Data Visualisation with R

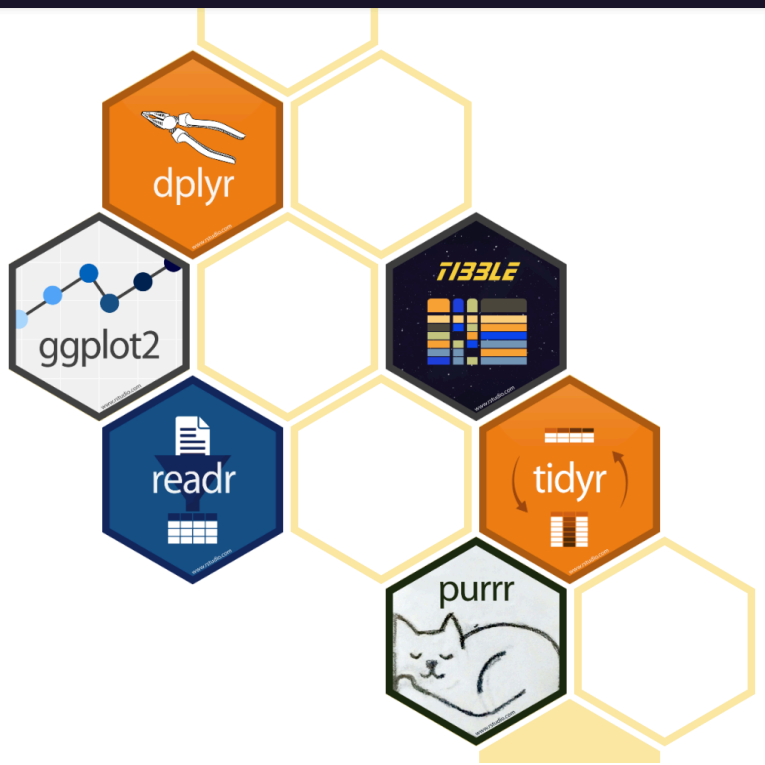
Richard White

Topics

- Data manipulation
  - tidy data and the pipe (%>%) operator
  - loading data
  - selecting, filtering and creating new columns
- ggplot2
  - aesthetics
  - geoms
  - shapes and colours
  - facets
  - themes

Tidyverse

Tidyverse Packages Blog Learn Help Contribute



R packages for data science

The tidyverse is an opinionated collection of R packages designed for data science. All packages share an underlying design philosophy, grammar, and data structures.

Install the complete tidyverse with:

```
install.packages("tidyverse")
```

https://www.tidyverse.org/

Tidy data

- Each variable forms a column
- Each observation forms a row
- Each type of observational unit forms a table

name	description	sample	normalised_count
slc35a5	ENSDARG00000000001	sample_1	36.2823
ccdc80	ENSDARG00000000002	sample_1	75.5064
nrf1	ENSDARG00000000018	sample_1	305.948
slc35a5	ENSDARG00000000001	sample_2	33.4323
ccdc80	ENSDARG00000000002	sample_2	113.155
nrf1	ENSDARG00000000018	sample_2	281.174
slc35a5	ENSDARG00000000001	sample_3	34.1082
ccdc80	ENSDARG00000000002	sample_3	102.324
nrf1	ENSDARG00000000018	sample_3	274.76

Tidy data

- Each variable forms a column
- Each observation forms a row
- Each type of observational unit forms a table

name	description	sample_1	sample_2	sample_3
slc35a5	ENSDARG00000000001	36.28229146	33.4323	34.1081598
ccdc80	ENSDARG00000000002	75.50639034	113.155	102.324479
nrf1	ENSDARG00000000018	305.9479712	281.174	274.760176

Tidy data

- Each variable forms a column
- Each observation forms a row
- Each type of observational unit forms a table

name	description	sample	count	normalised_count
slc35a5	ENSDARG00000000001	sample_1	35	36.2823
ccdc80	ENSDARG00000000002	sample_1	75	75.5064
nrf1	ENSDARG00000000018	sample_1	300	305.948
slc35a5	ENSDARG00000000001	sample_2	30	33.4323
ccdc80	ENSDARG00000000002	sample_2	115	113.155
nrf1	ENSDARG00000000018	sample_2	283	281.174
slc35a5	ENSDARG00000000001	sample_3	31	34.1082
ccdc80	ENSDARG00000000002	sample_3	107	102.324
nrf1	ENSDARG00000000018	sample_3	276	274.76

pipe

- %>%
- Equivalent of the Unix |
  - `cut –f1,2,4 data.txt | head`
  - `select(data, c(1,2,4)) %>% head()`
- Allows sending the results of one function into the next
- Makes code easier to read
  - `head(select(data, c(1,2,4)), 6)`
  - `select(data, c(1,2,4)) %>% head(6)`

%>%

```
eat(
  slice(
   bake(
     put(
      pour(
        mix(ingredients),
       into=baking_form),
      into=oven),
     time=30),
   pieces=6),
  1)
```

```
ingredients %>%
  mix() %>%
  pour(into=baking_form) %>%
  put(into=oven) %>%
  bake(time=30) %>%
  slice(pieces=6) %>%
  eat(1)
```

from @dmi3k on Twitter

readr

- read_tsv
  - reads in tab-delimited data and tries to guess the type of each column
    - character, integer etc.
- read_csv
  - same for comma-separated files

https://readr.tidyverse.org/

read_tsv

```
> read_tsv('rvis/Rvis_test_data.tsv')
Parsed with column specification:
cols(
  A = col_character(),
  B = col_character(),
  C = col_double(),
  D = col_double(),
  E = col_integer(),
  F = col_logical()
)
# A tibble: 50 x 6
   A     B         C     D     E F
   <chr> <chr> <dbl> <dbl> <int> <lgl>
 1 b     E     4.80   29.9    58 FALSE
 2 b     D     0.819  29.5    69 FALSE
 3 d     E     2.47   36.3    21 TRUE
 4 b     D     8.71   47.1    62 TRUE
 5 d     D     8.95   28.7    82 FALSE
 6 d     C     3.64   14.3    46 TRUE
 7 a     C     0.532  35.5    80 FALSE
 8 a     D     6.06   13.4    69 FALSE
 9 a     C     5.60   16.1    35 FALSE
10 c     E     4.87   44.4    26 FALSE
# ... with 40 more rows
```

factors

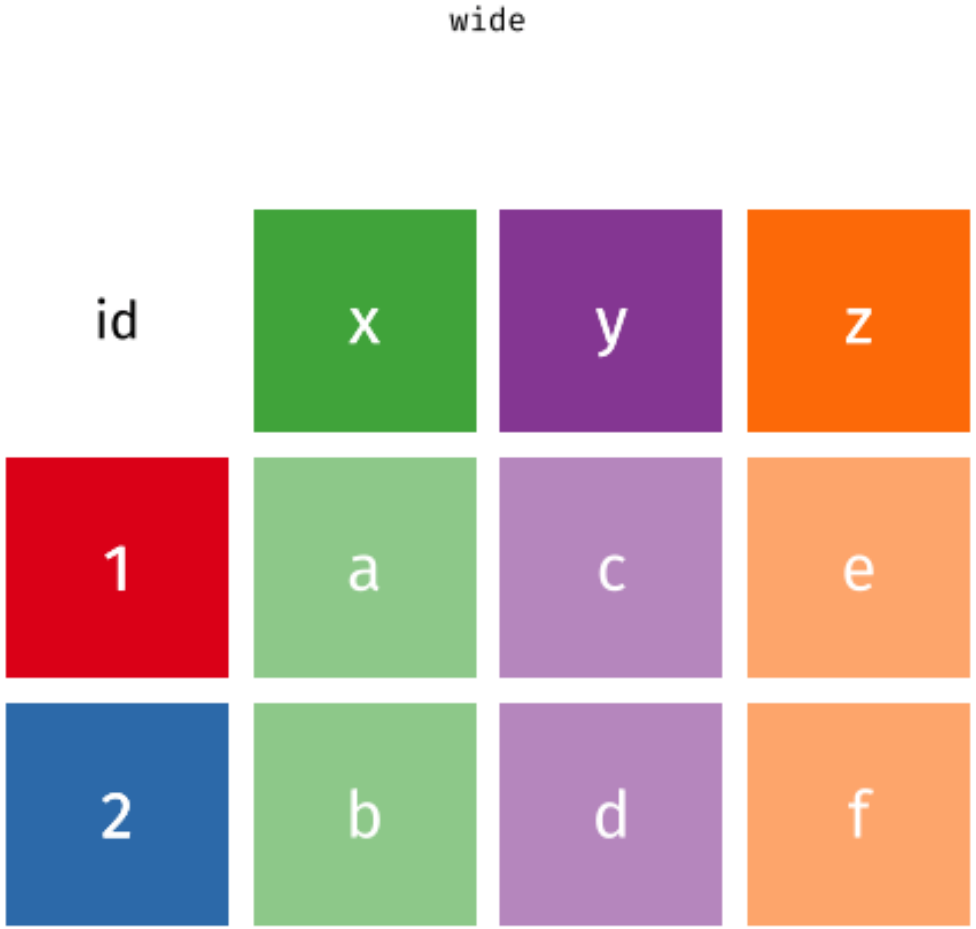
```
> samples <- read_tsv('rvis/Rvis_test_samples.tsv')
Parsed with column specification:
cols(
  sample_name = col_character(),
  genotype = col_character()
)
> head(samples)
# A tibble: 6 x 2
  sample_name genotype
  <chr>       <chr>
1 sample_1    wt
2 sample_2    wt
3 sample_3    wt
4 sample_4    wt
5 sample_5    het
6 sample_6    het
> samples$genotype
 [1] "wt"  "wt"  "wt"  "wt"  "het" "het" "het" "het" "hom" "hom" "hom" "hom"
> factor(samples$genotype)
 [1] wt  wt  wt  wt  het het het het hom hom hom hom
Levels: het hom wt
> factor(samples$genotype, levels = c('wt', 'het', 'hom'))
 [1] wt  wt  wt  wt  het het het het hom hom hom hom
Levels: wt het hom
> samples$genotype <- factor(samples$genotype, levels = c('wt', 'het', 'hom'))
```

wide vs long data

id	x	y	z
1	a	c	e
2	b	d	f

id	name	val
1	x	a
1	y	c
1	z	e
2	x	b
2	y	d
2	z	f

pivot_wider() and pivot_longer()



Garrick Aden-Buie and Mara Averick

https://github.com/batpigandme/tidyexplain/blob/pivot/images/tidyr-longer-wider.gif

Tidy data

name	description	sample_1	sample_2	sample_3
slc35a5	ENSDARG00000000001	36.28229146	33.4323	34.1081598
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ccdc80	ENSDARG00000000002	sample_2	113.155
nrf1	ENSDARG00000000018	sample_2	281.174
slc35a5	ENSDARG00000000001	sample_3	34.1082
ccdc80	ENSDARG00000000002	sample_3	102.324
nrf1	ENSDARG00000000018	sample_3	274.76

Data manipulation

- select(): pick variables
- filter(): pick rows
- mutate(): add new variables that are a function of existing ones
- arrange(): sort rows
- summarise(): reduce multiple values down to a single summary (mean, min, max, etc.)

https://dplyr.tidyverse.org/index.html

select()

- Choose variables from a table
  - use column names explicitly: `select(data, GeneID)`
  - or positions: `select(data, c(1,5,9))`
  - column names can be used like they are positions

    e.g. `select(data, GeneID:Name)`
  - or search functions
    - starts_with() `select(data, starts_with('uninf'))`
    - ends_with() `select(data, ends_with('count'))`
    - contains() `select(data, contains('3dpf'))`
    - matches() `select(data, matches('3dpf.*count'))`

select()

```
> head(iris, 4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
> summary(iris)
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width          Species
 Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100   setosa     :50
 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300   versicolor:50
 Median :5.800   Median :3.000   Median :4.350   Median :1.300   virginica :50
 Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
 3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
 Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
> select(iris, Sepal.Length, Sepal.Width) %>% head(4)
  Sepal.Length Sepal.Width
1          5.1         3.5
2          4.9         3.0
3          4.7         3.2
4          4.6         3.1
> select(iris, starts_with('Petal')) %>% head(4)
  Petal.Length Petal.Width
1          1.4         0.2
2          1.4         0.2
3          1.3         0.2
4          1.5         0.2
```

select()

```
> select(iris, ends_with('Width')) %>% head(4)
  Sepal.Width Petal.Width
1         3.5         0.2
2         3.0         0.2
3         3.2         0.2
4         3.1         0.2
> select(iris, -Species) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width
1          5.1         3.5          1.4         0.2
2          4.9         3.0          1.4         0.2
3          4.7         3.2          1.3         0.2
4          4.6         3.1          1.5         0.2
> select(iris, Species, ends_with('Width')) %>% head(4)
  Species Sepal.Width Petal.Width
1  setosa         3.5         0.2
2  setosa         3.0         0.2
3  setosa         3.2         0.2
4  setosa         3.1         0.2
```

filter()

- choose rows where conditions are true
  - check equality with ==
  - Also <, >, <=, >=
  - combine conditions with & (AND), | (OR)
  - ! (NOT)
  - e.g.

    adjustedp < 0.05 & log2fc > 2

filter()

```
> filter(iris, Species == "virginica") %>% dim()
[1] 50  5
> filter(iris, Species == "virginica") %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
1          6.3         3.3          6.0         2.5 virginica
2          5.8         2.7          5.1         1.9 virginica
3          7.1         3.0          5.9         2.1 virginica
4          6.3         2.9          5.6         1.8 virginica
> filter(iris, Species == "virginica" | Species == "versicolor") %>% dim()
[1] 100   5
> filter(iris, Sepal.Length > 6) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
1          7.0         3.2          4.7         1.4 versicolor
2          6.4         3.2          4.5         1.5 versicolor
3          6.9         3.1          4.9         1.5 versicolor
4          6.5         2.8          4.6         1.5 versicolor
> filter(iris, Sepal.Length > 6) %>% dim()
[1] 61  5
> filter(iris, Sepal.Length > 6 & Sepal.Width < 3) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
1          6.5         2.8          4.6         1.5 versicolor
2          6.6         2.9          4.6         1.3 versicolor
3          6.1         2.9          4.7         1.4 versicolor
4          6.2         2.2          4.5         1.5 versicolor
> filter(iris, Sepal.Length > 6 & Sepal.Width < 3) %>% dim()
[1] 25  5
```

mutate()

- mutate makes new columns that are functions of existing columns
  - mutate keeps the original column
  - transmute replaces the original column

mutate()

```
> mutate(iris, exp = 10^Sepal.Width) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species      exp
1          5.1         3.5          1.4         0.2  setosa 3162.278
2          4.9         3.0          1.4         0.2  setosa 1000.000
3          4.7         3.2          1.3         0.2  setosa 1584.893
4          4.6         3.1          1.5         0.2  setosa 1258.925
> mutate(iris, l2fc = log2(Sepal.Length)) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species     l2fc
1          5.1         3.5          1.4         0.2  setosa 2.350497
2          4.9         3.0          1.4         0.2  setosa 2.292782
3          4.7         3.2          1.3         0.2  setosa 2.232661
4          4.6         3.1          1.5         0.2  setosa 2.201634
> mutate(iris, cumulsum = cumsum(Petal.Length)) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species cumulsum
1          5.1         3.5          1.4         0.2  setosa      1.4
2          4.9         3.0          1.4         0.2  setosa      2.8
3          4.7         3.2          1.3         0.2  setosa      4.1
4          4.6         3.1          1.5         0.2  setosa      5.6
> mutate(iris, tenfold = Petal.Length * 10, tenth = tenfold / 100) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species tenfold tenth
1          5.1         3.5          1.4         0.2  setosa      14  0.14
2          4.9         3.0          1.4         0.2  setosa      14  0.14
3          4.7         3.2          1.3         0.2  setosa      13  0.13
4          4.6         3.1          1.5         0.2  setosa      15  0.15
```

arrange()

```
> arrange(iris, Sepal.Length) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          4.3         3.0          1.1         0.1  setosa
2          4.4         2.9          1.4         0.2  setosa
3          4.4         3.0          1.3         0.2  setosa
4          4.4         3.2          1.3         0.2  setosa
> arrange(iris, desc(Sepal.Length)) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
1          7.9         3.8          6.4         2.0 virginica
2          7.7         3.8          6.7         2.2 virginica
3          7.7         2.6          6.9         2.3 virginica
4          7.7         2.8          6.7         2.0 virginica
> arrange(iris, Sepal.Length, Petal.Length) %>% head(4)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          4.3         3.0          1.1         0.1  setosa
2          4.4         3.0          1.3         0.2  setosa
3          4.4         3.2          1.3         0.2  setosa
4          4.4         2.9          1.4         0.2  setosa
```

Exercises

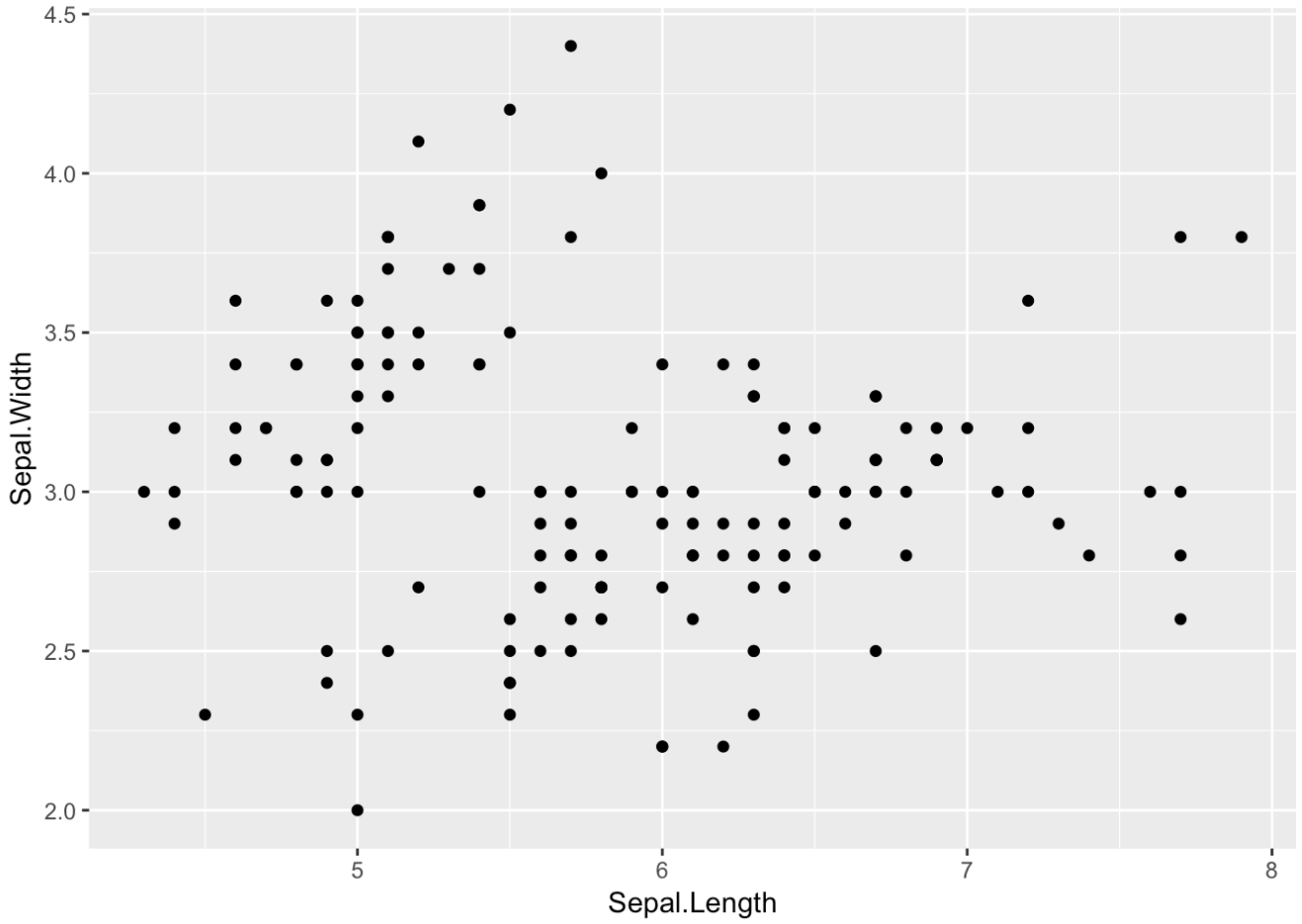
ggplot2

- Grammar of Graphics
  - Leland Wilkinson (2005)
- Components of a plot
  1. data
  2. aesthetics
     - attributes of a plot that variables in the data are mapped to
     - x, y, colour, shape, length, size, linetype
  3. theme

https://ggplot2.tidyverse.org/index.html

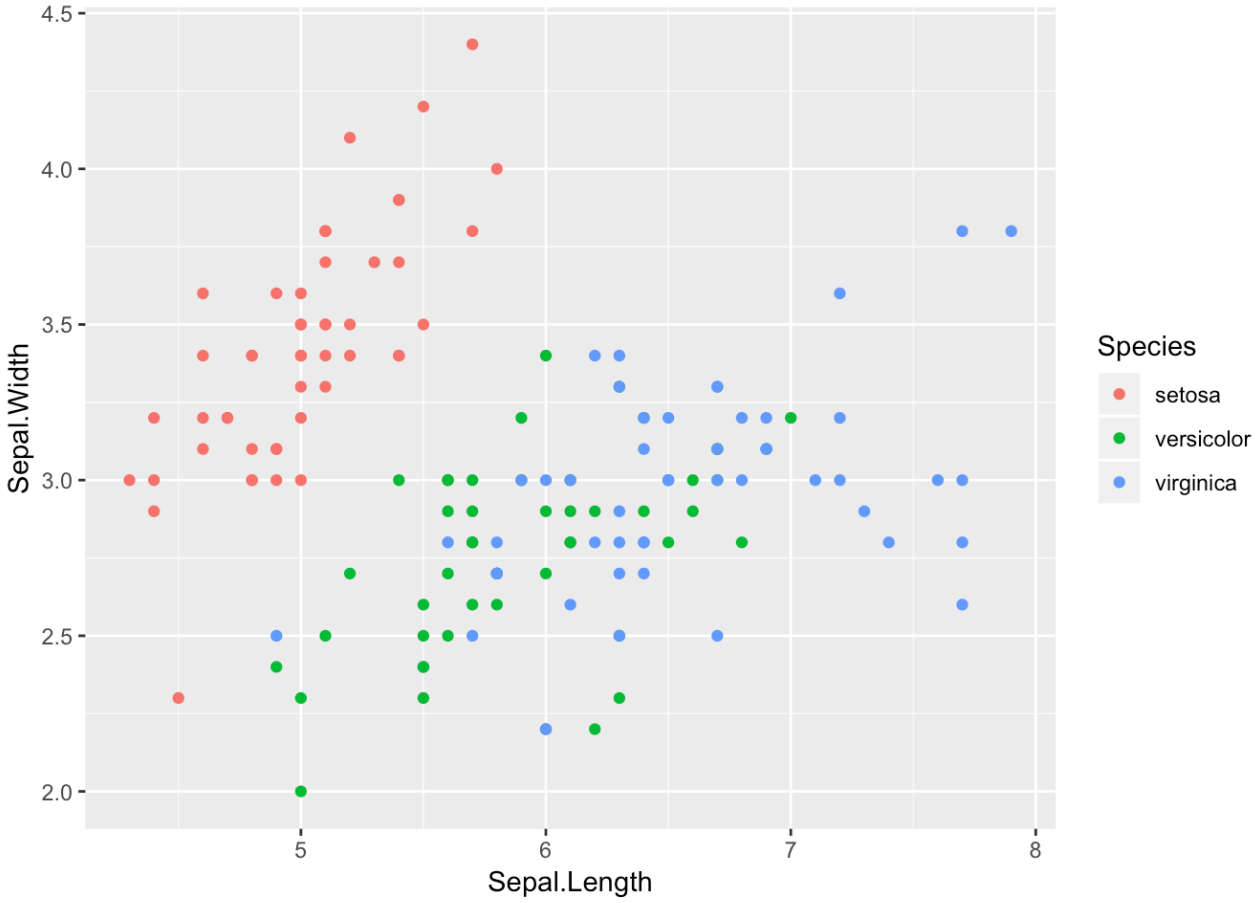
scatterplot

```
ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width) ) +
  geom_point()
```



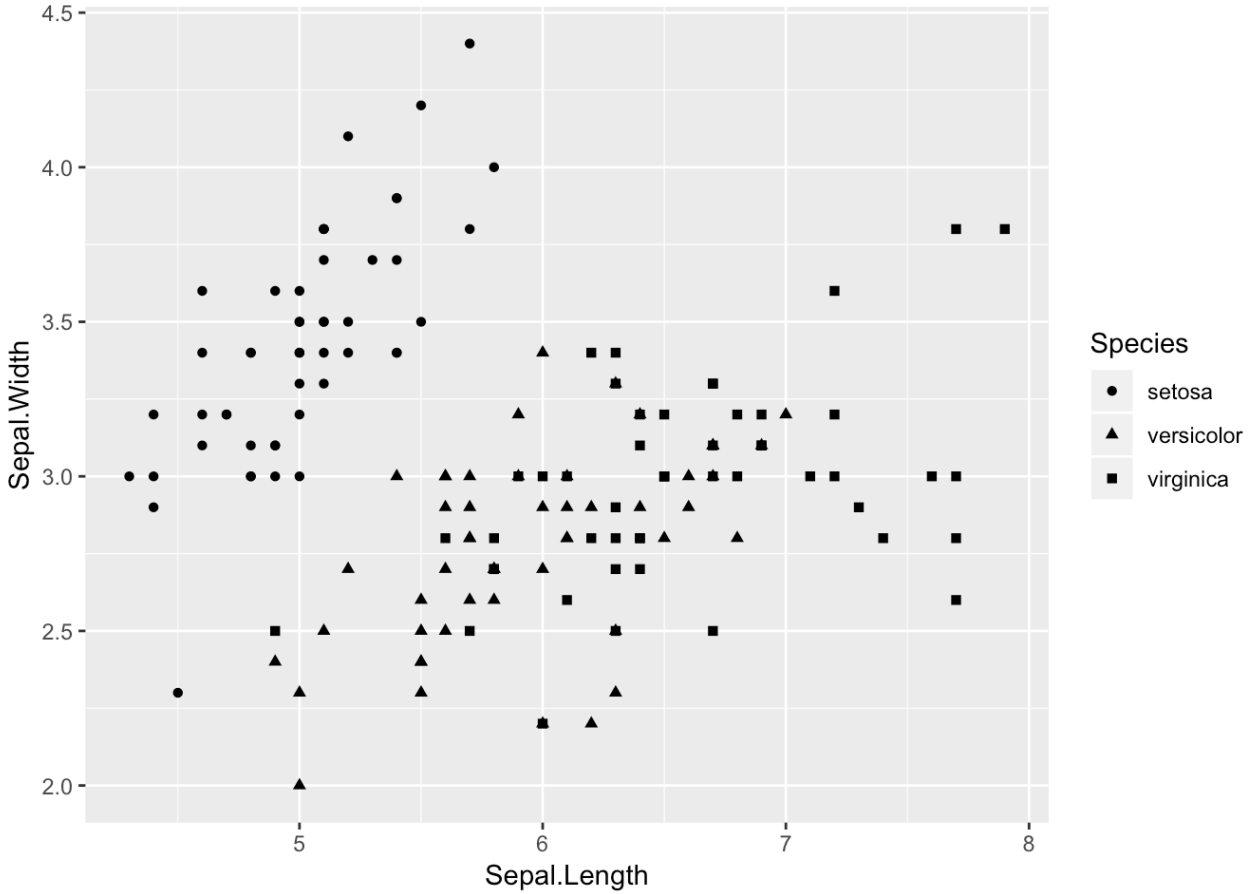
Map categorical variable to colour

```
ggplot(data = iris) +
  geom_point( aes(x = Sepal.Length, y = Sepal.Width,
                  colour = Species))
```



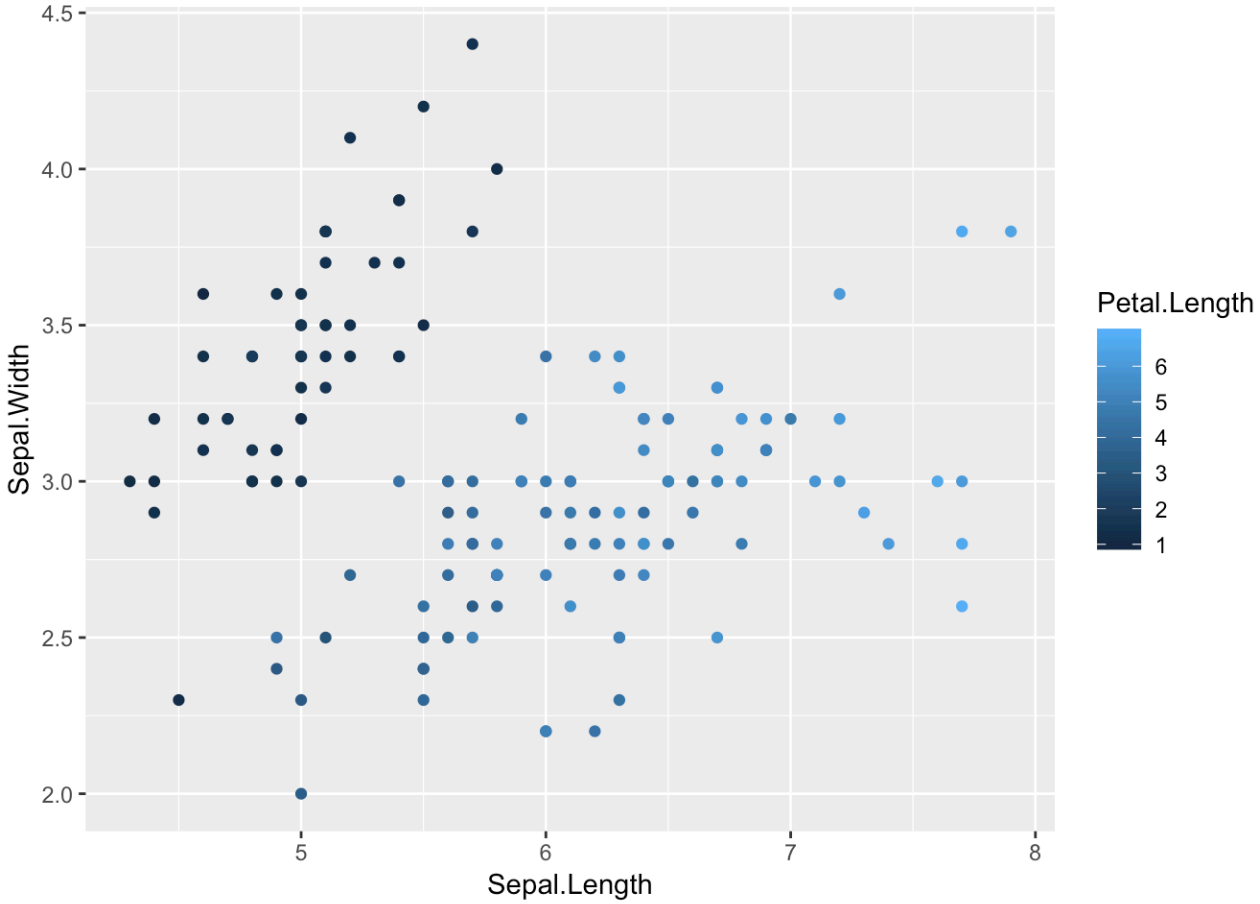
Map categorical variable to shape

```
ggplot(data = iris) +
  geom_point( aes(x = Sepal.Length, y = Sepal.Width,
                  shape = Species))
```



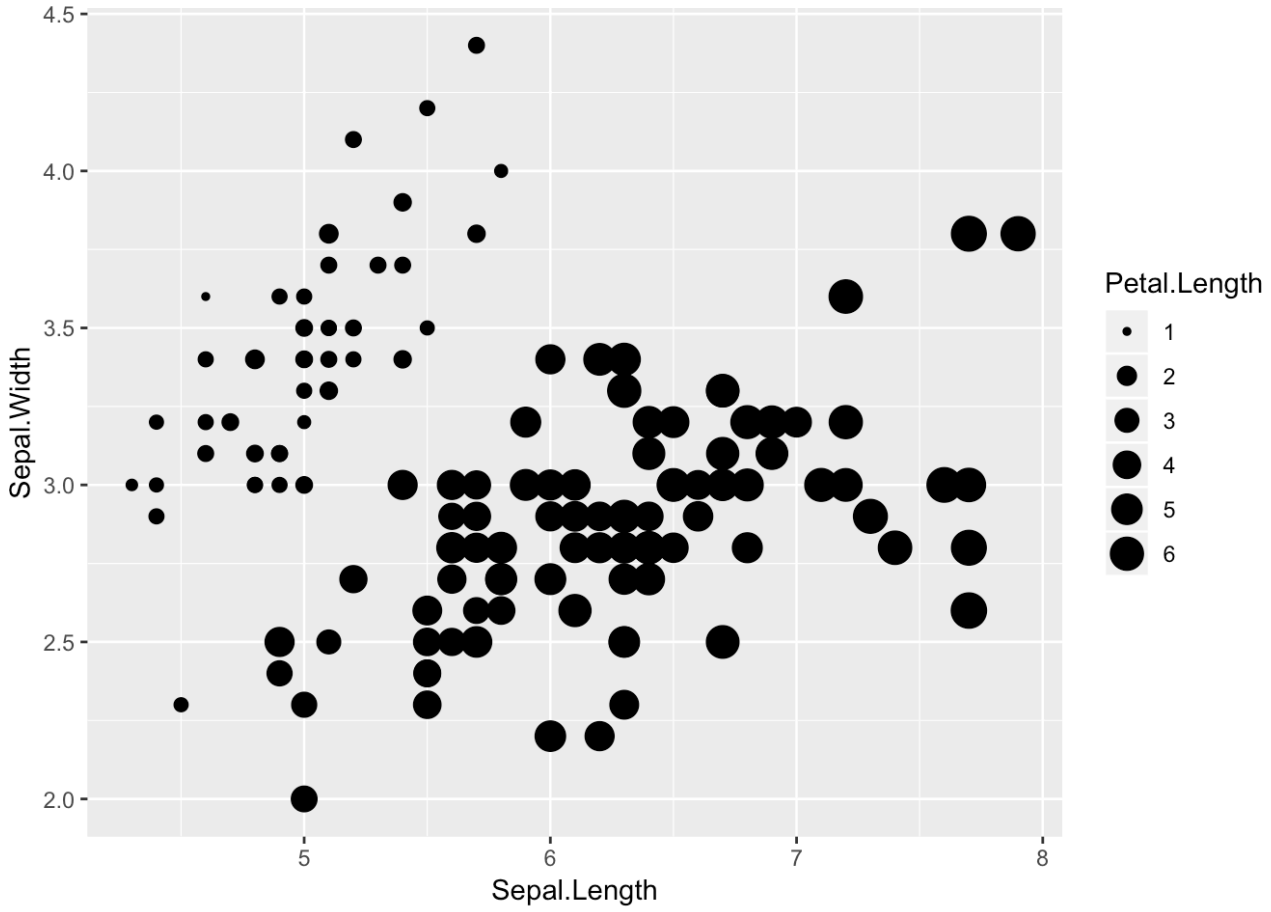
Map continuous variable to colour

```
ggplot(data = iris) +
  geom_point( aes(x = Sepal.Length, y = Sepal.Width,
                  colour = Petal.Length))
```



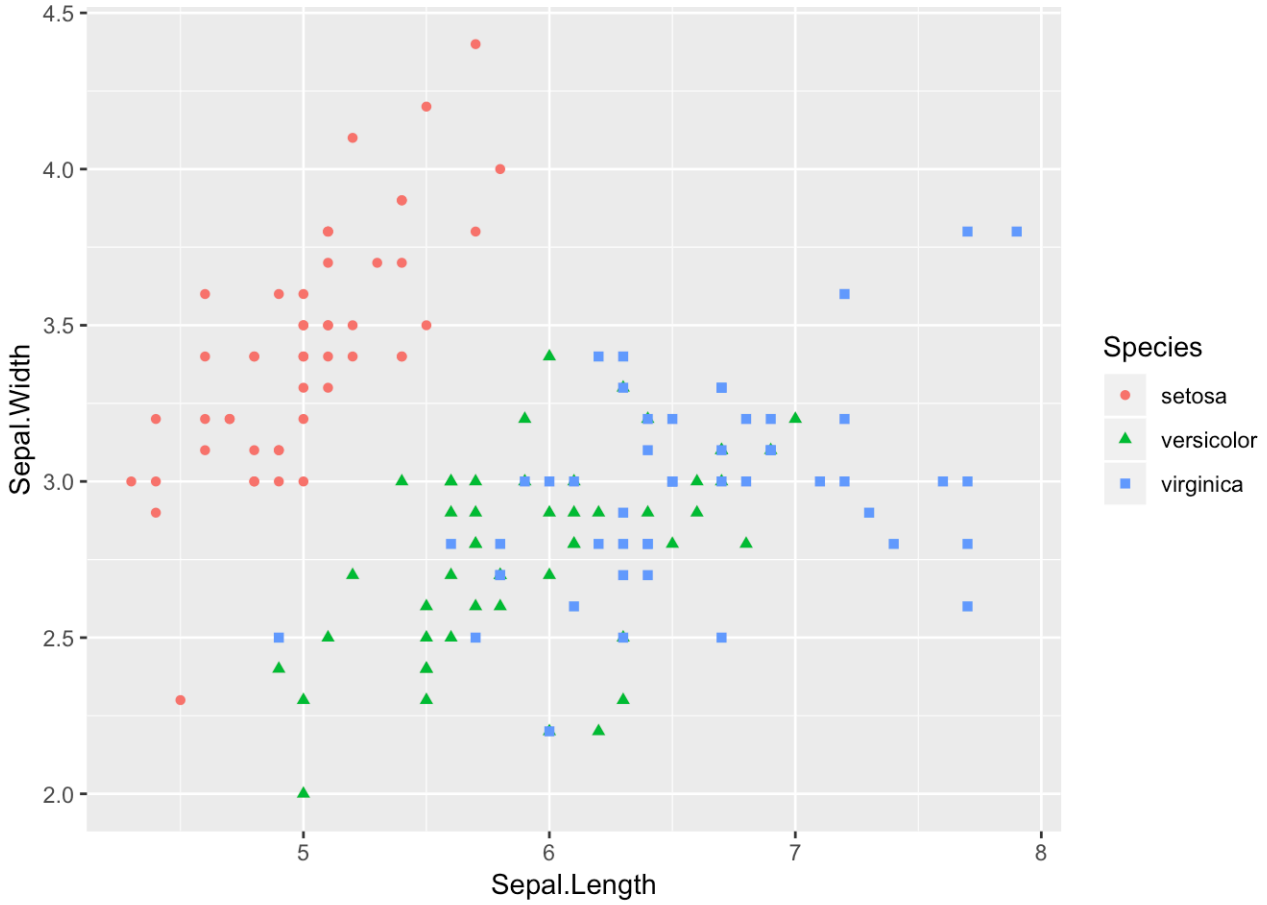
Map continuous variable to size

```
ggplot(data = iris) +
  geom_point( aes(x = Sepal.Length, y = Sepal.Width,
                  size = Petal.Length))
```



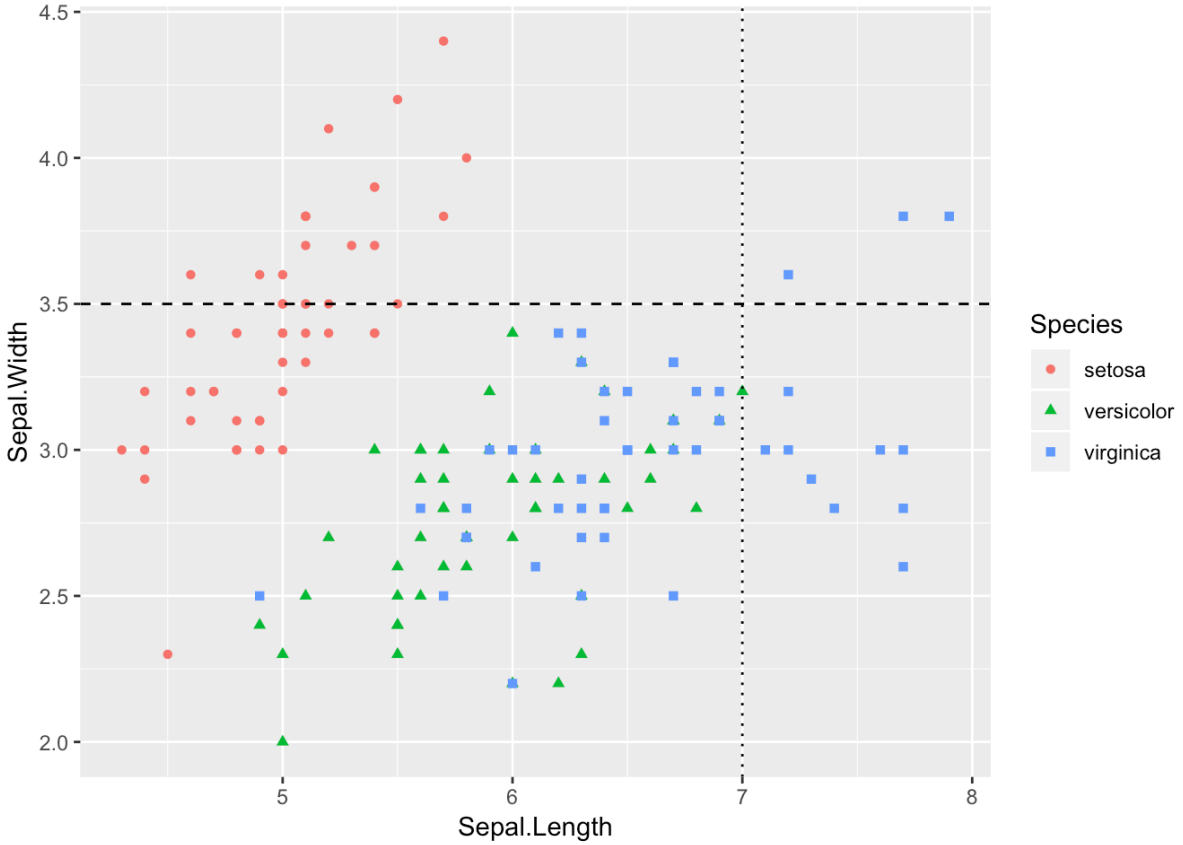
Map variable to colour and shape

```
ggplot(data = iris) +
  geom_point( aes(x = Sepal.Length, y = Sepal.Width,
                  shape = Species, colour = Species))
```



Add extra geoms

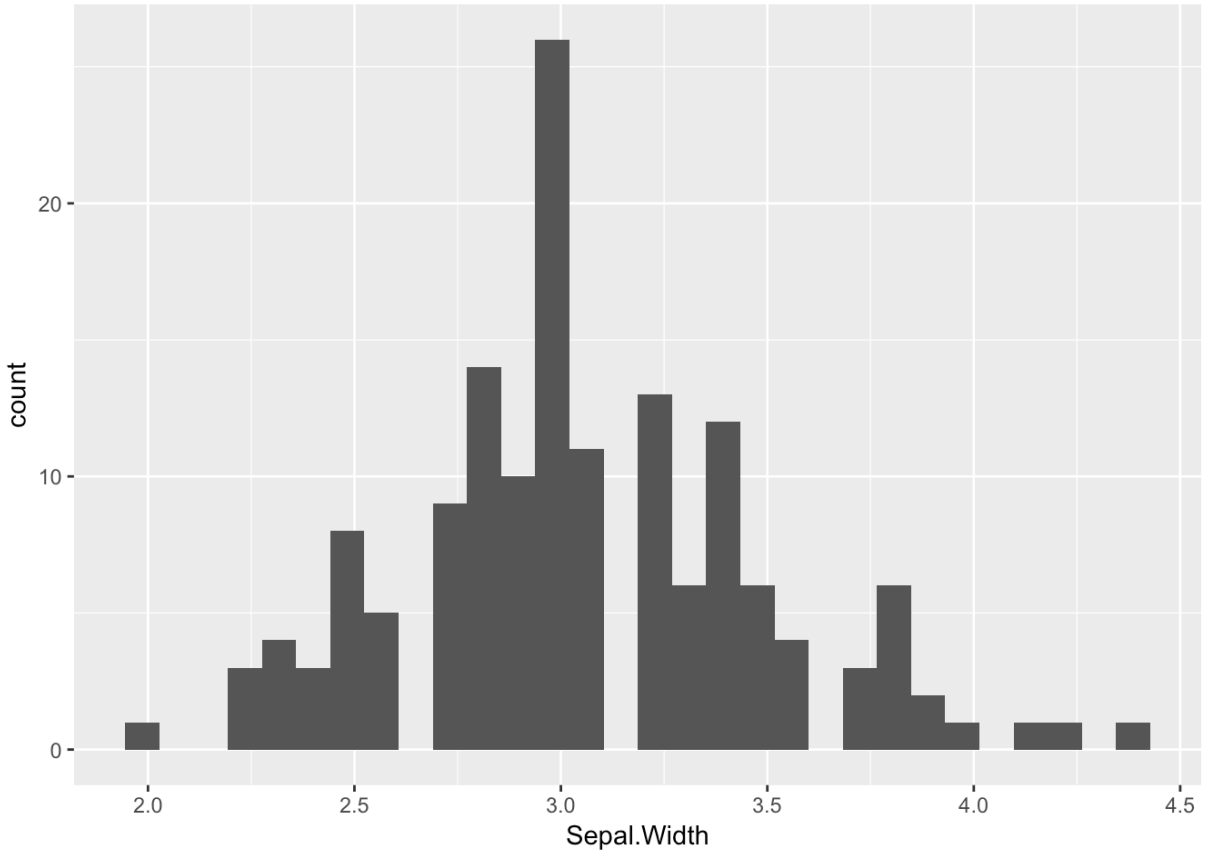
```
ggplot(data = iris) +
  geom_point( aes(x = Sepal.Length, y = Sepal.Width,
                  shape = Species, colour = Species)) +
  geom_hline(yintercept = 3.5, linetype = 'dashed') +
  geom_vline(xintercept = 7, linetype = 'dotted')
```



geom_histogram

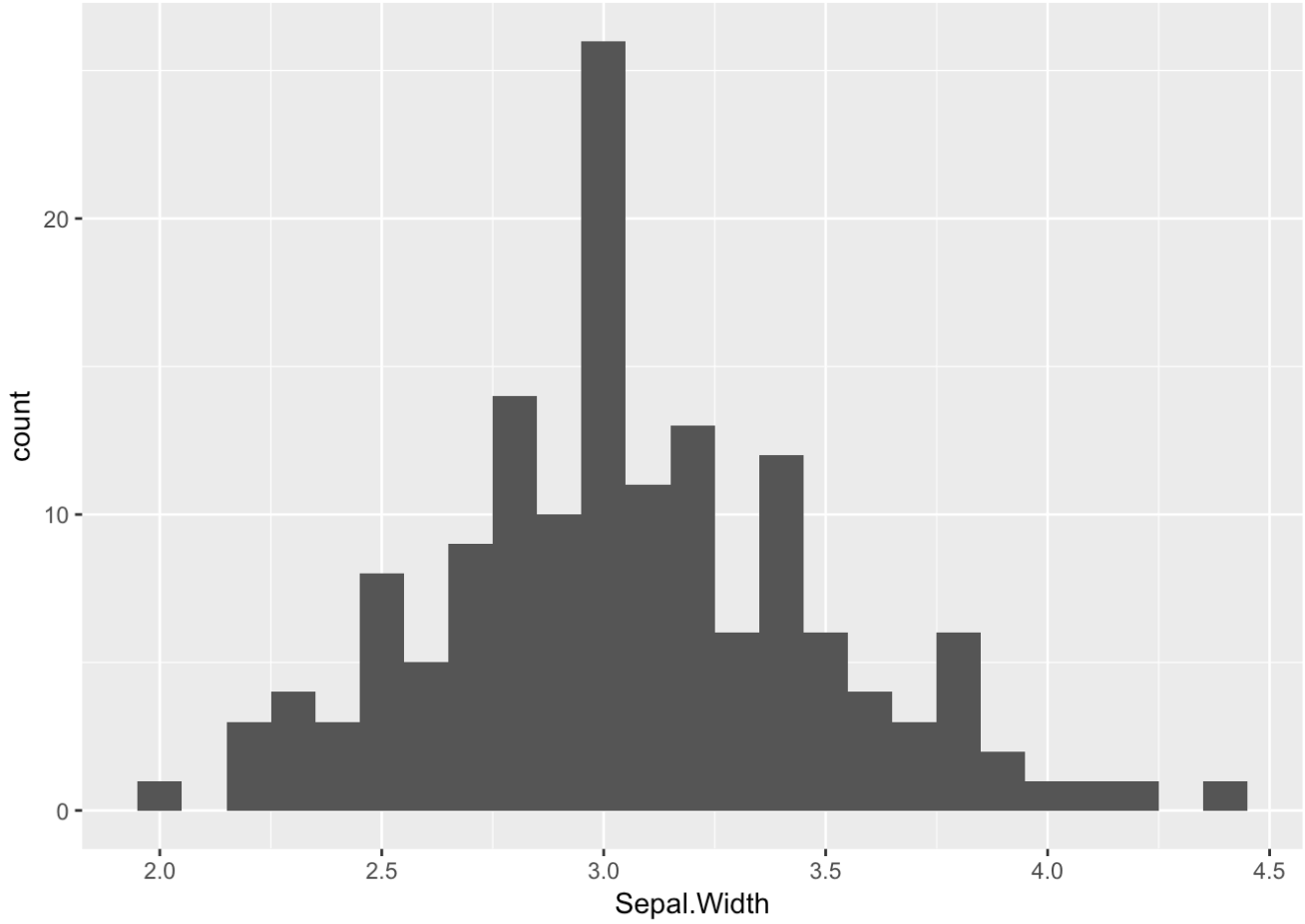
```
ggplot(data = iris) +
  geom_histogram( aes(x = Sepal.Width) )
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



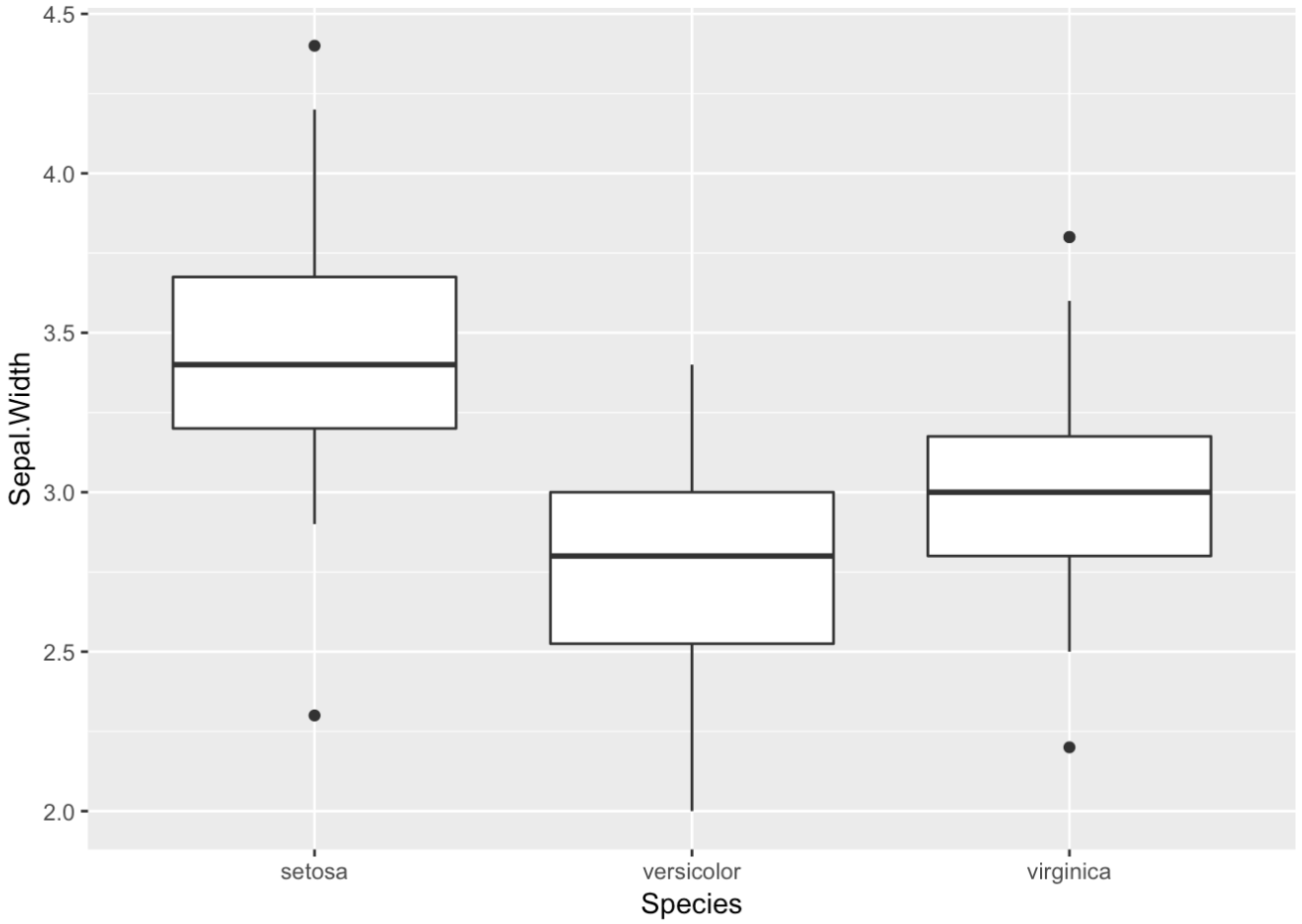
setting the binwidth of a histogram

```
ggplot(data = iris) +
  geom_histogram( aes(x = Sepal.Width), binwidth = 0.1 )
```



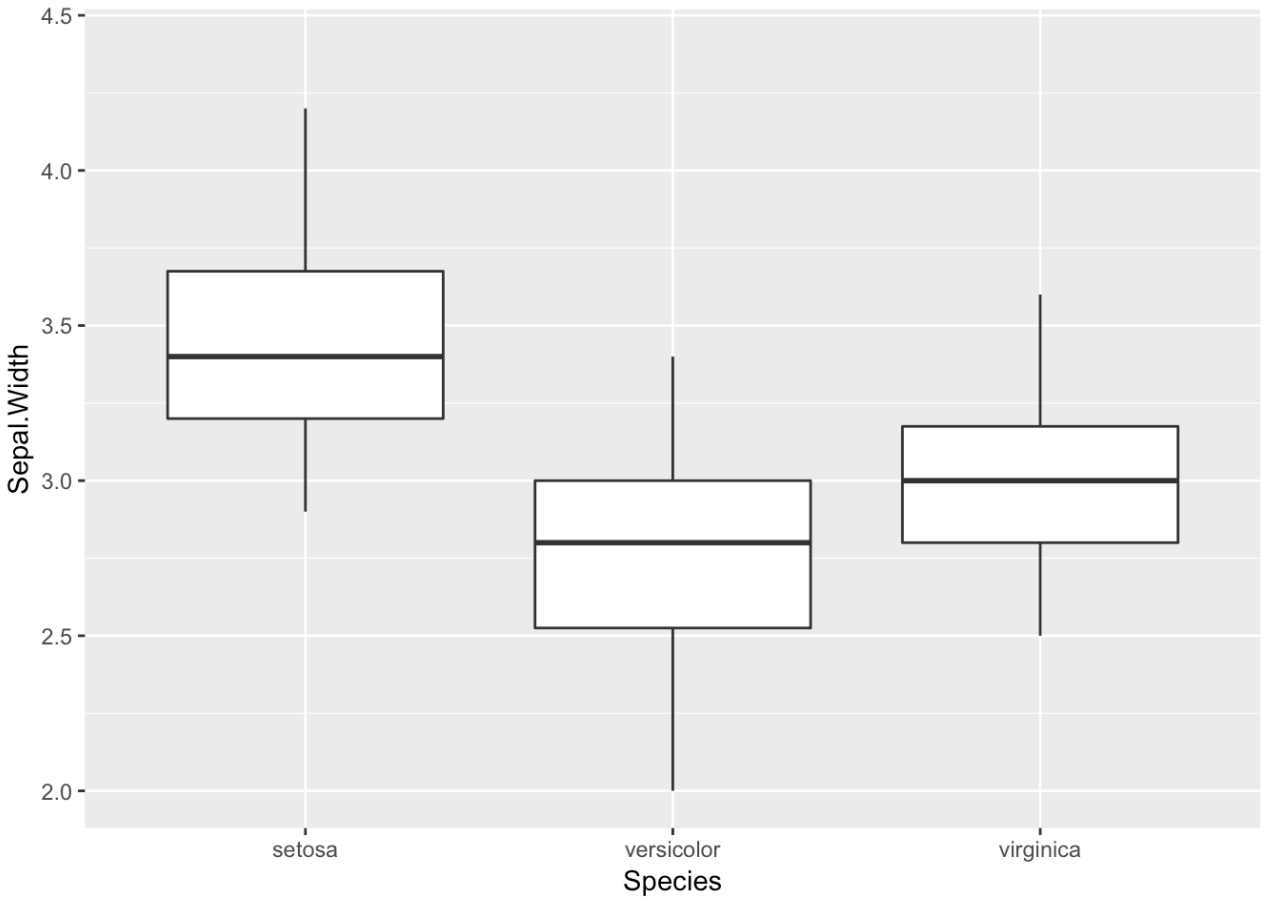
Boxplots

```
ggplot(data = iris) +
  geom_boxplot( aes(y = Sepal.Width, x = Species) )
```



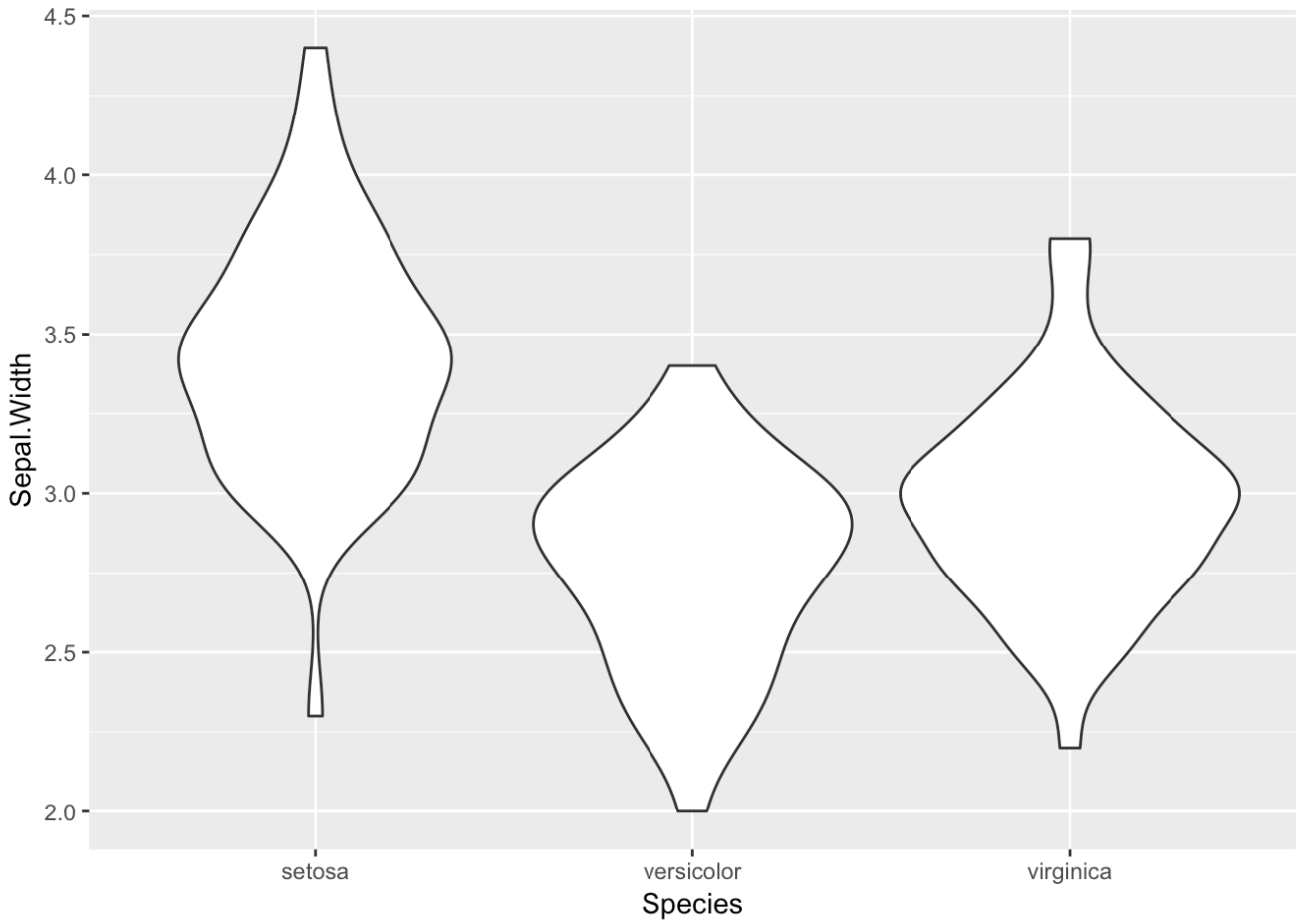
Remove outliers

```
ggplot(data = iris) +
  geom_boxplot( aes(y = Sepal.Width, x = Species),
                outlier.shape = NA)
```



Violin plot

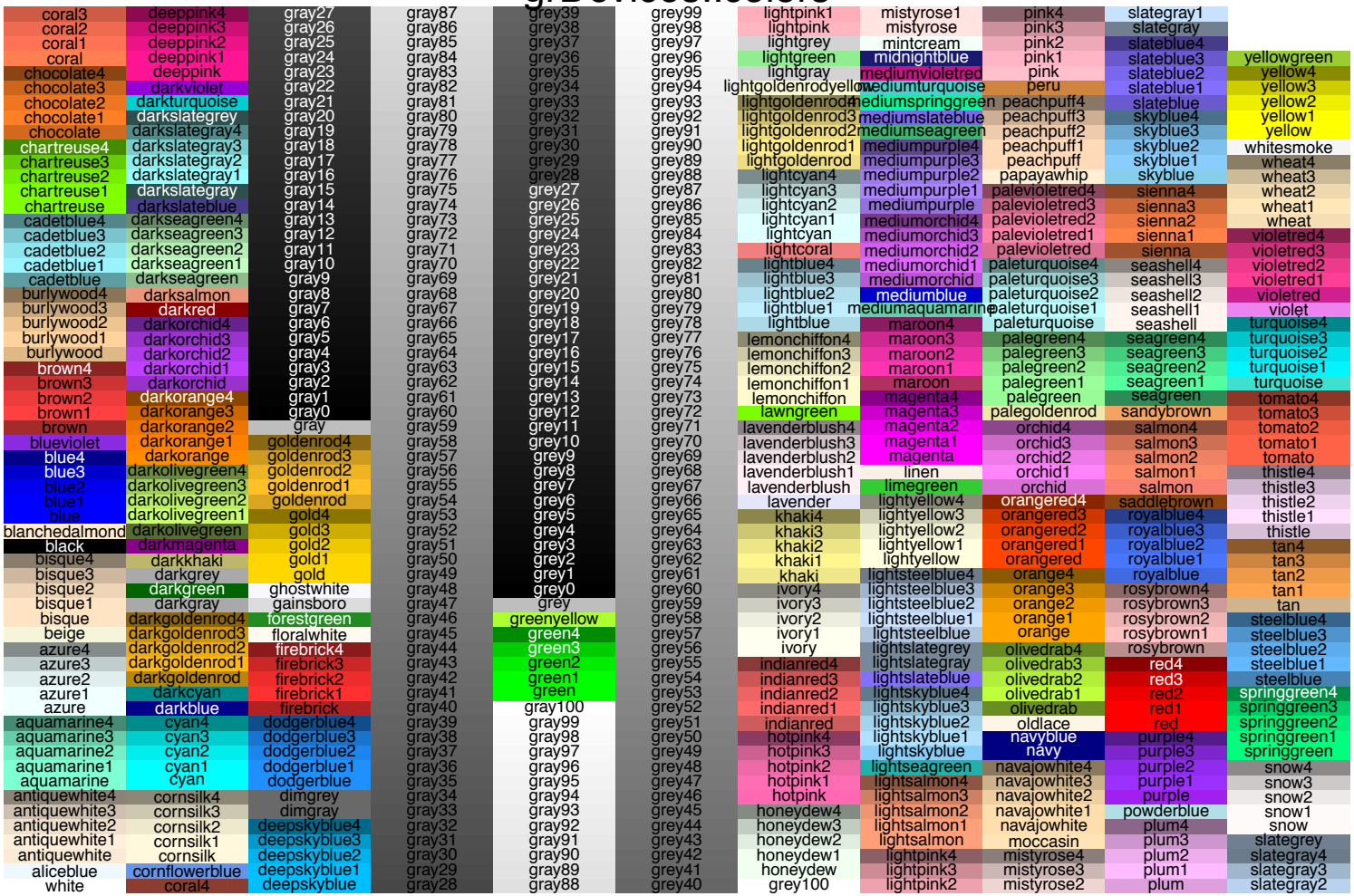
```
ggplot(data = iris) +
  geom_violin( aes(y = Sepal.Width, x = Species) )
```



Colours

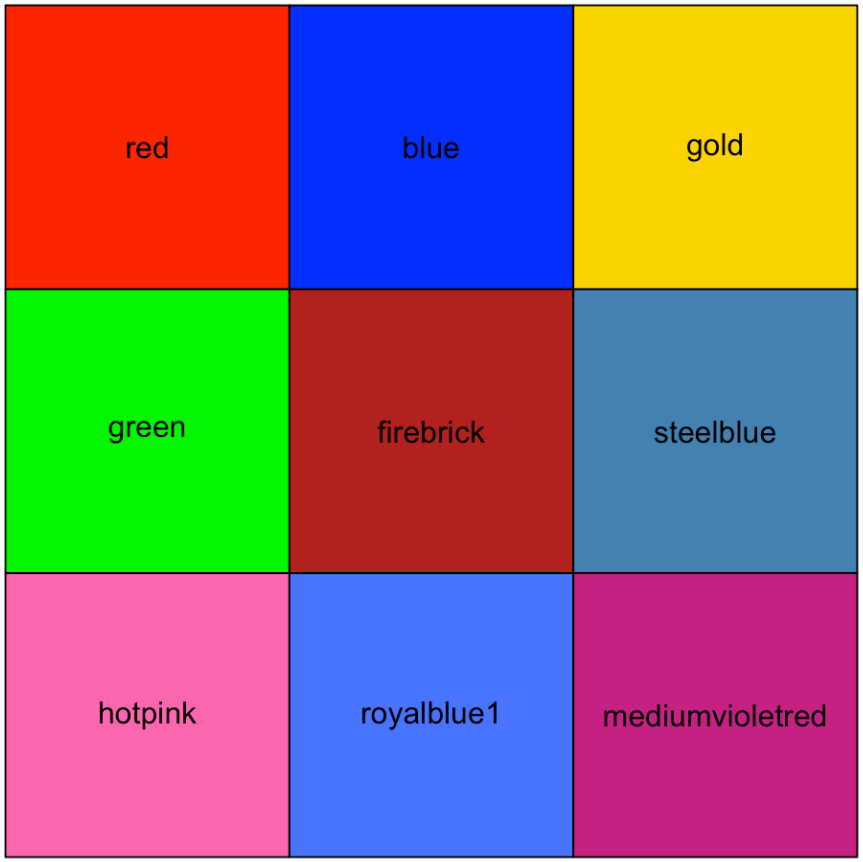
`colours()`

grDevices::colors



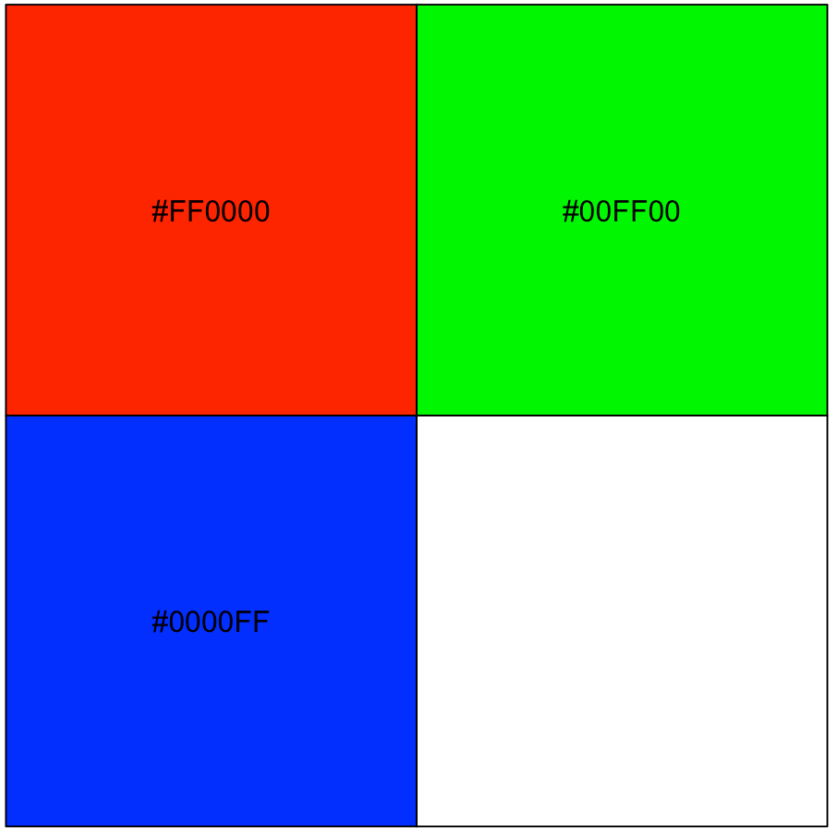
specify colours by name

```
library(scales)
show_col(c('red', 'blue', 'gold', 'green', 'firebrick', 'steelblue',
           'hotpink', 'royalblue1', 'mediumvioletred'))
```



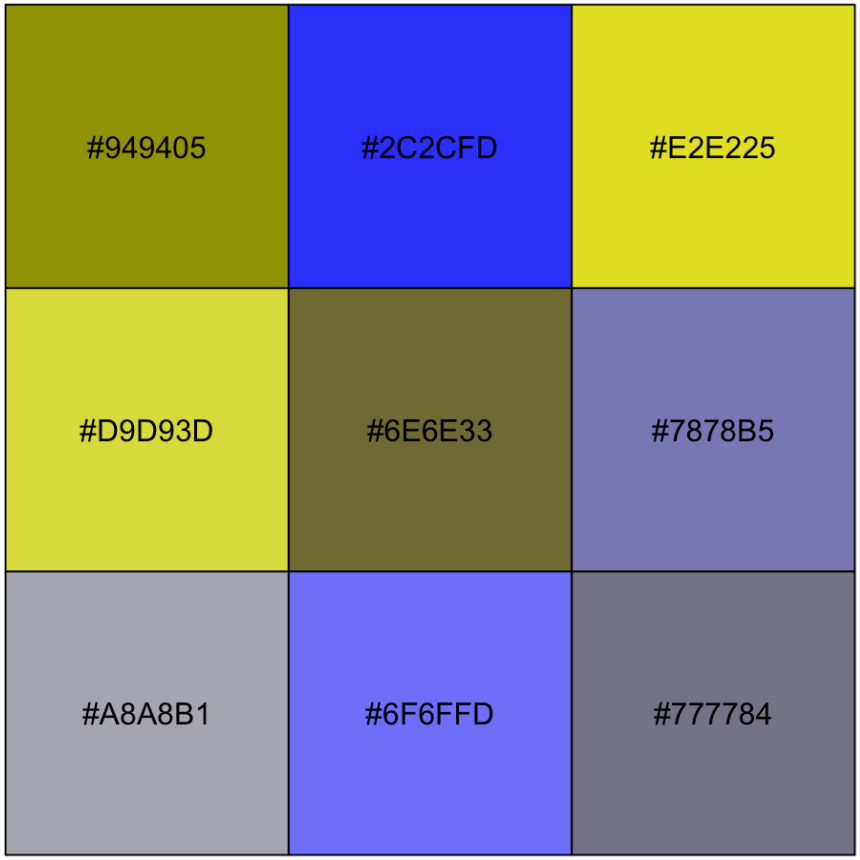
specify colours as RGB values

```
rgb_colours <- c(rgb(255,0,0, maxColorValue = 255),
                 rgb(0,255,0, maxColorValue = 255),
                 rgb(0,0,255, maxColorValue = 255))
show_col(rgb_colours)
```



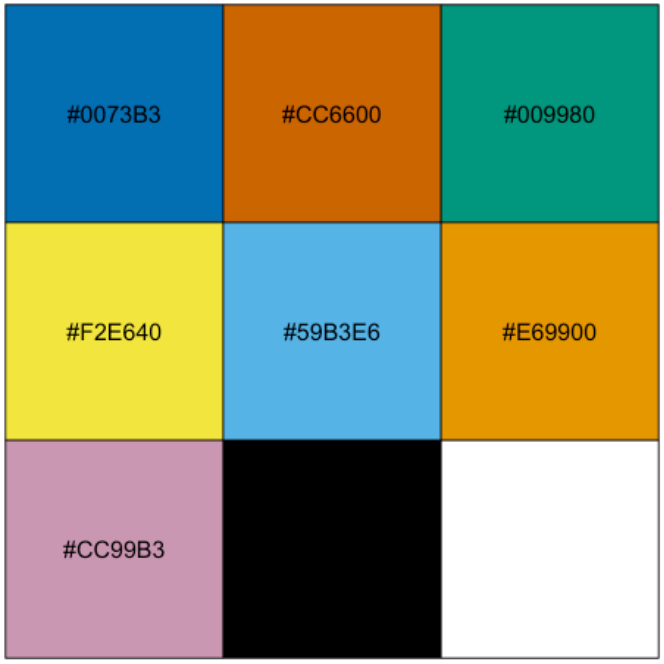
check how colour-blind friendly your palette is

```
library(dichromat)
show_col(dichromat(c('red', 'blue', 'gold', 'green', 'firebrick', 'steelblue',
           'hotpink', 'royalblue1', 'mediumvioletred')))
```

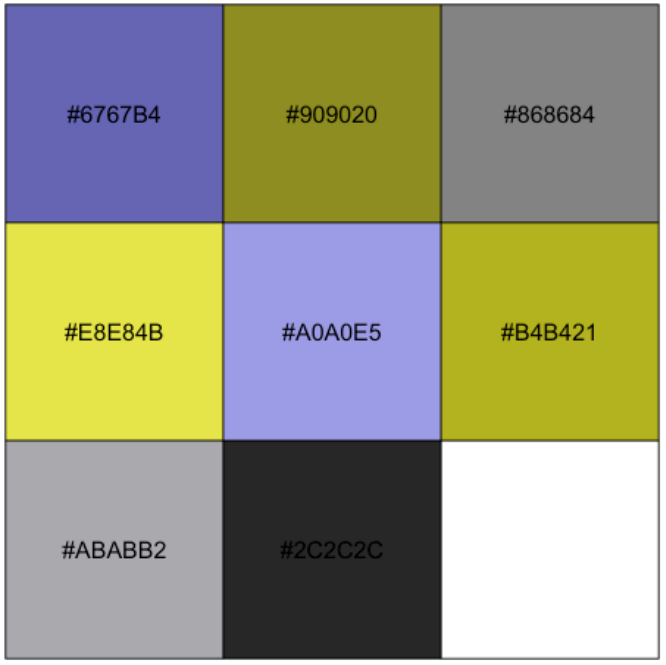


colour-blind friendly palette

```
colour_blind_palette <-
  c( 'blue' = rgb(0,0.45,0.7),
     'vermillion' = rgb(0.8, 0.4, 0),
     'blue_green' = rgb(0, 0.6, 0.5),
     'yellow' = rgb(0.95, 0.9, 0.25),
     'sky_blue' = rgb(0.35, 0.7, 0.9),
     'orange' = rgb(0.9, 0.6, 0),
     'purple' = rgb(0.8, 0.6, 0.7),
     'black' = rgb(0, 0, 0) )
show_col(colour_blind_palette)
```




```
show_col(dichromat(colour_blind_palette))
```



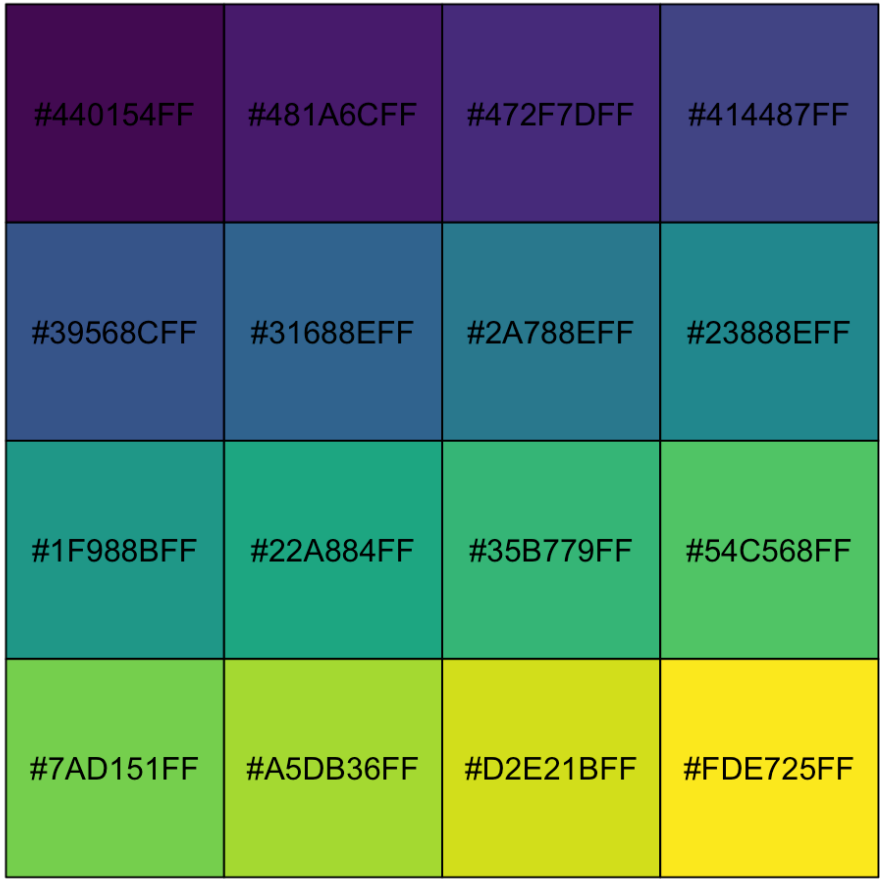
https://jfly.uni-koeln.de/color/#pallet

https://doi.org/10.1038/nmeth.1618

viridis: perceptually uniform colour scales

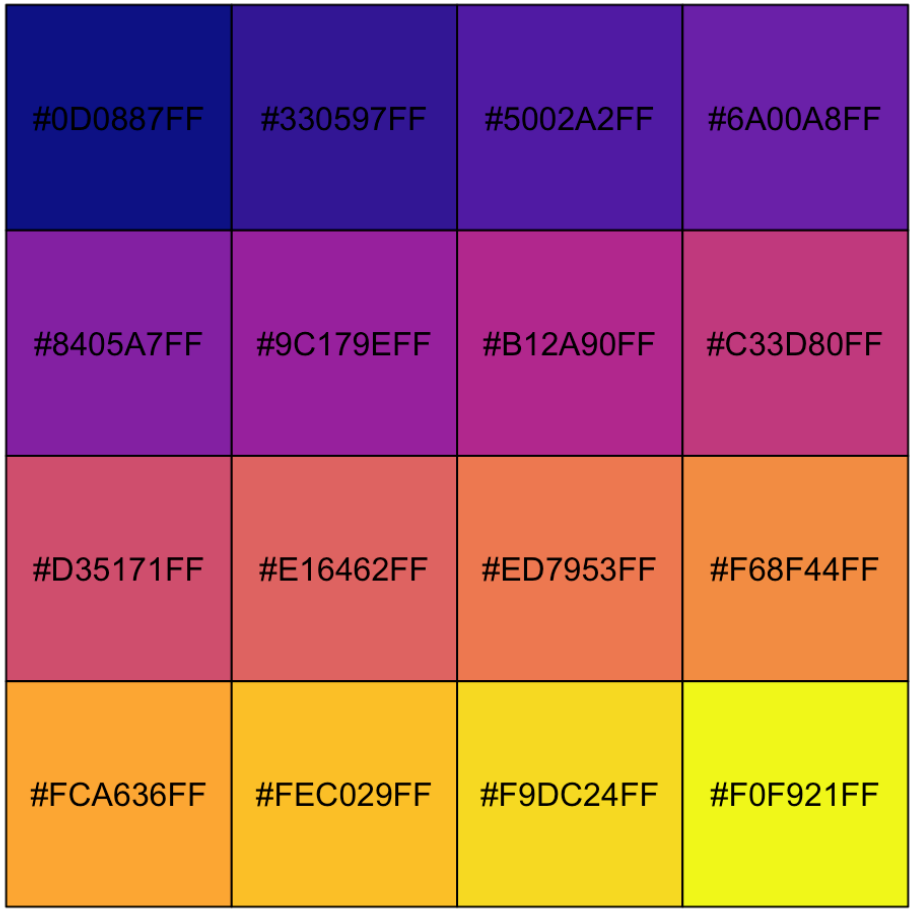
viridis: perceptually uniform colour scales

```
library(viridis)
show_col(viridis(16))
```

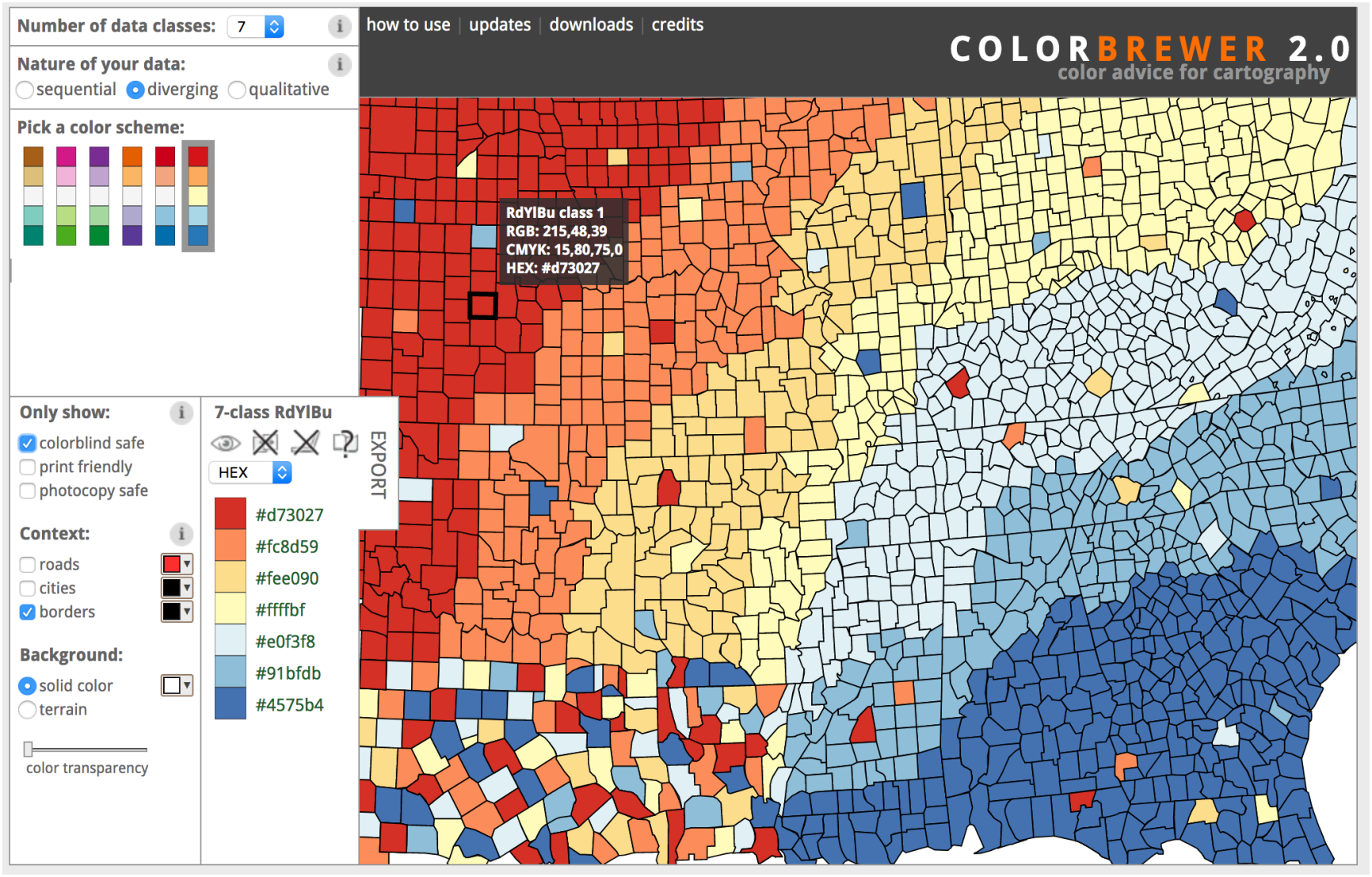


viridis-plasma

```
show_col(plasma(16))
```

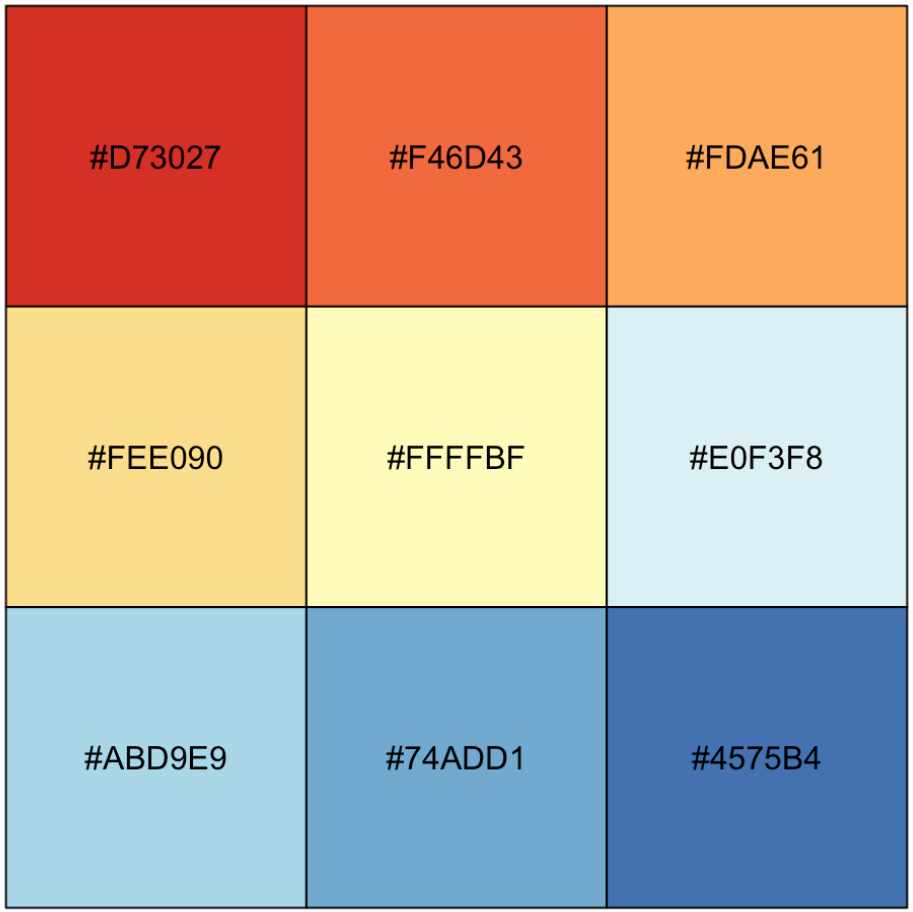


ColorBrewer



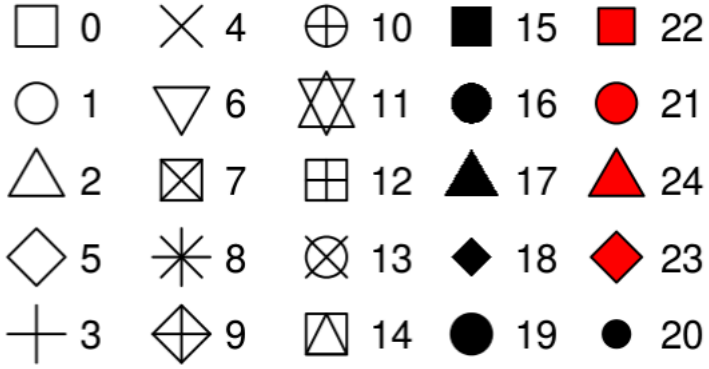
ColorBrewer colour schemes

```
show_col(brewer_pal(type = "div", palette = 'RdYlBu', direction = 1)(9))
```



Shapes

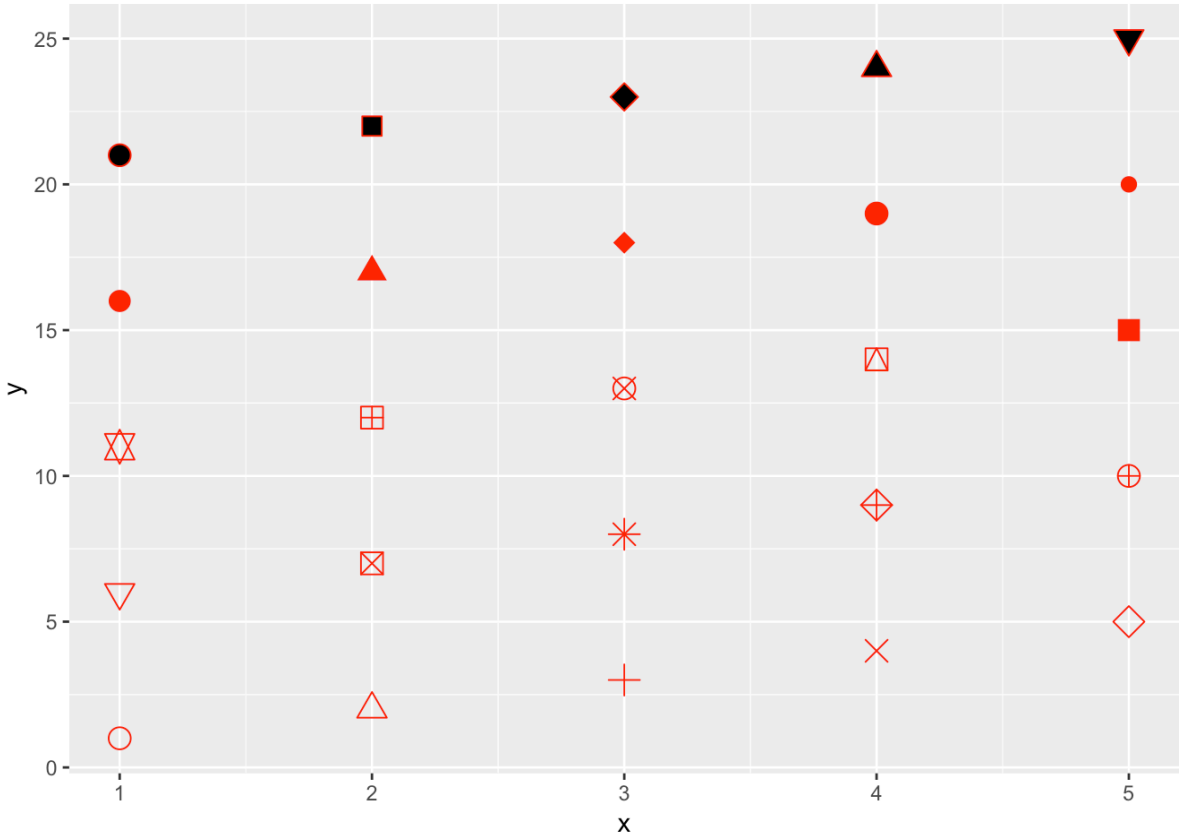
- There are 25 available shapes for plotting that are identified by numbers



- 0-14 are hollow. The border colour is determined by the colour aesthetic
- 15-20 are solid. The colour is determined by the colour aesthetic
- 21-24 are filled shapes that have a border colour and a fill colour

Shapes

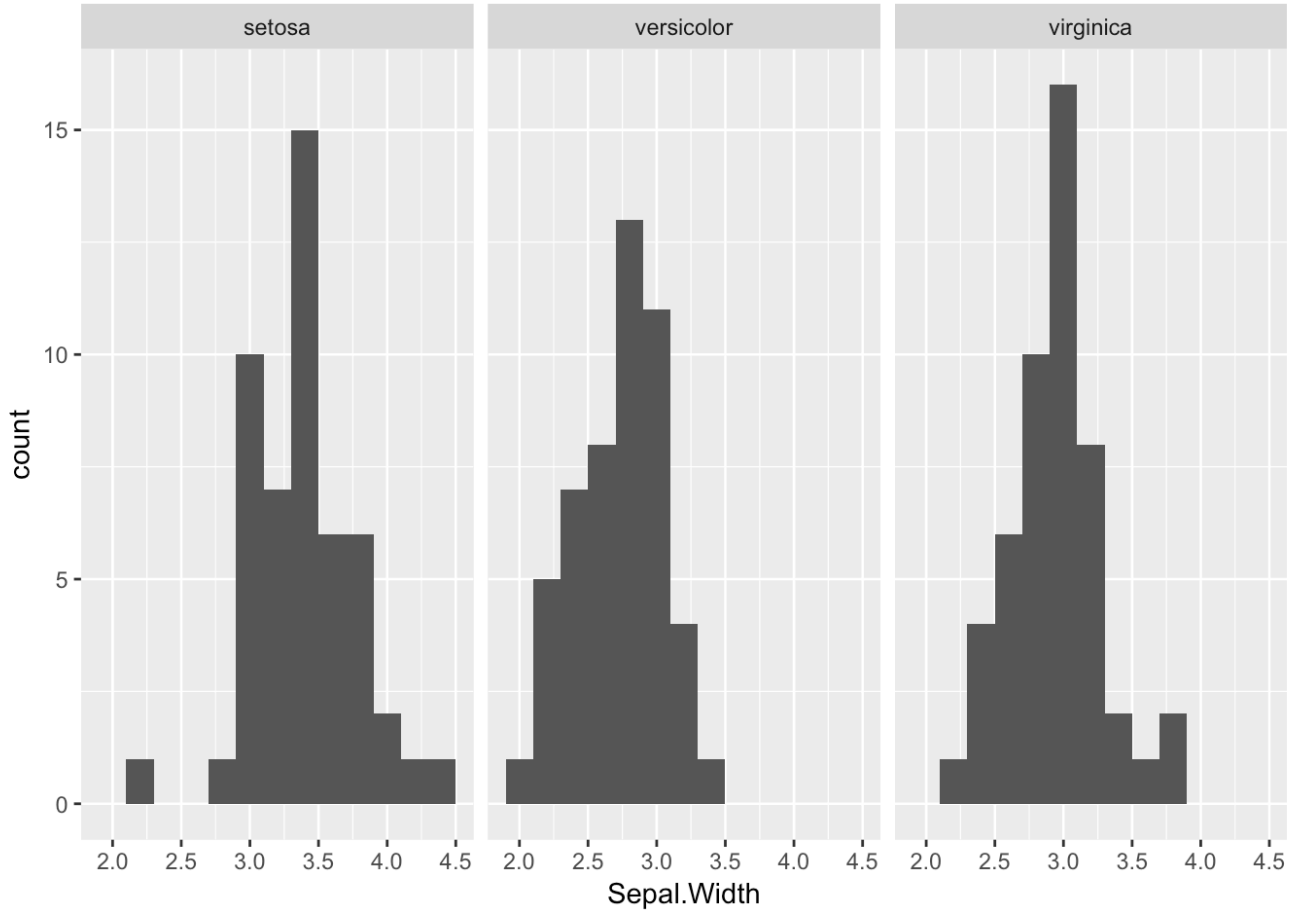
```
df2 <- data.frame(x = 1:5 , y = 1:25, z = 1:25)
ggplot(df2, aes(x, y)) +
  geom_point(aes(shape = z), size = 4,
             colour = "Red", fill = "Black") +
  scale_shape_identity()
```



https://ggplot2.tidyverse.org/reference/aes_linetype_size_shape.html

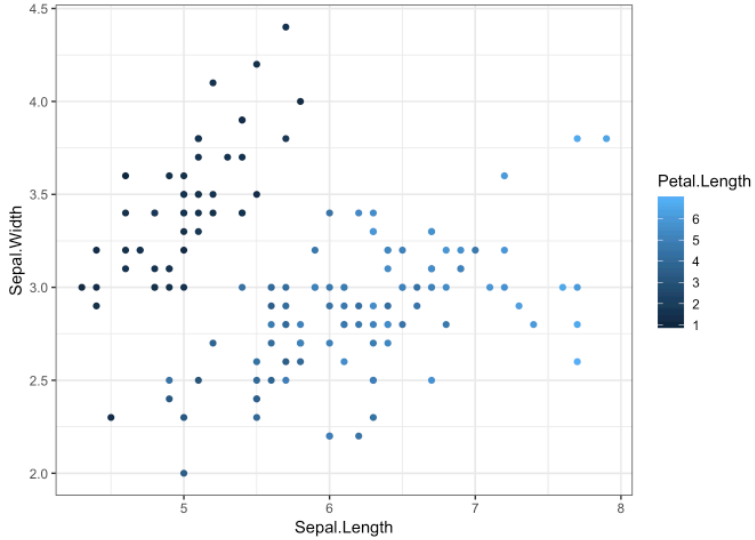
Facets

```
ggplot(data = iris) +
  geom_histogram( aes(x = Sepal.Width), binwidth = 0.2 ) +
  facet_wrap(~ Species)
```

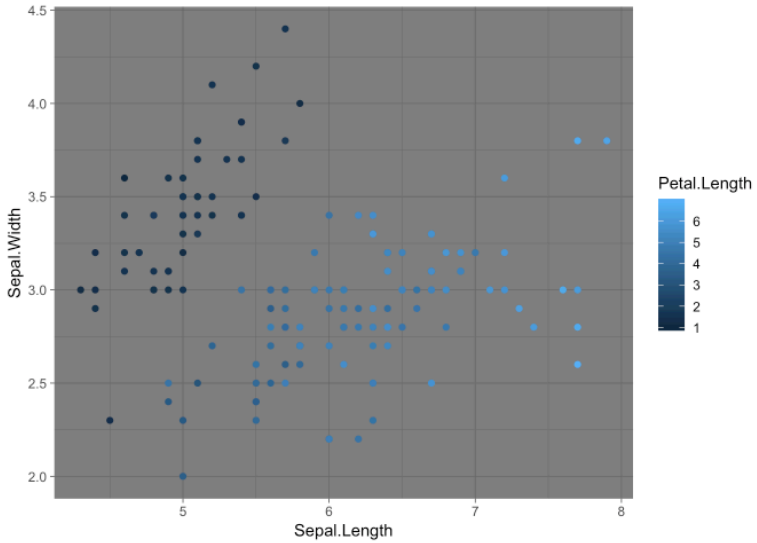


Themes

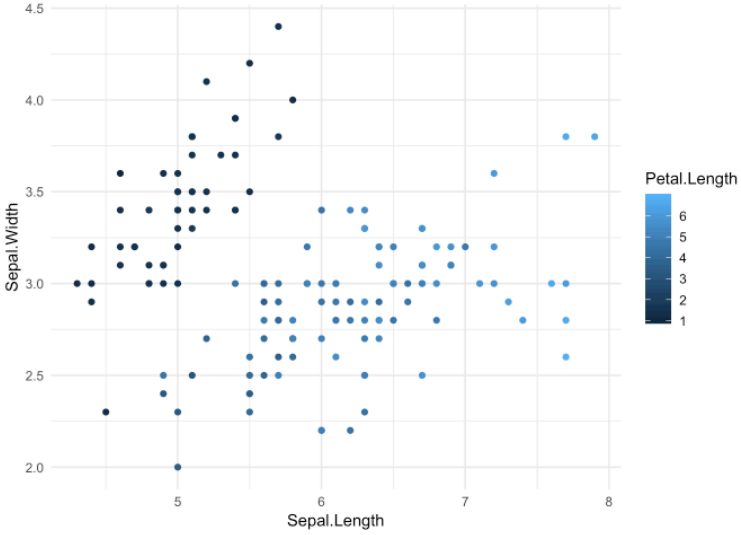
theme_bw()



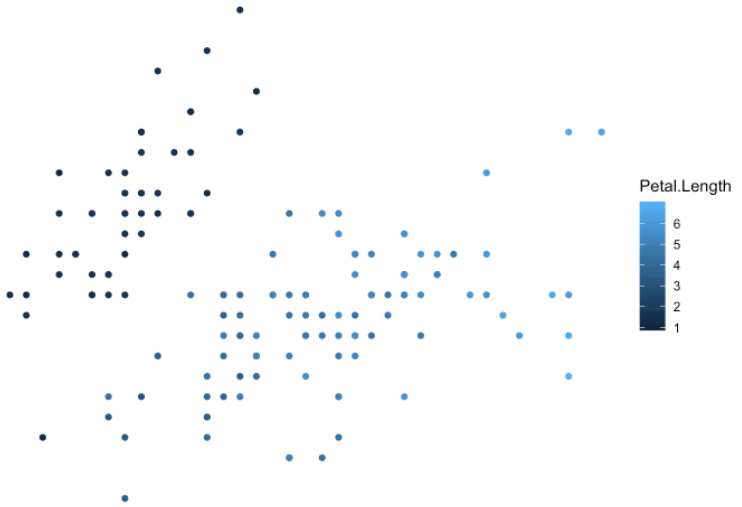
theme_dark()



theme_light()



theme_void()



Customising themes

```
theme(line, rect, text, title, aspect.ratio, axis.title, axis.title.x,
  axis.title.x.top, axis.title.x.bottom, axis.title.y, axis.title.y.left,
  axis.title.y.right, axis.text, axis.text.x, axis.text.x.top,
  axis.text.x.bottom, axis.text.y, axis.text.y.left, axis.text.y.right,
  axis.ticks, axis.ticks.x, axis.ticks.x.top, axis.ticks.x.bottom,
  axis.ticks.y, axis.ticks.y.left, axis.ticks.y.right, axis.ticks.length,
  axis.ticks.length.x, axis.ticks.length.x.top, axis.ticks.length.x.bottom,
  axis.ticks.length.y, axis.ticks.length.y.left, axis.ticks.length.y.right,
  axis.line, axis.line.x, axis.line.x.top, axis.line.x.bottom, axis.line.y,
  axis.line.y.left, axis.line.y.right, legend.background, legend.margin,
  legend.spacing, legend.spacing.x, legend.spacing.y, legend.key,
  legend.key.size, legend.key.height, legend.key.width, legend.text,
  legend.text.align, legend.title, legend.title.align, legend.position,
  legend.direction, legend.justification, legend.box, legend.box.just,
  legend.box.margin, legend.box.background, legend.box.spacing,
  panel.background, panel.border, panel.spacing, panel.spacing.x,
  panel.spacing.y, panel.grid, panel.grid.major, panel.grid.minor,
  panel.grid.major.x, panel.grid.major.y, panel.grid.minor.x,
  panel.grid.minor.y, panel.ontop, plot.background, plot.title,
  plot.subtitle, plot.caption, plot.tag, plot.tag.position, plot.margin,
  strip.background, strip.background.x, strip.background.y,
  strip.placement, strip.text, strip.text.x, strip.text.y,
  strip.switch.pad.grid, strip.switch.pad.wrap, ..., complete = FALSE,
  validate = TRUE)
```

https://ggplot2.tidyverse.org/reference/theme.html

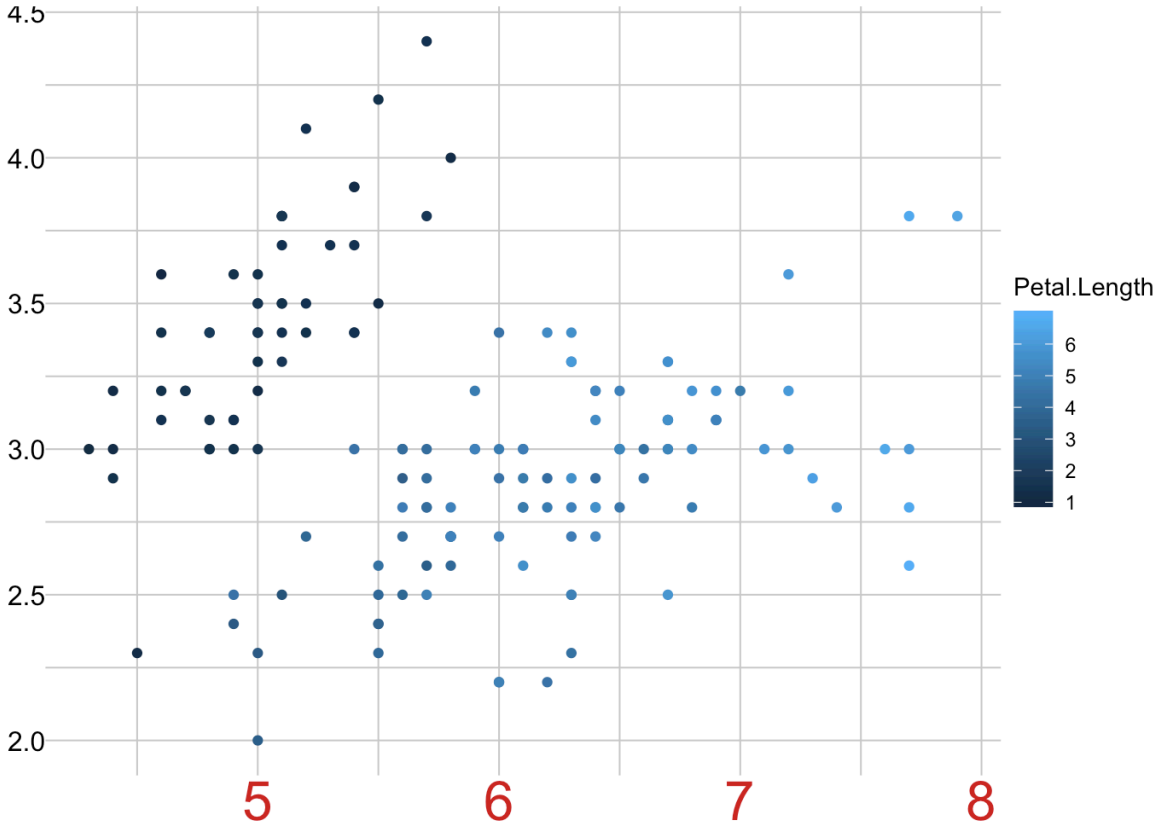
Theme elements

- element_text
  - font_family, colour, size, angle
- element_line
  - colour, size, linetype
- element_rect: borders and backgrounds
  - fill, colour, size, linetype

https://ggplot2.tidyverse.org/reference/element.html

Customising themes

```
ggplot(data = iris) +
  geom_point( aes(x = Sepal.Length, y = Sepal.Width,
                  colour = Petal.Length)) +
  theme_void() +
  theme(axis.text = element_text(colour = "black", size = 12),
        axis.text.x = element_text(colour = "firebrick3", size = 24),
        panel.grid = element_line(colour = "grey80"))
```



Further Reading

https://ggplot2.tidyverse.org/reference/

ggplot2 part of the tidyverse 3.2.1

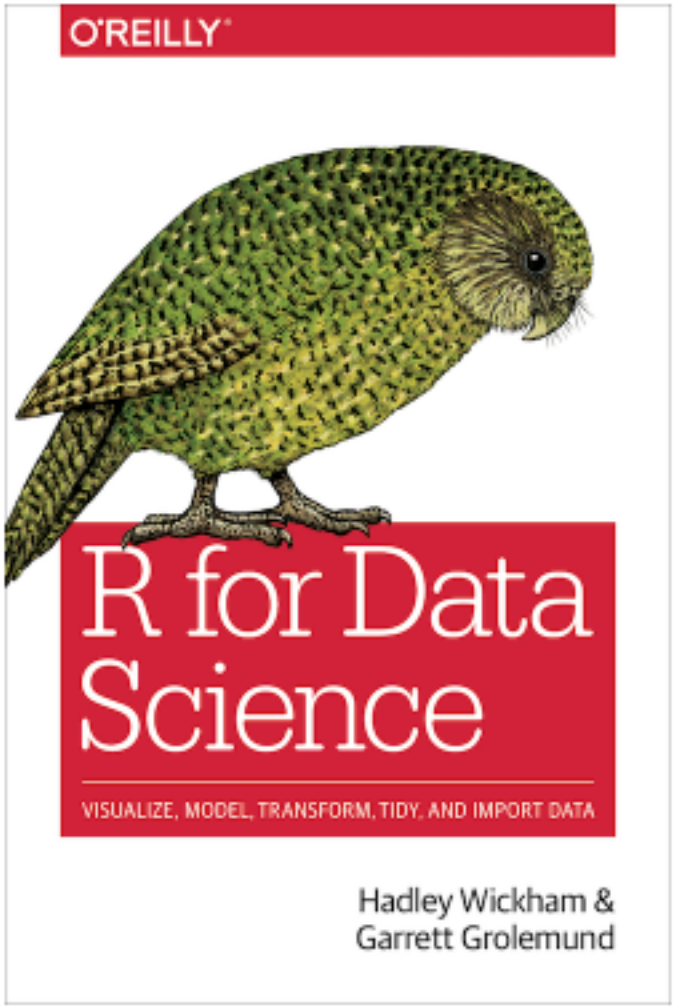
Layer: geoms

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

`geom_abline()` `geom_hline()` `geom_vline()`	Reference lines: horizontal, vertical, and diagonal
`geom_bar()` `geom_col()` `stat_count()`	Bar charts
`geom_bin2d()` `stat_bin_2d()`	Heatmap of 2d bin counts
`geom_blank()`	Draw nothing
`geom_boxplot()` `stat_boxplot()`	A box and whiskers plot (in the style of Tukey)
`geom_contour()` `stat_contour()`	2d contours of a 3d surface
`geom_count()` `stat_sum()`	Count overlapping points
`geom_density()` `stat_density()`	Smoothed density estimates

Further Reading

- https://r4ds.had.co.nz/



Exercises