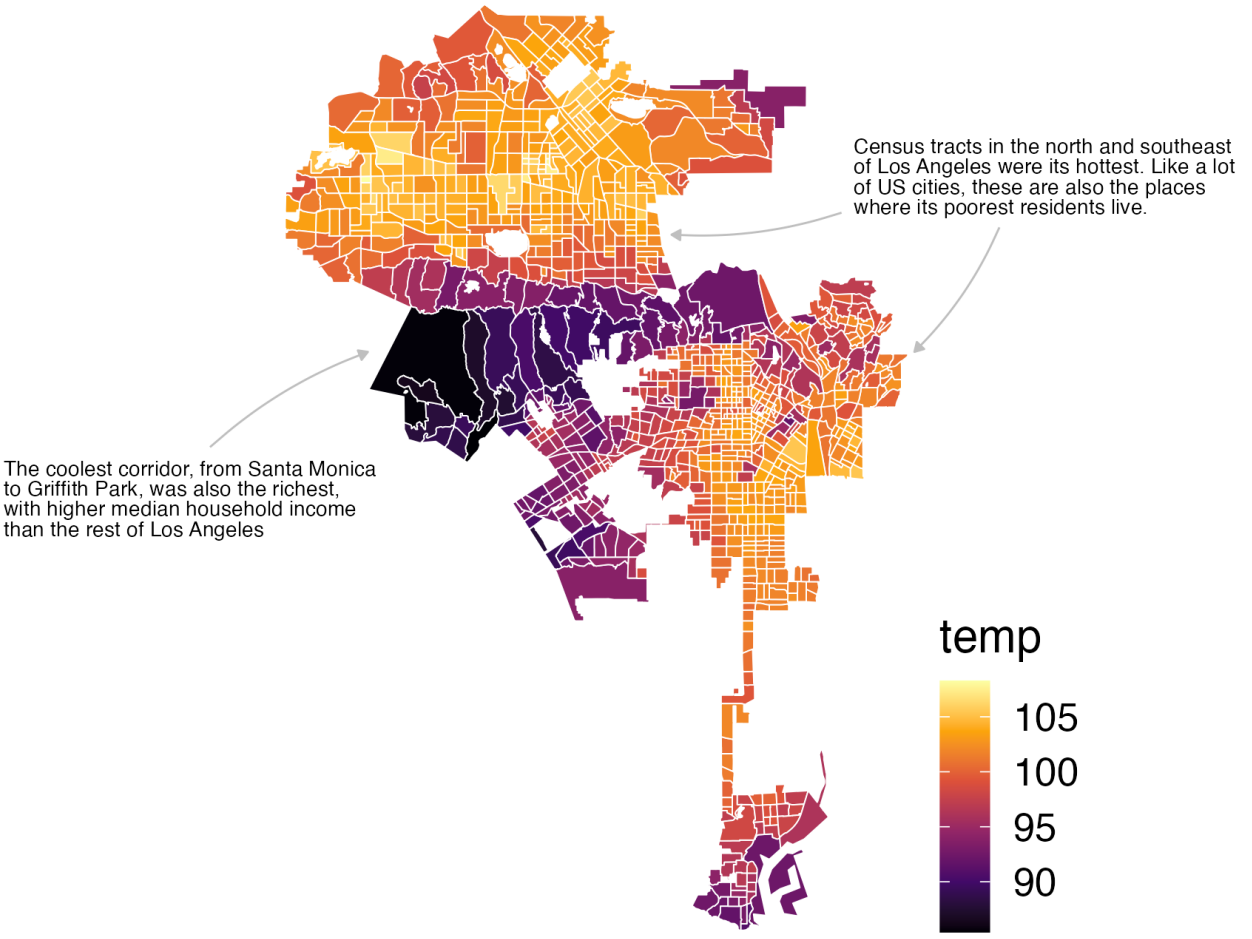
Add geom_text() **and** geom_curve() **to** base_map**. Give each geom the relevant data that you just named in (2).**

Let's clean up the geoms a bit. Reduce the lineheight **of the text geom to** 0.8**. Then, add arrows to the curve geom usiing the** arrow() **function. Give it two arguments:** length = unit(0.01, "npc") **and** type = "closed"**. Run the plot.**

One of the labels is being clipped because it runs off the main plotting panel. Add coord_sf(clip = "off") **to prevent clipping the text.**

```r
text_labels <- tibble::tribble(
  ~x,       ~y,    ~label,
  -118.90, 34.00, west_label,
  -118.20, 34.22, east_label
)

arrows <- tibble::tribble(
  ~x, ~y, ~xend, ~yend,
  -118.73, 34.035, -118.60, 34.10,
  -118.21, 34.195, -118.35, 34.18,
  -118.08, 34.185, -118.15, 34.10
)
```

```r
base_map +
  geom_text(
    data = text_labels,
    aes(x, y, label = label),
    hjust = 0,
    vjust = 0.5,
    lineheight = .8
  ) +
  geom_curve(
    data = arrows,
    aes(x = x, y = y, xend = xend, yend = yend),
    colour = "grey75",
    size = 0.3,
    curvature = -0.1,
    arrow = arrow(length = unit(0.01, "npc"), type = "closed")
  ) +
  coord_sf(clip = "off")
```


Census tracts in the north and southeast of Los Angeles were its hottest. Like a lot of US cities, these are also the places where its poorest residents live.
The coolest corridor, from Santa Monica to Griffith Park, was also the richest, with higher median household income than the rest of Los Angeles
temp
105
100
95
90

How do we augment plots to explain?

Annotate plots using text geoms and arrows

Combine plots to build a cohesive narrative

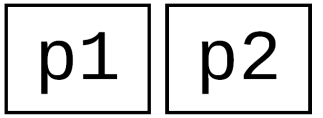
Combine plots to tell a story

1. **Build plots up from simpler to more complex**
2. **Don't use the same type of plot in each panel**
3. **Use consistent color**

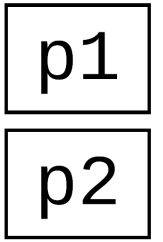
patchwork: Compose ggplots

```
library(patchwork)
```

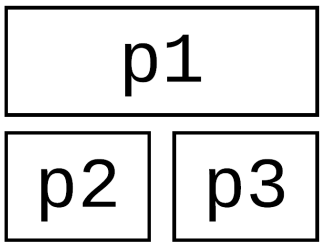
```
p1 + p2
```




```
p1 / p2
```




```
p1 /
(p2 + p3)
```

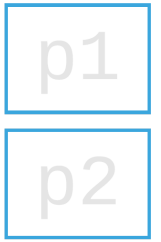


```
p1 + p2
```

combine with +

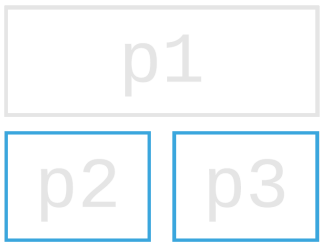

```
p1 / p2
```

stack with /

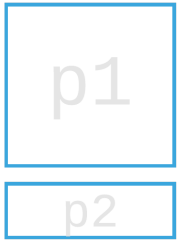



```
p1 /
(p2 + p3)
```

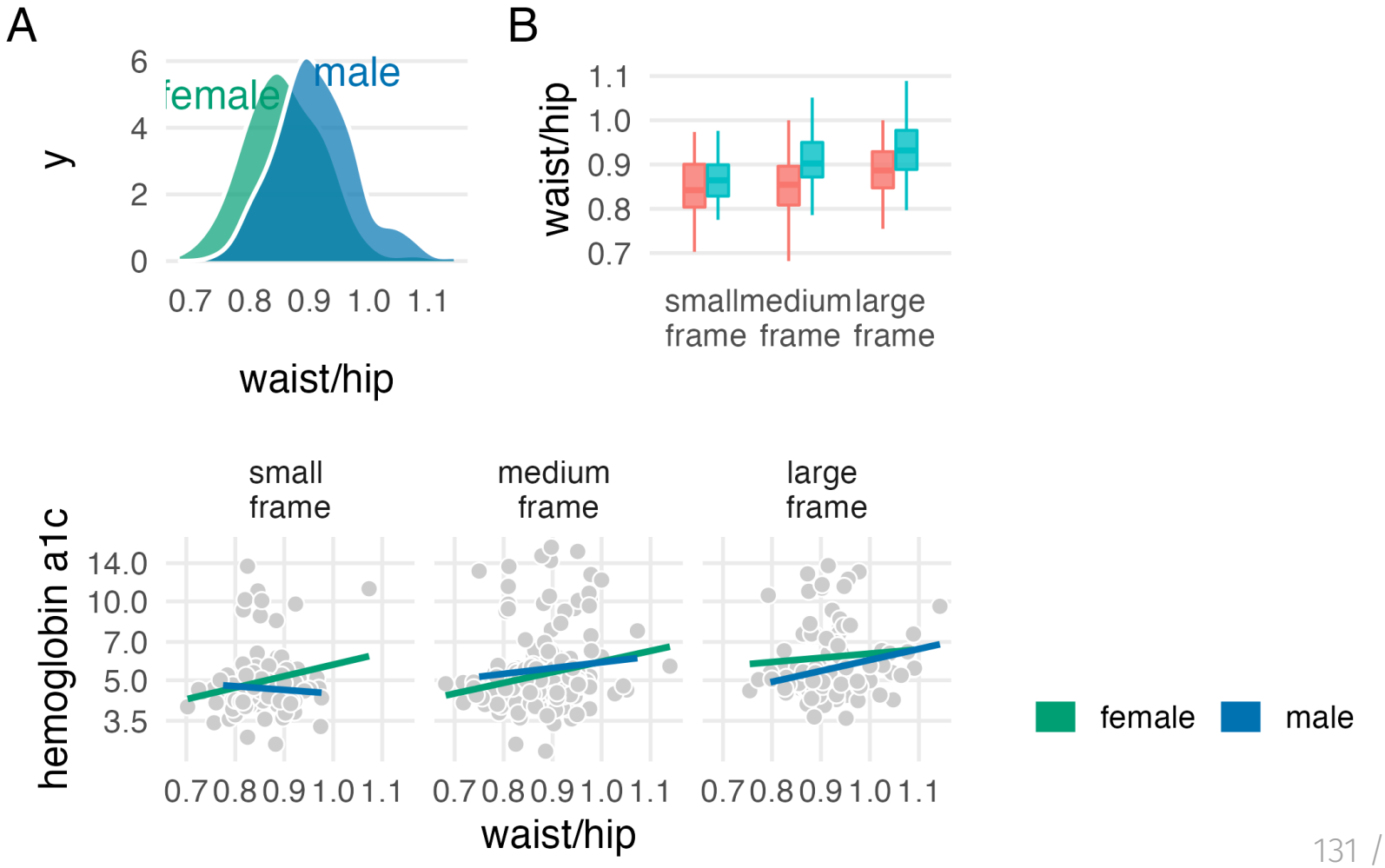
group with ()



```
p1 +
  plot_spacer() +
  p2

p1 / p2 +
 plot_layout(
  heights = c(3, 1)
 )

p1 /
(p2 + p3)
```



Your Turn 7


A
B
female
male
y
waist/hip
0.7 0.8 0.9 1.0 1.1
small frame
medium frame
large frame
hemoglobin a1c
14.0
10.0
7.0
5.0
3.5
female
male

Run the first code chunk. label_frames() **will help us label the** frame **variable better.** theme_multiplot() **is the theme we'll add to each plot. We'll use** diabetes_complete **for the plots (removing the missing values of the variables we're plotting produce the same plots as** diabetes **would, but it prevents ggplot2 from warning us that it's dropping the data internally). Nothing to change here!**

Run the code for plot_a **and take a look. Nothing to change here, either!**

The colors in plot_b **don't match** plot_a**. Add** scale_color_manual() **to make the colors consistent.**

Also add scale_fill_manual()**. For the fill colors, we'll add a bit of transparency. Paste "B3" to the end of the colors in** plot_colors**. "B3" is equivalent to 70% transparency (or** alpha = .7**) in hex code (see this GitHub page with translations from percent to hex, but note that in R you need to put the transparency at the end of the six character hex code).**

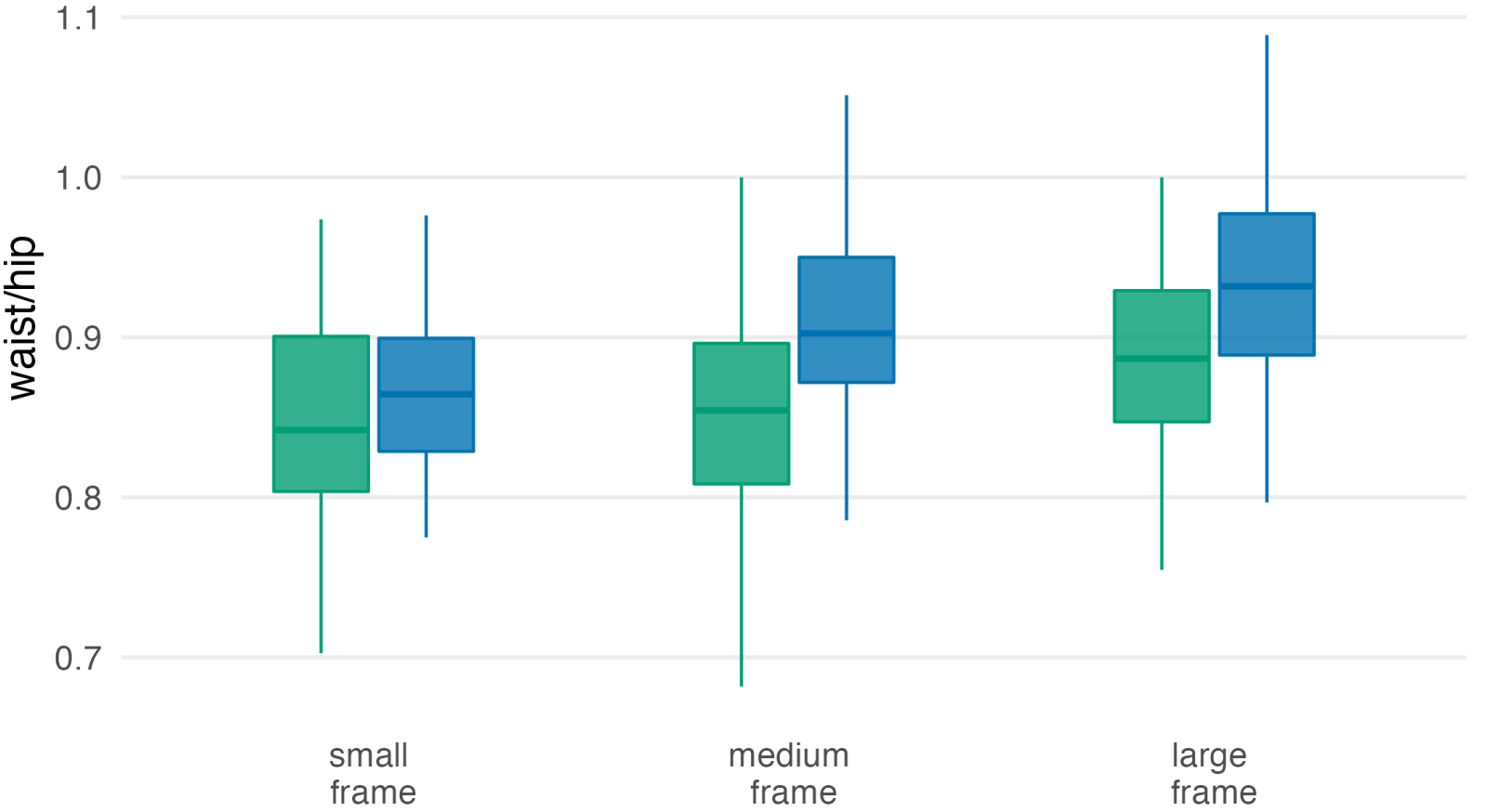
This plot doesn't have a tag **label like the other two plots. Add one to the** labs() **call.**

The legend isn't working well, but let's take advantage of it. We'll move the legend to above the plot by setting legend.position **to** c(1, 1.25) **in** theme()**. We wont' be able to see it in** plot_c**, but it will show up in the combined plot!**

Finally, combine the 3 plots using patchwork. Have plot_a **and** plot_b **on top and** plot_c **on the bottom.**

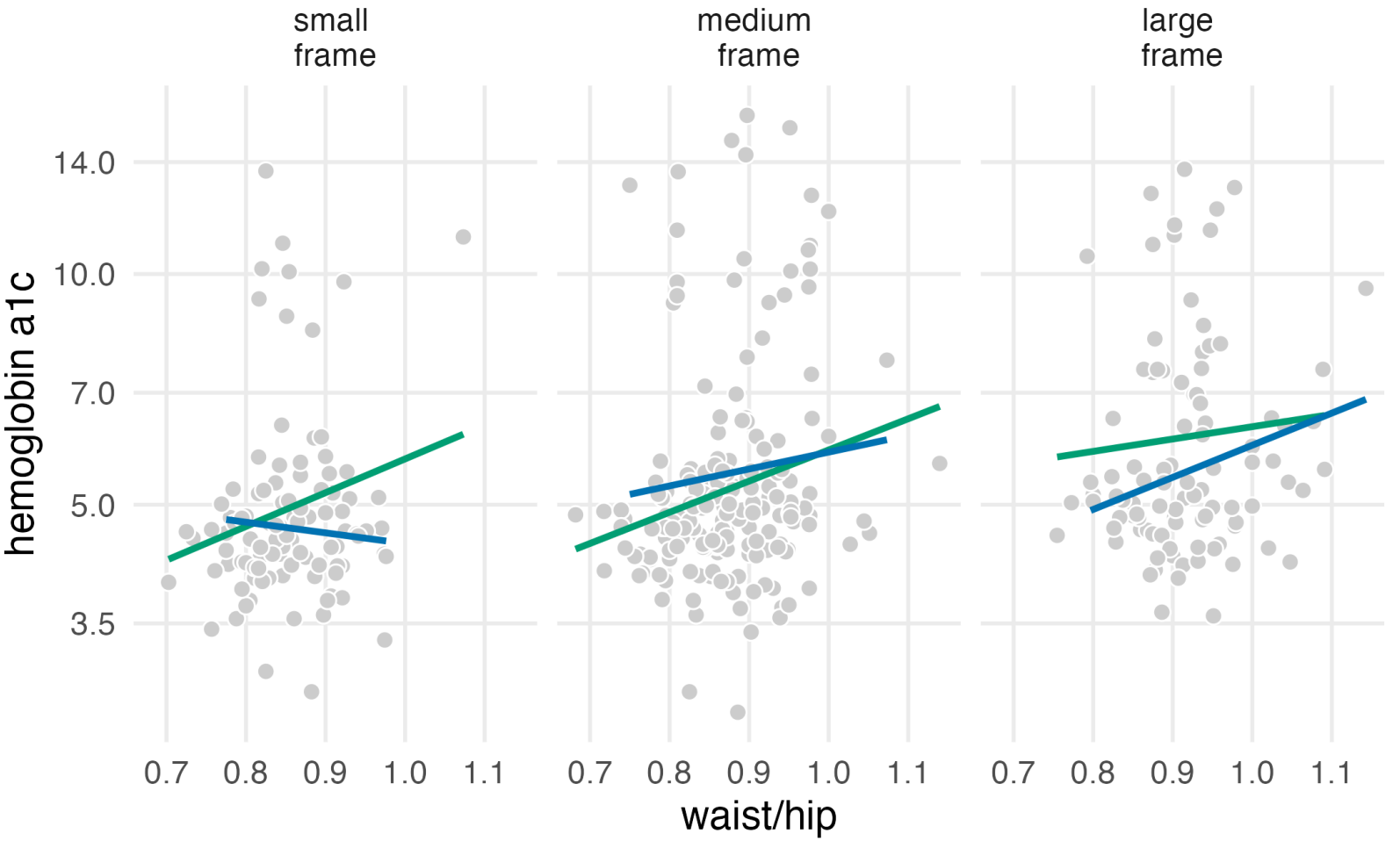
```r
plot_b <- diabetes_complete %>%
  ggplot(
    aes(fct_rev(frame),
      waist / hip,
      fill = gender,
      col = gender
    )
  ) +
  geom_boxplot(
    outlier.color = NA,
    alpha = .8,
    width = .5
  ) +
  theme_multiplot() +
  theme(axis.title.x = element_blank()) +
  scale_color_manual(values = plot_colors) +
  scale_fill_manual(values = clr_alpha(plot_colors, .69)) +
  scale_x_discrete(labels = label_frames) +
  labs(tag = "B")

plot_b
```

B

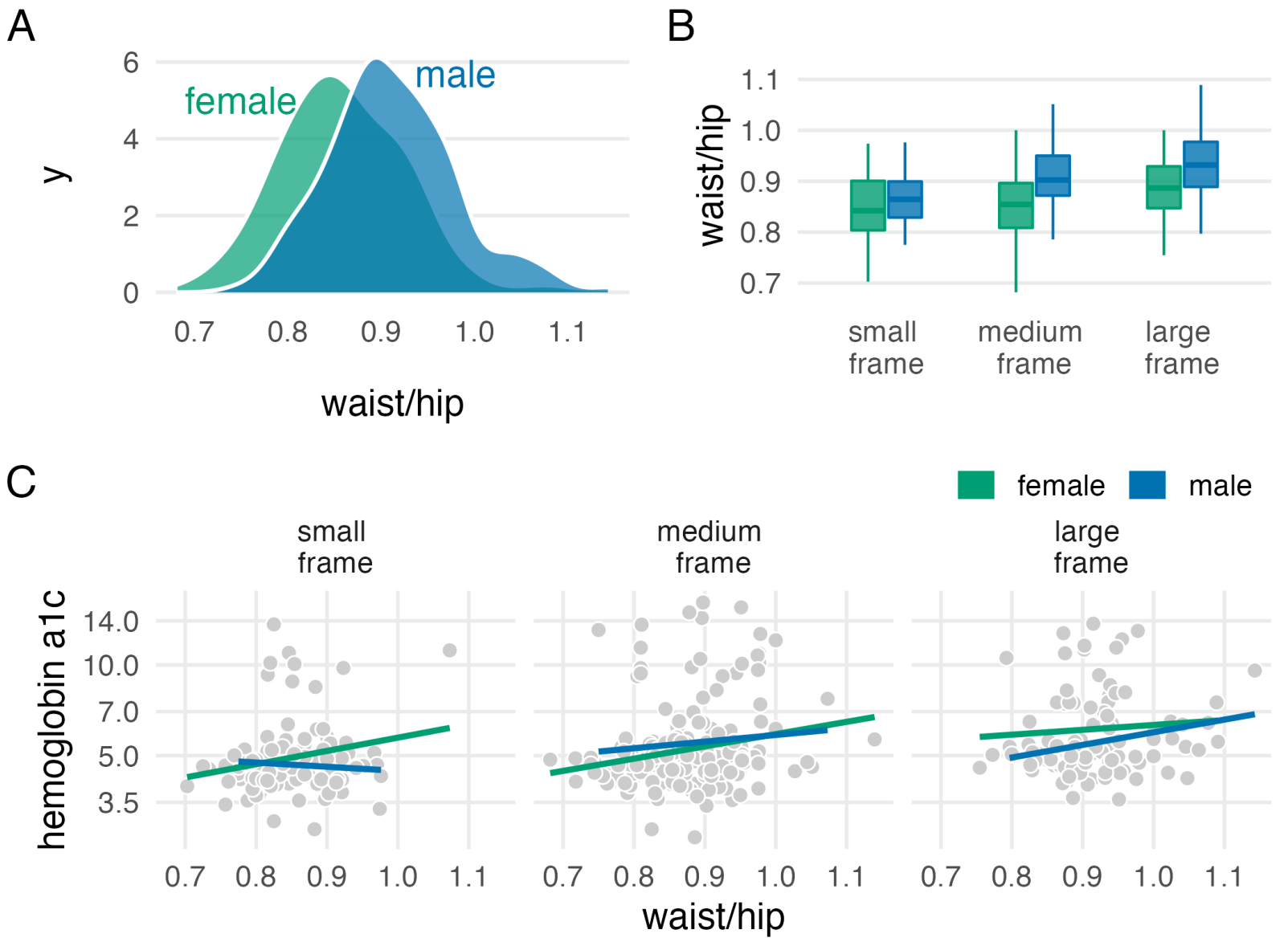


```r
plot_c <- diabetes_complete %>%
  ggplot(aes(waist / hip, glyhb, col = gender)) +
  geom_point(
    shape = 21,
    col = "white",
    fill = "grey80",
    size = 2.5
  ) +
  geom_smooth(
    method = "lm",
    formula = y ~ x,
    se = FALSE,
    size = 1.1
  ) +
  theme_minimal(base_size = 14) +
  theme(
    legend.position = c(1, 1.25),
    legend.justification = c(1, 0),
    legend.direction = "horizontal",
    panel.grid.minor = element_blank()
  ) +
  facet_wrap(~ fct_rev(frame), labeller = as_labeller(label_frames)) +
  scale_y_log10(breaks = c(3.5, 5.0, 7.0, 10.0, 14.0)) +
  scale_color_manual(name = "", values = plot_colors) +
  guides(color = guide_legend(override.aes = list(size = 5))) +
  labs(y = "hemoglobin a1c", tag = "C")

plot_c
```

C


small frame
medium frame
large frame
hemoglobin a1c
14.0
10.0
7.0
5.0
3.5
0.7
0.8
0.9
1.0
1.1
waist/hip

```r
library(patchwork)
(plot_a + plot_b) / plot_c
```


A
female
male
y
6
4
2
0
0.7
0.8
0.9
1.0
1.1
waist/hip
B
waist/hip
1.1
1.0
0.9
0.8
0.7
small frame
medium frame
large frame
C
female
male
small frame
medium frame
large frame
hemoglobin a1c
14.0
10.0
7.0
5.0
3.5
0.7
0.8
0.9
1.0
1.1
waist/hip

Resources

Fundamentals of Data Visualization by Claus O. Wilke

Storytelling with Data by Cole Nussbaumer Knaflic

Better Presentations by Jonathan Schwabish