# Lab 2: More ggplot and dplyr

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## Annoucments

1. We encourage you to be active on Piazza, asking and answering homework questions.
2. When asking a homework question, gather all relevant information to your problem **to make it reproduceable**
    - What operating system are you using (Windows/Mac)
    - What version of R are you using?
    - What versions of packages are you using? (run `sessionInfo()` after loading packages to see)
    - What code did you run before running into your problem?
    - What does the output say?
    - Take a screenshot or picture for best results
    - Bonus: Piazza lets you upload files, so upload your Jupyter notebook to help us help you
3. Demo on homework submission.
4. Demo on Zoom links

## Review : Lab 1 Exercise

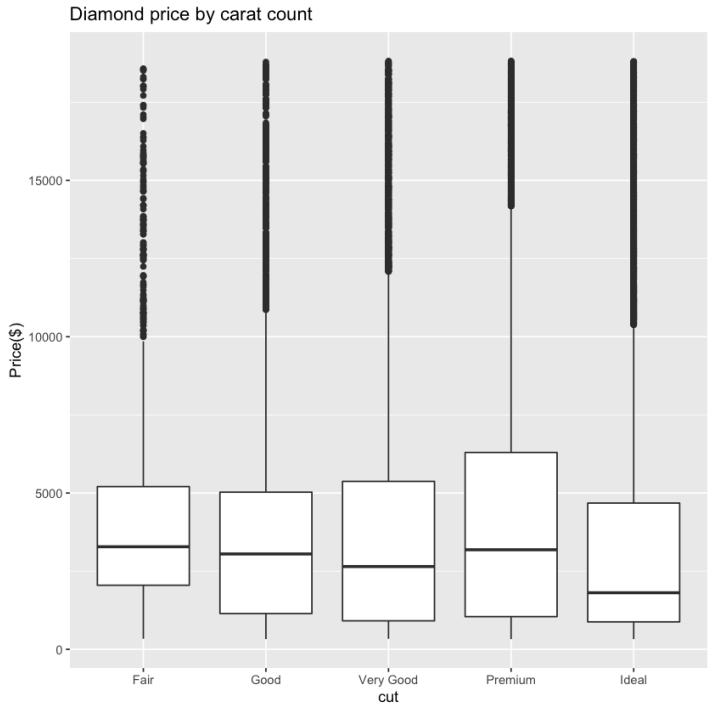
Question 1: What is the default value of the mean and standard deviation used by the `rnorm` function in R to generate a value from a normal distribution?

Answer: `?rnorm` will tell you that the mean is $0$ and the standard deviation is $1$.

In [122]:
```
library(tidyverse)
```

Question 2: Create a boxplot of `price` grouped by the levels in the `cut` variable.

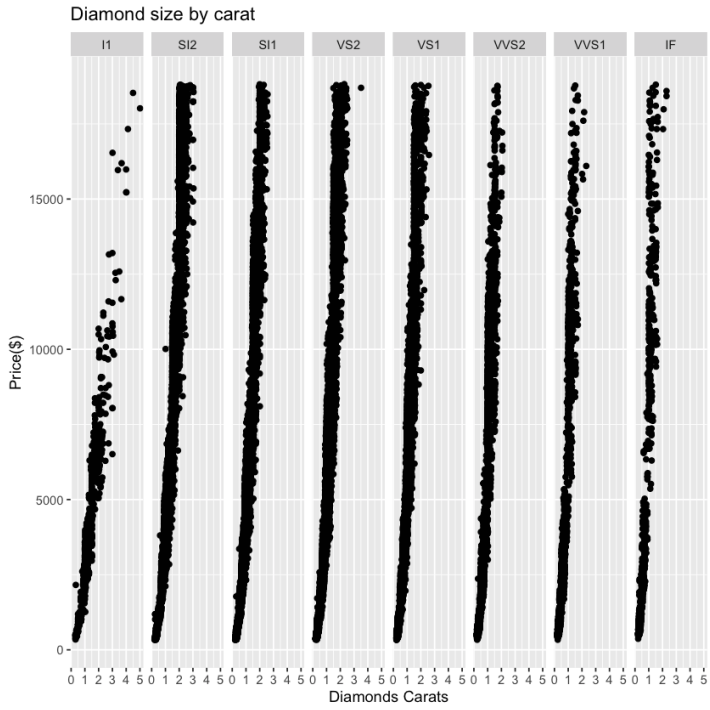
In [123]:
```
# boxplot helps to visualize the variability of a price for each cut
ggplot(data = diamonds) +
    geom_boxplot(mapping = aes(x = cut, y = price)) +
    labs(x = 'cut', y = 'Price($)') +
    ggtitle('Diamond price by carat count')
```



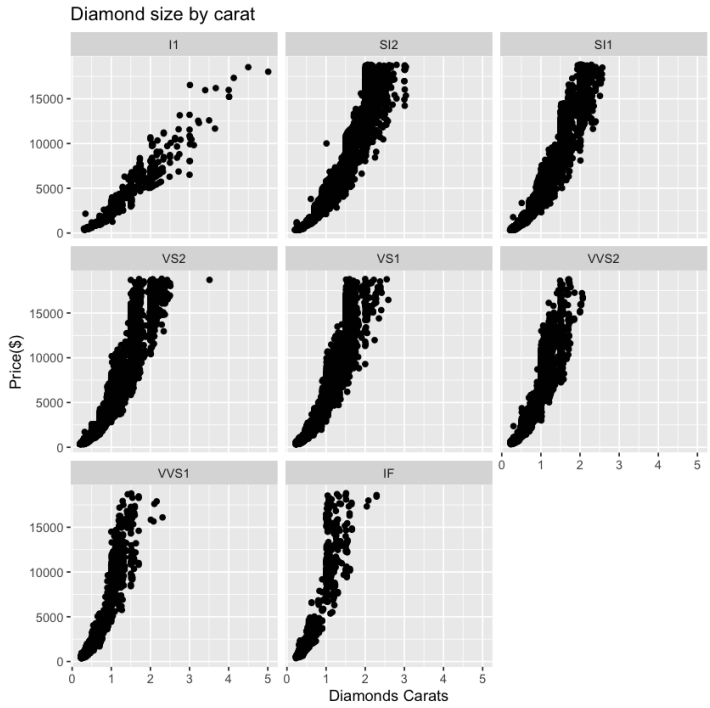

## Facets

- Facets create subplots which are group by a specified variable.
- `facet_wrap` takes one variable in the formula `~vars` and will wrap it to best fit the plotting area
- `facet_grid` forms a grid of subplots with the formula `rows~columns`

In [124]:
```
ggplot(data = diamonds) +
    geom_point(mapping = aes(x = carat, y = price)) +
    labs(x = 'Diamonds Carats', y = 'Price($)') +
    ggtitle('Diamond size by carat') +
    facet_grid(.~clarity)
```




In [125]:
```
ggplot(data = diamonds) +
    geom_point(mapping = aes(x = carat, y = price)) +
    labs(x = 'Diamonds Carats', y = 'Price($)') +
    ggtitle('Diamond size by carat') +
    facet_wrap(~clarity)
```



## Subset generation

- Say we want to take a random subset of diamonds

In [126]:
```
nrow(diamonds)
```

53940

## Sampling

- We can use the `sample` function in R to randomly sample from a list of numbers from 1 to 53940
- This sample can then be used to index the diamonds dataset

In [127]:
```
rand_idx = sample(x = 1:nrow(diamonds), # What we're sampling from,
       size = 1000, # How many to sample
       replace = TRUE) # After we sample one number, do we place it back in the po
pulation (TRUE) or remove it (FALSE)
head(rand_idx)
```

46136 49352 20077 45494 53062 4533

In [128]:
```
dm = diamonds[rand_idx, ]
print(names(dm))
print(dim(dm))
```

```
 [1] "carat"   "cut"     "color"   "clarity" "depth"   "table"   "price"
 [8] "x"       "y"       "z"
[1] 1000   10
```

In [129]:
```
summary(dm)
```

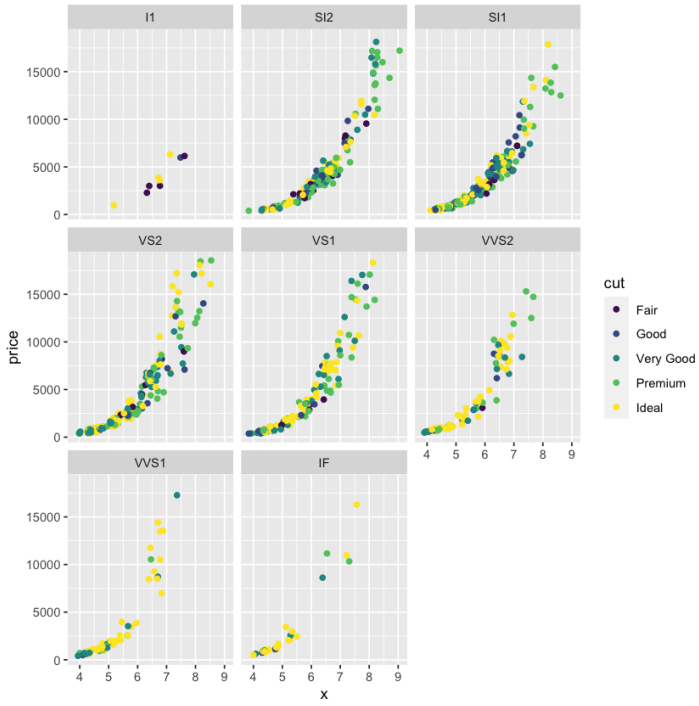
```
     carat               cut        color      clarity        depth      
 Min.   :0.2100   Fair      : 40   D:127   VS2    :246   Min.   :43.00  
 1st Qu.:0.4100   Good      : 91   E:179   SI1    :231   1st Qu.:61.10  
 Median :0.7100   Very Good:207   F:197   SI2    :171   Median :61.90  
 Mean   :0.8081   Premium   :249   G:199   VS1    :156   Mean   :61.82  
 3rd Qu.:1.0500   Ideal     :413   H:139   VVS2   : 91   3rd Qu.:62.60  
 Max.   :2.6000                   I:102   VVS1   : 61   Max.   :72.90  
                                  J: 57   (Other): 44                  
     table           price             x                y        
 Min.   :49.00   Min.   :  373   Min.   :3.840   Min.   :3.820  
 1st Qu.:56.00   1st Qu.: 1016   1st Qu.:4.770   1st Qu.:4.780  
 Median :57.00   Median : 2604   Median :5.740   Median :5.725  
 Mean   :57.33   Mean   : 4021   Mean   :5.763   Mean   :5.764  
 3rd Qu.:59.00   3rd Qu.: 5395   3rd Qu.:6.562   3rd Qu.:6.562  
 Max.   :69.00   Max.   :18559   Max.   :9.050   Max.   :8.940  

       z        
 Min.   :2.310  
 1st Qu.:2.940  
 Median :3.550  
 Mean   :3.564  
 3rd Qu.:4.050  
 Max.   :5.440  
```

In [130]:
```
summary(diamonds)
```

```
     carat               cut        color        clarity          depth      
 Min.   :0.2000   Fair      : 1610   D: 6775   SI1     :13065   Min.   :43.00  
 1st Qu.:0.4000   Good      : 4906   E: 9797   VS2     :12258   1st Qu.:61.00  
 Median :0.7000   Very Good:12082   F: 9542   SI2     : 9194   Median :61.80  
 Mean   :0.7979   Premium   :13791   G:11292   VS1     : 8171   Mean   :61.75  
 3rd Qu.:1.0400   Ideal     :21551   H: 8304   VVS2    : 5066   3rd Qu.:62.50  
 Max.   :5.0100                     I: 5422   VVS1    : 3655   Max.   :79.00  
                                    J: 2808   (Other): 2531                  
     table           price             x                y         
 Min.   :43.00   Min.   :  326   Min.   : 0.000   Min.   : 0.000  
 1st Qu.:56.00   1st Qu.:  950   1st Qu.: 4.710   1st Qu.: 4.720  
 Median :57.00   Median : 2401   Median : 5.700   Median : 5.710  
 Mean   :57.46   Mean   : 3933   Mean   : 5.731   Mean   : 5.735  
 3rd Qu.:59.00   3rd Qu.: 5324   3rd Qu.: 6.540   3rd Qu.: 6.540  
 Max.   :95.00   Max.   :18823   Max.   :10.740   Max.   :58.900  

       z         
 Min.   : 0.000  
 1st Qu.: 2.910  
 Median : 3.530  
 Mean   : 3.539  
 3rd Qu.: 4.040  
 Max.   :31.800  
```

## More about Facets

In [131]:
```
p1 = ggplot(data = dm) +
    geom_point(mapping = aes(x = x, y = price, color = cut)) +
    facet_wrap(~clarity)
print(p1)
```

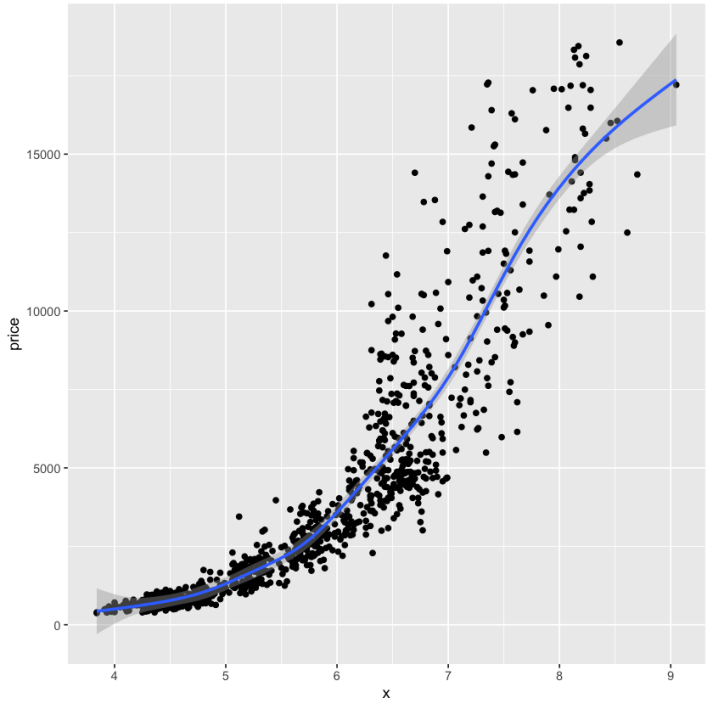


# geom_smooth

- Scatterplots can be useful as a quick glance at the data, but so many points can often be distracting.
- The `geom_smooth` function automatically fits a curve with standard-error bounds on the estimated mean function

In [132]:
```
p2 = ggplot(data = dm) +
    geom_point(mapping = aes(x = x, y = price)) +
    geom_smooth(mapping = aes(x = x, y = price))
print(p2)
```

```
`geom_smooth()` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```

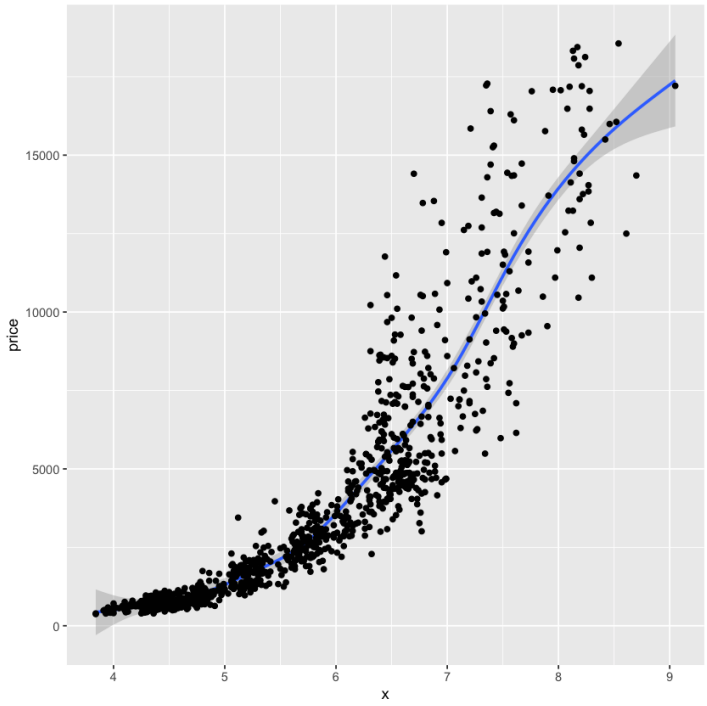



In [133]:
```
?geom_smooth
```

How can we reduce the code duplication above? "(x=x, y=price)" is in both lines.

In [134]:
```
ggplot(data = dm, mapping = aes(x = x, y= price)) +
  geom_smooth() + geom_point()
```

```
`geom_smooth()` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```



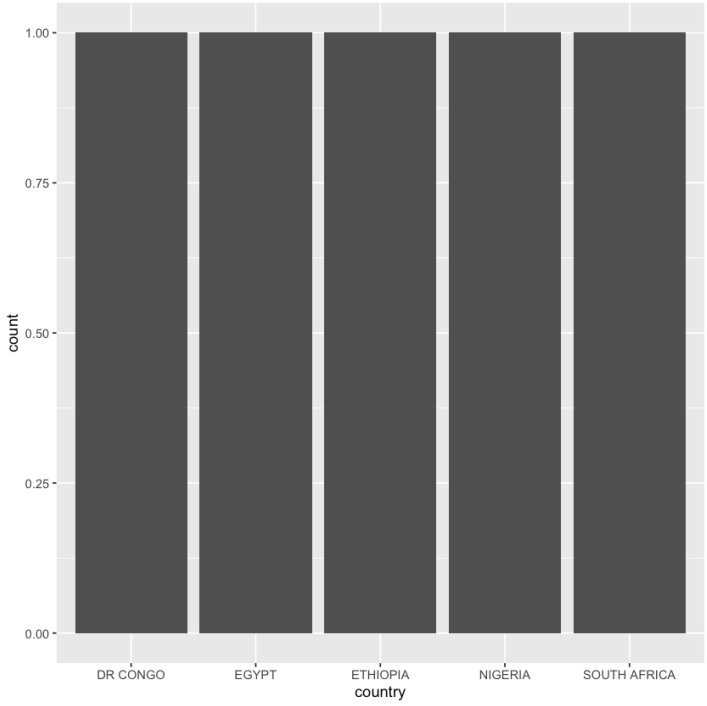

## Geometric Plots

- Many graphs, like scatterplots and lines, plot the raw values of your dataset. ( `geom_point` , `geom_line` )
- Other graphs, like bar charts, calculate new values to plot. ( `geom_bar` , `geom_smooth` )
- You can learn which stat a geom uses by inspecting the default value for the 'stat' argument. For example, ?geom_bar shows that the default value for stat is 'count', which means that geom_bar() uses stat_count().
- stat_count() is documented on the same page as geom_bar(), and if you scroll down you can find a section called "computed variables." That describes how it computes two new variables: count and prop.
- Let's use the following case where we override the default stat and instead want to use a value within the dataset of the y-axis (instead of a count).

In [135]:
```
popn <- tribble(
~country, ~population,
"ETHIOPIA", 102000000,
"NIGERIA", 186000000,
"EGYPT", 96000000,
"DR CONGO", 78000000,
"SOUTH AFRICA", 56000000
)
popn
```

| country | population |
|---|---|
| ETHIOPIA | 1.02e+08 |
| NIGERIA | 1.86e+08 |
| EGYPT | 9.60e+07 |
| DR CONGO | 7.80e+07 |
| SOUTH AFRICA | 5.60e+07 |

In [136]:
```
ggplot(popn) + geom_bar(aes(x=country))
```

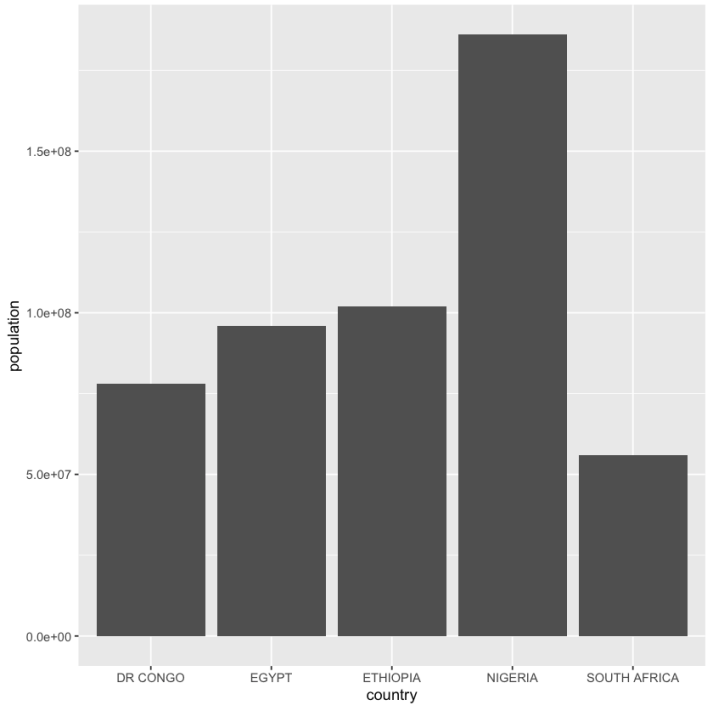


In [137]:
```
ggplot(popn) + geom_bar(aes(x=country, y=population))
```

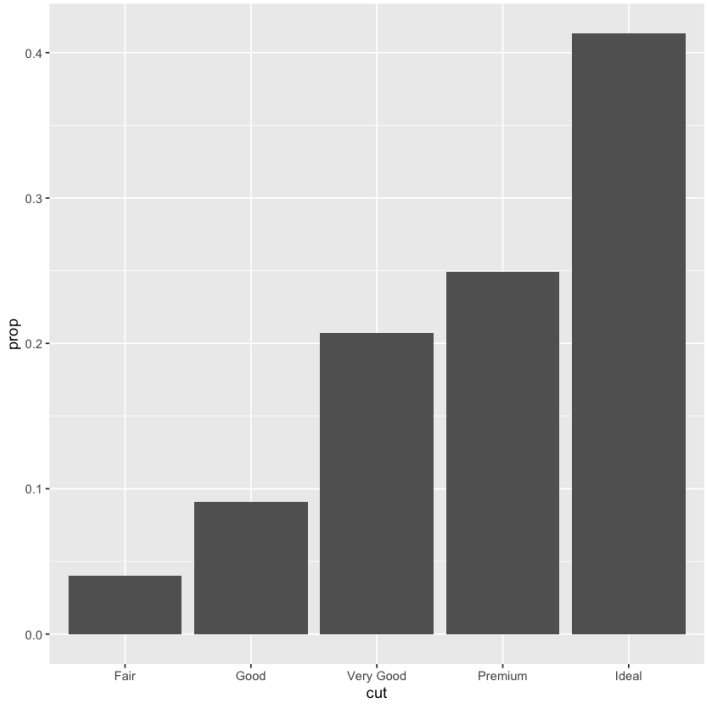
```
ERROR while rich displaying an object: Error: stat_count() can only have an x or
y aesthetic.

Traceback:
1. FUN(X[[i]], ...)
2. tryCatch(withCallingHandlers({
 .     if (!mime %in% names(repr::mime2repr))
 .         stop("No repr_* for mimetype ", mime, " in repr::mime2repr")
 .     rpr <- repr::mime2repr[[mime]](obj)
 .     if (is.null(rpr))
 .         return(NULL)
 .     prepare_content(is.raw(rpr), rpr)
 . }, error = error_handler), error = outer_handler)
3. tryCatchList(expr, classes, parentenv, handlers)
4. tryCatchOne(expr, names, parentenv, handlers[[1L]])
5. doTryCatch(return(expr), name, parentenv, handler)
6. withCallingHandlers({
 .     if (!mime %in% names(repr::mime2repr))
 .         stop("No repr_* for mimetype ", mime, " in repr::mime2repr")
 .     rpr <- repr::mime2repr[[mime]](obj)
 .     if (is.null(rpr))
 .         return(NULL)
 .     prepare_content(is.raw(rpr), rpr)
 . }, error = error_handler)
7. repr::mime2repr[[mime]](obj)
8. repr_text.default(obj)
9. paste(capture.output(print(obj)), collapse = "\n")
10. capture.output(print(obj))
11. evalVis(expr)
12. withVisible(eval(expr, pf))
13. eval(expr, pf)
14. eval(expr, pf)
15. print(obj)
16. print.ggplot(obj)
17. ggplot_build(x)
18. ggplot_build.ggplot(x)
19. by_layer(function(l, d) l$compute_statistic(d, layout))
20. f(l = layers[[i]], d = data[[i]])
21. l$compute_statistic(d, layout)
22. f(..., self = self)
23. self$stat$setup_params(data, self$stat_params)
24. f(...)
25. abort("stat_count() can only have an x or y aesthetic.")
26. signal_abort(cnd)
```

In [138]:
```
ggplot(data = popn) +
  geom_bar(mapping = aes(x = country, y = population), stat = "identity")
  ggtitle('Most populous countries in Africa')
```

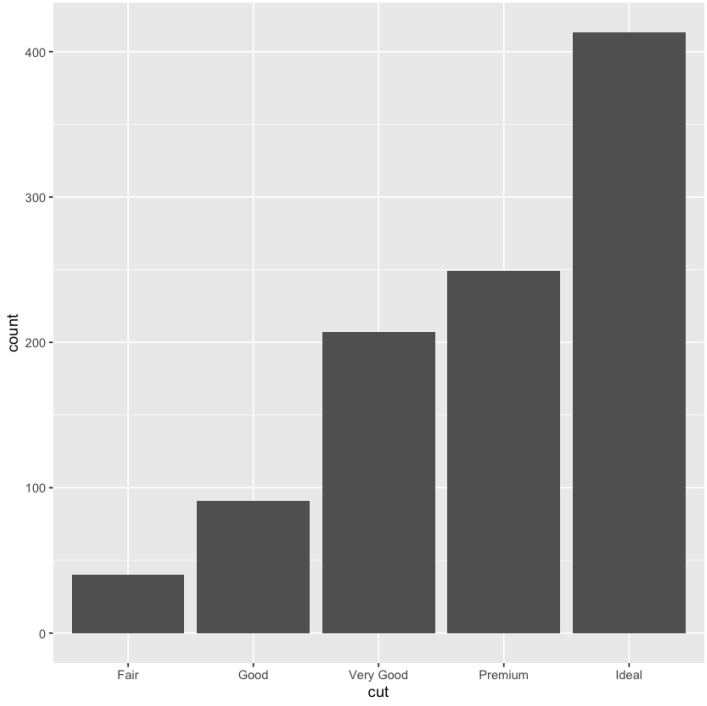
```
$title
[1] "Most populous countries in Africa"

attr(,"class")
[1] "labels"
```



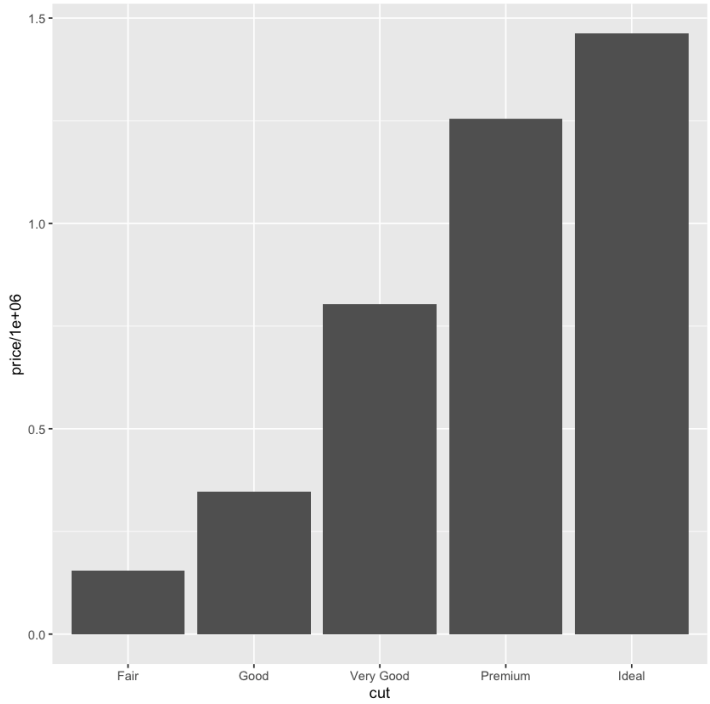
In [139]:
```
ggplot(data = dm) +
    geom_bar(mapping = aes(x=cut, y=..prop.., group=1))
```




In [140]:
```
ggplot(data = dm) +
    stat_count(mapping = aes(x = cut))
```

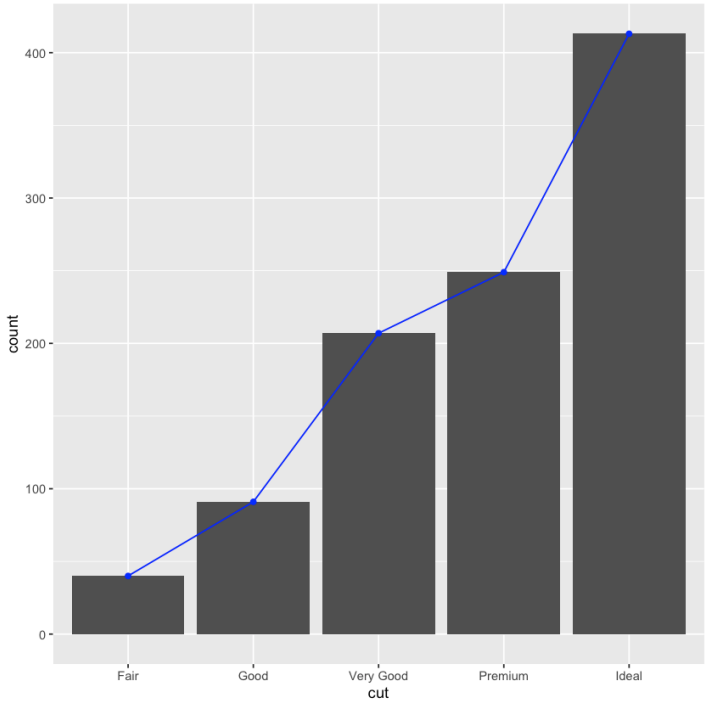


In [141]:
```
ggplot(data = dm) +
    geom_col(mapping = aes(x = cut, y = price / 1e6))
```




- A `geom_` function is tied to specific plot, with a modifiable underlying stat
  - e.g. `geom_bar` and `geom_col` only differ in their default underlying stat ("count and "identity" respectively)
- A `stat_` function is tied to a specific statistical transformation, with a modifiable geom (i.e. plot)
  - e.g. `stat_count` has a default geom of "bar", but this can be overridden if we want to display count data differently

In [142]:
```
ggplot(data = dm) +
    stat_count(mapping = aes(x = cut, group=1)) +
    stat_count(mapping = aes(x = cut, group=1), geom="point", color="blue") +
    stat_count(mapping = aes(x = cut, group=1), geom="line", color="blue")
```



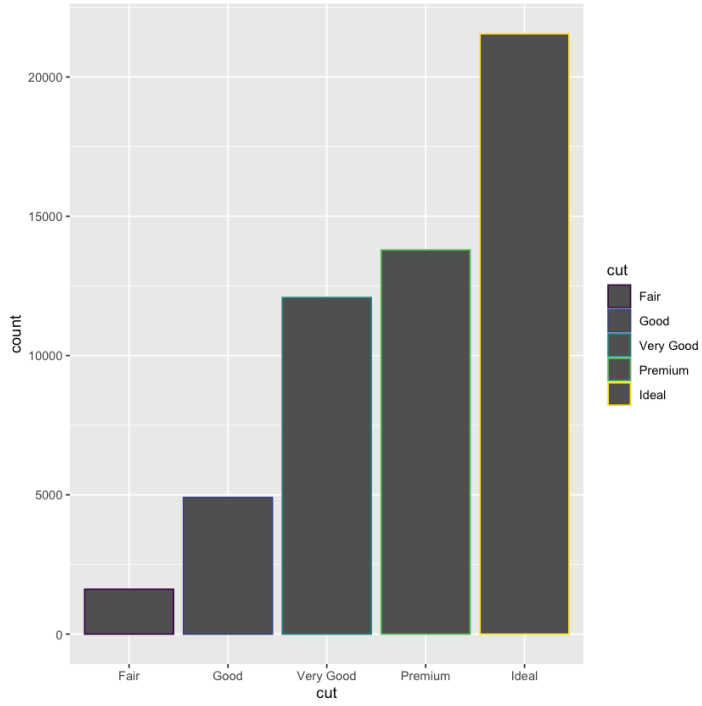

### Exercise

1. What does geom_col() do? How is it different to geom_bar()?
2. Most geoms and stats come in pairs that are almost always used in concert. Read through the documentation and make a list of all the pairs. What do they have in common?
3. What variables does stat_smooth() compute? What parameters control its behaviour?
4. In our proportion bar chart, we need to set group = 1. Why? In other words, what is the problem with these two graphs?

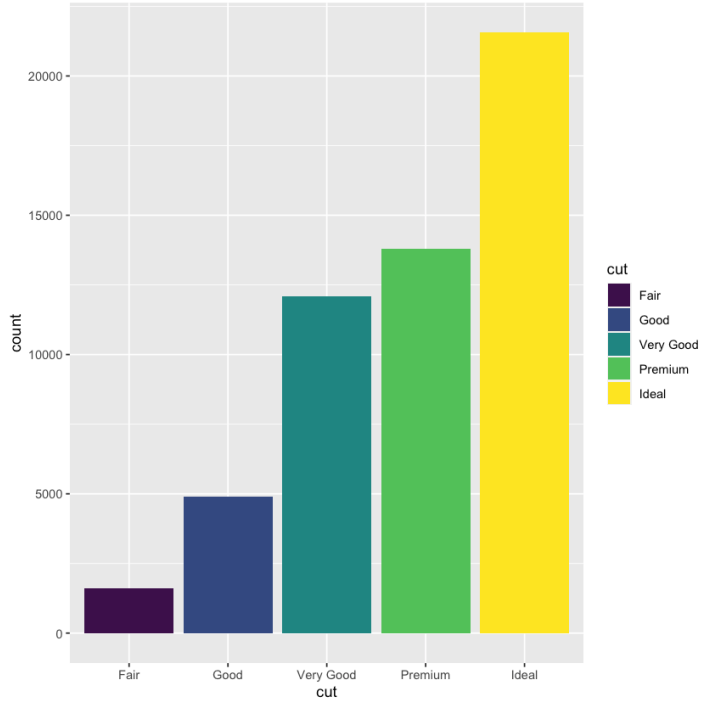
## More settings: fill, color, and position

- "fill" corresponds to the color of the volume within a geom
- "color" corresponds to the color of the lines bordering a geom

In [143]:
```
ggplot(data = diamonds) +
  geom_bar(mapping = aes(x = cut, colour = cut))
```

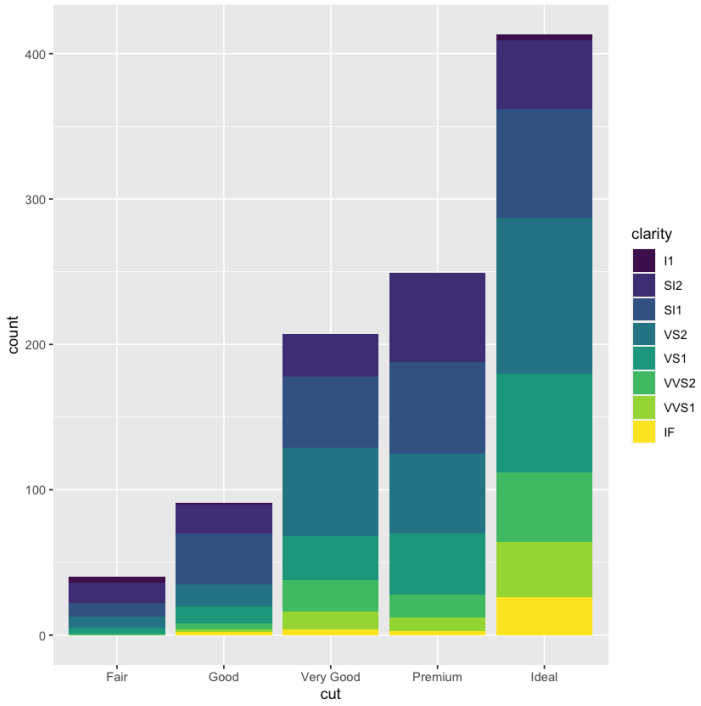



In [144]:
```
ggplot(data = diamonds) +
  geom_bar(mapping = aes(x = cut, fill = cut))
```



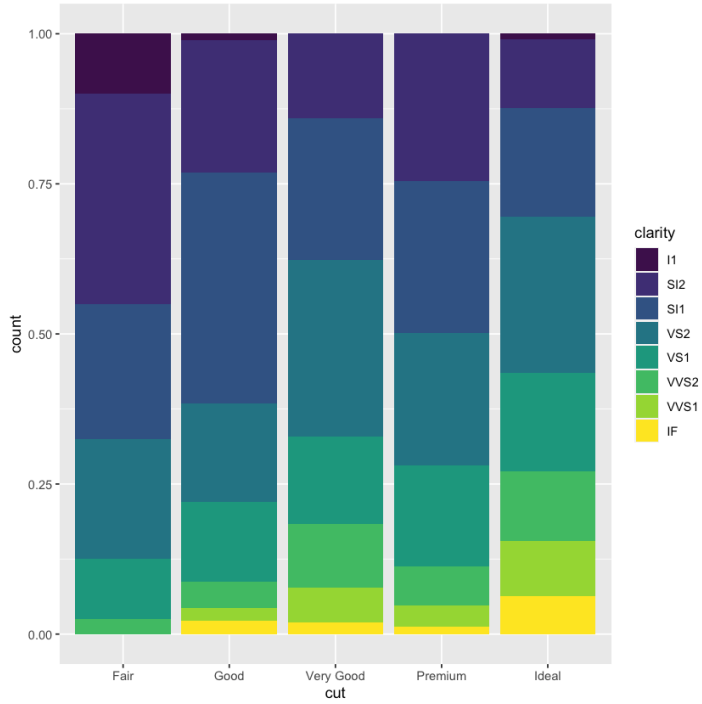
- Remember that we can "color by" a different variable - in this case, clarity.
- By default, it stacks the bars for each clarity level.
- This is done using the positional adjustment specified by the position argument of geom_bar.
- If you don't want a stacked bar chart, you can use one of three other options:
  - "identity"
  - "dodge"
  - "fill

In [145]:
```
ggplot(data = dm) +
    geom_bar(mapping = aes(x = cut, fill = clarity)) # this "fill" is different fr
om the following one.
```




*position 'fill'* This works like stacking, but makes each set of stacked bars the same height. This makes it easier to compare proportions across groups.

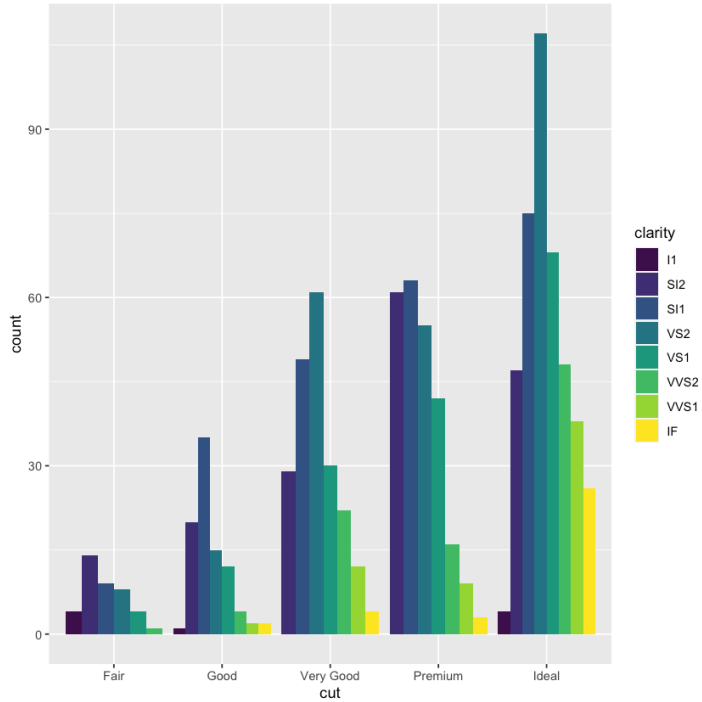
In [146]:
```
ggplot(data = dm) +
  geom_bar(mapping = aes(x = cut, fill = clarity), position = "fill")
```




*position* = '*dodge*'

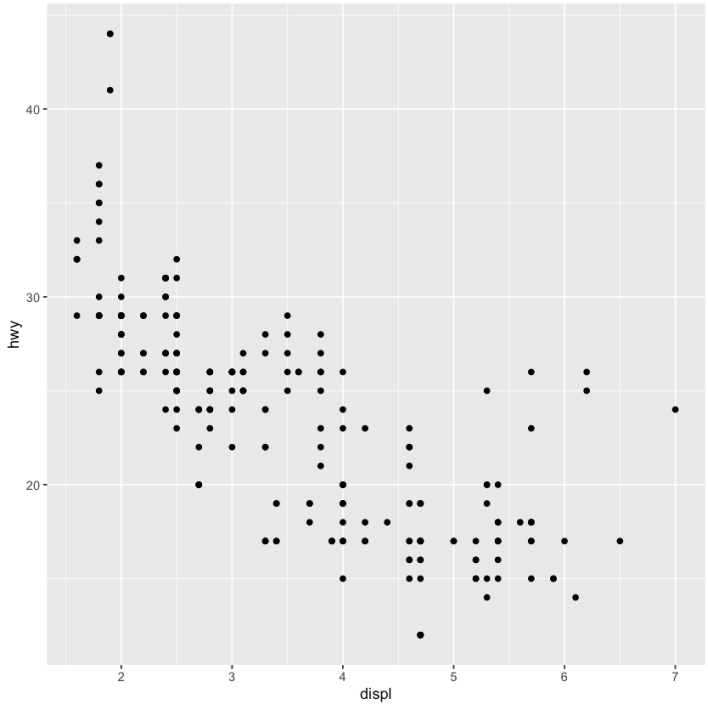
This places overlapping objects directly beside one another, which makes it easier to compare individual values.

In [147]:
```
ggplot(data = dm) +
  geom_bar(mapping = aes(x = cut, fill = clarity), position = "dodge")
```

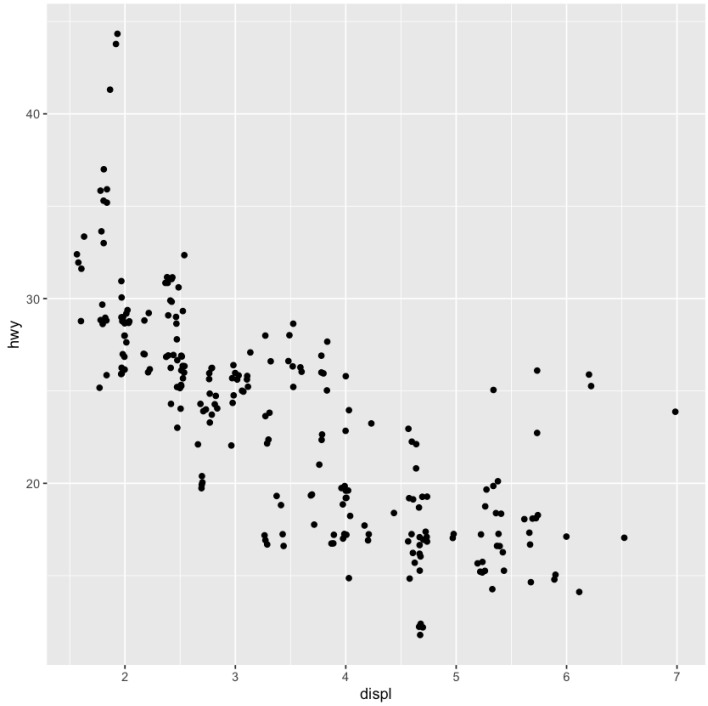


A positional adjustment that is very useful for scatterplots with overlaps is the 'jitter' argument.

In [148]:
```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy))
```




In [149]:
```
ggplot(data = mpg) +
  geom_point(mapping = aes(x = displ, y = hwy), position = "jitter")
```



# dplyr for data manipulation

In [150]:
```
dim(dm)
head(dm)
```

1000 10

| carat | cut | color | clarity | depth | table | price | x | y | z |
|---|---|---|---|---|---|---|---|---|---|
| 0.41 | Ideal | E | VVS1 | 61.1 | 56 | 1745 | 4.80 | 4.82 | 2.94 |
| 0.54 | Ideal | H | IF | 60.9 | 57 | 2096 | 5.26 | 5.31 | 3.22 |
| 1.00 | Very Good | F | VVS2 | 60.0 | 62 | 8553 | 6.43 | 6.46 | 3.87 |
| 0.52 | Ideal | D | VS2 | 62.0 | 56 | 1679 | 5.17 | 5.19 | 3.21 |
| 0.75 | Good | D | SI1 | 64.1 | 54 | 2608 | 5.78 | 5.76 | 3.70 |
| 0.91 | Premium | E | SI2 | 62.8 | 61 | 3639 | 6.09 | 6.07 | 3.82 |

There are five main functions in dplyr:

- filter
- arrange
- select
- mutate
- summarise.

All of them have the following properties:

1. The first argument is a data frame.
2. The subsequent arguments describe what to do with the data frame
3. The result is a new data frame.

## Filter

Used if you want to create a new dataset only containing rows which pass a given condition.

Note: Make sure to use '==' instead of '=' when checking equality.

In [151]:
```
worst_diamonds <- filter(dm, cut == 'Fair', color == 'J')
worst_diamonds
```

| carat | cut | color | clarity | depth | table | price | x | y | z |
|---|---|---|---|---|---|---|---|---|---|
| 1.03 | Fair | J | SI2 | 64.6 | 62 | 3149 | 6.3 | 6.21 | 4.06 |

## More examples

In [152]:
```
a = filter(dm, cut == 'Fair'| color == 'J')
# filtering for rows that satisfy one or both of the conditions

b = filter(dm, color == 'D' & color == 'J')
# filtering for rows that satisfy both conditions

best_cuts = filter(dm, cut == 'Ideal')
# filtering using membership condition

not_worst_cuts = filter(dm, cut > 'Fair')
# can do this because cut is an ordinal variable
```

In [153]:
```
head(not_worst_cuts)
```

| carat | cut | color | clarity | depth | table | price | x | y | z |
|---|---|---|---|---|---|---|---|---|---|
| 0.41 | Ideal | E | VVS1 | 61.1 | 56 | 1745 | 4.80 | 4.82 | 2.94 |
| 0.54 | Ideal | H | IF | 60.9 | 57 | 2096 | 5.26 | 5.31 | 3.22 |
| 1.00 | Very Good | F | VVS2 | 60.0 | 62 | 8553 | 6.43 | 6.46 | 3.87 |
| 0.52 | Ideal | D | VS2 | 62.0 | 56 | 1679 | 5.17 | 5.19 | 3.21 |
| 0.75 | Good | D | SI1 | 64.1 | 54 | 2608 | 5.78 | 5.76 | 3.70 |
| 0.91 | Premium | E | SI2 | 62.8 | 61 | 3639 | 6.09 | 6.07 | 3.82 |

# Missing Values and TRUE/FALSE

- In R, if there is a chance that a value equals NA, use the is.na() function to check
- In particular, do not check for equality with NA, because this won't be true or false, but NA

In [154]:
```
x = 4
x == NA
is.na(x)
```

<NA>

FALSE

## Exercise

1. Write code using filter that will allow you to output diamonds with colors D or E and cuts Good or Very Good
2. Write code using filter that wil allow you to output diamonds with even-numbered prices

# Arrange

Useful for ordering rows instead of filtering for a subset of them

In [155]:
```
head(arrange(dm, cut, color))
# can be done since clarity is an ordinal variable
```

| carat | cut | color | clarity | depth | table | price | x | y | z |
|---|---|---|---|---|---|---|---|---|---|
| 1.01 | Fair | D | SI2 | 64.7 | 57 | 3871 | 6.31 | 6.27 | 4.07 |
| 0.90 | Fair | D | SI2 | 65.7 | 60 | 3205 | 5.98 | 5.93 | 3.91 |
| 0.53 | Fair | E | SI1 | 64.5 | 53 | 1363 | 5.16 | 5.15 | 3.33 |
| 0.45 | Fair | E | VS2 | 65.8 | 58 | 951 | 4.81 | 4.74 | 3.14 |
| 0.41 | Fair | E | SI2 | 64.7 | 55 | 818 | 4.70 | 4.67 | 3.03 |
| 0.72 | Fair | E | SI2 | 68.4 | 64 | 2125 | 5.38 | 5.32 | 3.66 |

In [156]:
```
# arranging in the descending order of carat and then cut
head(arrange(dm,desc(carat), cut))
```

| carat | cut | color | clarity | depth | table | price | x | y | z |
|---|---|---|---|---|---|---|---|---|---|
| 2.60 | Premium | J | SI2 | 58.3 | 61 | 17209 | 9.05 | 8.94 | 5.24 |
| 2.55 | Premium | I | SI2 | 62.9 | 58 | 14351 | 8.70 | 8.59 | 5.44 |
| 2.38 | Premium | J | VS2 | 62.1 | 58 | 18559 | 8.54 | 8.49 | 5.29 |
| 2.37 | Ideal | J | VS2 | 62.2 | 57 | 16059 | 8.52 | 8.58 | 5.32 |
| 2.30 | Premium | J | SI1 | 59.6 | 59 | 12499 | 8.61 | 8.56 | 5.12 |
| 2.30 | Premium | H | SI2 | 62.7 | 56 | 15992 | 8.46 | 8.42 | 5.29 |

Missing values are always sorted at the end:

In [157]:
```
df = tibble(x = c(5, NA, 2))
arrange(df, x)
```

| x |
|---|
| 2 |
| 5 |
| NA |

In [158]:
```
arrange(df, desc(x))
```

| x |
|---|
| 5 |
| 2 |
| NA |

## Exercise

1. Use arrange to sort the dm dataset by describing order of the product of the x, y, and z variables. Output the first 20 rows of the new dataset.

## Select

This is used to reduce the number of columns that we're dealing with. Useful for things like genetic data

In [159]:
```
names(dm)
```

'carat' 'cut' 'color' 'clarity' 'depth' 'table' 'price' 'x' 'y' 'z'

In [160]:
```
head(select(dm, carat, price))
```

| carat | price |
|---|---|
| 0.41 | 1745 |
| 0.54 | 2096 |
| 1.00 | 8553 |
| 0.52 | 1679 |
| 0.75 | 2608 |
| 0.91 | 3639 |

In [161]:
```
head(select(dm, carat:price))
```

| carat | cut | color | clarity | depth | table | price |
|---|---|---|---|---|---|---|
| 0.41 | Ideal | E | VVS1 | 61.1 | 56 | 1745 |
| 0.54 | Ideal | H | IF | 60.9 | 57 | 2096 |
| 1.00 | Very Good | F | VVS2 | 60.0 | 62 | 8553 |
| 0.52 | Ideal | D | VS2 | 62.0 | 56 | 1679 |
| 0.75 | Good | D | SI1 | 64.1 | 54 | 2608 |
| 0.91 | Premium | E | SI2 | 62.8 | 61 | 3639 |

In [162]:
```
head(select(dm, -(carat:price)))
```

| x | y | z |
|---|---|---|
| 4.80 | 4.82 | 2.94 |
| 5.26 | 5.31 | 3.22 |
| 6.43 | 6.46 | 3.87 |
| 5.17 | 5.19 | 3.21 |
| 5.78 | 5.76 | 3.70 |
| 6.09 | 6.07 | 3.82 |

Use rename(), which is a variant of select(), to rename a column and keep all the variables that aren't explicitly mentioned:

In [163]:
```
head(rename(dm, width=x))
```

| carat | cut | color | clarity | depth | table | price | width | y | z |
|---|---|---|---|---|---|---|---|---|---|
| 0.41 | Ideal | E | VVS1 | 61.1 | 56 | 1745 | 4.80 | 4.82 | 2.94 |
| 0.54 | Ideal | H | IF | 60.9 | 57 | 2096 | 5.26 | 5.31 | 3.22 |
| 1.00 | Very Good | F | VVS2 | 60.0 | 62 | 8553 | 6.43 | 6.46 | 3.87 |
| 0.52 | Ideal | D | VS2 | 62.0 | 56 | 1679 | 5.17 | 5.19 | 3.21 |
| 0.75 | Good | D | SI1 | 64.1 | 54 | 2608 | 5.78 | 5.76 | 3.70 |
| 0.91 | Premium | E | SI2 | 62.8 | 61 | 3639 | 6.09 | 6.07 | 3.82 |

In [164]:
```
head(select(dm, width = x))
```

| width |
|---|
| 4.80 |
| 5.26 |
| 6.43 |
| 5.17 |
| 5.78 |
| 6.09 |

Another option is to use select() in conjunction with the everything() helper. This is useful if you have a handful of variables you would like to move to the start of the dtaframe

In [165]:
```
head(select(dm, price, carat, everything()))
```

| price | carat | cut | color | clarity | depth | table | x | y | z |
|---|---|---|---|---|---|---|---|---|---|
| 1745 | 0.41 | Ideal | E | VVS1 | 61.1 | 56 | 4.80 | 4.82 | 2.94 |
| 2096 | 0.54 | Ideal | H | IF | 60.9 | 57 | 5.26 | 5.31 | 3.22 |
| 8553 | 1.00 | Very Good | F | VVS2 | 60.0 | 62 | 6.43 | 6.46 | 3.87 |
| 1679 | 0.52 | Ideal | D | VS2 | 62.0 | 56 | 5.17 | 5.19 | 3.21 |
| 2608 | 0.75 | Good | D | SI1 | 64.1 | 54 | 5.78 | 5.76 | 3.70 |
| 3639 | 0.91 | Premium | E | SI2 | 62.8 | 61 | 6.09 | 6.07 | 3.82 |

There are some helper functions for select():

- `starts_with("xyz")` : any column that starts with "xyz"
- `ends_with("xyz")` : any column that ends with "xyz"
- `contains("xyz")` : any column that contains "xyz"

## Exercise:

1. Write code that will have price as the first column and the columns starting with the letter 'c' as the following columns. Output the first 20 rows of such a datset.

### Mutate

`mutate()` is used to create a new column as a function of other columns in the dataset.

In [166]:
```
dm_dimensions = select(dm,
  -(carat:price)
)
head(mutate(dm_dimensions,
  volume = x*y*z
))
```

| x | y | z | volume |
|---|---|---|---|
| 4.80 | 4.82 | 2.94 | 68.01984 |
| 5.26 | 5.31 | 3.22 | 89.93653 |
| 6.43 | 6.46 | 3.87 | 160.75129 |
| 5.17 | 5.19 | 3.21 | 86.13168 |
| 5.78 | 5.76 | 3.70 | 123.18336 |
| 6.09 | 6.07 | 3.82 | 141.21127 |

If you only want to keep the new variables, use transmute()

In [167]:
```
head(transmute(dm_dimensions,
          volume = x*y*z))
```

| volume |
|---|
| 68.01984 |
| 89.93653 |
| 160.75129 |
| 86.13168 |
| 123.18336 |
| 141.21127 |

## Summarise

Generally used in concert with group_by() function to output summaries by group. Group summaries are seen in many applications

In [168]:
```
by_color = group_by(dm, color)
summarise(by_color, avg_price = mean(price, na.rm = TRUE))
```

```
`summarise()` ungrouping output (override with `.groups` argument)
```

| color | avg_price |
|---|---|
| D | 3426.551 |
| E | 2780.503 |
| F | 3700.203 |
| G | 4279.628 |
| H | 4495.496 |
| I | 5263.480 |
| J | 6067.912 |

In [169]:
```
by_maker_yr = group_by(mpg, manufacturer, year)
hwy_summary = summarise(by_maker_yr,
                        count = n(),
                        hwy = mean(hwy, na.rm = TRUE),
                        cty = mean(cty, na.rm = TRUE))
head(hwy_summary)
```

```
`summarise()` regrouping output by 'manufacturer' (override with `.groups` argum
ent)
```

| manufacturer | year | count | hwy | cty |
|---|---|---|---|---|
| audi | 1999 | 9 | 26.11111 | 17.11111 |
| audi | 2008 | 9 | 26.77778 | 18.11111 |
| chevrolet | 1999 | 7 | 21.57143 | 15.14286 |
| chevrolet | 2008 | 12 | 22.08333 | 14.91667 |
| dodge | 1999 | 16 | 18.43750 | 13.37500 |
| dodge | 2008 | 21 | 17.57143 | 12.95238 |

# Pipes

- Often times we create intermediate data frames which are not needed for the final output
- We can use the **pipe** operator ( `%>%` ) to succinctly chain together functions
- `x %>% f(y,z)` is equivalent to `f(x, y, z)`
- The transformations above can rewritten with the pipe

In [170]:
```
hwy_summary_ag2 = mpg %>%
    group_by(manufacturer, year) %>%
    summarise(
        count = n(),
        hwy = mean(hwy, na.rm = TRUE),
        cty = mean(cty, na.rm = TRUE)) %>%
    filter(substring(manufacturer,1,1) %in% c('a','b','c','d','e','f','g'))
```

```
`summarise()` regrouping output by 'manufacturer' (override with `.groups` argum
ent)
```

In [171]:
```
head(hwy_summary_ag2)
```

| manufacturer | year | count | hwy | cty |
|---|---|---|---|---|
| audi | 1999 | 9 | 26.11111 | 17.11111 |
| audi | 2008 | 9 | 26.77778 | 18.11111 |
| chevrolet | 1999 | 7 | 21.57143 | 15.14286 |
| chevrolet | 2008 | 12 | 22.08333 | 14.91667 |
| dodge | 1999 | 16 | 18.43750 | 13.37500 |
| dodge | 2008 | 21 | 17.57143 | 12.95238 |