Data visualization

R for Data Science

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Data distribution (categorical)

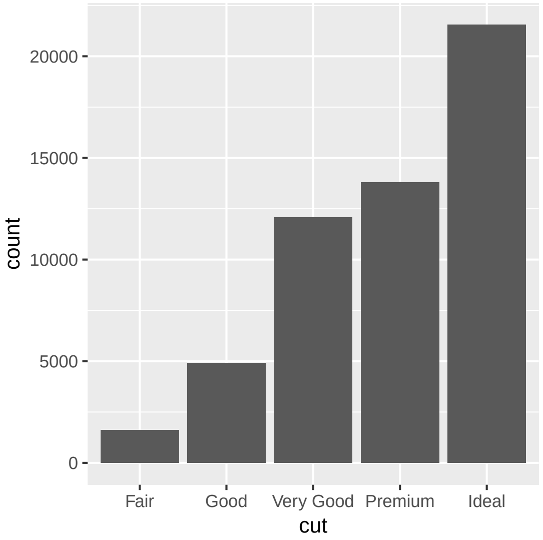
```r
library(tidyverse)
diamonds
```

```
# A tibble: 53,940 x 10
   carat cut       color clarity depth table price     x     y     z
   <dbl> <ord>     <ord> <ord>   <dbl> <dbl> <int> <dbl> <dbl> <dbl>
 1 0.23  Ideal     E     SI2      61.5    55   326  3.95  3.98  2.43
 2 0.21  Premium   E     SI1      59.8    61   326  3.89  3.84  2.31
 3 0.23  Good      E     VS1      56.9    65   327  4.05  4.07  2.31
 4 0.290 Premium   I     VS2      62.4    58   334  4.2   4.23  2.63
 5 0.31  Good      J     SI2      63.3    58   335  4.34  4.35  2.75
 6 0.24  Very Good J     VVS2     62.8    57   336  3.94  3.96  2.48
 7 0.24  Very Good I     VVS1     62.3    57   336  3.95  3.98  2.47
 8 0.26  Very Good H     SI1      61.9    55   337  4.07  4.11  2.53
 9 0.22  Fair      E     VS2      65.1    61   337  3.87  3.78  2.49
10 0.23  Very Good H     VS1      59.4    61   338  4     4.05  2.39
# ... with 53,930 more rows
```

```r
count(diamonds, cut)
```

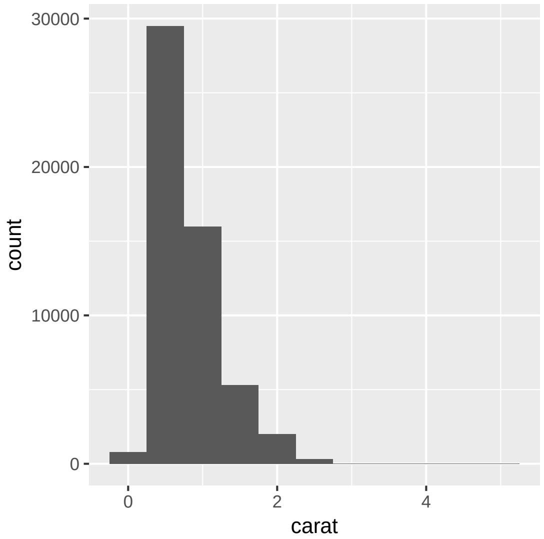
```
# A tibble: 5 x 2
  cut           n
  <ord>     <int>
1 Fair       1610
2 Good       4906
3 Very Good 12082
4 Premium   13791
5 Ideal     21551
```

```r
ggplot(data = diamonds) +
  geom_bar(mapping = aes(x = cut))
```



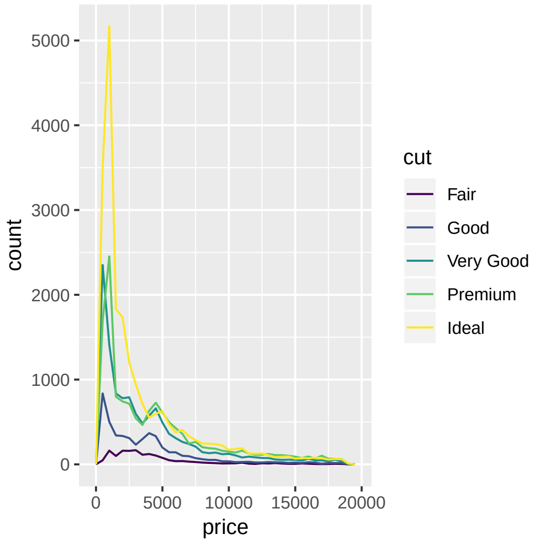
Data distribution (continous)

```
ggplot(data = diamonds) +
  geom_histogram(mapping = aes(x = carat), binwidth = 0.5)
```



Data distribution (categorical and continous)

```r
ggplot(data = diamonds, mapping = aes(x = price)) +
  geom_freqpoly(mapping = aes(colour = cut), binwidth = 500)
```



Data distribution (categorical and continous)

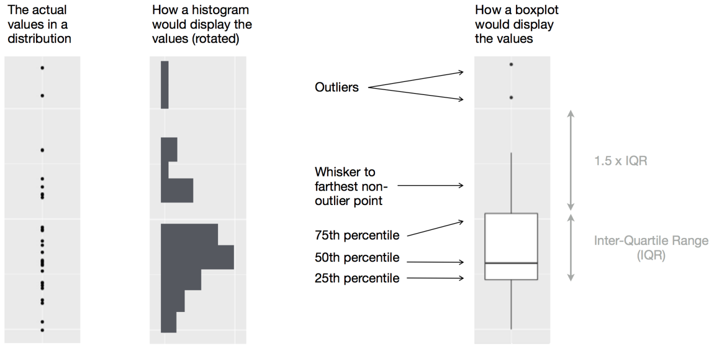
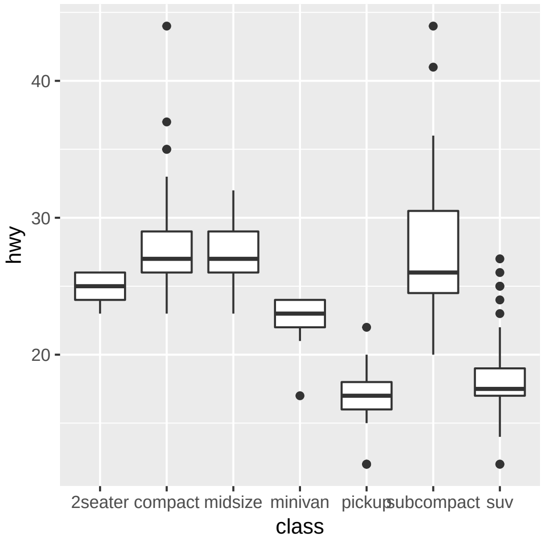

The actual values in a distribution
How a histogram would display the values (rotated)
How a boxplot would display the values
Outliers
Whisker to farthest non-outlier point
75th percentile
50th percentile
25th percentile
1.5 x IQR
Inter-Quartile Range (IQR)

Figure 1: Box-plot

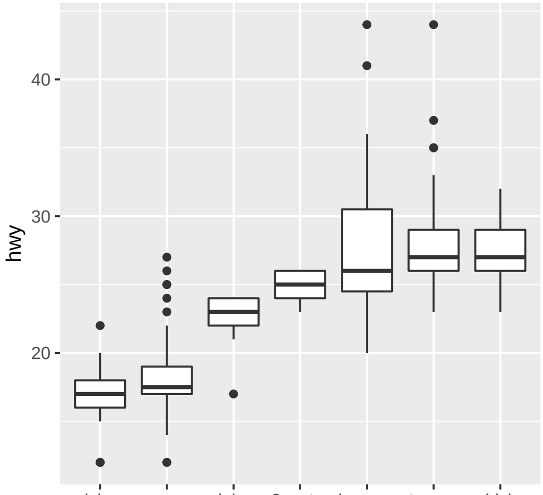
Boxplot

```
ggplot(data = mpg, mapping = aes(x = class, y = hwy)) +
  geom_boxplot()
```

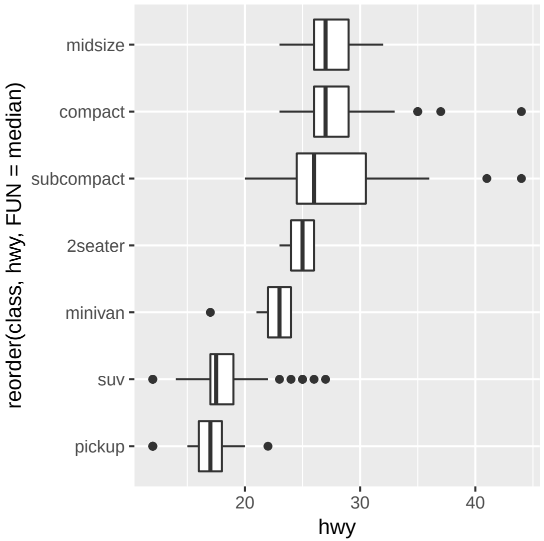


Reordered boxplot (improves interpretation)

```
ggplot(data = mpg) +
  geom_boxplot(mapping = aes(x = reorder(class, hwy,
                                         FUN = median),
                             y = hwy))
```

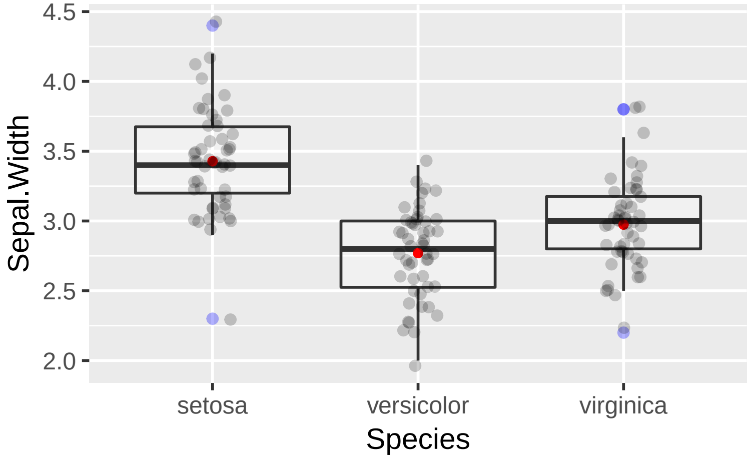


```r
ggplot(data = mpg) +
  geom_boxplot(mapping = aes(x = reorder(class, hwy,
                                          FUN = median),
                             y = hwy)) +  coord_flip()
```



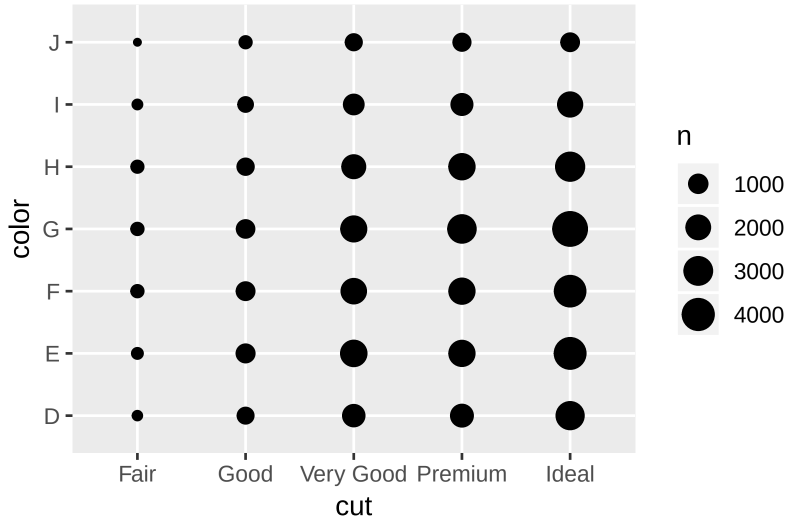
Improved boxplot

```
ggplot(iris, aes(x=Species, y=Sepal.Width) ) +
  geom_boxplot(alpha=0.3, outlier.colour = "blue") +
  geom_point(stat= "summary", fun.y=mean,
             shape=16, size=1.5, color="red") +
  geom_jitter(width = 0.1, alpha = 0.2)
```



Two categorical variables

```r
ggplot(data = diamonds) +
  geom_count(mapping = aes(x = cut, y = color))
```



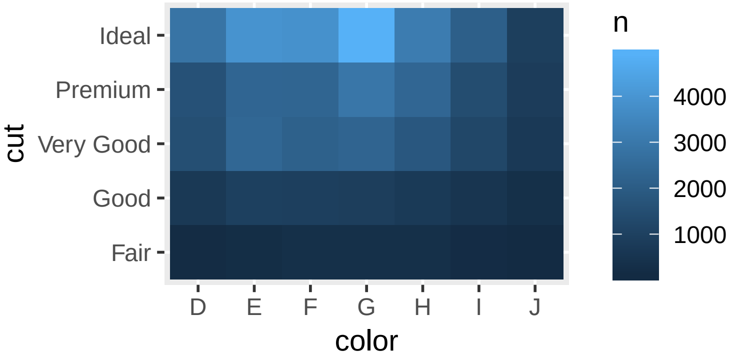
Another approach is to compute the count with `dplyr`:

```r
diamonds %>%
  count(color, cut)
```

```
# A tibble: 35 x 3
   color cut           n
   <ord> <ord>     <int>
 1 D     Fair        163
 2 D     Good        662
 3 D     Very Good  1513
 4 D     Premium    1603
 5 D     Ideal      2834
 6 E     Fair        224
 7 E     Good        933
 8 E     Very Good  2400
 9 E     Premium    2337
10 E     Ideal      3903
# ... with 25 more rows
```

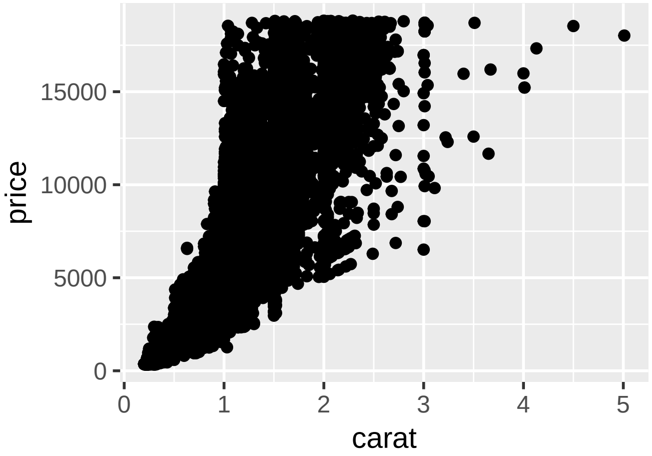
and then visuallize with `geom_tile()` and the fill aesthetic:

```
diamonds %>%
  count(color, cut) %>%
  ggplot(mapping = aes(x = color, y = cut)) +
    geom_tile(mapping = aes(fill = n))
```



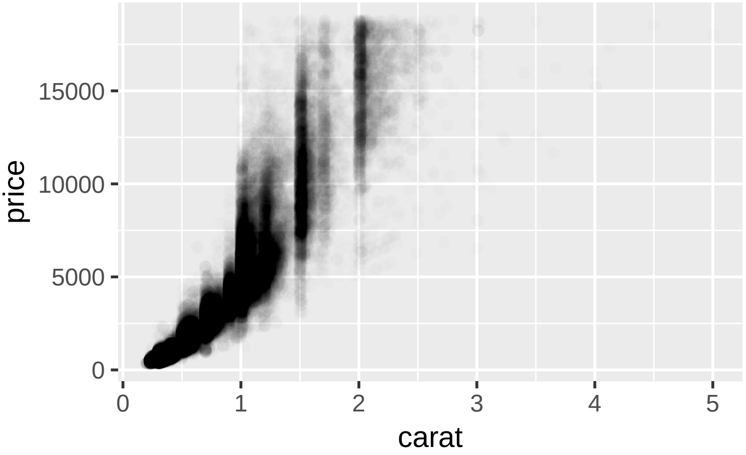
Two continuos variables

```r
ggplot(data = diamonds) +
  geom_point(mapping = aes(x = carat, y = price))
```



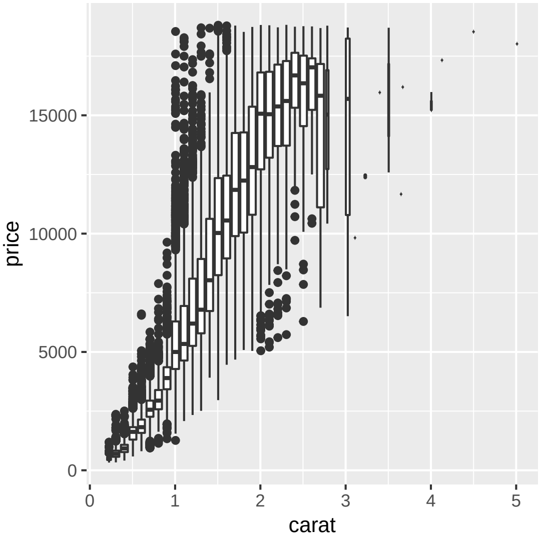
Scatterplots become less useful as the size of your dataset grows because points begin to overplot: use `alpha` aesthetic:

```r
ggplot(data = diamonds) +
  geom_point(mapping = aes(x = carat, y = price),
             alpha = 1 / 100)
```



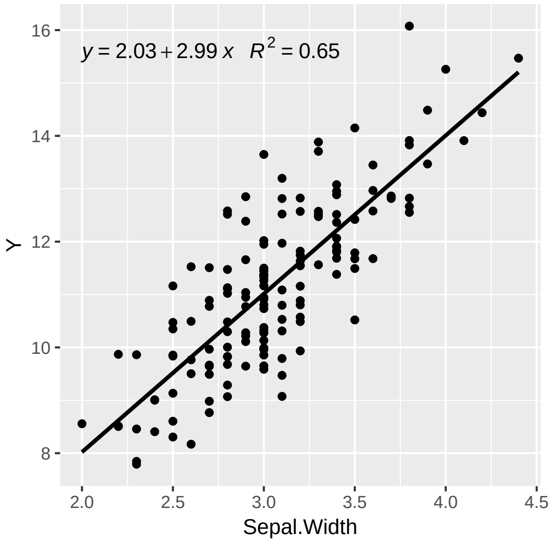
Another option is to bin one continuous variable and use `boxplot`

```
ggplot(data = diamonds, mapping = aes(x = carat, y = price)) +
  geom_boxplot(mapping = aes(group = cut_width(carat, 0.1)))
```



Fitting regression line

```r
library(ggpmisc)
set.seed(1234)
iris <- mutate(iris,
               Y = 1.5 + 3.2*Sepal.Width +
                 rnorm(nrow(iris)))
ggplot(iris, aes(x = Sepal.Width, y = Y)) +
  geom_smooth(method = "lm", se=FALSE, color="black",
              formula = y ~ x) +
  stat_poly_eq(formula = y ~ x,
               aes(label = paste(..eq.label.., ..rr.label..,
                                 sep = "~~~")),
               parse = TRUE) +
  geom_point()
```



$y = 2.03 + 2.99\,x \quad R^2 = 0.65$
Y
16
14
12
10
8
2.0
2.5
3.0
3.5
4.0
4.5
Sepal.Width

Why using ggplot2?

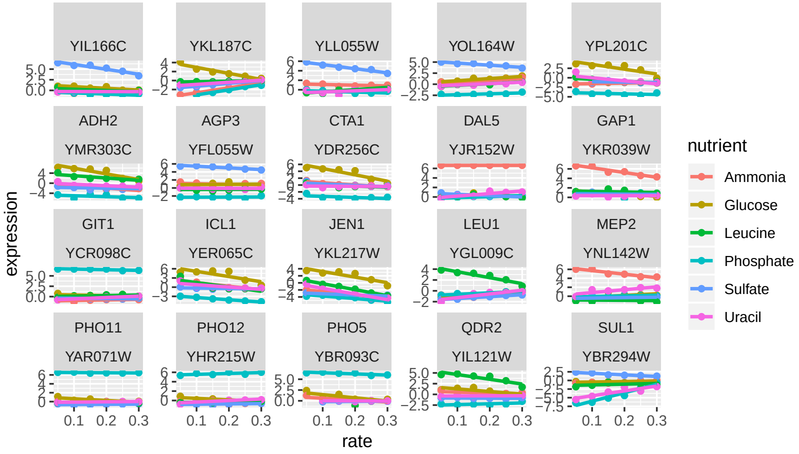
Let's image we want to compare gene expression by growth rate in twenty genes in six conditions[1]example obtained from http://varianceexplained.org/r/why-I-use-ggplot2/)

```r
load("../../data/genes.Rdata")
genes
```

```
# A tibble: 711 x 7
   name  BP             MF              systematic_name nutrient  rate expression
   <chr> <chr>          <chr>           <chr>           <chr>    <dbl>      <dbl>
 1 SUL1  sulfate tran~ sulfate trans~ YBR294W         Glucose   0.05      -0.32
 2 ""    biological p~ molecular fun~ YKL187C         Glucose   0.05       4.13
 3 QDR2  multidrug tr~ multidrug eff~ YIL121W         Glucose   0.05       1.07
 4 LEU1  leucine bios~ 3-isopropylma~ YGL009C         Glucose   0.05      -1.12
 5 PHO5  phosphate me~ acid phosphat~ YBR093C         Glucose   0.05       2.39
 6 PHO12 biological p~ acid phosphat~ YHR215W         Glucose   0.05       0.9
 7 PHO11 phosphate me~ acid phosphat~ YAR071W         Glucose   0.05       1.14
 8 GIT1  glycerophosp~ glycerophosph~ YCR098C         Glucose   0.05       0.77
 9 AGP3  amino acid t~ amino acid tr~ YFL055W         Glucose   0.05       0.570
10 ""    biological p~ molecular fun~ YOL164W         Glucose   0.05       0.53
# ... with 701 more rows
```

[1](

```r
ggplot(genes, aes(rate, expression, color = nutrient)) +
    geom_point() +
    geom_smooth(method = "lm", se = FALSE) +
    facet_wrap(~name + systematic_name, scales = "free_y")
```



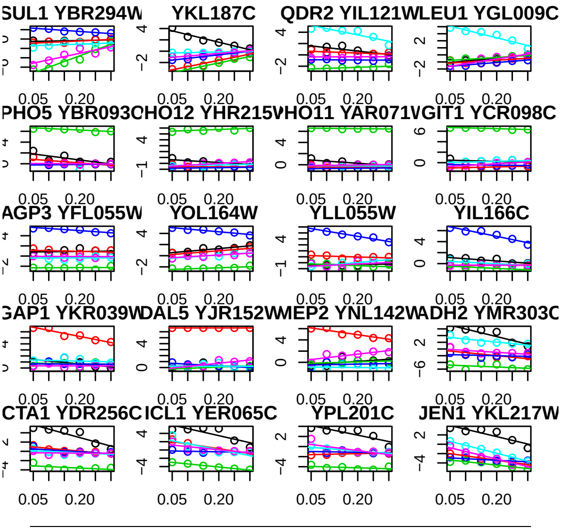
```r
par(mar = c(1.5, 1.5, 1.5, 1.5))

colors <- 1:6
names(colors) <- unique(genes$nutrient)

m <- matrix(c(1:20, 21, 21, 21, 21), nrow = 6,
            ncol = 4, byrow = TRUE)
layout(mat = m, heights = c(.18, .18, .18, .18, .18, .1))

genes$combined <- paste(genes$name, genes$systematic_name)
for (gene in unique(genes$combined)) {
    sub_data <- filter(genes, combined == gene)
    plot(expression ~ rate, sub_data,
         col = colors[sub_data$nutrient], main = gene)
    for (n in unique(sub_data$nutrient)) {
        m <- lm(expression ~ rate,
                filter(sub_data, nutrient == n))
        if (!is.na(m$coefficients[2])) {
            abline(m, col = colors[n])
        }
    }
}

# create a new plot for legend
plot(1, type = "n", axes = FALSE, xlab = "", ylab = "")
legend("top", names(colors), col = colors, horiz = TRUE, lwd = 4
```

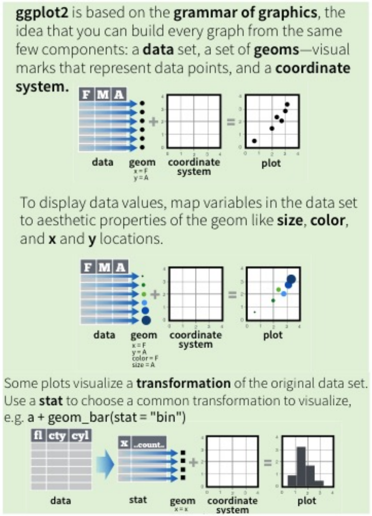

SUL1 YBR294W
YKL187C
QDR2 YIL121W
LEU1 YGL009C
PHO5 YBR093C
PHO12 YHR215W
PHO11 YAR071W
GIT1 YCR098C
AGP3 YFL055W
YOL164W
YLL055W
YIL166C
GAP1 YKR039W
DAL5 YJR152W
MEP2 YNL142W
ADH2 YMR303C
CTA1 YDR256C
ICL1 YER065C
YPL201C
JEN1 YKL217W
0.05
0.20

ggplot2

Every visualization in ggplot2 is composed of the following:

- Data: the raw material of your visualization
- Layers: what you see on the plot (e.g., points, lines, . . .)
- Scales: Maps the data to graphical output
- Coordinates: The visualization's perspective (e.g., grids)
- Faceting: Provides "visual drill-down" into the data
- Themes: Controls the details of the display (e.g. fonts)

plot = data + Aesthetics + geometry



ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same few components: a **data** set, a set of **geoms**—visual marks that represent data points, and a **coordinate system.**

To display data values, map variables in the data set to aesthetic properties of the geom like **size**, **color**, and **x** and **y** locations.

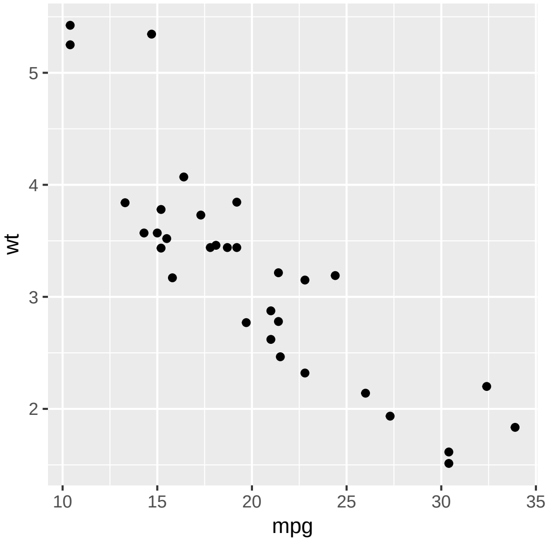
Some plots visualize a **transformation** of the original data set. Use a **stat** to choose a common transformation to visualize, e.g. a + geom_bar(stat = "bin")

Figure 2: ggplot cheat seet:
https://www.rstudio.com/resources/cheatsheets/

```r
mtcars[1:5,1:8]
```

```
                   mpg cyl disp  hp drat    wt  qsec vs
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0
```

```r
ggplot(mtcars) +              # data
  aes(x = mpg, y=wt) +        # Aesthetics
  geom_point()                # geometry (layer)
```

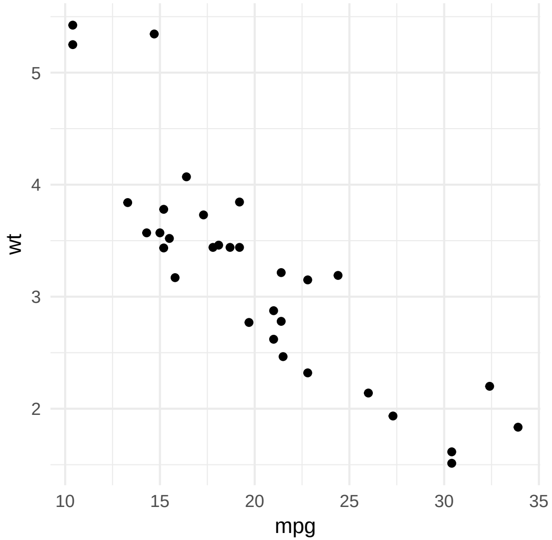


Possible aesthetics

These are some:

- `theme_dark()`
- `theme_minimal()`
- `theme_classic()`
- `theme_void()`
- `theme_test()`

```r
ggplot(mtcars) +               # data
  aes(x = mpg, y=wt) +    # Aesthetics
  geom_point() +               # geometry (layer)
  theme_minimal()              # theme
```



Possible geometry (layers)

- For one continuous variable:
  - `geom_area()` for area plot
  - `geom_density()` for density plot
  - `geom_dotplot()` for dot plot
  - `geom_freqpoly()` for frequency polygon
  - `geom_histogram()` for histogram plot
  - `stat_ecdf()` for empirical cumulative density function
  - `stat_qq()` for quantile - quantile plot
- For one discrete variable:
  - `geom_bar()` for bar plot

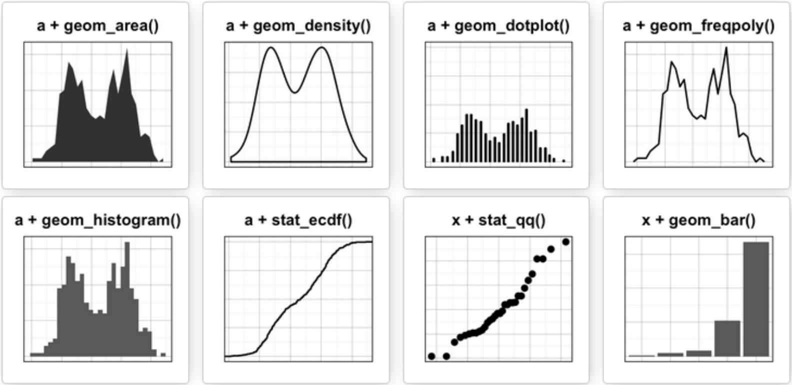
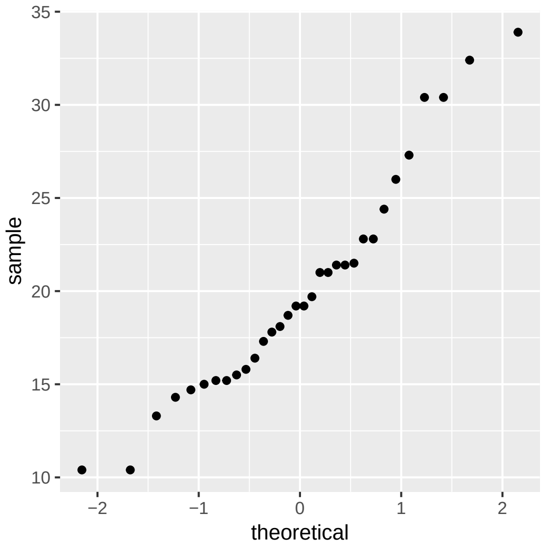


Figure 3: Possible layers

```r
ggplot(mtcars) +
  aes(sample = mpg) + stat_qq()
```

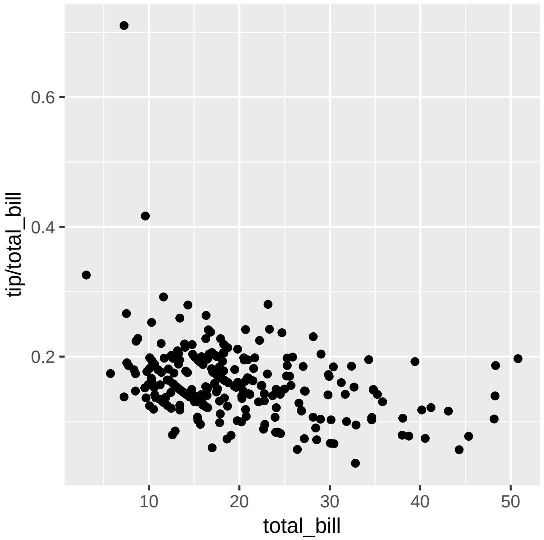


Facets

```r
data(tips, package="reshape2")
head(tips)
```

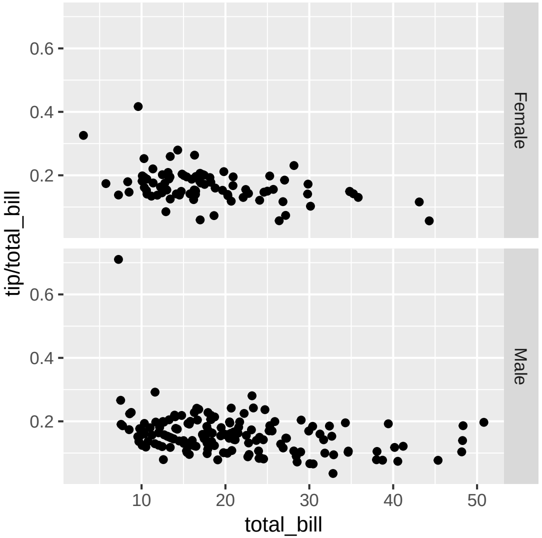
```
  total_bill  tip    sex smoker day   time size
1      16.99 1.01 Female     No Sun Dinner    2
2      10.34 1.66   Male     No Sun Dinner    3
3      21.01 3.50   Male     No Sun Dinner    3
4      23.68 3.31   Male     No Sun Dinner    2
5      24.59 3.61 Female     No Sun Dinner    4
6      25.29 4.71   Male     No Sun Dinner    4
```

```
sp <- ggplot(tips, aes(x=total_bill, y=tip/total_bill)) +
  geom_point()
sp
```

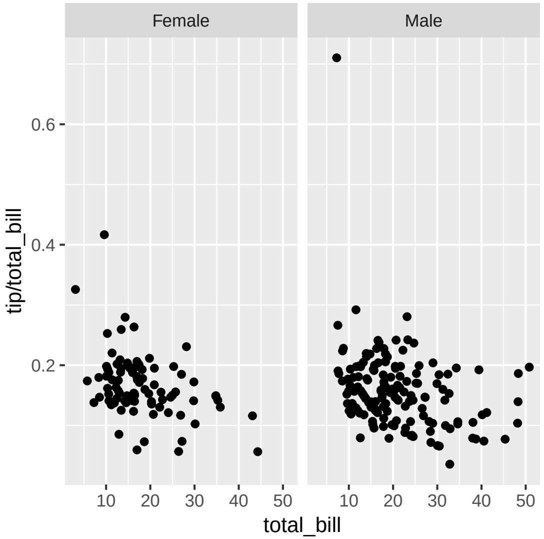


Facet grid

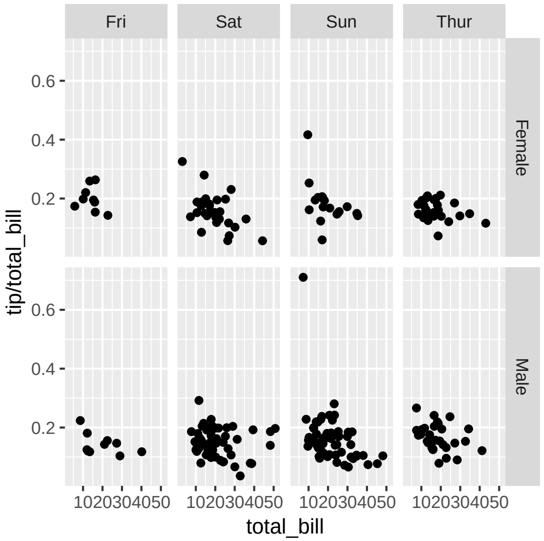
```r
# vertical direction
sp + facet_grid(sex ~ .)
```



```r
# horizontal direction
sp + facet_grid(. ~ sex)
```



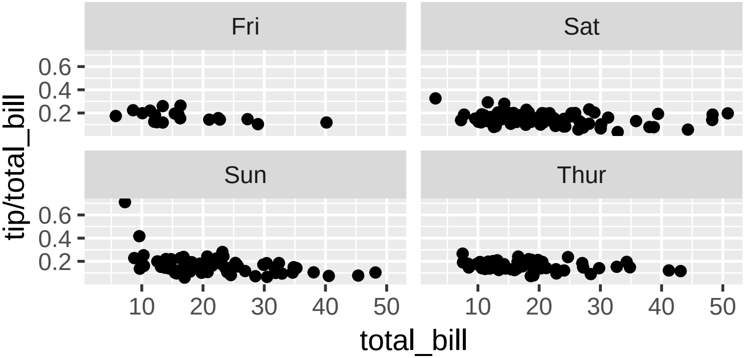
```r
# Divide with "sex" vertical, "day" horizontal
sp + facet_grid(sex ~ day)
```



Facet wrap

Instead of faceting with a variable in the horizontal or vertical direction, facets can be placed next to each other, wrapping with a certain number of columns or rows. The label for each plot will be at the top of the plot.

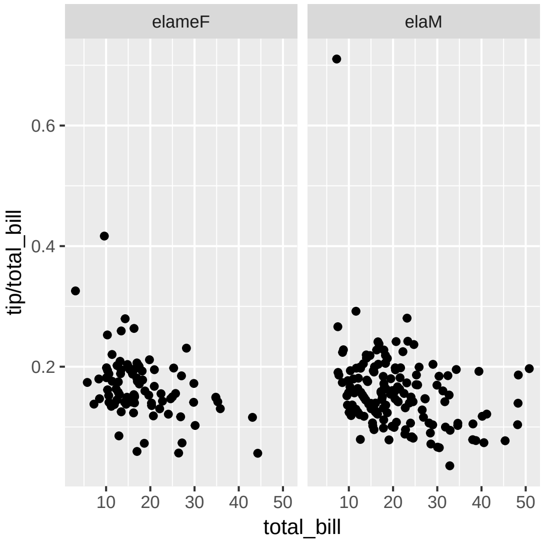
```
# Divide by day, going horizontally and wrapping with 2 columns
sp + facet_wrap( ~ day, ncol=2)
```



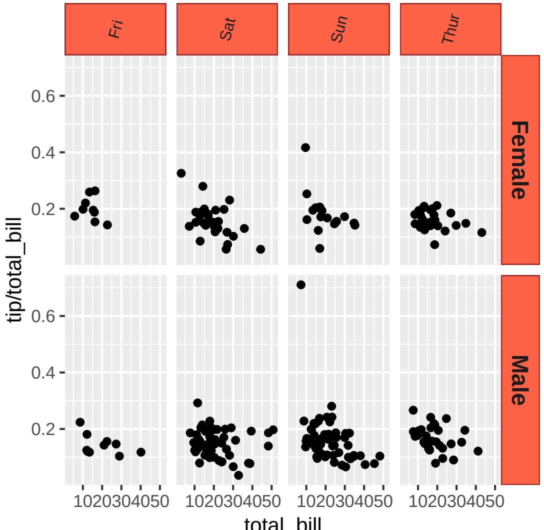
`labeller()` can use any function that takes a character vector as input and returns a character vector as output (e.g. `gsub`). We can also define our own custom functions, like this one, which reverses strings:

```r
# Reverse each strings in a character vector
reverse <- function(strings) {
    strings <- strsplit(strings, "")
    vapply(strings, function(x) {
        paste(rev(x), collapse = "")
    }, FUN.VALUE = character(1))
}

sp + facet_grid(. ~ sex, labeller=labeller(sex = reverse))
```


elameF
elaM
tip/total_bill
0.6
0.4
0.2
10
20
30
40
50
total_bill

```r
sp + facet_grid(sex ~ day) +
    theme(strip.text.x = element_text(size=8, angle=75),
          strip.text.y = element_text(size=12, face="bold"),
          strip.background = element_rect(colour="brown",
                                          fill="tomato"))
```



More about ggplot2 . . . .

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

Exercises (data visualization)

1. Use what you've learned to improve the visualisation of the departure times of cancelled vs. non-cancelled flights (NOTE: missing values in the `dep_time` variable indicate that the flight was cancelled).
2. What variable in the diamonds dataset is most important for predicting the price of a diamond? How is that variable correlated with `cut`? Why does the combination of those two relationships lead to lower quality diamonds being more expensive?. NOTE: variable `cut` describes the quality (see `?diamonds`).
3. Visualize the number of flights of each airline by month.
4. Instead of summarising the conditional distribution with a boxplot, you could use a frequency polygon. What do you need to consider when using `cut_width()` vs `cut_number()`? How does that impact a visualisation of the 2d distribution of carat and price (`diamonds` dataset)?
5. Visualise the distribution of carat, partitioned by price on `diamonds` dataset .

6. Download genome data (https://github.com/isglobal-brge/TeachingMaterials/blob/master/Master_Modelling/data/genome.txt) into your computer and load it into RStudio by using `read_delim` function (NOTE: data are tab-delimited).

The file is containing information about

- Name: genomic variant (single nucleotide polymorphism)
- Chr: chromosome
- Position: chromosome position
- Log.R.Ratio: log-ratio intensity of the two alleles
- B.Allele.Freq: frequency of the alternative allele
    - 6.1 Which is the expected value of `Log.R.Ratio` and `B.Allel.Freq` for each chromosome? (show the R code to get your answer)
    - 6.2 Create a facet plot that represent the `Log.R.Ratio` for each chromosome
    - 6.3 Create a facet plot of `B.Allele.Freq` for chromosomes 1, 2, 3, . . . , 6 drawing `B.Allele.Freq` information in red color.

Session info

```r
sessionInfo()
```

```
R version 3.5.0 (2018-04-23)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 17134)

Matrix products: default

locale:
[1] LC_COLLATE=Spanish_Spain.1252  LC_CTYPE=Spanish_Spain.1252
[3] LC_MONETARY=Spanish_Spain.1252 LC_NUMERIC=C
[5] LC_TIME=Spanish_Spain.1252

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
 [1] bindrcpp_0.2.2  ggpmisc_0.3.0   forcats_0.3.0   stringr_1.3.1
 [5] dplyr_0.7.6     purrr_0.2.4     readr_1.1.1     tidyr_0.8.0
 [9] tibble_1.4.2    ggplot2_3.0.0   tidyverse_1.2.1

loaded via a namespace (and not attached):
 [1] tidyselect_0.2.4 reshape2_1.4.3   haven_1.1.1      lattice_0.20-35
 [5] colorspace_1.3-2 viridisLite_0.3.0 htmltools_0.3.6  yaml_2.1.19
 [9] utf8_1.1.3       rlang_0.2.2      pillar_1.2.2     foreign_0.8-70
[13] glue_1.2.0       withr_2.1.2      modelr_0.1.2     readxl_1.1.0
[17] bindr_0.1.1      plyr_1.8.4       munsell_0.5.0    gtable_0.2.0
[21] cellranger_1.1.0 rvest_0.3.2      codetools_0.2-15 psych_1.8.4
[25] evaluate_0.10.1  labeling_0.3     knitr_1.20       parallel_3.5.0
[29] broom_0.4.4      Rcpp_0.12.18     polynom_1.3-9    scales_1.0.0
[33] backports_1.1.2  jsonlite_1.5     mnormt_1.5-5     hms_0.4.2
```