

Class 5: Data visualization

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##Plotting in R

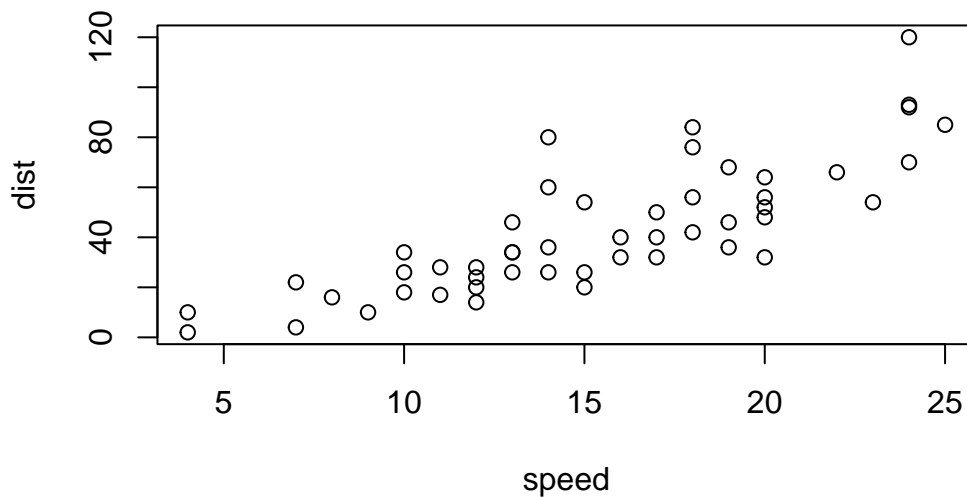
R has many plotting and visualization systems including “base” R. #Head function to print out first few rows, can also specify number of rows #head(dataset, n = i)

codechunks for management

```
head(cars, n=10)
```

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10
7	10	18
8	10	26
9	10	34
10	11	17

```
plot(cars)
```



Base R plots can be quite simple for basic plots when compared to systems like ggplot.

`#how to not plot in ggplot`

```
#ggplot2(cars)
```

It will produce an error because ggplot is not installed. To use an add-on package like ggplot, I have to first install it onto the computer.

##How to install a package

We use the function `'install.packages()'` with the name of the package we want to install.

Packages like ggplot need to be loaded from the library before every use, using the library function.

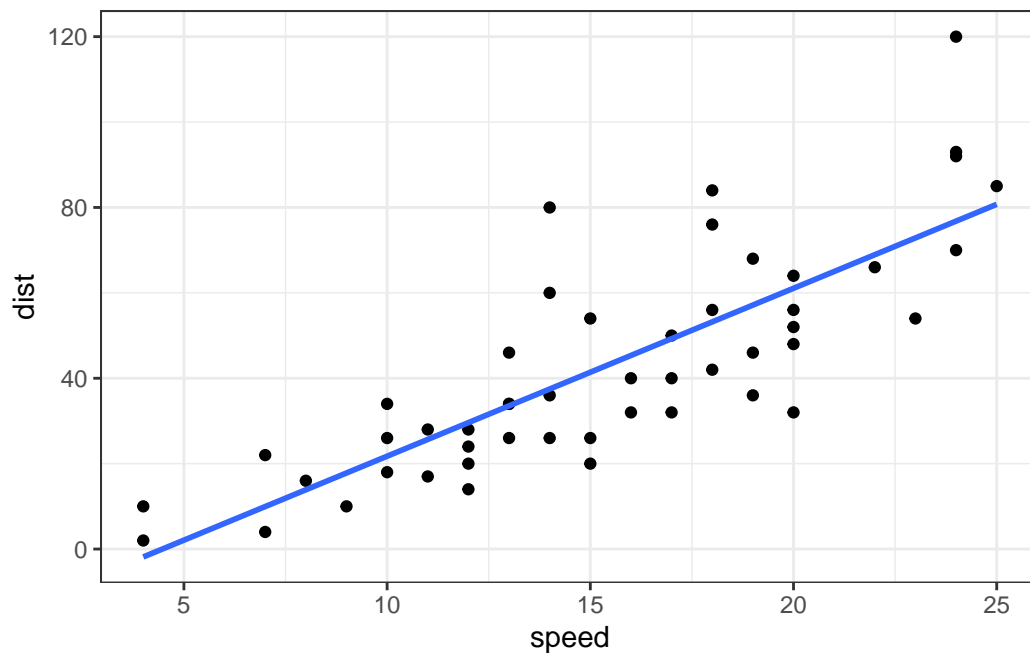
```
library(ggplot2)
```

##**ggplot minimum inputs** ggplot is much more requires more inputs than base R plot function. Ggplot requires 3 inputs at minimum:

- **Data** (this is the data.frame with the stuff we want to plot)
- **Aesthetics** or `aes()` for short (how the data map to the plot)
- **Geometery** (`geom_point()`, `geomline()` the plot type)

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  theme_bw() +
  geom_smooth(se=FALSE, method = lm)
```

`geom_smooth()` using formula = 'y ~ x'



A plot of some gene expression data

The code to read the data:

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

	Gene	Condition1	Condition2	State
1	A4GNT	-3.6808610	-3.4401355	unchanging
2	AAAS	4.5479580	4.3864126	unchanging

```

3      AASDH  3.7190695  3.4787276  unchanging
4      AATF   5.0784720  5.0151916  unchanging
5      AATK   0.4711421  0.5598642  unchanging
6 AB015752.4 -3.6808610 -3.5921390  unchanging

```

Q. How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

#Example of inline code

There are 5196 genes in this dataset.

How many genes are up-regulated?

```
table(genes$State)
```

```

down  unchanging      up
   72      4997      127

```

```
sum(genes$State == "up")
```

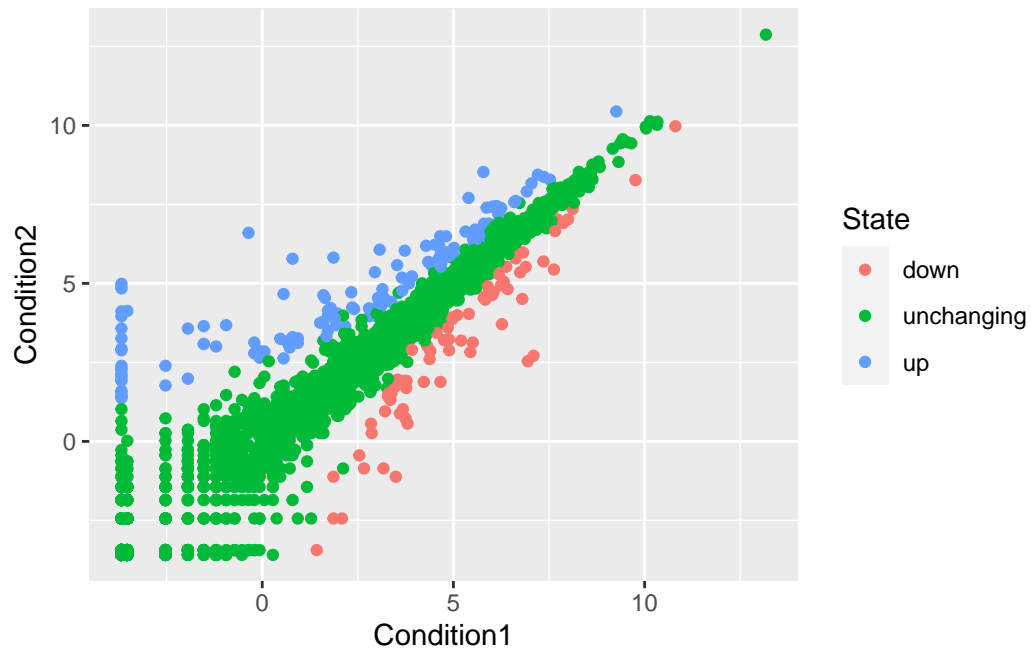
```
[1] 127
```

plotting

```

ggplot(genes) +
  aes(x = Condition1, y=Condition2, color=State) +
  geom_point(alpha = 1.0)

```



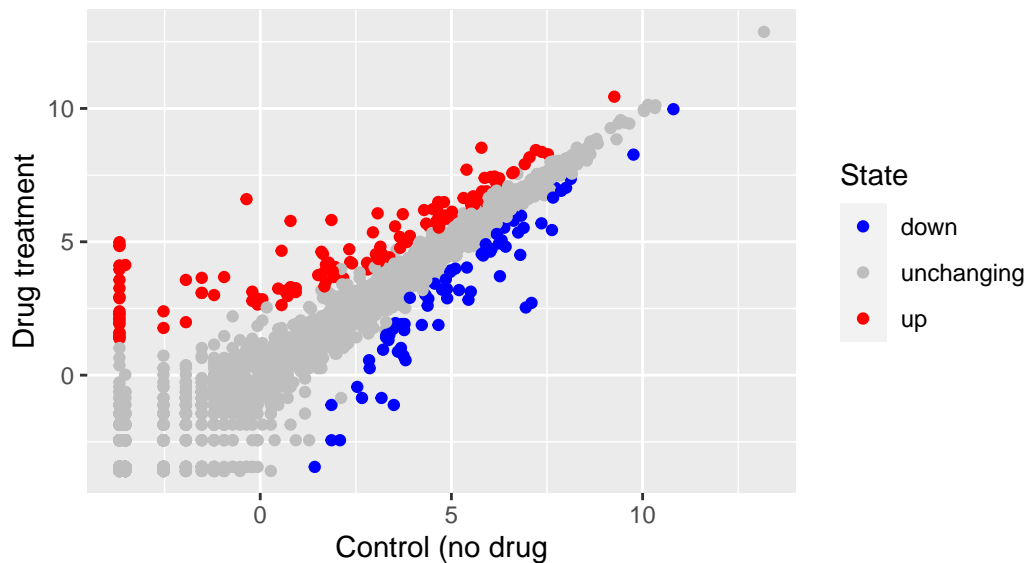
I can save any ggplot object for use later so I don't need to type it all out again. Here I save my starting plot to object `p` then I can add layers to `p` later on.

```
p <- ggplot(genes) +
  aes(x = Condition1, y=Condition2, color=State) +
  geom_point(alpha = 1.0)

p + scale_color_manual(
  values=c("blue","gray","red")) +
  labs(title = "Gene expression changes upon drug treatment", subtitle = "some subtitle",
```

Gene expression changes upon drug treatment

some subtitle



A more complex ggplot example

One of the big wins with ggplot is how easy it is to facet your data into sub-plots.

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.  
gapminder <- read.delim(url)
```

Q. How many countries are in this dataset?

```
length(unique(gapminder$country))
```

```
[1] 142
```

Q. How many years are in this dataset?

```
length(unique(gapminder$year))
```

```
[1] 12
```

```
range(gapminder$year)
```

```
[1] 1952 2007
```

Q. How to find country with smallest population

```
min(gapminder$pop)
```

```
[1] 60011
```

#how to index - first where is this min value in the popvector

```
ind <- which.min(gapminder$pop)
```

```
gapminder$country[ind]
```

```
[1] "Sao Tome and Principe"
```

```
gapminder[ind,]
```

	country	continent	year	lifeExp	pop	gdpPercap
1297	Sao Tome and Principe	Africa	1952	46.471	60011	879.5836

Plotting gdb vs. life expectancy

```
ggplot(gapminder) +  
  aes(x=gdpPercap, y=lifeExp ,color=continent) +  
  geom_point(alpha = 0.7) +  
  facet_wrap(~continent)
```

