

Class 05: Data Visualization with GGPLOT

Ethan Ashley (PID: A15939817)

Today we are playing with plotting and graphics in R.

There are lots of ways to make cool figures in R. There is “base” R graphics (`plot()`, `hist()`, `boxplot()`, etc.)

There are also add-on packages, like `ggplot`.

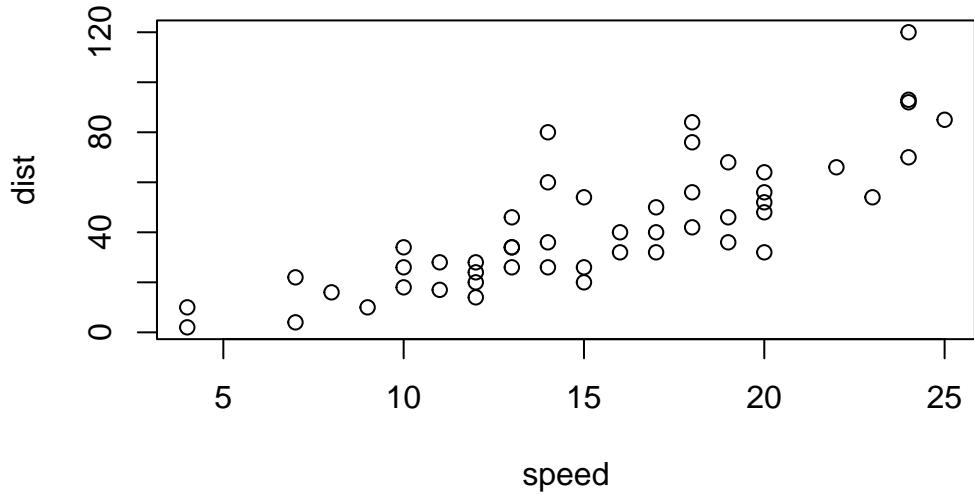
```
cars
```

	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
11	11	28
12	12	14
13	12	20
14	12	24
15	12	28
16	13	26
17	13	34
18	13	34
19	13	46
20	14	26
21	14	36
22	14	60
23	14	80

24	15	20
25	15	26
26	15	54
27	16	32
28	16	40
29	17	32
30	17	40
31	17	50
32	18	42
33	18	56
34	18	76
35	18	84
36	19	36
37	19	46
38	19	68
39	20	32
40	20	48
41	20	52
42	20	56
43	20	64
44	22	66
45	23	54
46	24	70
47	24	92
48	24	93
49	24	120
50	25	85

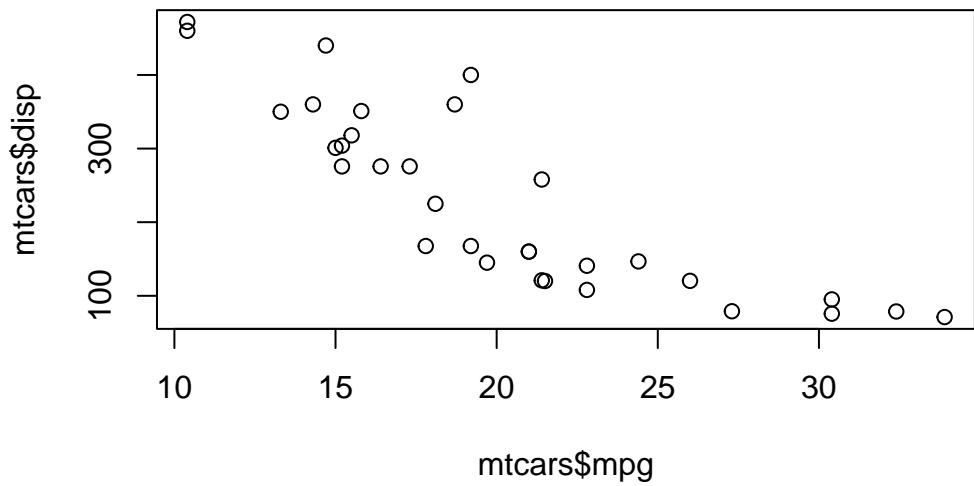
Let;s plot this with “base” R:

```
plot(cars)
```



Plot of mpg vs. displacement

```
plot(mtcars$mpg, mtcars$disp)
```



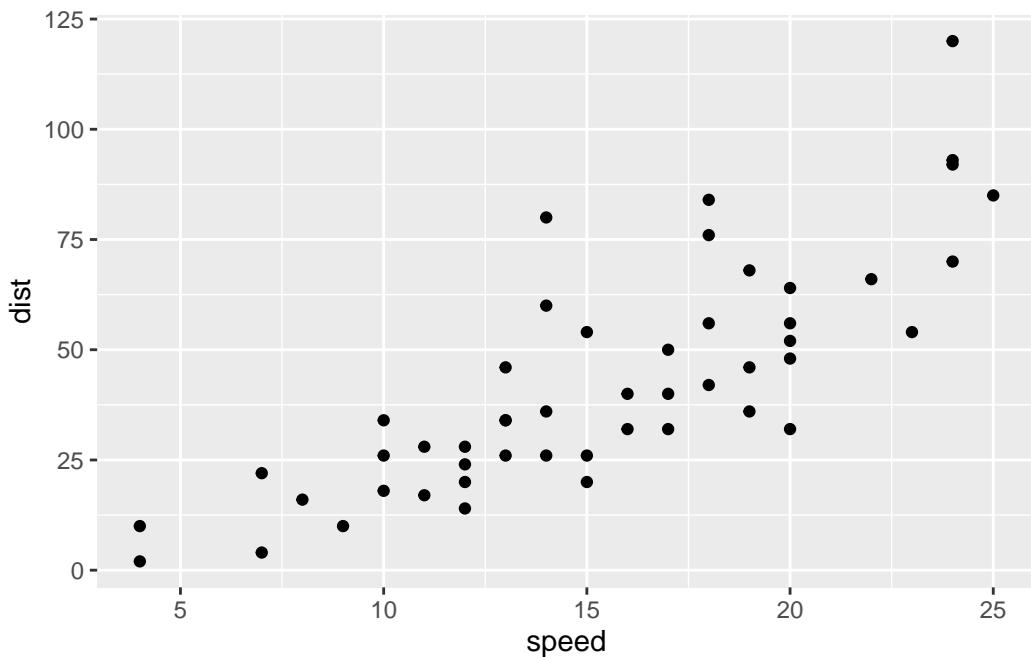
GGPLOT

The main function in the GGPLOT2 package is `ggplot`. **GGPLOT2 needs to be installed first.** Packages can be installed with the function `install.packages()`

Note Do not install packages in individual files, install them in the global R console

Must call packages with a `library()` call in order to use their functions

```
#install.packages("ggplot2")
library(ggplot2)
ggplot(cars) + aes(x=speed, y=dist) + geom_point()
```



Every ggplot needs at least 3 things:

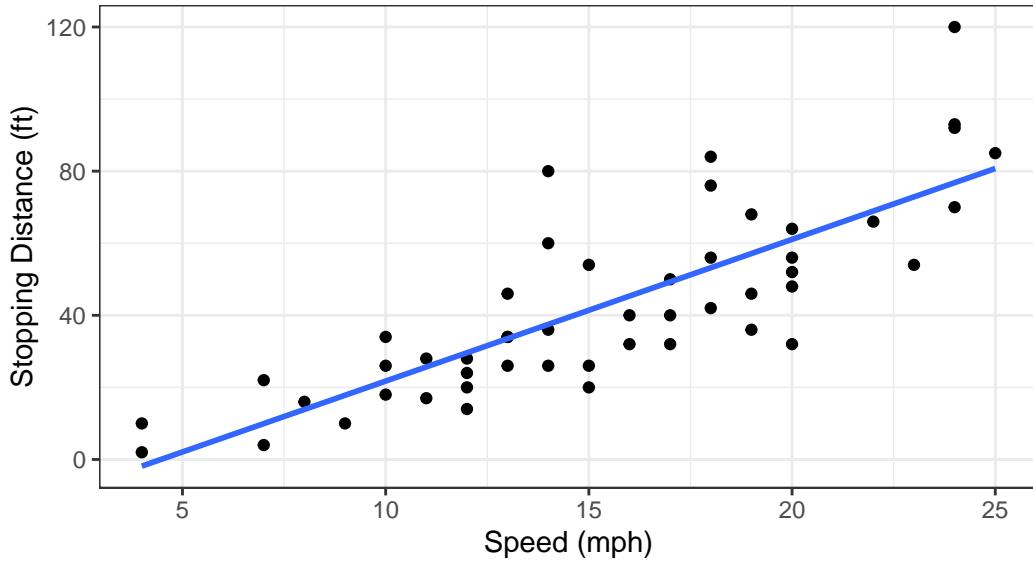
- The **data** (given with `ggplot(cars)`)
- The **aesthetic** mapping (given with `aes()`)
- The **geometry** (given with `geom_...`)

For simple canned graphs “base” R is nearly always faster

Adding more layers

```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(method="lm", se=FALSE) +  
  labs(x="Speed (mph)", y="Stopping Distance (ft)", title="Speed and Stopping Distance of Cars")  
  theme_bw()  
  
`geom_smooth()` using formula = 'y ~ x'
```

Speed and Stopping Distance of Cars



Plotting more relevant gene data

Loading in the dataset

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

Interrogating the shape of the data

```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

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

```
FALSE  TRUE  
5069   127
```

```
round(table(genes$State)/nrow(genes) * 100, 2)
```

	down	unchanging	up
	1.39	96.17	2.44

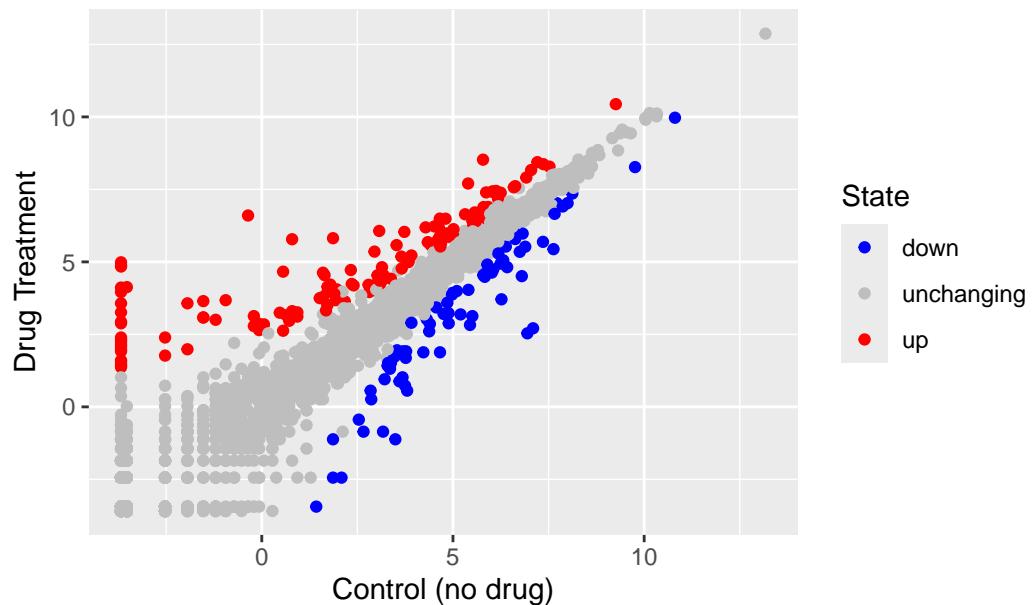
There are 5196 genes in this dataset

There are 127 upregulated genes in this dataset

Plotting the data in the genes dataframe

```
library(ggrepel)  
p <- ggplot(genes) + aes(Condition1, Condition2, col=State) + geom_point()  
p + scale_color_manual(values=c("blue", "gray", "red")) +  
  labs(x="Control (no drug)", y="Drug Treatment", title="Gene Expression Changes Upon Drug T
```

Gene Expression Changes Upon Drug Treatment



Gap Minder Dataset Plotting

Importing the data

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts"

gapminder <- read.delim(url)

#install.packages("dplyr")

# install.packages("dplyr") ## un-comment to install if needed
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

```
The following objects are masked from 'package:base':
```

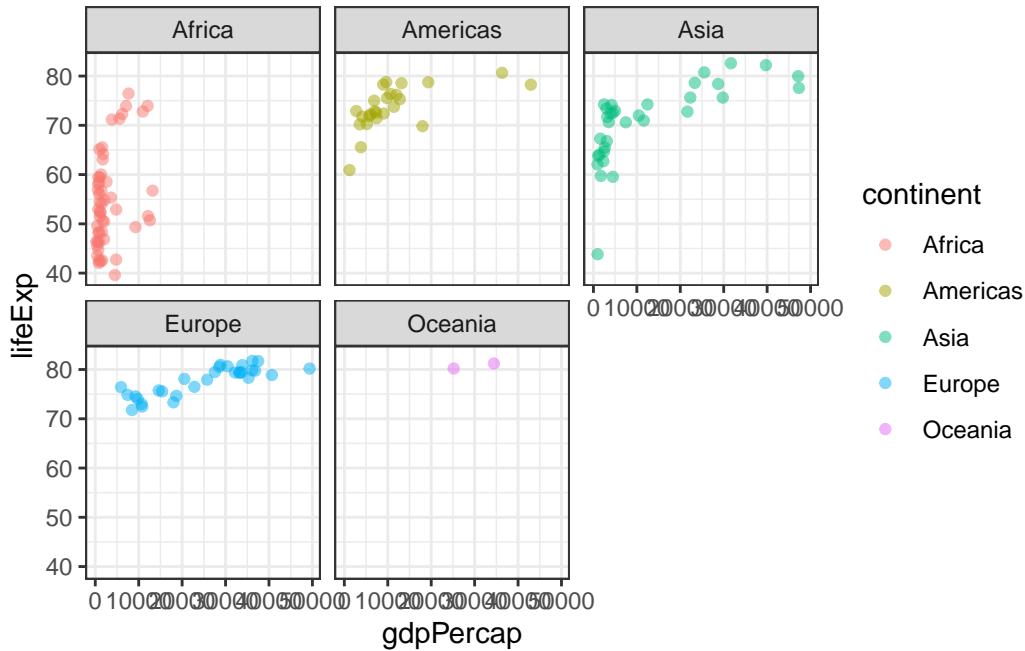
```
intersect, setdiff, setequal, union
```

```
ggplot
```

```
function (data = NULL, mapping = aes(), ..., environment = parent.frame())
{
  UseMethod("ggplot")
}
<bytecode: 0x000001ce9507ccb0>
<environment: namespace:ggplot2>
```

```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent) +
  geom_point(alpha=0.5) +
  facet_wrap(~continent) +
  theme_bw()
```



The Patchwork package can be useful for assembling multi-panel figures