

Lecture 5: Exploratory Data Analysis

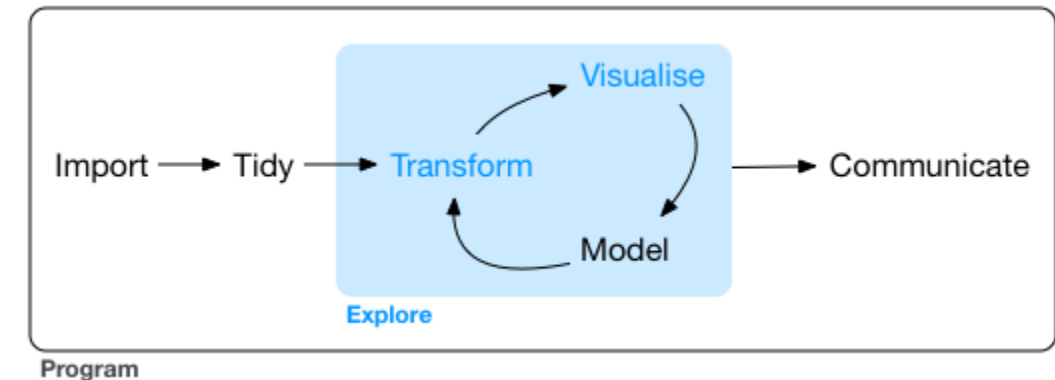
CME/STATS 195

Lan Huong Nguyen

October 11, 2018

Contents

- Data Manipulation
 - Programming with `purrr`
 - Handling missing values
 - Merging datasets
- Exploratory Data Analysis
 - Variation
 - Covariation
- Interactive graphics
- Data Export



Data Manipulation

The `purrr` package

Package `purrr` is part of the `tidyverse`. Handles tasks similar to ones performed by `apply`-family functions in base R.

It enhances R's functional programming toolkit by providing a complete and consistent set of tools for working with functions and vectors. `map`-functions allow you to replace many `for` loops with code that is easier to read.

- `map()`, `map_if()`, `map_at()` returns a list
- `map_lgl()` returns a logical vector,
- `map_int()` returns a integer vector,
- `map_dbl()` returns a double vector,
- `map_chr()` returns a character vector,
- `map_dfr()`, `map_df()` returns a `data.frame` by binding rows or columns respectively.

The map functions

Example: column-wise mean

```
df <- tibble(a=rnorm(10), b=rnorm(10), c=rnorm(10), d=rnorm(10))
map_dbl(df, mean) # or equivalently: df %>% map_dbl(mean)
```

```
##           a           b           c           d
## -0.53592399 -0.04025187  0.25081582 -0.05770421
```

Focus is on the operation being performed, not the book-keeping:

- purrr functions are implemented in C.
- the second argument, .f, can be a function, a formula, a character vector, or an integer vector.

```
map(1:3, ~ rnorm(7, .x))
```

```
## [[1]]
## [1] 1.0782558 0.2743947 0.3041190 1.0134683 1.1395083 1.3808201 2.1555289
##
## [[2]]
## [1] 3.0128433 1.1747387 -0.2547562 0.4858909 2.1740475 3.0109330
## [7] 1.5207914
##
## [[3]]
## [1] 3.843500 3.187574 1.161702 3.463796 3.584169 4.298590 2.210775
```

- `map` can pass additional parameters to the function

```
map_dbl(df, mean, trim = 0.25)
```

```
##           a           b           c           d
## -0.36711034  0.14183991  0.43717035  0.03812828
```

- other inputs/outputs:

```
mtcars %>%
  split(.$cyl)
```

```
## $`4`
##           mpg cyl  disp  hp drat   wt
## Datsun 710    22.8   4 108.0  93 3.85 2.320
## Merc 240D     24.4   4 146.7  62 3.69 3.190
## Merc 230      22.8   4 140.8  95 3.92 3.150
## Fiat 128      32.4   4  78.7  66 4.08 2.200
## Honda Civic   30.4   4  75.7  52 4.93 1.615
## Toyota Corolla 33.9   4  71.1  65 4.22 1.835
## Toyota Corona 21.5   4 120.1  97 3.70 2.465
## Fiat X1-9     27.3   4  79.0  66 4.08 1.935
## Porsche 914-2 26.0   4 120.3  91 4.43 2.140
## Lotus Europa  30.4   4  95.1 113 3.77 1.513
## Volvo 142E    21.4   4 121.0 109 4.11 2.780
##
## $`6`
##           mpg cyl  disp  hp drat   wt
## Mazda RX4     21.0   6 160.0 110 3.90 2.620
## Mazda RX4 Wag 21.0   6 160.0 110 3.90 2.875
## Hornet 4 Drive 21.4   6 258.0 110 3.08 3.215
## Valiant        18.1   6 225.0 105 2.76 3.460
## Merc 280       19.2   6 167.6 123 3.92 3.440
## Merc 280C      17.8   6 167.6 123 3.92 3.440
## Ferrari Dino   19.7   6 145.0 175 3.62 2.770
##
```

```
mtcars %>%
  split(.$cyl) %>%
  map_df(dim)
```

```
## # A tibble: 2 x 3
##   `4`   `6`   `8`
##   <int> <int> <int>
## 1    11     7    14
## 2    11    11    11
```

```
##
## $`8`
##      mpg  cyl  disp  hp drat
## Hornet Sportabout 18.7    8 360.0 175 3.15 3
## Duster 360        14.3    8 360.0 245 3.21 3
## Merc 450SE        16.4    8 275.8 180 3.07 4
## Merc 450SL        17.3    8 275.8 180 3.07 3
## Merc 450SLC       15.2    8 275.8 180 3.07 3
## Cadillac Fleetwood 10.4    8 472.0 205 2.93 5
## Lincoln Continental 10.4    8 460.0 215 3.00 5
## Chrysler Imperial 14.7    8 440.0 230 3.23 5
## Dodge Challenger  15.5    8 318.0 150 2.76 3
## AMC Javelin        15.2    8 304.0 150 3.15 3
## Camaro Z28         13.3    8 350.0 245 3.73 3
## Pontiac Firebird   19.2    8 400.0 175 3.08 3
## Ford Pantera L     15.8    8 351.0 264 4.22 3
## Maserati Bora      15.0    8 301.0 335 3.54 3
```

Base-R maps vs. purrr maps

However, `purrr` is more consistent, so you should learn it.

A quick reference of similar base R functions:

- `lapply` is basically identical to `map`
- `sapply` is a wrapper around `lapply` and it tries to simplify the output.
Downside: you never know what you'll get
- `vapply`: like `sapply`, but you can supply an additional argument that defines the type

You can learn more about `purrr` here: (<http://r4ds.had.co.nz/iteration.html>)

Handling missing values

Missing values

Two types of missingness

```
stocks <- tibble(  
  year = c(2015, 2015, 2015, 2015, 2016, 2016, 2016),  
  qtr = c(1, 2, 3, 4, 2, 3, 4),  
  return = c(1.88, 0.59, 0.35, NA, 0.92, 0.17, 2.66)  
)
```

The return for the fourth quarter of 2015 is **explicitly missing**

The return for the first quarter of 2016 is **implicitly missing**

The way that a dataset is represented can make implicit values explicit.

```
stocks %>% spread(year, return)
```

```
## # A tibble: 4 x 3  
##   qtr `2015` `2016`  
##   <dbl> <dbl> <dbl>  
## 1     1  1.88    NA  
## 2     2  0.59    0.92  
## 3     3  0.35    0.17  
## 4     4   NA    2.66
```

Gathering missing data

Recall the functions we learned from `tidyr` package.

You can use `spread()` and `gather()` to retain only non-missing records, i.e. to turn all explicit missing values into implicit ones.

```
stocks %>% spread(year, return) %>%  
  gather(year, return, `2015`:`2016`, na.rm = TRUE)
```

```
## # A tibble: 6 x 3  
##   qtr year  return  
##   <dbl> <chr>  <dbl>  
## 1     1 2015    1.88  
## 2     2 2015    0.59  
## 3     3 2015    0.35  
## 4     2 2016    0.92  
## 5     3 2016    0.17  
## 6     4 2016    2.66
```

Completing missing data

`complete()` takes a set of columns, and finds all unique combinations. It then ensures the original dataset contains all those values, **filling in explicit NAs** where necessary.

```
stocks %>% complete(year, qtr)
```

```
## # A tibble: 8 x 3
##   year    qtr return
##   <dbl> <dbl>   <dbl>
## 1  2015     1   1.88
## 2  2015     2   0.59
## 3  2015     3   0.35
## 4  2015     4    NA
## 5  2016     1    NA
## 6  2016     2   0.92
## 7  2016     3   0.17
## 8  2016     4   2.66
```

Different interpretations of NA

Sometimes when a data source has primarily been used for data entry, missing values indicate that the previous value should be carried forward:

```
# tribble() constructs a tibble by filling by rows
treatment <- tribble(
  ~ person,      ~ treatment, ~response,
  "Derrick Whitmore", 1,      7,
  NA,                2,      10,
  NA,                3,      9,
  "Katherine Burke", 1,      4
)
```

You can fill in these missing values with `fill()`

```
treatment %>% fill(person)
```

```
## # A tibble: 4 x 3
##   person      treatment response
##   <chr>         <dbl>     <dbl>
## 1 Derrick Whitmore         1         7
## 2 Derrick Whitmore         2        10
## 3 Derrick Whitmore         3         9
## 4 Katherine Burke         1         4
```

Merging datasets

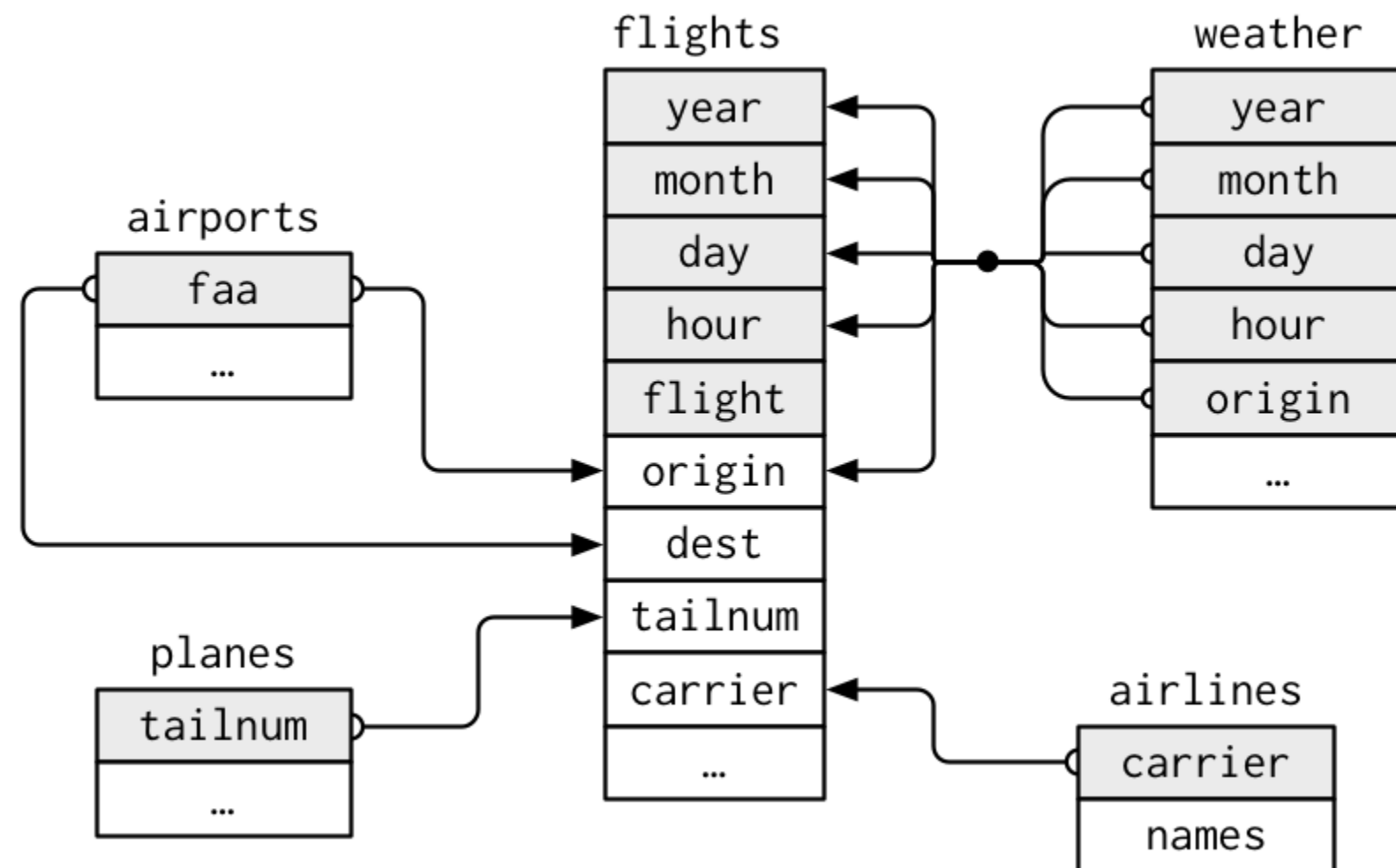
Relational data

- Rarely does a data analysis involve only a single table of data.
- Collectively, multiple tables of data are called **relational data** because the relations, not just the individual datasets, that are important.
- Relations are always defined between a pair of tables.
- All other relations are built up from this simple idea: the relations of three or more tables are always a property of the relations between each pair.

Example

the `nycflights13` package contains a collection of related datasets.

```
library(nycflights13)
```



Source: (<http://r4ds.had.co.nz/relational-data.html>)

Keys

A **key** is a variable (or set of variables) that uniquely identifies an observation.

For example, each plane is uniquely determined by its tailnum, but an observation in 'weather' is identified by five variables: year, month, day, hour, and origin

Keys can be used to connect each pair of tables together.

There are two types of keys:

- **Primary:** identifies an observation in its own table. Example: `planes$tailnum`
- **Foreign:** identifies an observation in another table. Example: `flights$tailnum`, this is because `tailnum` does not enough to identify a record in `flights` dataset.

A variable can be both a primary key and a foreign key.

Identify primary keys

It's good practice to verify that chosen keys do indeed uniquely identify each observation.

One way to do that is to `count ()` the primary keys and look for entries where `n` is greater than one:

```
planes %>%  
  count(tailnum) %>%  
  filter(n > 1)
```

```
## # A tibble: 0 x 2  
## # ... with 2 variables: tailnum <chr>, n <int>
```

```
weather %>%  
  count(year, month, day, hour, origin) %>%  
  filter(n > 1)
```

```
## # A tibble: 3 x 6  
##   year month   day hour origin      n  
##   <dbl> <dbl> <int> <int> <chr>  <int>  
## 1  2013    11     3     1 EWR      2  
## 2  2013    11     3     1 JFK      2  
## 3  2013    11     3     1 LGA      2
```

No primary key

Sometimes a table doesn't have an explicit primary key, e.g. in `flights` dataset each row is an observation, but no combination of variables reliably identifies it, (even the flight numbers).

In this case, you can add an extra `identifier` column:

```
flights %>%  
  count(flight) %>%  
  filter(n > 1)
```

```
## # A tibble: 3,493 x 2  
##   flight      n  
##   <int> <int>  
## 1     1    701  
## 2     2     51  
## 3     3   631  
## 4     4   393  
## 5     5   324  
## 6     6   210  
## 7     7   237  
## 8     8   236  
## 9     9   153  
## 10    10    61  
## # ... with 3,483 more rows
```

```
flights %>%  
  mutate(flight_id= paste0("F", row_number())) %>%  
  select(flight_id, year:flight)
```

```
## # A tibble: 336,776 x 12  
##   flight_id year month   day dep_time sched  
##   <chr>      <int> <int> <int>    <int>  
## 1 F1        2013     1     1     517  
## 2 F2        2013     1     1     533  
## 3 F3        2013     1     1     542  
## 4 F4        2013     1     1     544  
## 5 F5        2013     1     1     554  
## 6 F6        2013     1     1     554  
## 7 F7        2013     1     1     555  
## 8 F8        2013     1     1     557  
## 9 F9        2013     1     1     557  
## 10 F10       2013     1     1     558  
## # ... with 336,766 more rows, and 4 more variables:  
## #   arr_delay <dbl>, carrier <chr>, flight <int>
```

Merging two tables

There are three families of functions designed to merge relational data:

- **Mutating joins**, which add new variables to one data frame from matching observations in another.
- **Filtering joins**, which filter observations from one data frame based on whether or not they match an observation in the other table.
- **Set operations**, which treat observations as if they were set elements.

Mutating joins

A **mutating join** allows you to combine variables from two tables, by matching observations by their keys, and then copying across variables from one table to the other. e.g.

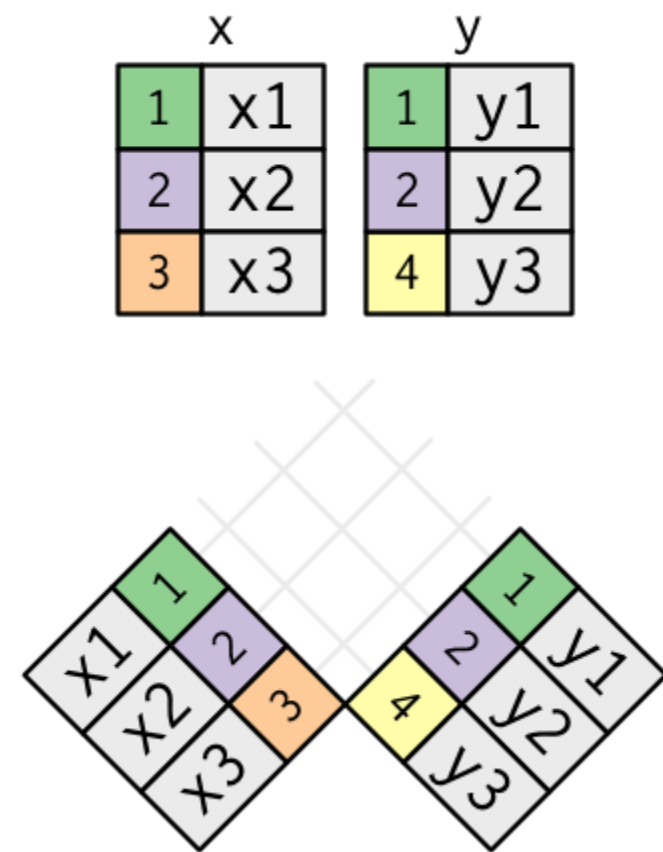
```
flights %>%  
  select(year:day, hour, origin, dest, tailnum, carrier) %>%  
  left_join(airlines, by = "carrier")
```

```
## # A tibble: 336,776 x 9  
##   year month   day hour origin dest tailnum carrier name  
##   <int> <int> <int> <dbl> <chr> <chr> <chr>   <chr>   <chr>  
## 1  2013     1     1     5 EWR   IAH  N14228  UA      United Air Lines ...  
## 2  2013     1     1     5 LGA   IAH  N24211  UA      United Air Lines ...  
## 3  2013     1     1     5 JFK   MIA  N619AA  AA      American Airlines...  
## 4  2013     1     1     5 JFK   BQN  N804JB  B6      JetBlue Airways  
## 5  2013     1     1     6 LGA   ATL  N668DN  DL      Delta Air Lines I...  
## 6  2013     1     1     5 EWR   ORD  N39463  UA      United Air Lines ...  
## 7  2013     1     1     6 EWR   FLL  N516JB  B6      JetBlue Airways  
## 8  2013     1     1     6 LGA   IAD  N829AS  EV      ExpressJet Airlin...  
## 9  2013     1     1     6 JFK   MCO  N593JB  B6      JetBlue Airways  
## 10 2013     1     1     6 LGA   ORD  N3ALAA  AA      American Airlines...  
## # ... with 336,766 more rows
```

There are four mutating join functions: - `inner_join()`, - outer joins; + `left_join()` + `right_join()` + `full_join()`

A simple example

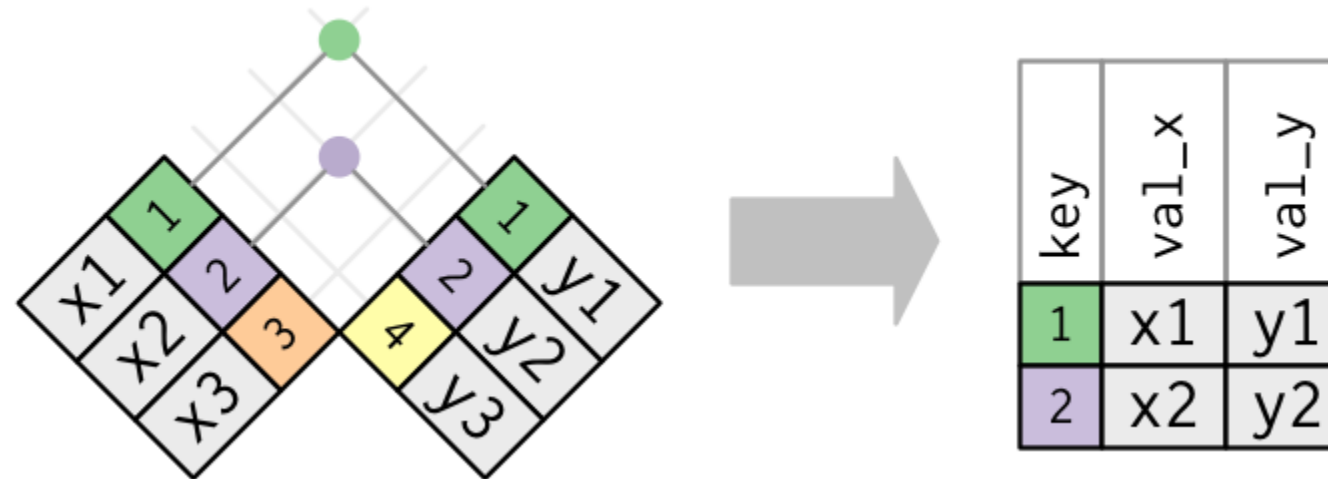
```
x <- tribble(  
  ~key, ~val_x,  
  1, "x1",  
  2, "x2",  
  3, "x3"  
)  
  
y <- tribble(  
  ~key, ~val_y,  
  1, "y1",  
  2, "y2",  
  4, "y3"  
)
```



Inner join

```
x %>% inner_join(y, by = "key")
```

```
## # A tibble: 2 x 3  
##   key val_x val_y  
##   <dbl> <chr> <chr>  
## 1     1 x1    y1  
## 2     2 x2    y2
```



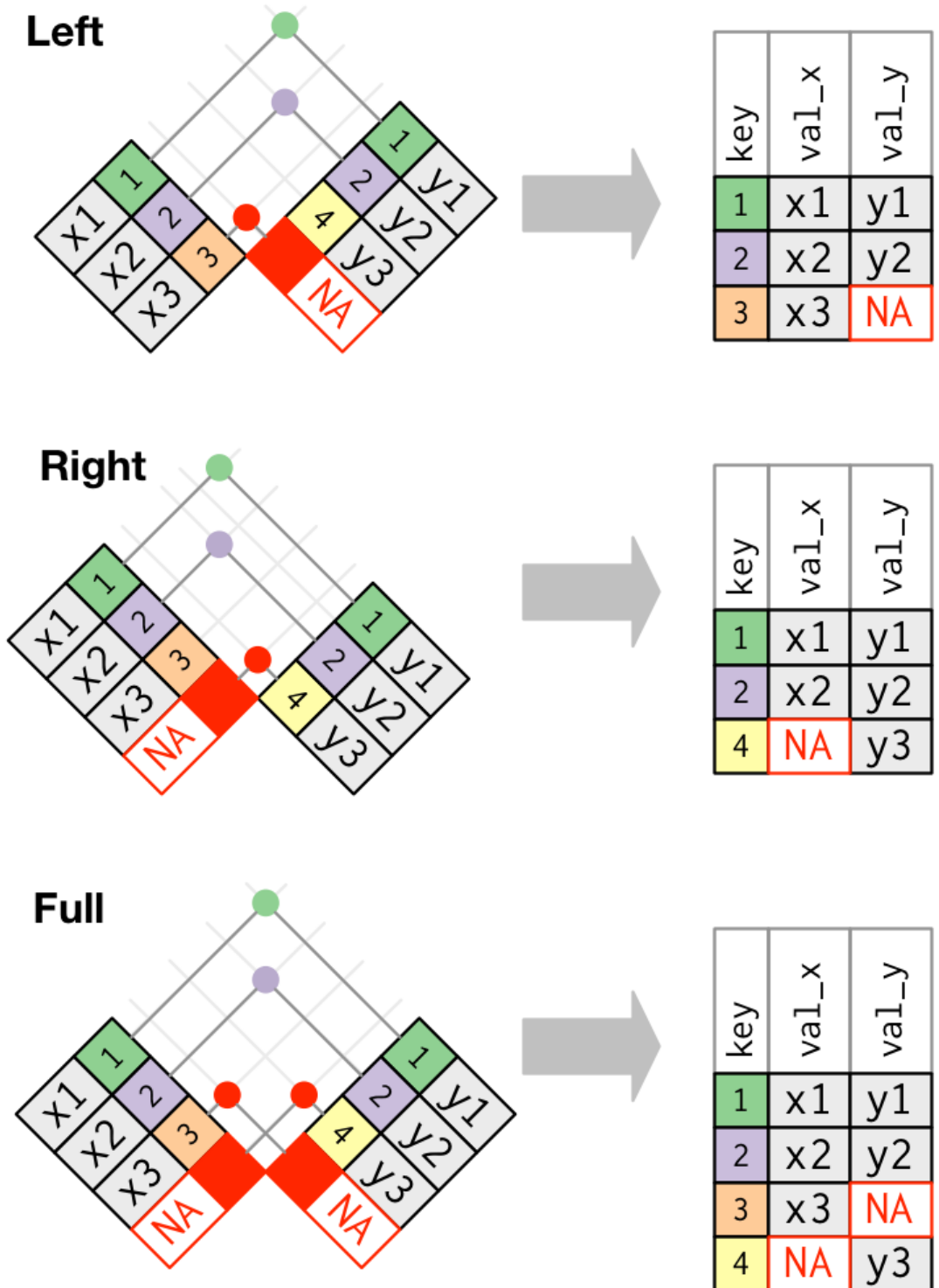
Source: (<http://r4ds.had.co.nz/relational-data.html>)

Outer join

An outer join keeps observations that appear in at least one of the tables:

- A `left_join()` keeps all observations in the table on the left
- A `right_join()` keeps all observations in the table on the right
- A `full_join()` keeps all observations in both tables

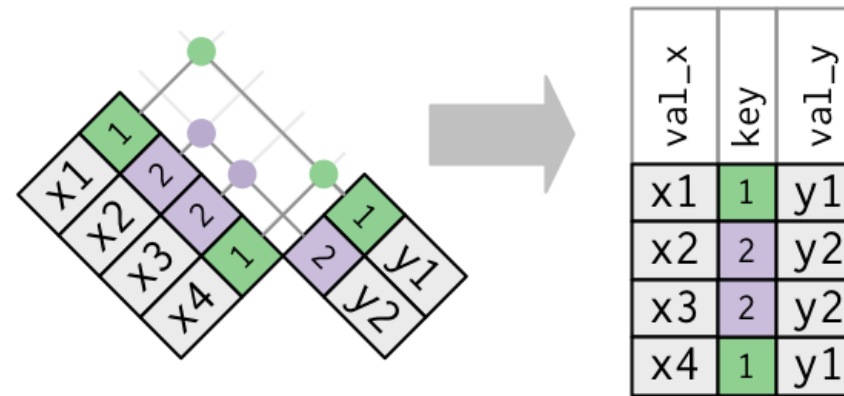
Source: <http://r4ds.had.co.nz/relational-data.html>



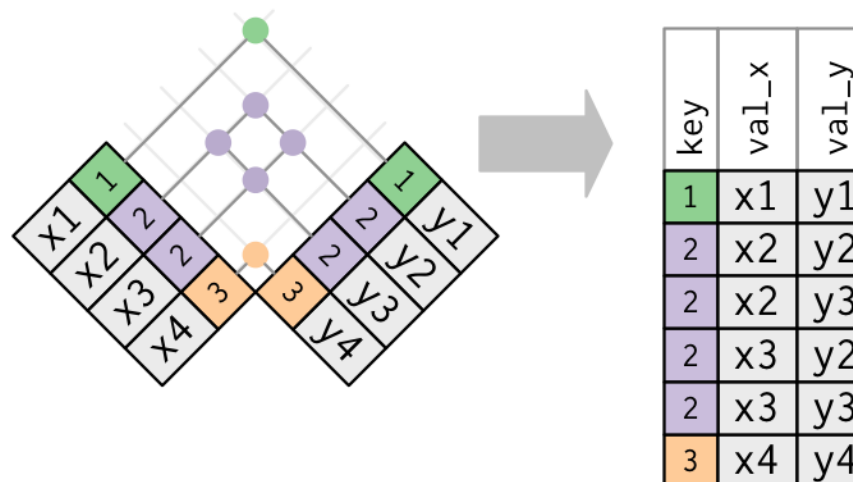
Duplicate keys

What happens when there are duplicate keys?

- One table has duplicate keys. There may be a one-to-many relation.



- Both tables have duplicate keys. When you join duplicated keys, you get all possible combinations:



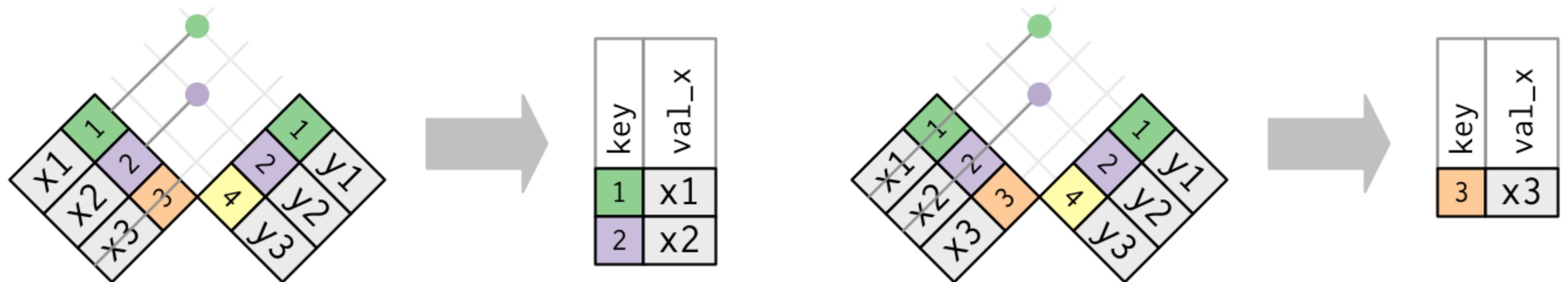
Source: <http://r4ds.had.co.nz/relational-data.html>

Filtering joins

Filtering joins match observations in the same way as mutating joins, but affect the observations, not the variables.

There are two types:

- `semi_join(x, y)` keeps all observations in x that have a match in y.
- `anti_join(x, y)` drops all observations in x that have a match in y.

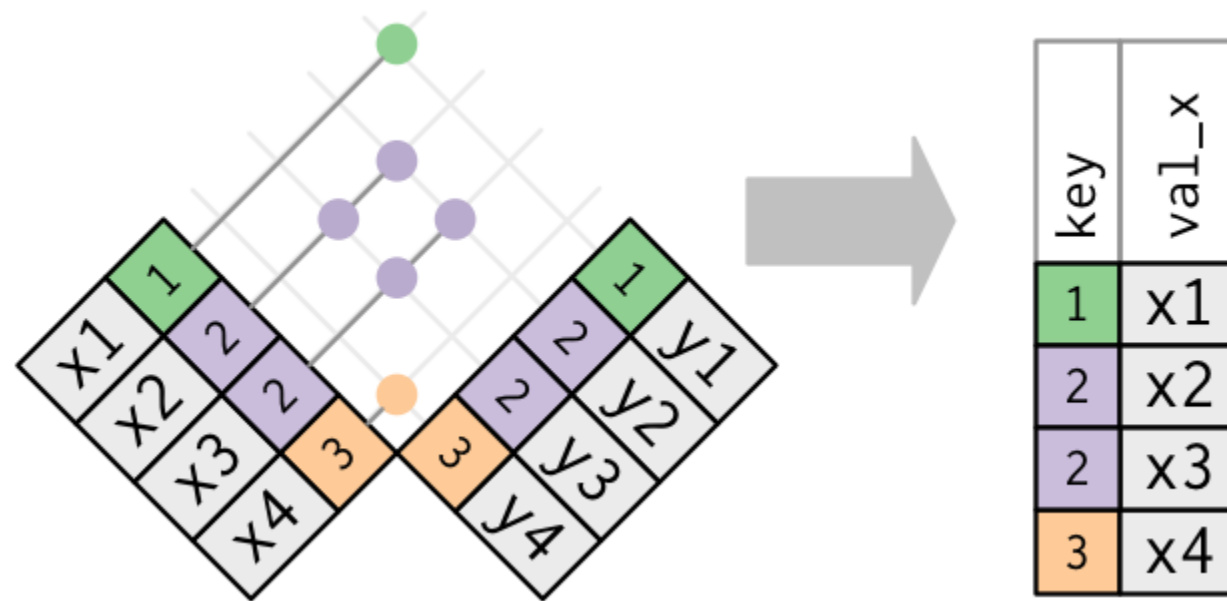


Multiple matches

In filtering joins, only the existence of a match is important.

It doesn't matter which observation is matched.

Filtering joins never duplicate rows like mutating joins do:



Set operations

Set operations apply to rows; they expect the `x` and `y` inputs to have the same variables, and treat the observations like sets.

- `intersect(x, y)`: returns only observations in both `x` and `y`.
- `union(x, y)`: returns unique observations in `x` and `y`.
- `setdiff(x, y)`: returns observations in `x`, but not in `y`.

All these operations work with a complete row, comparing the values of every variable.

Example

```
df1 <- tribble(
  ~x, ~y,
  1,  1,
  2,  1
)
df2 <- tribble(
  ~x, ~y,
  1,  1,
  1,  2
)
```

```
intersect(df1, df2)
```

```
## # A tibble: 1 x 2
##       x     y
##   <dbl> <dbl>
## 1     1     1
```

```
union(df1, df2)
```

```
## # A tibble: 3 x 2
##       x     y
##   <dbl> <dbl>
## 1     1     2
## 2     2     1
## 3     1     1
```

```
setdiff(df1, df2)
```

```
## # A tibble: 1 x 2
##       x     y
##   <dbl> <dbl>
## 1     2     1
```

```
setdiff(df2, df1)
```

```
## # A tibble: 1 x 2
##       x     y
##   <dbl> <dbl>
## 1     1     2
```

Exploratory data analysis

What is exploratory data analysis (EDA)?

EDA is an iterative process:

- Generate questions about your data
- Search for answers by visualising, transforming, and modelling data

Use what you learn to refine your questions or generate new ones.

Some comments about EDA:

- It is not a formal process with a strict set of rules.
- Explore many ideas: some will pan out, others will be dead ends.
- Even if questions are predefined, quality of data still needs to be assessed

Asking questions

Your goal during EDA is to develop an understanding of your data.

“There are no routine statistical questions, only questionable statistical routines.”

— Sir David Cox

EDA is fundamentally a creative process. And like most creative processes, the key to asking quality questions is to generate a large quantity of questions. ^[^1] ^[^1]:

(<http://r4ds.had.co.nz/exploratory-data-analysis.html#questions>)

Two types of questions will always be useful for making discoveries within your data:

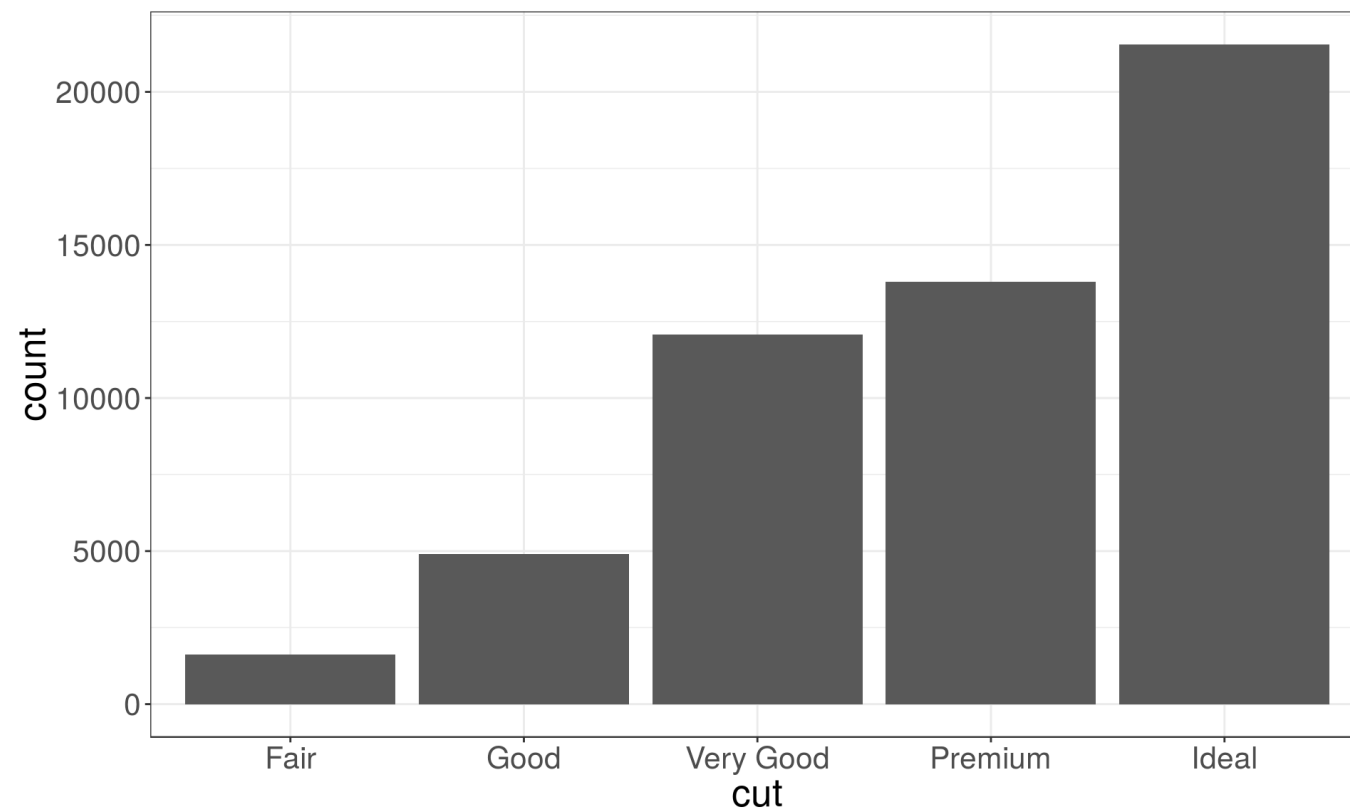
1. What type of variation occurs within my variables?
2. What type of covariation occurs between my variables?

Variation

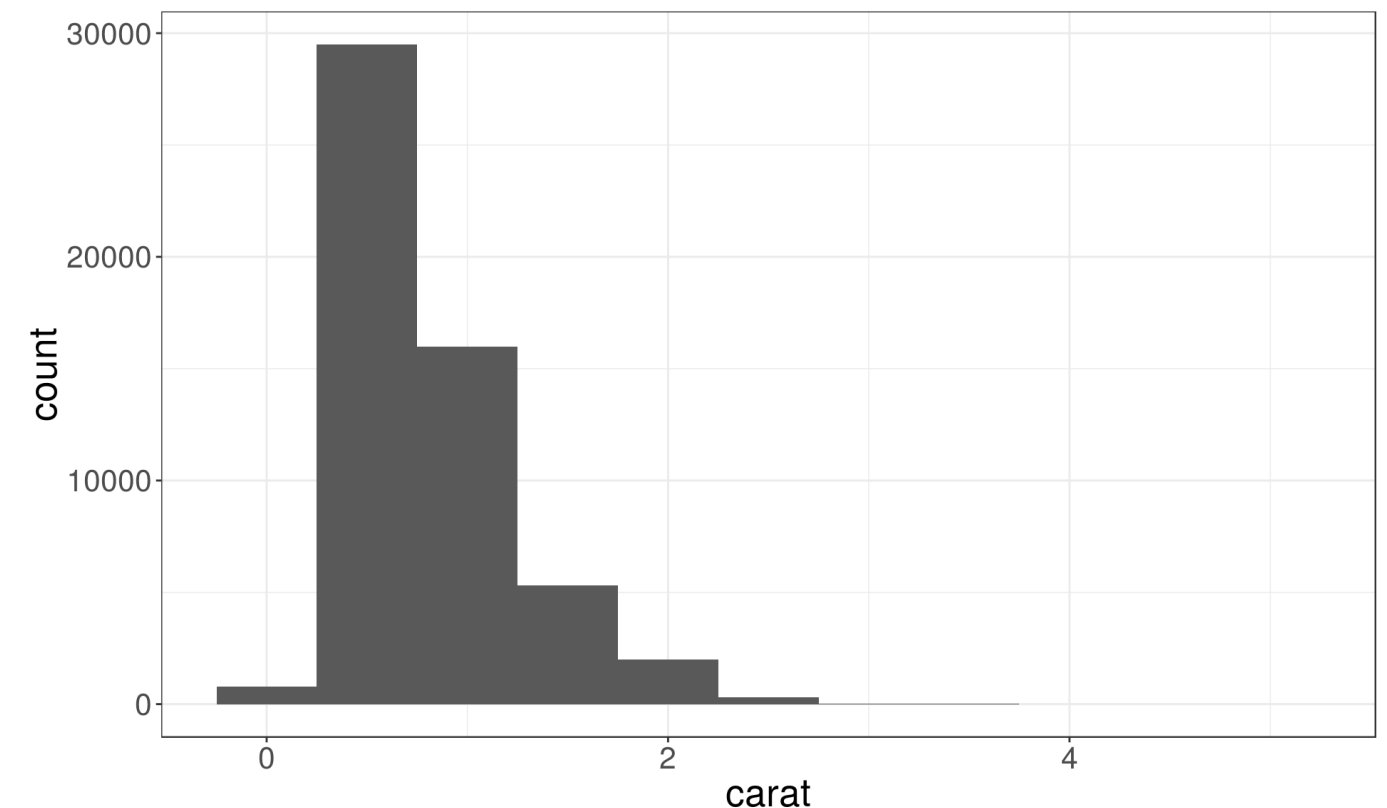
Variation is the tendency of the values of a variable to change from measurement to measurement. Every variable has its own pattern of variation, which can reveal interesting information.¹

Recall the `diamonds` dataset. Use a bar chart, to examine the distribution of a **categorical variable**, and a histogram that of a **continuous** one.

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



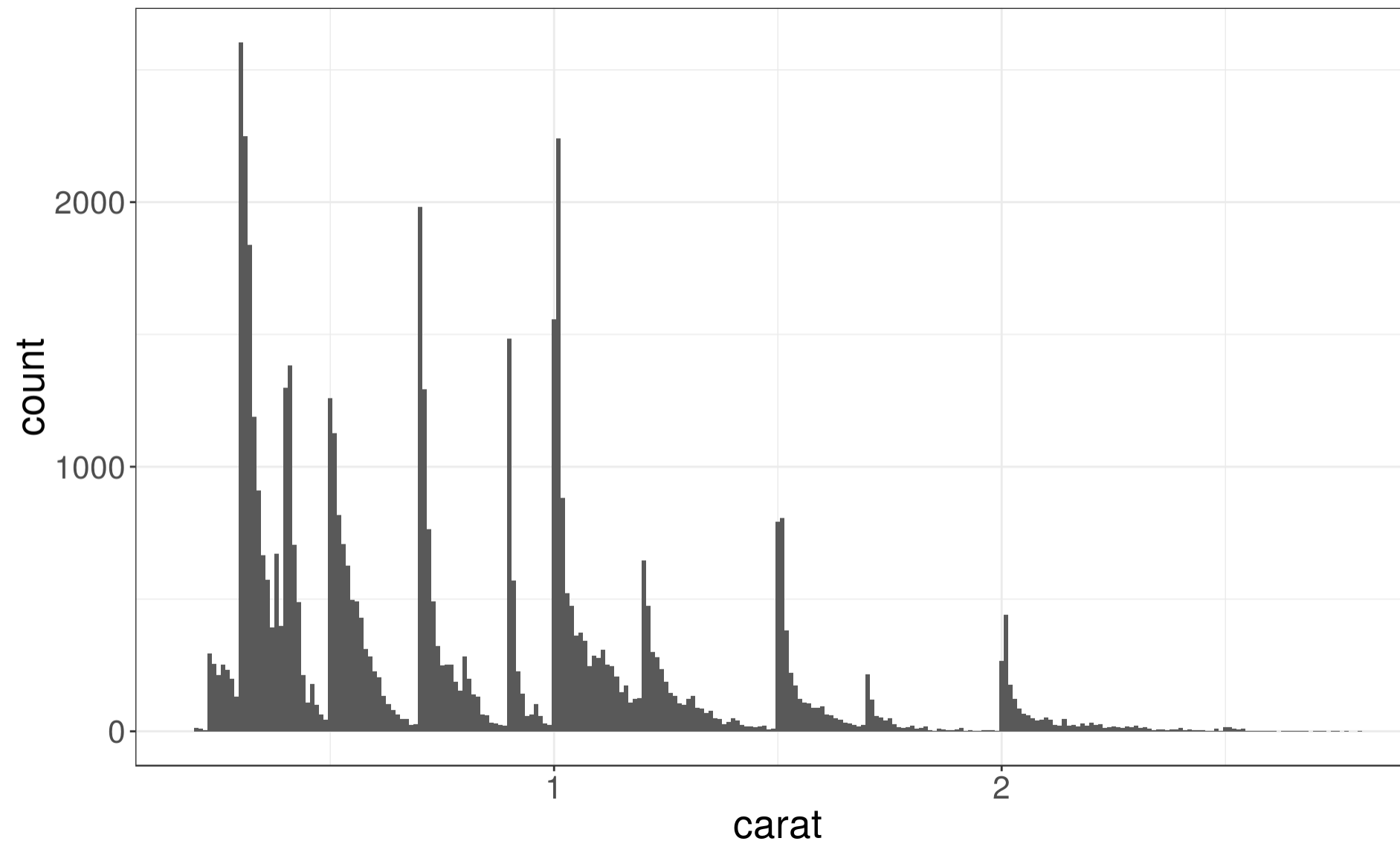
```
ggplot(data = diamonds) +  
  geom_histogram(mapping = aes(x = carat), binwidth = 0.2)
```



Identifying typical values

- Which values are the most common? Why?
- Which values are rare? Why? Does that match your expectations?
- Can you see any unusual patterns? What might explain them?

```
diamonds %>% filter(carat < 3) %>%  
  ggplot(aes(x = carat)) + geom_histogram(binwidth = 0.01)
```



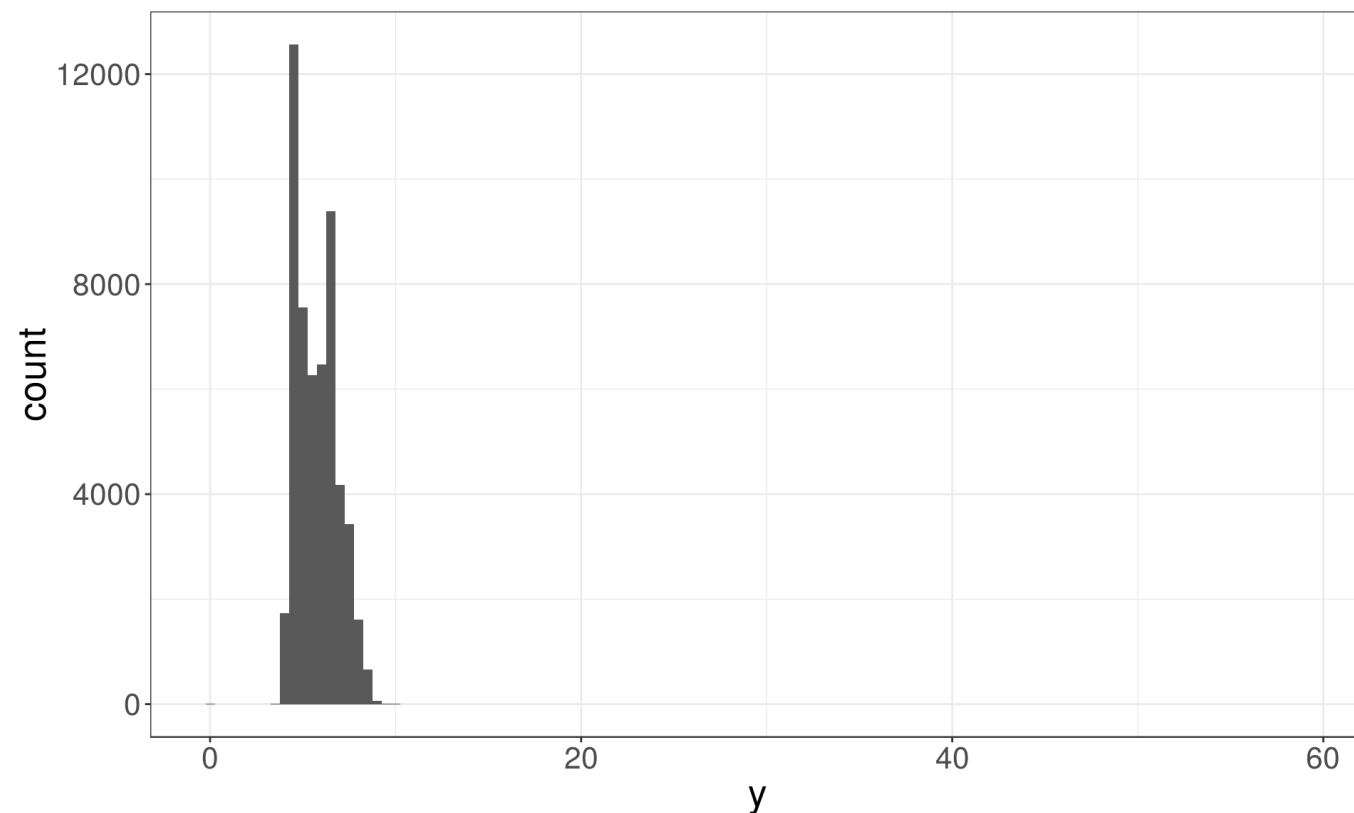
Look for anything unexpected!

Identify outliers

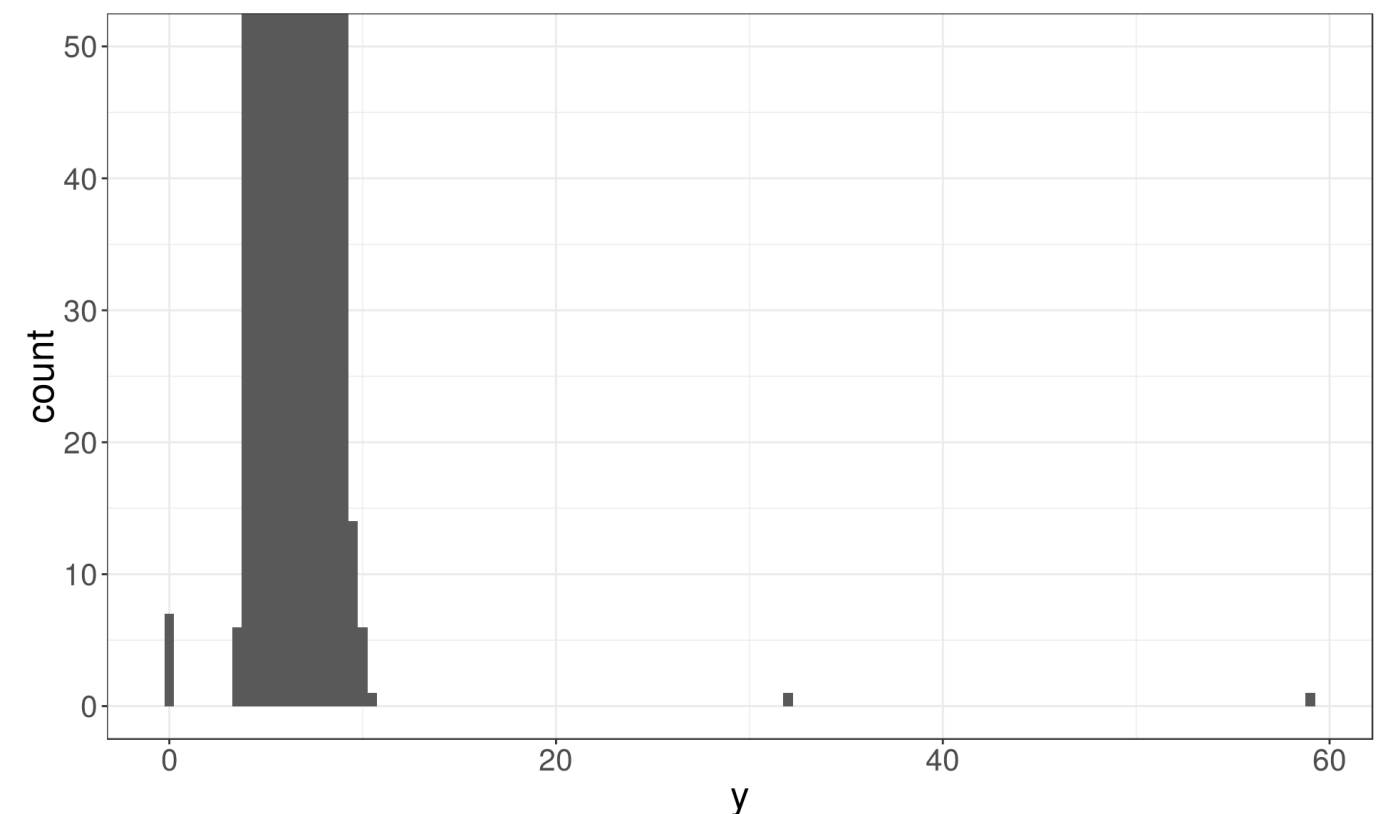
Outliers are observations that are unusual – data points that don't seem to fit the general pattern.

Sometimes outliers are data entry errors; other times outliers suggest important new science.

```
ggplot(diamonds) +  
  geom_histogram(mapping = aes(x = y), binwidth
```



```
ggplot(diamonds) +  
  geom_histogram(mapping = aes(x = y), binwidth  
  coord_cartesian(ylim = c(0, 50))
```



Identifying outliers

Now that we have seen the usual values, we can try to understand them.

```
diamonds %>% filter(y < 3 | y > 20) %>%  
  select(price, carat, x, y, z) %>% arrange(y)
```

```
## # A tibble: 9 x 5  
##   price carat      x      y      z  
##   <int> <dbl> <dbl> <dbl> <dbl>  
## 1  5139    1      0      0      0  
## 2  6381  1.14    0      0      0  
## 3 12800  1.56    0      0      0  
## 4 15686  1.2     0      0      0  
## 5 18034  2.25    0      0      0  
## 6  2130  0.71    0      0      0  
## 7  2130  0.71    0      0      0  
## 8  2075  0.51    5.15  31.8    5.12  
## 9 12210   2     8.09  58.9    8.06
```

The y variable measures the length (in mm) of one of the three dimensions of a diamond.

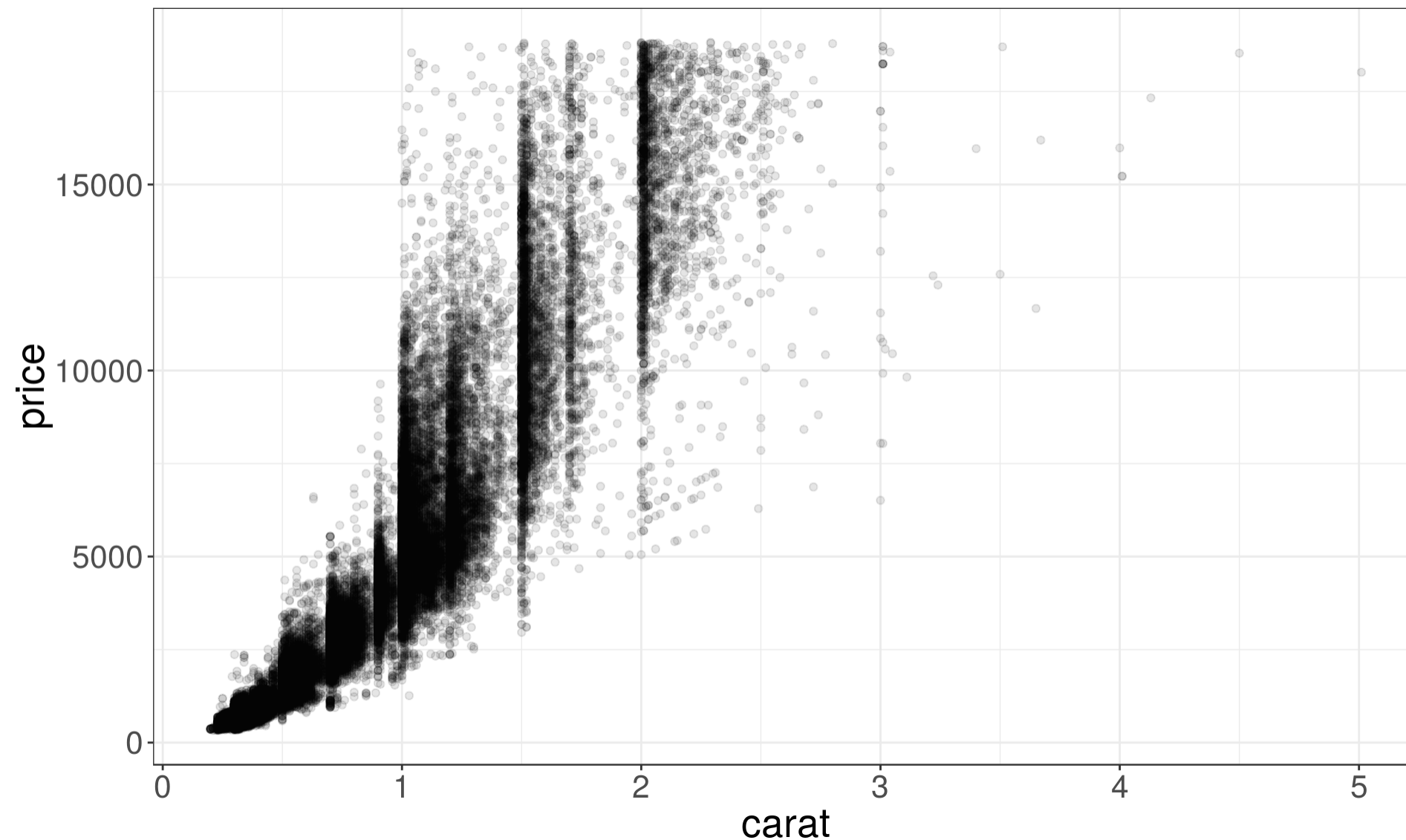
Therefore, these must be entry errors! Why?

It's good practice to repeat your analysis with and without the outliers.

Covariation

Covariation is the tendency for the values of two or more variables to vary together in a related way.

```
ggplot(data = diamonds) +  
  geom_point(aes(x=carat, y=price), alpha=0.1)
```

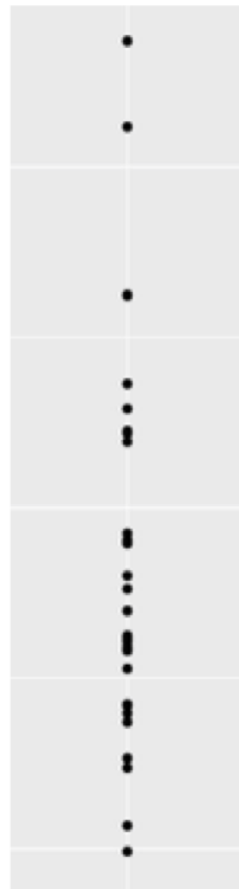


Boxplots

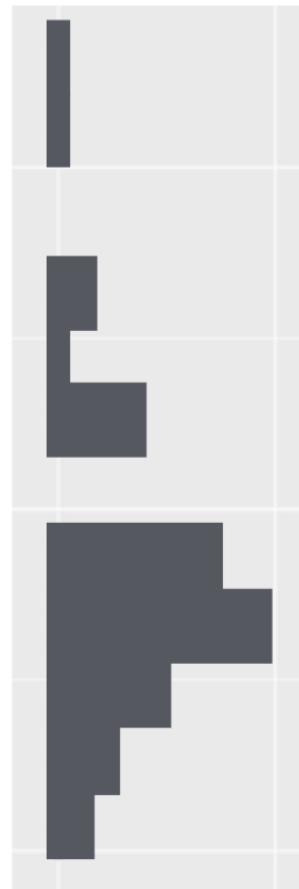
Boxplot are used to display visual shorthand for a distribution of a continuous variable broken down by categories.

They mark the distribution's quartiles.

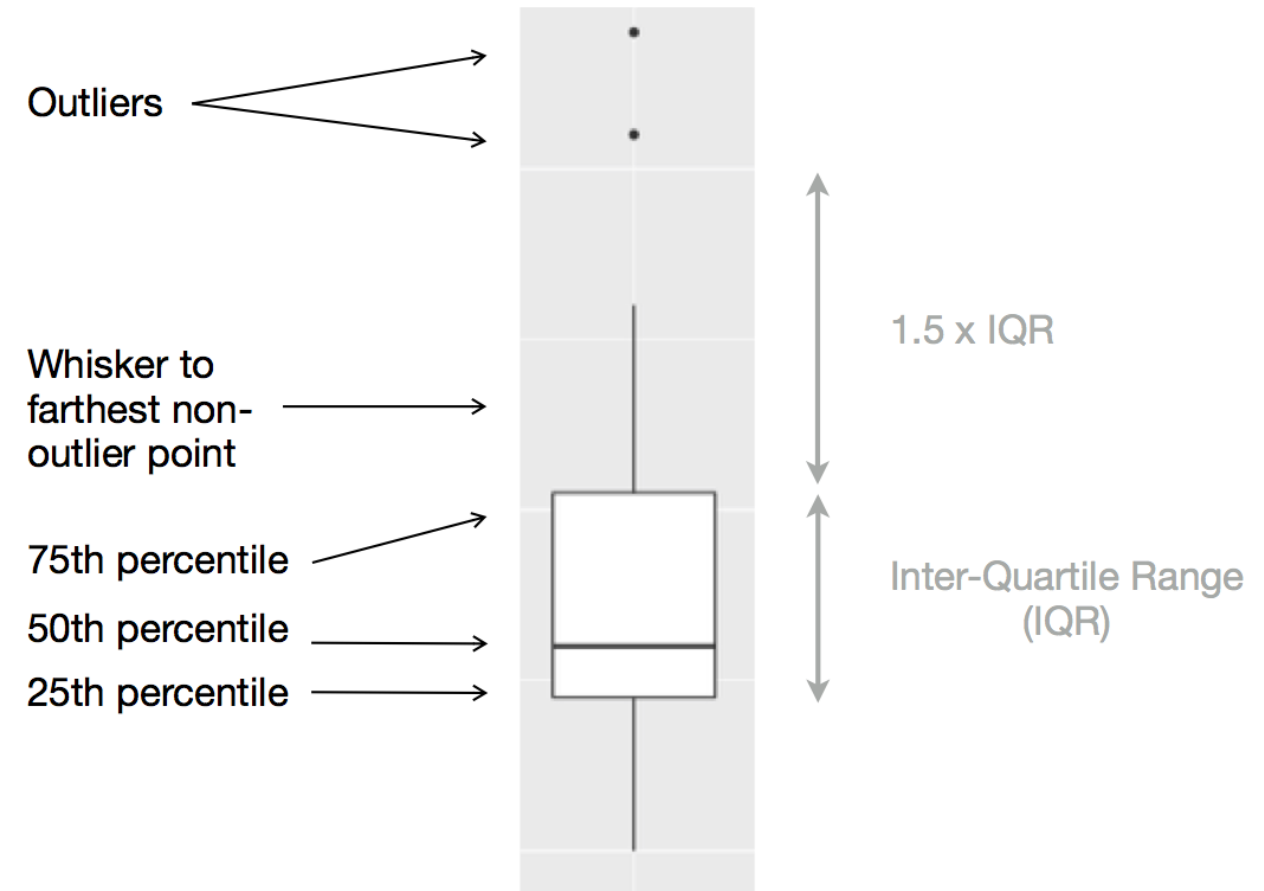
The actual
values in a
distribution



How a histogram
would display the
values (rotated)



How a boxplot
would display
the values

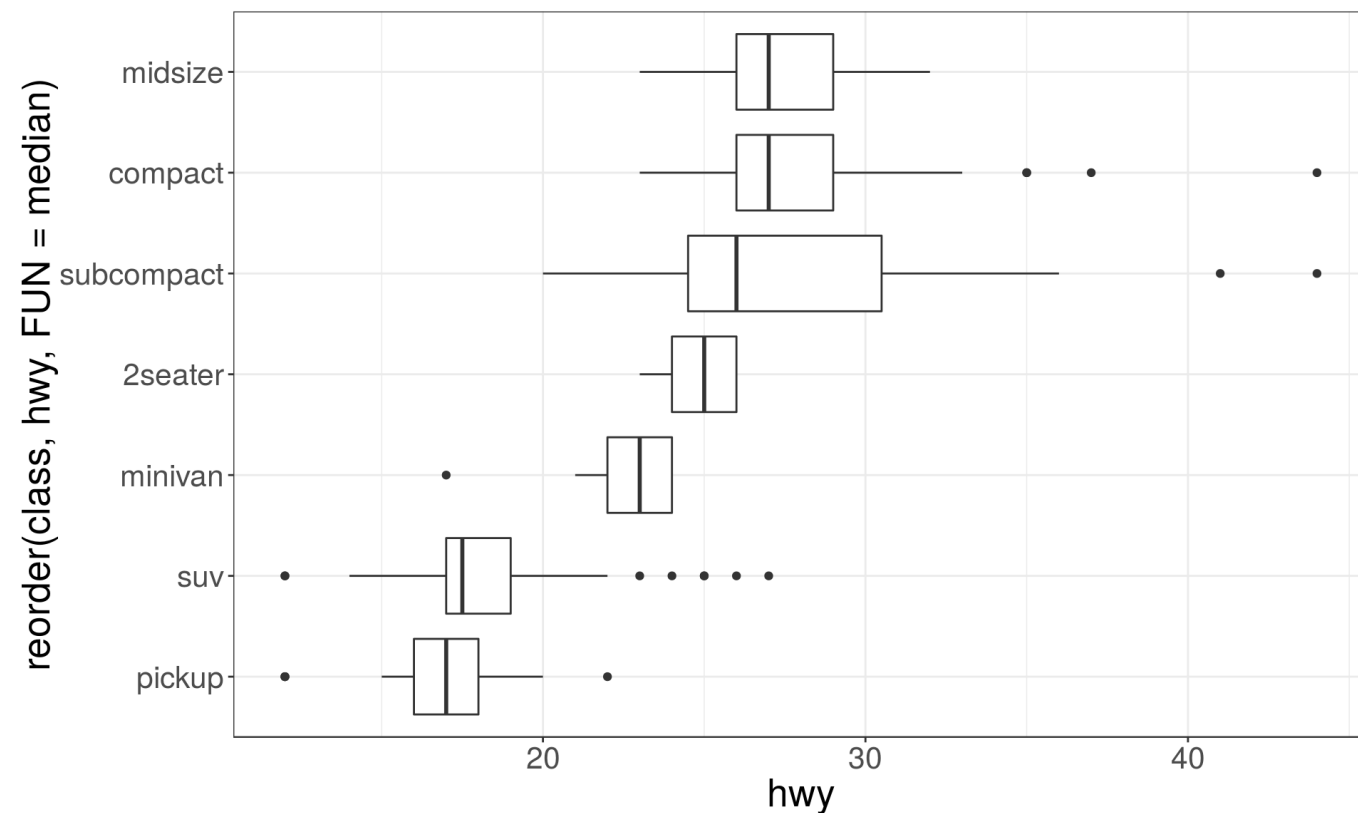


A categorical and a continuous variable

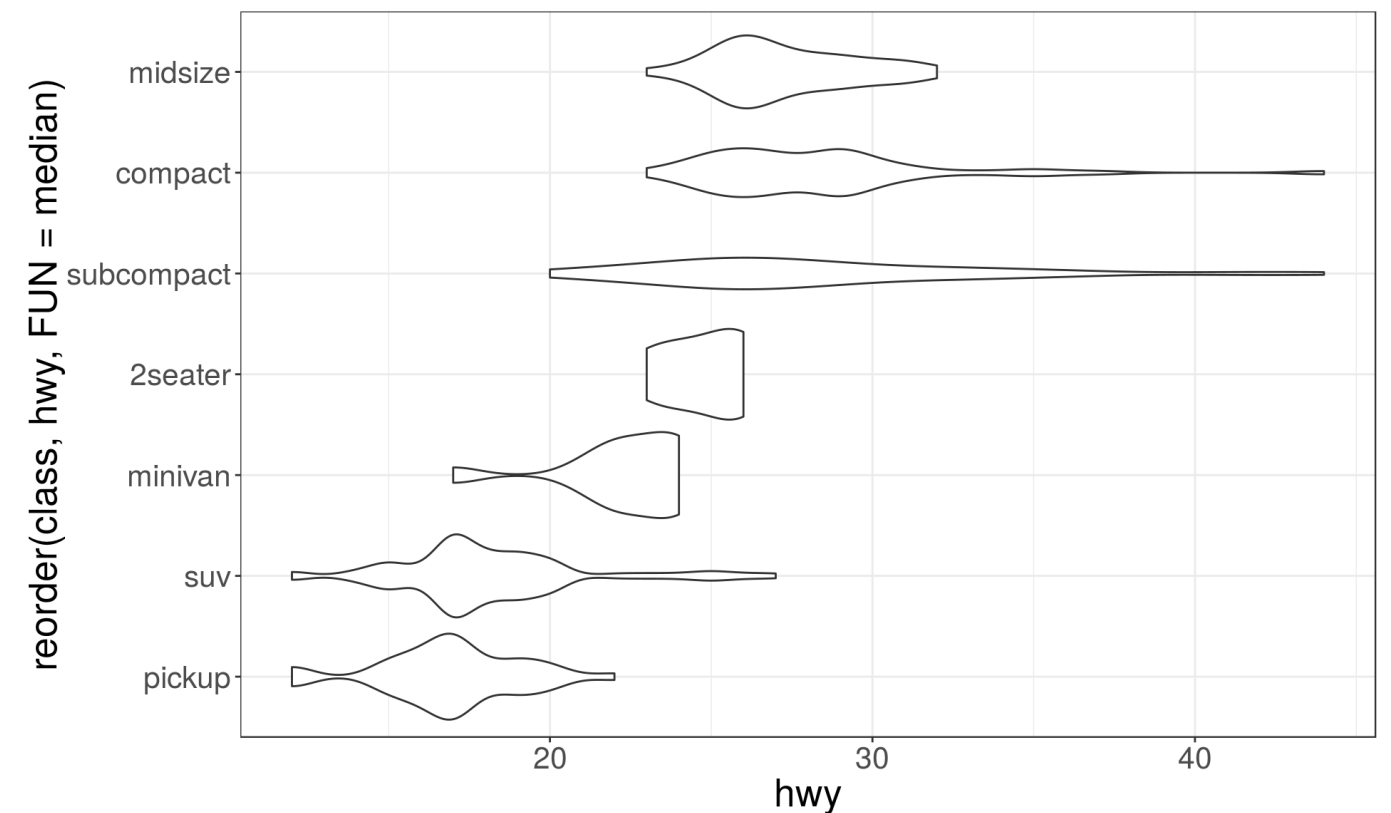
Use a boxplot or a violin plot to display the covariation between a categorical and a continuous variable.

Violin plots give more information, as they show the entire estimated distribution.

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



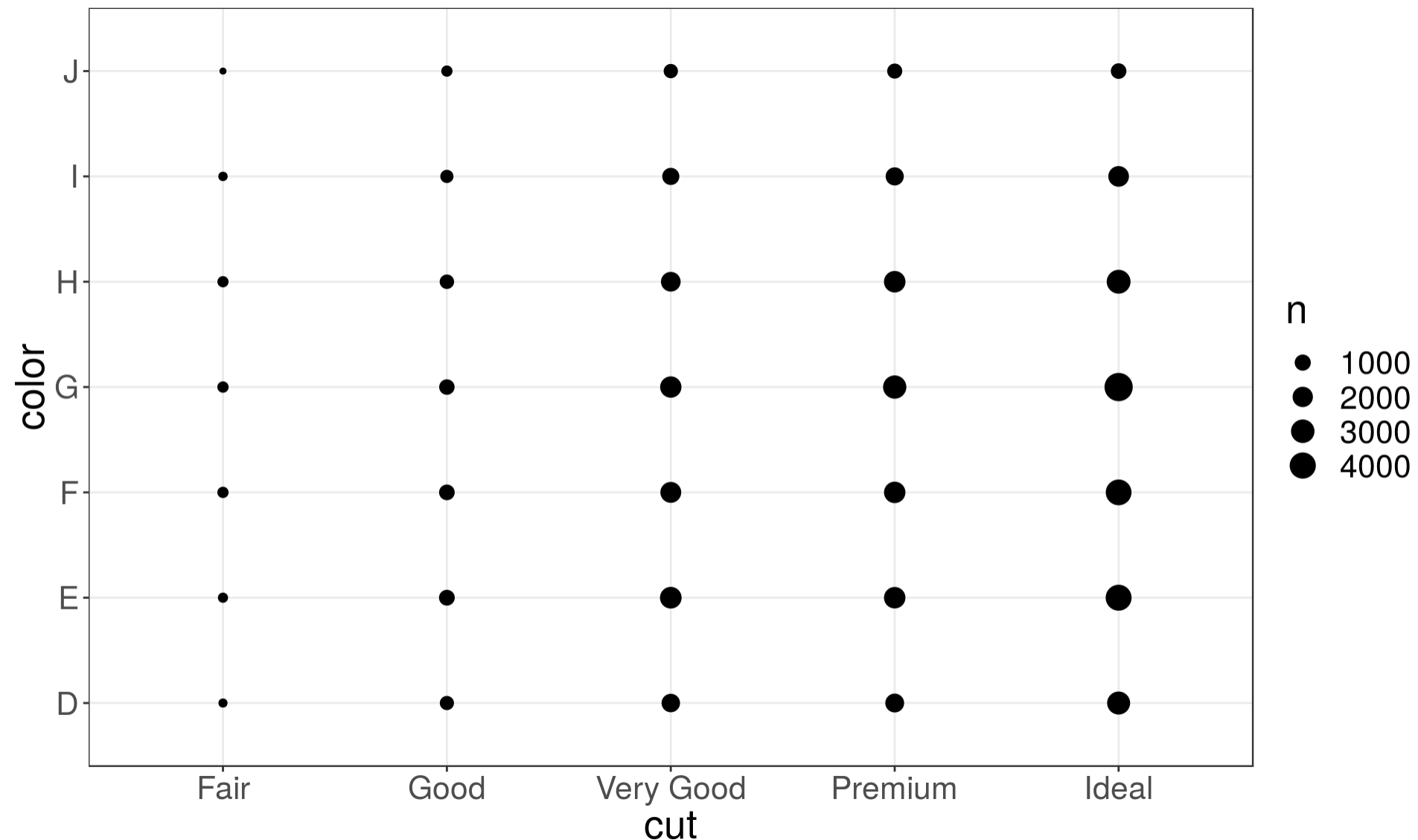
```
ggplot(mpg, aes(  
  x = reorder(class, hwy, FUN = median), y = hwy  
  geom_violin() + coord_flip()
```



Two categorical variables

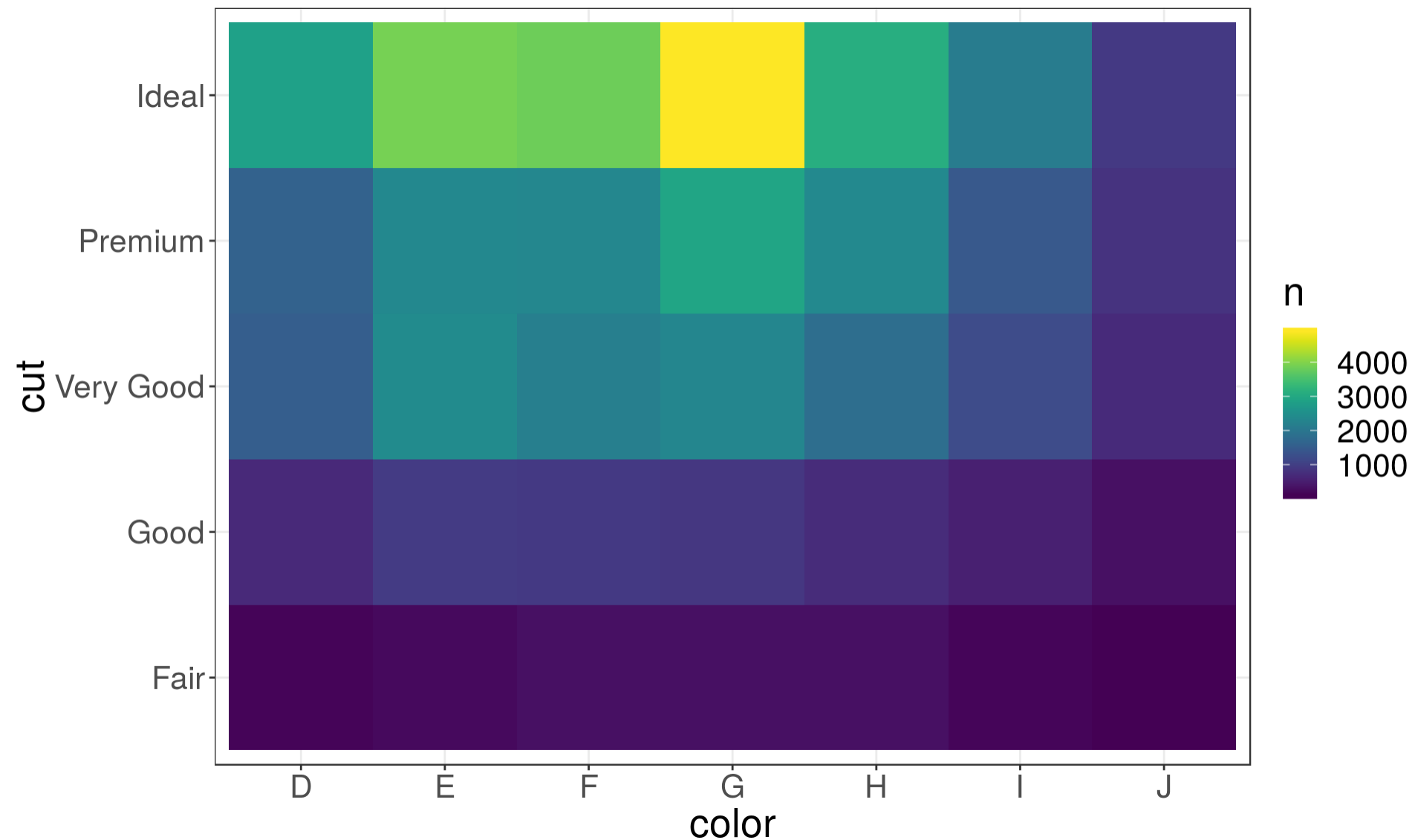
To visualise the **covariation between categorical variables**, you need to count the number of observations for each combination, e.g. using `geom_count()`:

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



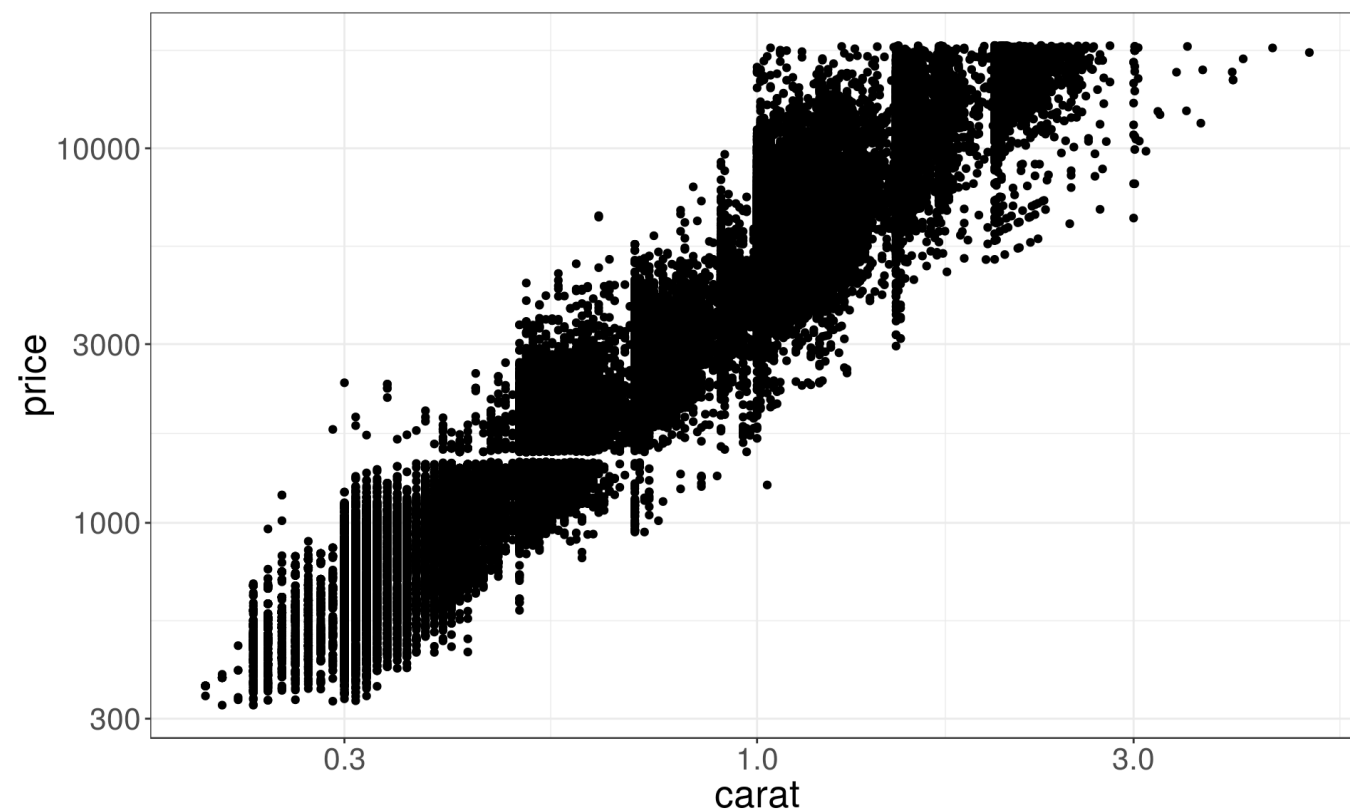
Another approach is to first, compute the count and then visualise it by coloring with `geom_tile()` and the fill aesthetic:

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

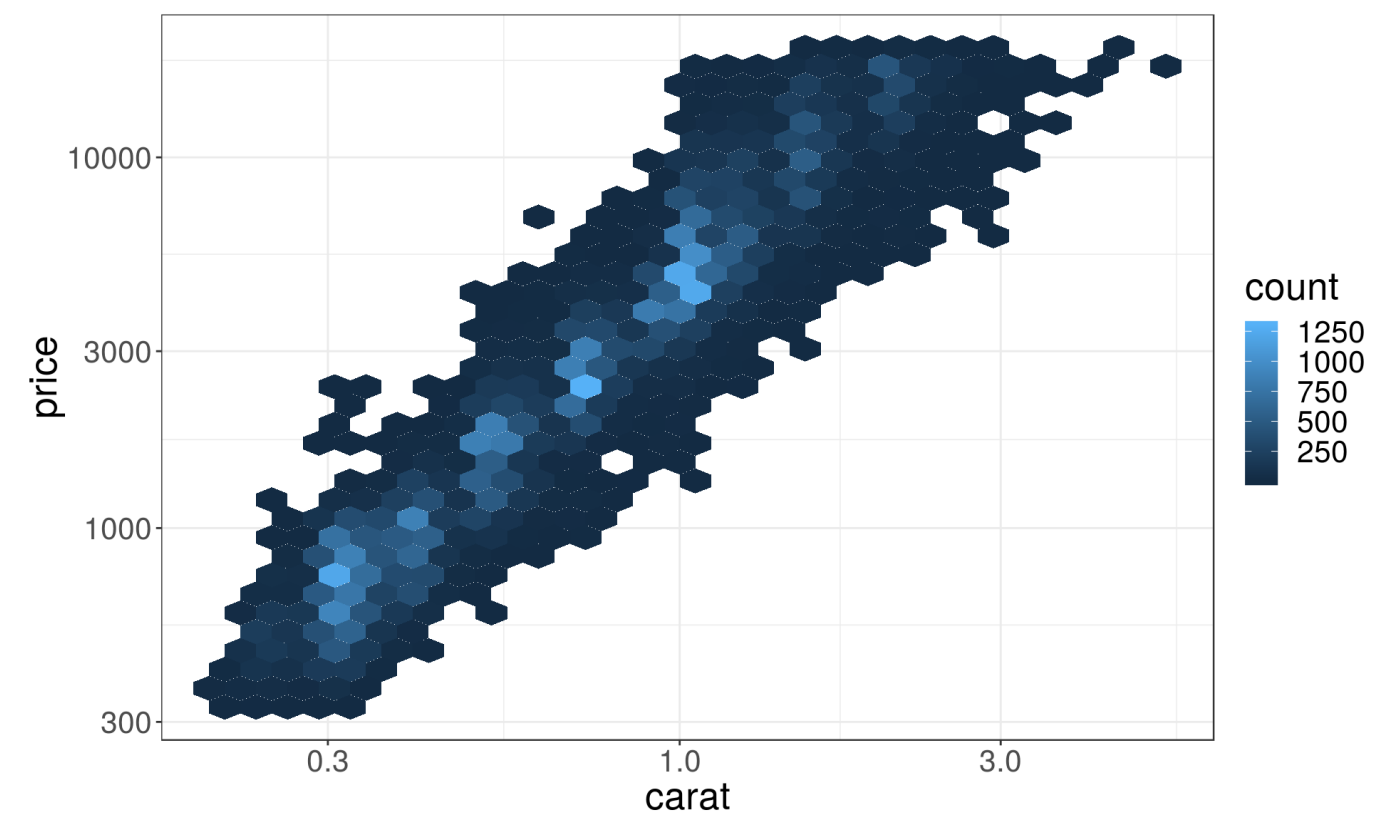


Two continuous variables

```
ggplot(data = diamonds) +  
  geom_point(mapping = aes(x = carat, y = price))  
  scale_y_log10() + scale_x_log10()
```



```
# install.packages("hexbin")  
ggplot(data = diamonds) +  
  geom_hex(mapping = aes(x = carat, y = price))  
  scale_y_log10() + scale_x_log10()
```



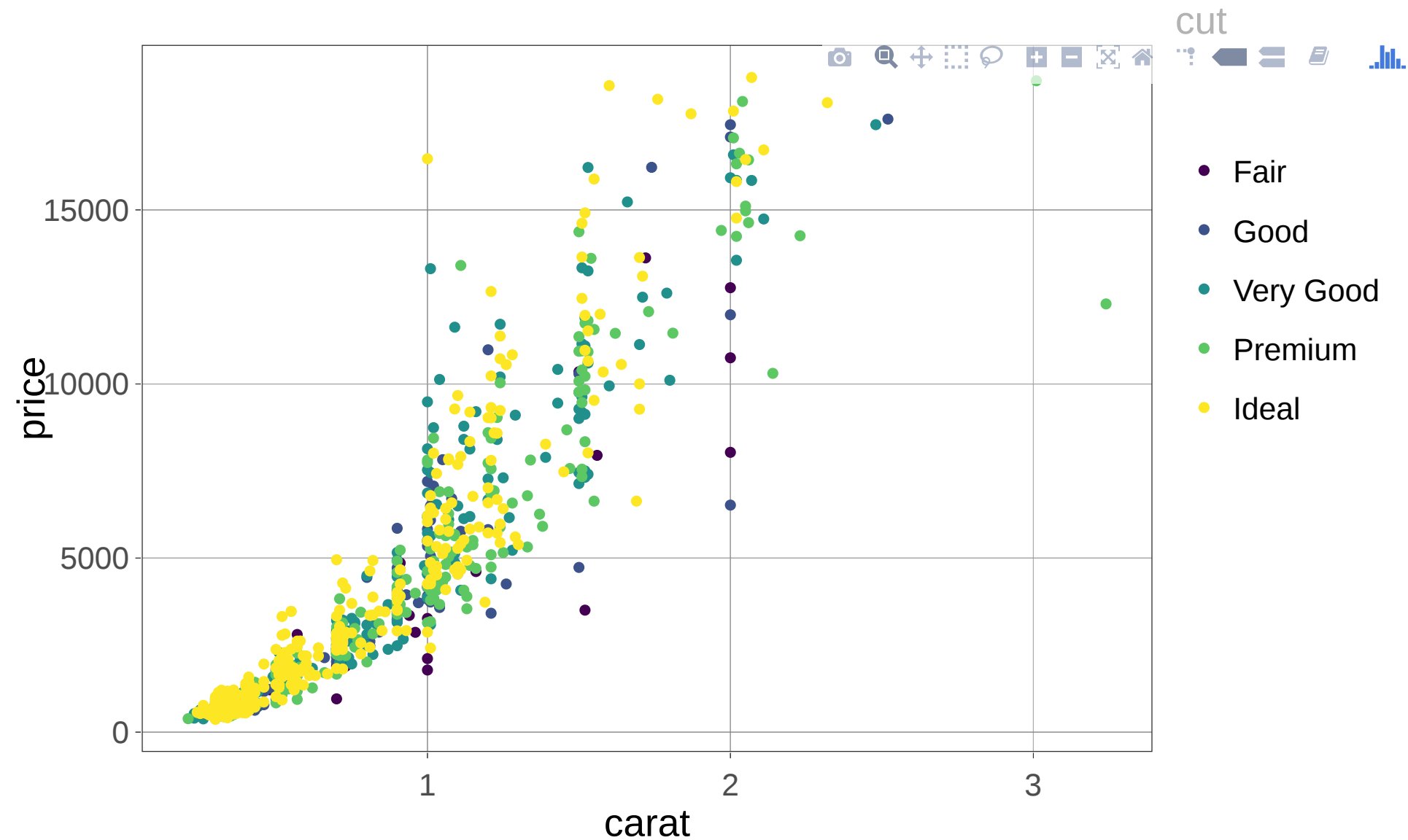
Interactive graphics

The `plotly` package

- `plotly` is a **package for visualization** and a collaboration platform for data science
- Available in **R, python, MATLAB, scala**.
- You can produce **interactive graphics including 3D plots** (with zooming and rotating).
- You can open a '**plotly**' **account** to upload 'plotly' graphs and view or modify them in a web browser.
- Resources: [cheatsheet](#), [book](#)

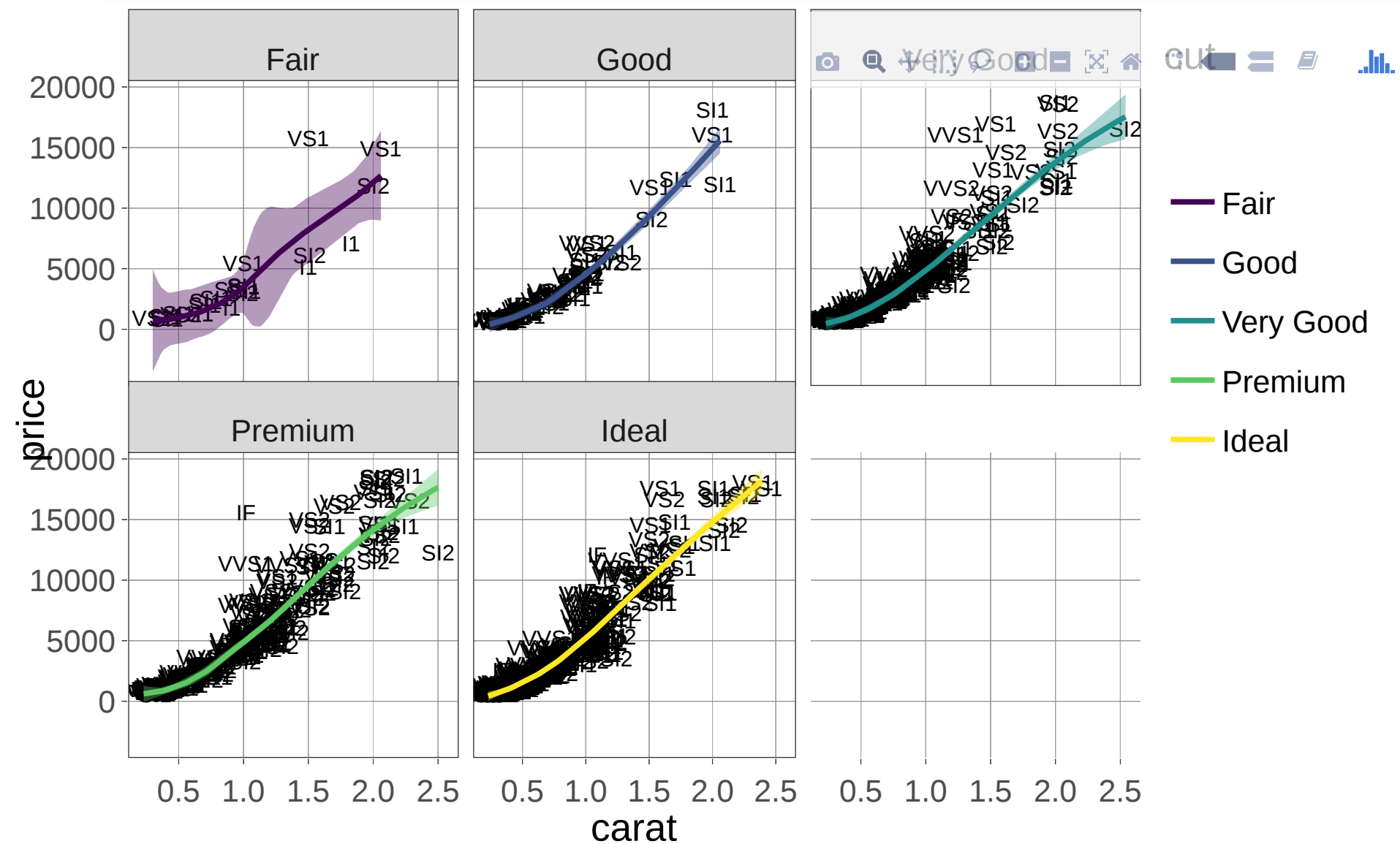
plotly integration with ggplot2

```
library(plotly); library(tidyverse) # or library(ggplot2); library(dplyr)
plt <- ggplot(diamonds %>% sample_n(1000), aes(x = carat, y = price)) +
  geom_point(aes(color = cut))
ggplotly(plt)
```



```
plt <- ggplot(diamonds %>% sample_n(1000), aes(x = carat, y = price)) +
  geom_text(aes(label = clarity), size = 4) +
  geom_smooth(aes(color = cut, fill = cut)) +
  facet_wrap(~cut)
ggplotly(plt)
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



3D Scatter plots

```
theta <- seq(0, 10, 0.2);  
df <- data.frame(U = theta, V = cos(theta), W = sin(theta)*theta)  
plot_ly(df, x = ~V, y = ~W, z = ~U, type = "scatter3d", mode = "markers",  
         marker = list(size = 3))
```



```
df$cols <- rep_len(c("orange", "blue", "green"), length.out = length(theta))  
(plt <- plot_ly(df, x = ~V, y = ~W, z = ~U, color = ~cols,  
  type = "scatter3d", mode = "markers+lines",  
  marker = list(size = 5), line = list(width = 5)))
```



Adding layers

```
dbl.helix <- data.frame(t = rep(seq(0, 2*pi, length.out = 100), 3)) %>%  
  mutate(x1 = sin(t), y1 = cos(t), z = (1:length(t))/10,  
         x2 = sin(t + pi/2), y2 = cos(t + pi/2))  
plot_ly(dbl.helix, x = ~x1, y = ~y1, z = ~z, type = "scatter3d", mode = "lines",  
        color = "green", colors = c("green", "purple"), line = list(width = 5)) %>%  
  add_trace(x = ~x2, y = ~y2, z = ~z+0.2, color = "purple")
```



Volcano dataset

- **volcano** - a built-in dataset storing topographic information for Maunga Whau (Mt Eden), one of 50 volcanos in Auckland, New Zealand.
- It consist of a 87 x 61 matrix with entries corresponding to the mountain's altitudes [m] on a 10m by 10m grid.
- rows run east to west, and columns south to north

```
dim(volcano)
```

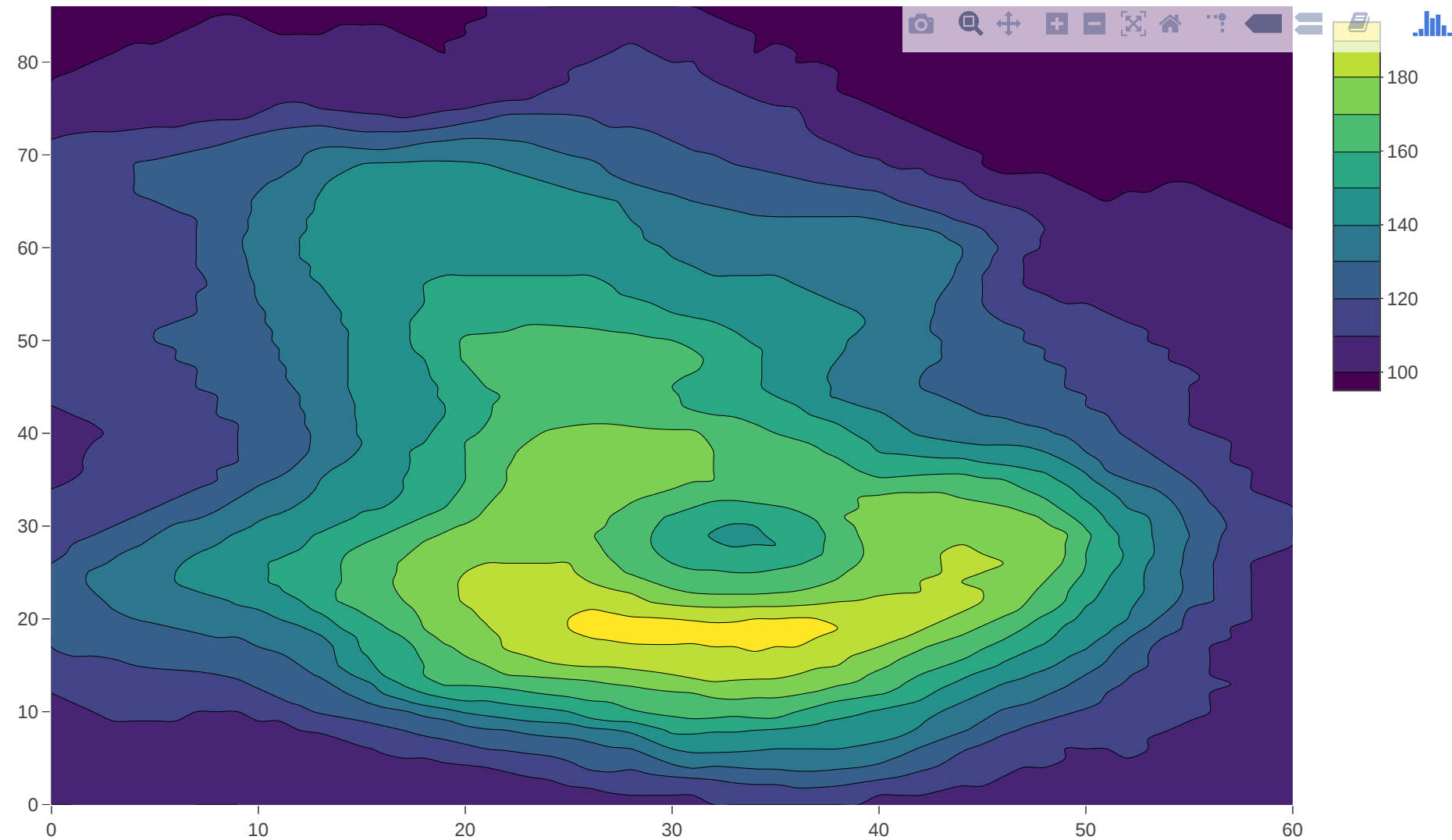
```
## [1] 87 61
```

```
volcano[1:5, 1:5]
```

```
##      [,1] [,2] [,3] [,4] [,5]  
## [1,]  100  100  101  101  101  
## [2,]  101  101  102  102  102  
## [3,]  102  102  103  103  103  
## [4,]  103  103  104  104  104  
## [5,]  104  104  105  105  105
```

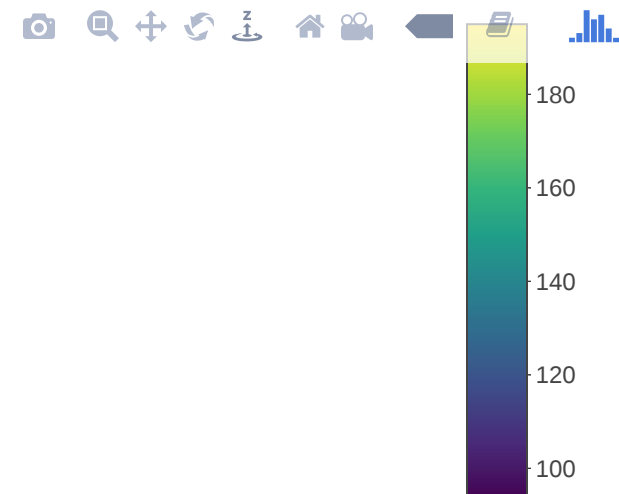
2D contour plots

```
plot_ly(z = volcano) %>% add_contour()
```



3D surface plots

```
plot_ly(z = volcano) %>% add_surface()
```



Data Export

Exporting Data

After working with a dataset and doing all data manipulation, you might want to save your new data table.

Recall the `readr` package. Besides functions for reading data in, `readr` has utilities for **saving your data to a text file**:

```
write_tsv(mydata, "path/to/filename.tsv")      # tab-delimited
write_csv(mydata, "path/to/filename.csv")      # comma-delimited
write_delim(mydata, "path/to/filename.csv", delim = " ") # general delimiter
```

To save your data in other types of files, you need to install and use other packages:

- to export an **Excel spreadsheet**, use `xlsx` package, and follow this [guide](#).

```
# install.packages(xlsx)
library(xlsx)
write.xlsx(mydata, "path/to/filename.xlsx")
```

- to export **SAS**, **SPSS** and **Stata** files use the [haven](#) package.

```
# install.packages(haven)
library(haven)
read_sas("mtcars.sas7bdat")
write_sas(mtcars, "mtcars.sas7bdat")
```

Saving the workspace

- You can also choose to **save all objects** currently in the workspace (variables, functions, etc.) into a file e.g. `filename.rda`.
- The file `filename.rda` can be easily loaded next time you work with R.
- You can also save a single object or a subset of specified objects currently in the workspace.

```
# save the workspace to file  
save.image(file = "path/to/filename.rda")  
  
# save specific objects to a file  
save(object_list, file = "path/to/filename.rda")  
  
# save just a single object  
saveRDS(object, file = "path/to/filename.rds")
```

- Saved objects/workspace can be loaded back in a new R session.

```
# load a workspace into the current session  
load("path/to/filename.rda")  
  
# read just the previously saved 1 object  
object <- readRDS("path/to/filename.rds")
```

1. (<http://r4ds.had.co.nz/exploratory-data-analysis.html#variation>)↩