## **Exploratory Data Analysis**



Jonathan Kropko (jkropko@virginia.edu)

District Data Labs

The summary() function
The dfSummary() function
Quick calculations
Percentiles
Frequency tables
Cross tabulations
Correlation

# Correlation Inferential statistics

Student's *t*-test  $\chi^2$  test of association

#### Beautiful graphics with ggplot2

The ggplot() function
Aesthetics
Different kinds of plots with geom functions
Axis labels and titles
Using colors, shapes, or line types for groups
Creating a grid of plots
Saving graphics as PDF, JPEG, BMP, or PNG files
Using ggplot() within an R markdown document

A descriptive statistic is a quantity that **summarizes** some feature of data. These statistics are usually quick and easy to calculate.

A descriptive statistic is a quantity that **summarizes** some feature of data. These statistics are usually quick and easy to calculate.

<u>Examples</u>: mean, median, standard deviation, correlation, quantiles, frequency tables, cross-tabulations

A descriptive statistic is a quantity that **summarizes** some feature of data. These statistics are usually quick and easy to calculate.

<u>Examples</u>: mean, median, standard deviation, correlation, quantiles, frequency tables, cross-tabulations

Descriptive statistics contrast with inferential statistics, which involve hypothesis tests, *p*-values, etc. **Simple** inferential statistics are great ways to explore data quickly, without spending much time worrying about model design (we'll have plenty of chances for that later!)

A descriptive statistic is a quantity that **summarizes** some feature of data. These statistics are usually quick and easy to calculate.

<u>Examples</u>: mean, median, standard deviation, correlation, quantiles, frequency tables, cross-tabulations

Descriptive statistics contrast with inferential statistics, which involve hypothesis tests, *p*-values, etc. **Simple** inferential statistics are great ways to explore data quickly, without spending much time worrying about model design (we'll have plenty of chances for that later!)

Examples: t-tests,  $\chi^2$  tests of association

### The summary() function

The summary() function is one of the most useful R commands to run after loading and cleaning data.

### The summary() function

The summary() function is one of the most useful R commands to run after loading and cleaning data.

It gives different output depending on the class of the object passed to it. For a data frame, it provides the mean, median, min, and max, and quartiles for **continuous** variables:

```
> summary(anes$fthrc)
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
0.00 3.00 44.00 42.99 76.00 100.00 1
```

And it displays frequencies for factor variables:

### The dfSummary() function

The dfSummary() from the summarytools package provides many descriptive statistics in a neat HTML format.

### The dfSummary() function

The dfSummary() from the summarytools package provides many descriptive statistics in a neat HTML format.

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
1	sex [factor]	1. female 2. male	1586 (55.5%) 1273 (44.5%)		o (o%)
2	age [numeric]	Mean (sd): 49.1 (17.7) min < med < max: 18 < 49 < 89 IQR (CV): 28 (0.4)	72 distinct values		10 (0.35%)
3	artexbt [factor]	1. no 2. yes	987 (67.2%) 481 (32.8%)		1391 (48.65%)
4	class [factor]	1. lower class 2. middle class 3. upper class 4. working class	286 (10.1%) 1143 (40.3%) 80 ( 2.8%) 1328 (46.8%)		22 (0.77%)

### Quick calculations

There are several functions that quickly calculate summary statistics. They have straightforward names:

### Quick calculations

There are several functions that quickly calculate summary statistics. They have straightforward names:

- ▶ mean() calculates the mean
- ▶ median() calculates the median
- sd() calculates the standard deviation
- var() calculates the variance
- ▶ min() calculates the minimum value
- ▶ max() calculates the maximum value

### Quick calculations

There are several functions that quickly calculate summary statistics. They have straightforward names:

- ▶ mean() calculates the mean
- median() calculates the median
- sd() calculates the standard deviation
- var() calculates the variance
- ▶ min() calculates the minimum value
- ▶ max() calculates the maximum value

If there are missing values for an object, these functions will return NA unless you also specify the argument na.rm=TRUE, in which case it ignores the missing values.

A percentile is a statistic that **ranks** the observations from lowest to highest, counts from the lowest to a specified percent, and reports the value of the observation at that percent.

A percentile is a statistic that **ranks** the observations from lowest to highest, counts from the lowest to a specified percent, and reports the value of the observation at that percent.

The median is the **50th percentile**. 50% of the observations have a value lower than or equal to the median.

A percentile is a statistic that **ranks** the observations from lowest to highest, counts from the lowest to a specified percent, and reports the value of the observation at that percent.

The median is the **50th percentile**. 50% of the observations have a value lower than or equal to the median.

To find percentiles, use the quantile() function. Use the probs argument to specify the percentiles you want to see.

A percentile is a statistic that **ranks** the observations from lowest to highest, counts from the lowest to a specified percent, and reports the value of the observation at that percent.

The median is the **50th percentile**. 50% of the observations have a value lower than or equal to the median.

To find percentiles, use the quantile() function. Use the probs argument to specify the percentiles you want to see.

Here are the 10th, 40th, and 85th percentiles for Hillary Clinton's thermometer scores in the 2016 ANES pilot study:

```
> quantile(anes$fthrc, probs=c(.1, .4, .85), na.rm=TRUE)
10% 40% 85%
0 20 89
```

A frequency table is the most useful way to describe a categorical (factor) variable. It is simply a count of the number of observations with each category.

A frequency table is the most useful way to describe a categorical (factor) variable. It is simply a count of the number of observations with each category.

There are three functions that report frequencies:

- ▶ table()
- plyr::count()
- xtabs()

A frequency table is the most useful way to describe a categorical (factor) variable. It is simply a count of the number of observations with each category.

There are three functions that report frequencies:

- ▶ table()
- plyr::count()
- xtabs()

table() displays these frequencies side by side:

```
> table(anes$vote12)

Mitt Romney Barack Obama Someone else
371 512 68
```

plyr::count() displays these frequencies vertically:

plyr::count() displays these frequencies vertically:

xtabs() also displays these frequencies side by side, but requires a slightly different syntax:

```
> xtabs(~ vote12, data=anes)
vote12
Mitt Romney Barack Obama Someone else
371 512 68
```

A cross tabulation is a method for examining the **relationship** between two categorical variables.

A cross tabulation is a method for examining the **relationship** between two categorical variables.

You specify two variables, one for the rows and one for the columns. The cells in the tables contain the **number of observations** that have the category represented by the row AND the category represented by the column.

A cross tabulation is a method for examining the **relationship** between two categorical variables.

You specify two variables, one for the rows and one for the columns. The cells in the tables contain the **number of observations** that have the category represented by the row AND the category represented by the column.

Both table() and xtabs() can create cross tabulations. For table(), write the rows variable first, the columns variable second:

```
> table(anes$gender, anes$vote12)

Mitt Romney Barack Obama Someone else
Male 191 236 46
Female 180 276 22
```

For xtabs(), write a

 $\sim$ 

first, then rows variable, then +, then the columns variable:

```
> xtabs( ~ gender + vote12, data=anes)
vote12
gender Mitt Romney Barack Obama Someone else
Male 191 236 46
Female 180 276 22
```

For xtabs(), write a

 $\sim$ 

first, then rows variable, then +, then the columns variable:

You get a slightly cleaner display by placing this function within ftable() (this creates a "flat table"):

```
ftable(xtabs( ~ gender + vote12, data=anes))
vote12 Mitt Romney Barack Obama Someone else
gender
Male 191 236 46
Female 180 276 22
```

If you write a third variable in the formula, it displays a different cross-tab for each value of the third variable:

```
> xtabs( ~ gender + vote12 + sign, data=anes)
, , sign = Have done this in the past 12 months
        vot.e12
gender
       Mitt Romney Barack Obama Someone else
 Male
                  50
                               69
                                            15
  Female
                  35
                               75
, , sign = Have not done this in the past 12 months
        vote12
gender
       Mitt Romney Barack Obama Someone else
 Male
                              167
                 141
                                            31
  Female
                145
                              201
                                            21
```

Row percents are the percent that each cell comprises of the row total. Column percents are the percent that each cell comprises of the column total. And cell percents are the percent that each cell comprises of the overall total.

Row percents are the percent that each cell comprises of the row total. Column percents are the percent that each cell comprises of the column total. And cell percents are the percent that each cell comprises of the overall total.

To calculate these percents, save the table as a separate object

```
my.table <- table(anes$gender, anes$vote12)</pre>
```

Row percents are the percent that each cell comprises of the row total. Column percents are the percent that each cell comprises of the column total. And cell percents are the percent that each cell comprises of the overall total.

To calculate these percents, save the table as a separate object

```
\verb|my.table <- table(anes$gender, anes$vote12)|\\
```

Then use the prop.table() function. By default it gives cell proportions (percents/100)

```
> prop.table(my.table)

Mitt Romney Barack Obama Someone else
Male     0.20084122     0.24815983     0.04837014
Female     0.18927445     0.29022082     0.02313354
```

For row proportions, use the argument margin=1:

For row proportions, use the argument margin=1:

```
> prop.table(my.table, margin=1)

Mitt Romney Barack Obama Someone else
Male 0.40380550 0.49894292 0.09725159
Female 0.37656904 0.57740586 0.04602510
```

For column proportions, use the argument margin=2:

For row proportions, use the argument margin=1:

```
> prop.table(my.table, margin=1)

Mitt Romney Barack Obama Someone else
Male 0.40380550 0.49894292 0.09725159
Female 0.37656904 0.57740586 0.04602510
```

For column proportions, use the argument margin=2:

For percents, multiply by 100:

```
> 100*prop.table(my.table, margin=2)

Mitt Romney Barack Obama Someone else
Male 51.48248 46.09375 67.64706
Female 48.51752 53.90625 32.35294
```



#### Correlation

Correlation is a statistic that measures the extent to which two continuous variables move with one another or opposed to one another.

#### Correlation

Correlation is a statistic that measures the extent to which two continuous variables move with one another or opposed to one another.

**Positive** correlation means that as one variable changes, the other changes in the same direction. If the correlation is 1, there's a perfect upward-sloping linear formula that describes this relationship.

Correlation is a statistic that measures the extent to which two continuous variables move with one another or opposed to one another.

**Positive** correlation means that as one variable changes, the other changes in the <u>same</u> direction. If the correlation is 1, there's a perfect <u>upward-sloping</u> linear formula that describes this relationship.

**Negative** correlation means that as one variable changes, the other changes in the opposite direction. If the correlation is -1, there's a perfect downward-sloping linear formula that describes this relationship.

To use R to calculate correlation, create a separate data frame with all of the continuous variables you want to calculate correlations between.

To use R to calculate correlation, create a separate data frame with all of the continuous variables you want to calculate correlations between.

The use na.omit() to remove rows with missing values.

To use R to calculate correlation, create a separate data frame with all of the continuous variables you want to calculate correlations between.

The use na.omit() to remove rows with missing values.

Then use the cor() function on the data.

A *t*-test is a way to test whether or not two variables **have equal means**.

A *t*-test is a way to test whether or not two variables **have equal means**.

We could spend a semester talking about the math behind a *t*-test. Many of you probably already have! We'll cover just the rudimentary basics here.

A *t*-test is a way to test whether or not two variables **have equal means**.

We could spend a semester talking about the math behind a *t*-test. Many of you probably already have! We'll cover just the rudimentary basics here.

A *t*-test is a way to test whether or not two variables **have equal means**.

We could spend a semester talking about the math behind a *t*-test. Many of you probably already have! We'll cover just the rudimentary basics here.

A *t*-test takes the following steps:

 Calculate the mean of both variables and the difference between these two means

A *t*-test is a way to test whether or not two variables **have equal means**.

We could spend a semester talking about the math behind a *t*-test. Many of you probably already have! We'll cover just the rudimentary basics here.

- Calculate the mean of both variables and the difference between these two means
- Suppose the means are equal in the population, and that the sample is random

A *t*-test is a way to test whether or not two variables **have equal means**.

We could spend a semester talking about the math behind a *t*-test. Many of you probably already have! We'll cover just the rudimentary basics here.

- Calculate the mean of both variables and the difference between these two means
- Suppose the means are equal in the population, and that the sample is random
- ► <u>Ask</u>: how likely is it that the difference could have been as far from 0 as it is? Calculate a probability called a *p*-**value**.

A *t*-test is a way to test whether or not two variables **have equal means**.

We could spend a semester talking about the math behind a *t*-test. Many of you probably already have! We'll cover just the rudimentary basics here.

- Calculate the mean of both variables and the difference between these two means
- Suppose the means are equal in the population, and that the sample is random
- ► <u>Ask</u>: how likely is it that the difference could have been as far from 0 as it is? Calculate a probability called a *p*-**value**.
- If p < .05 (or another standard), then it's not likely the mean could have been this far from 0. In that case conclude that the means weren't equal in the population after all.

When working with data frames, we usually test whether the means of variables are equal. In this case, the test should be paired, since the observations correspond.

When working with data frames, we usually test whether the means of variables are equal. In this case, the test should be paired, since the observations correspond.

To run a paired *t*-test, use the t.test() function with the paired=TRUE argument:

```
> t.test(anes$fthrc, anes$fttrump, paired=TRUE)
        Paired t-test
data: anes$fthrc and anes$fttrump
t = 2.5485, df = 1195, p-value = 0.01094
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
1.055163 8.113733
sample estimates:
mean of the differences
               4.584448
```

A  $\chi^2$  test of association provides an inference about whether two categorical variables have a statistically significant relationship with one another.

A  $\chi^2$  test of association provides an inference about whether two categorical variables have a statistically significant relationship with one another.

### Consider this table again:

```
> table(anes$gender, anes$vote12)

Mitt Romney Barack Obama Someone else
Male 191 236 46
Female 180 276 22
```

A  $\chi^2$  test of association provides an inference about whether two categorical variables have a statistically significant relationship with one another.

Consider this table again:

```
> table(anes$gender, anes$vote12)

Mitt Romney Barack Obama Someone else
Male 191 236 46
Female 180 276 22
```

Does gender appear to have anything to do with voting?

Are men more likely than women to vote for Romney?

Is there enough evidence here to conclude the relationship is real?

To run a  $\chi^2$  test of association in R, save the table as a separate object. Then use the chisq.test() function to run the test:

Edward Tufte, a Professor Emeritus of statistics at Yale, is the world's leading authority on data visualization. In his books he outlines four properties of good visualizations:

(1) Graphical Excellence -

Edward Tufte, a Professor Emeritus of statistics at Yale, is the world's leading authority on data visualization. In his books he outlines four properties of good visualizations:

(1) Graphical Excellence – the graphic must be usable, and covey information efficiently.

- (1) Graphical Excellence the graphic must be usable, and covey information efficiently.
- (2) Visual Integrity -

- (1) Graphical Excellence the graphic must be usable, and covey information efficiently.
- (2) Visual Integrity the graphic should neither distort the underlying data nor create a false impression or interpretation of that data.

- (1) Graphical Excellence the graphic must be usable, and covey information efficiently.
- (2) Visual Integrity the graphic should neither distort the underlying data nor create a false impression or interpretation of that data.
- (3) Maximizing the Data-Ink Ratio remove superfluous elements that do not report or describe the data.

- (1) Graphical Excellence the graphic must be usable, and covey information efficiently.
- (2) Visual Integrity the graphic should neither distort the underlying data nor create a false impression or interpretation of that data.
- (3) Maximizing the Data-Ink Ratio remove superfluous elements that do not report or describe the data.
- (4) Aesthetic Elegance -

- (1) Graphical Excellence the graphic must be usable, and covey information efficiently.
- (2) Visual Integrity the graphic should neither distort the underlying data nor create a false impression or interpretation of that data.
- (3) Maximizing the Data-Ink Ratio remove superfluous elements that do not report or describe the data.
- **(4)** Aesthetic Elegance use as simple a design as possible to convey a complex data structure.



ggplot() is a system for making graphics in R easily, and following Tufte's principles as closely as possible.

ggplot() is a system for making graphics in R easily, and following Tufte's principles as closely as possible.

This is NOT the only way to create graphics in R. Some alternatives:

- ▶ The base plotting system, which uses the plot() function
- ► The lattice package
- Numerous smaller plotting packages

ggplot() is a system for making graphics in R easily, and following Tufte's principles as closely as possible.

This is NOT the only way to create graphics in R. Some alternatives:

- ▶ The base plotting system, which uses the plot() function
- ► The lattice package
- Numerous smaller plotting packages

Like anything else in R, there are many ways to do the same thing. The advantage of ggplot() is that it is relatively simple, prettier, and more elegant than the other systems are by default.

ggplot() is a system for making graphics in R easily, and following Tufte's principles as closely as possible.

This is NOT the only way to create graphics in R. Some alternatives:

- ► The base plotting system, which uses the plot() function
- ► The lattice package
- Numerous smaller plotting packages

Like anything else in R, there are many ways to do the same thing. The advantage of ggplot() is that it is relatively simple, prettier, and more elegant than the other systems are by default.

The disadvantage of ggplot() is it's **inflexibility** when you want to customize elements of the graphic.

There are two ways to run a ggplot() function. If you call ggplot() directly:

```
ggplot(data, aes(x, y)) + . . .
```

then the graphic will appear immediately in the plot window in R Studio, or in the markdown file output.

There are two ways to run a ggplot() function. If you call ggplot() directly:

```
ggplot(data, aes(x, y)) + . . .
```

then the graphic will appear immediately in the plot window in R Studio, or in the markdown file output.

If you save the ggplot() output to an object, then the graphic won't display until you call the object directly.

$$g \leftarrow ggplot(data, aes(x, y)) + . . .$$

Nothing will be displayed until I type g. That's useful if I want to create the graphic, but I don't want to slow down compilation by displaying it right away.

#### The ggplot() function has three parts:

- 1. The data frame that contains the data to be plotted
- 2. An aesthetics statement: which variable is x? which is y? which is a grouping variable? etc
- 3. Additional information about the type of plot, labels, grids

The ggplot() function has three parts:

- 1. The data frame that contains the data to be plotted
- 2. An aesthetics statement: which variable is x? which is y? which is a grouping variable? etc
- 3. Additional information about the type of plot, labels, grids

Just like all the tidyverse commands, the first argument is the data frame. To make a plot from the ANES data we've been using, begin the command by typing

g <- ggplot(anes,

#### **Aesthetics**

The second thing to type in the ggplot() function is aes(), which is a function for the "aesthetics" of the plot.

#### **Aesthetics**

The second thing to type in the ggplot() function is aes(), which is a function for the "aesthetics" of the plot.

This is where you specify the x variable, the y variable (if you are making a plot that needs one), and optionally, variables that define colors, shapes, line styles, etc.

### **Aesthetics**

The second thing to type in the ggplot() function is aes(), which is a function for the "aesthetics" of the plot.

This is where you specify the x variable, the y variable (if you are making a plot that needs one), and optionally, variables that define colors, shapes, line styles, etc.

To make a plot (such as a scatterplot, more on this later) with Hillary Clinton's thermometer score on the x axis and Donald Trump's thermometer on the y axis, type

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump))</pre>
```

### **Aesthetics**

The second thing to type in the ggplot() function is aes(), which is a function for the "aesthetics" of the plot.

This is where you specify the x variable, the y variable (if you are making a plot that needs one), and optionally, variables that define colors, shapes, line styles, etc.

To make a plot (such as a scatterplot, more on this later) with Hillary Clinton's thermometer score on the x axis and Donald Trump's thermometer on the y axis, type

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump))</pre>
```

It's easy to forget about aes(), but it's required. Don't forget!

ggplot() works differently from other functions in one important way. Most functions use options, separated by commas, within the function itself.

ggplot() works differently from other functions in one important way. Most functions use options, separated by commas, within the function itself.

ggplot() uses options, but uses different functions for different options, and separates the options with plus signs. As far as I know, ggplot() is the only function that works this way.

ggplot() works differently from other functions in one important way. Most functions use options, separated by **commas**, within the function itself.

ggplot() uses options, but uses different functions for different options, and separates the options with plus signs. As far as I know, ggplot() is the only function that works this way.

There are currently 44 different functions that all begin geom\_...(), where the dots are replaced by different words. Each geom function works with ggplot() to create a different graph.

# Here's a few of the $geom_{-}...()$ functions

geom\_point() — creates a scatterplot for two **continuous variables**. Draws a point for every observation, with the two variables providing the *x* and *y* coordinates.

geom\_smooth() - draw best-fit lines or curves

geom\_line() and geom\_path() - create line plots

geom\_bar() - create bar charts

geom\_histogram() - create histograms

geom\_boxplot() - create box plots

geom\_density() and geom\_violin() - draws the density of a continuous variable (shows the relative frequency of values)



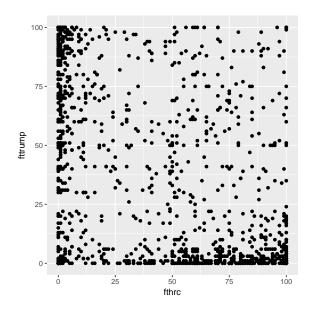
Different geom\_...() require different options, and there are too many to memorize right away. You will have to look up examples for a while – that's fine.

Different geom\_...() require different options, and there are too many to memorize right away. You will have to look up examples for a while – that's fine.

To create a scatterplot of Clinton and Trump's thermometer scores, add geom\_point() to the code:

Style point: I like to press enter after every + sign to make the code easier to look at.

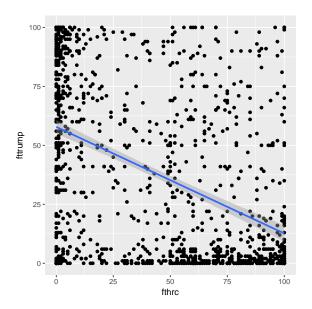
Then to display the graphic, type g in the script, console, or markdown file



You can use more than one geom...() function within one graphic. This overlays one graph over another.

You can use more than one geom\_...() function within one graphic. This overlays one graph over another.

To superimpose a best-fit line over the scatterplot, add geom\_smooth(method="lm") to the code:



The axis labels for our working example right now are the raw variable names. We can make a nicer-looking graph by replacing these labels with better names, and by giving the graph a title.

The axis labels for our working example right now are the raw variable names. We can make a nicer-looking graph by replacing these labels with better names, and by giving the graph a title.

To label the x and y axes, add xlab("x-axis label") and ylab("y-axis label") to the code.

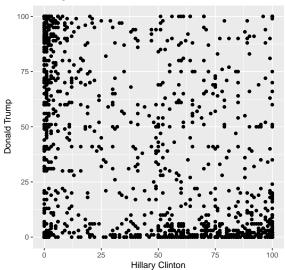
The axis labels for our working example right now are the raw variable names. We can make a nicer-looking graph by replacing these labels with better names, and by giving the graph a title.

To label the x and y axes, add xlab("x-axis label") and ylab("y-axis label") to the code.

To give the graph a title, add ggtitle("title") to the code.

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump)) +
        geom_point() +
        xlab("Hillary Clinton") +
        ylab("Donald Trump") +
        ggtitle("Feeling Thermometers for Candidates")</pre>
```





Sometimes it makes sense to distinguish between groups in a graphic.

Sometimes it makes sense to distinguish between groups in a graphic.

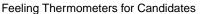
In the scatterplot, we can distinguish men and women, Democrats and Republicans, voters from non-voters, and so on. We can use **colors, shapes, or both** to distinguish these groups.

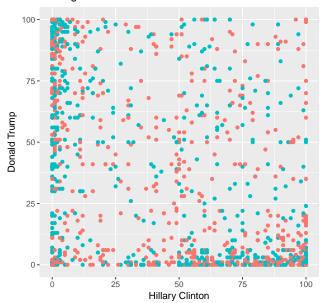
Sometimes it makes sense to distinguish between groups in a graphic.

In the scatterplot, we can distinguish men and women, Democrats and Republicans, voters from non-voters, and so on. We can use colors, shapes, or both to distinguish these groups.

Inside the aes() function, after specifying x and y, type col=gender to use different colors for the points that refer to men and the points that refer to women:

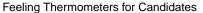
```
g <- ggplot(anes, aes(x=fthrc, y=fttrump, col=gender)) +
     geom_point() +
     xlab("Hillary Clinton") +
     ylab("Donald Trump") +
     ggtitle("Feeling Thermometers for Candidates")</pre>
```

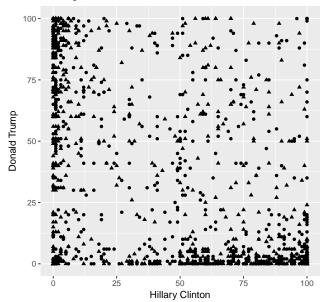




gender
Female
Male

To use different shapes, type pch=gender.



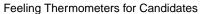


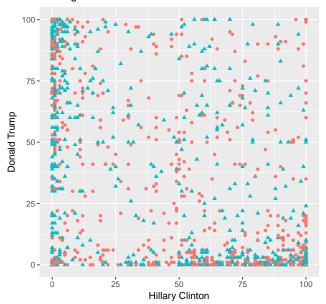
# gender • Female

▲ Male

You can set both colors and shapes to vary based on the same variable:

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump, col=gender, pch=gender)) +
    geom_point() +
    xlab("Hillary Clinton") +
    ylab("Donald Trump") +
    ggtitle("Feeling Thermometers for Candidates")</pre>
```





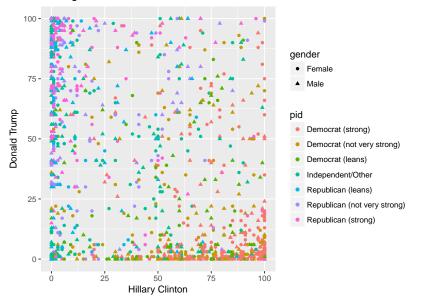
gender • Female

Male

You can set both colors and shapes to vary based on the two different variables:

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump, col=pid, pch=gender)) +
    geom_point() +
    xlab("Hillary Clinton") +
    ylab("Donald Trump") +
    ggtitle("Feeling Thermometers for Candidates")</pre>
```

#### Feeling Thermometers for Candidates

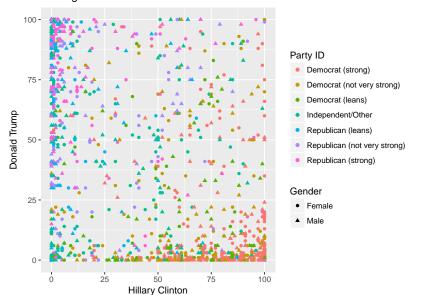


Notice that when you use colors or shapes to denote groups, ggplot() automatically creates a legend. You might want to change the legend title.

To do that, type labs(color = "Party ID") to change the legend title for the colors, and type labs(pch = "Gender") to change the legend title for the shapes:

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump, col=pid, pch=gender)) +
    geom_point() +
    xlab("Hillary Clinton") +
    ylab("Donald Trump") +
    ggtitle("Feeling Thermometers for Candidates") +
    labs(color = "Party ID") +
    labs(pch = "Gender")</pre>
```

#### Feeling Thermometers for Candidates



Colors and shapes are good ways to distinguish groups, but they aren't the only ways to do it. Another option is to create a grid of corresponding graphs, one for each category of a group.

Colors and shapes are good ways to distinguish groups, but they aren't the only ways to do it. Another option is to create a grid of corresponding graphs, one for each category of a group.

ggplot() will automatically format the graphs to fit perfectly next to each other, and will put the category name at the top of each graph.

Colors and shapes are good ways to distinguish groups, but they aren't the only ways to do it. Another option is to create a grid of corresponding graphs, one for each category of a group.

ggplot() will automatically format the graphs to fit perfectly next to each other, and will put the category name at the top of each graph.

To create a grid, use a facet\_...() function. There are  $\underline{\text{four}}$  ways to use these functions:

Colors and shapes are good ways to distinguish groups, but they aren't the only ways to do it. Another option is to create a grid of corresponding graphs, one for each category of a group.

ggplot() will automatically format the graphs to fit perfectly next to each other, and will put the category name at the top of each graph.

To create a grid, use a facet\_...() function. There are four ways to use these functions:

(1) facet\_grid(.  $\sim$  gender) will place the plots for men and women in different columns

Colors and shapes are good ways to distinguish groups, but they aren't the only ways to do it. Another option is to create a grid of corresponding graphs, one for each category of a group.

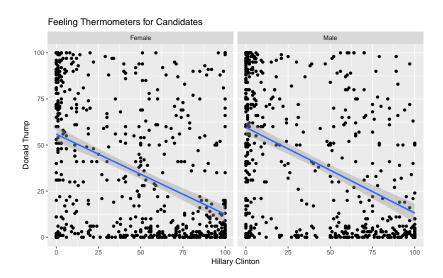
ggplot() will automatically format the graphs to fit perfectly next to each other, and will put the category name at the top of each graph.

To create a grid, use a facet...() function. There are four ways to use these functions:

- (1) facet\_grid(.  $\sim$  gender) will place the plots for men and women in different columns
- (2) facet\_grid(gender  $\sim$  .) will place the plots for men and women in different rows

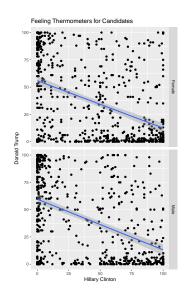
Here's an example breaking up gender into columns:

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump)) +
        geom_point() +
        geom_smooth(method="lm") +
        xlab("Hillary Clinton") +
        ylab("Donald Trump") +
        ggtitle("Feeling Thermometers for Candidates") +
        facet_grid(. ~ gender)</pre>
```



Here's an example breaking up gender into rows:

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump)) +
        geom_point() +
        geom_smooth(method="lm") +
        xlab("Hillary Clinton") +
        ylab("Donald Trump") +
        ggtitle("Feeling Thermometers for Candidates") +
        facet_grid(gender ~ .)</pre>
```

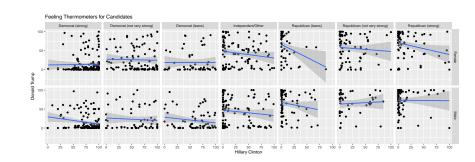


(3) facet\_grid(gender  $\sim$  pid) will create a plot for each combination of party ID and gender, and will place them in a grid where the rows represent genders and the columns represent party IDs.

(3) facet\_grid(gender  $\sim$  pid) will create a plot for each combination of party ID and gender, and will place them in a grid where the rows represent genders and the columns represent party IDs.

Here's an example:

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump)) +
    geom_point() +
    geom_smooth(method="lm") +
    xlab("Hillary Clinton") +
    ylab("Donald Trump") +
    ggtitle("Feeling Thermometers for Candidates") +
    facet_grid(gender ~ pid)</pre>
```

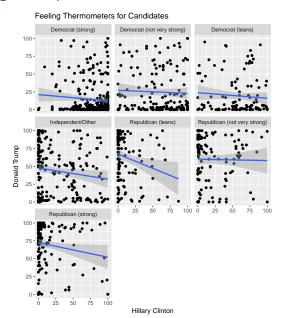


(4) facet\_wrap(  $\sim$  pid) will make a graph for every party ID, but will automatically fill several rows to make it look good.

(4) facet\_wrap(  $\sim$  pid) will make a graph for every party ID, but will automatically fill several rows to make it look good.

Here's an example:

```
g <- ggplot(anes, aes(x=fthrc, y=fttrump)) +
    geom_point() +
    geom_smooth(method="lm") +
    xlab("Hillary Clinton") +
    ylab("Donald Trump") +
    ggtitle("Feeling Thermometers for Candidates") +
    facet_wrap(~ pid)</pre>
```



If you've saved your plot an an object (named g or something else), you can use R code to save the graphic as a PDF, JPEG, BMP, or PNG file.

If you've saved your plot an an object (named g or something else), you can use R code to save the graphic as a PDF, JPEG, BMP, or PNG file.

For a PDF, the code is

```
pdf("filename.pdf", width=5, height=5)
g
dev.off()
```

If you've saved your plot an an object (named g or something else), you can use R code to save the graphic as a PDF, JPEG, BMP, or PNG file.

For a PDF, the code is

```
pdf("filename.pdf", width=5, height=5)
g
dev.off()
```

The pdf() function has three arguments. First, write the name of the file you want to create. Then specify the width and height you want this image to be, in inches.

If you've saved your plot an an object (named g or something else), you can use R code to save the graphic as a PDF, JPEG, BMP, or PNG file.

For a PDF, the code is

```
pdf("filename.pdf", width=5, height=5)
g
dev.off()
```

The pdf() function has three arguments. First, write the name of the file you want to create. Then specify the width and height you want this image to be, in inches.

g is just the name of your ggplot graphic object.

If you've saved your plot an an object (named g or something else), you can use R code to save the graphic as a PDF, JPEG, BMP, or PNG file.

For a PDF, the code is

```
pdf("filename.pdf", width=5, height=5)
g
dev.off()
```

The pdf() function has three arguments. First, write the name of the file you want to create. Then specify the width and height you want this image to be, in inches.

g is just the name of your ggplot graphic object.

dev.off() turns off the PDF recording device that R uses. If you don't write this function, R will continue to print all visual output to the same PDF as new pages.

To save as a JPEG, use this code:

```
jpeg("filename.jpg", width=5, height=5, units="in")
g
dev.off()
```

To save as a JPEG, use this code:

```
jpeg("filename.jpg", width=5, height=5, units="in")
g
dev.off()
```

This command works similarly to pdf(), but you have to specify units="in" for R to understand that the width and heights are in inches.

To save as a JPEG, use this code:

```
jpeg("filename.jpg", width=5, height=5, units="in")
g
dev.off()
```

This command works similarly to pdf(), but you have to specify units="in" for R to understand that the width and heights are in inches.

To save a BMP or PNG file, use the same code as above, but replace jpeg with bmp or png.

### Using ggplot() within an R markdown document

ggplot() works really well within code chunks in an R markdown file.

#### Using ggplot() within an R markdown document

ggplot() works really well within code chunks in an R markdown file.

You can control the width, height, and position of the graphic directly in the **code chunk options**. For example, to set a figure to be 4 inches wide, 6 inches tall, and centered, type this code chunk:

```
'''{r chunkname, fig.width=4, fig.height=6, fig.align="center"}
g <- ggplot(anes, aes(x=fthrc, y=fttrump)) +
        geom_point() +
        xlab("Hillary Clinton") +
        ylab("Donald Trump") +
        ggtitle("Feeling Thermometers for Candidates")
g
'''</pre>
```