

Class05: Data Vis with ggplot

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Graphics systems in R

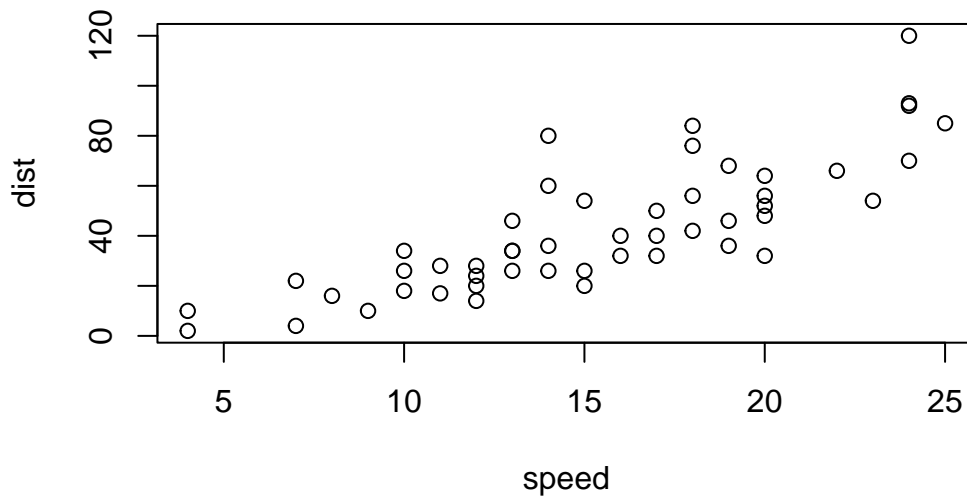
There are many graphics systems in R for making plots and figures.

We have already played a little bit with “**base R**” graphics and the `plot()` function.

Today we will start learning about a popular graphics package called `ggplot2()`

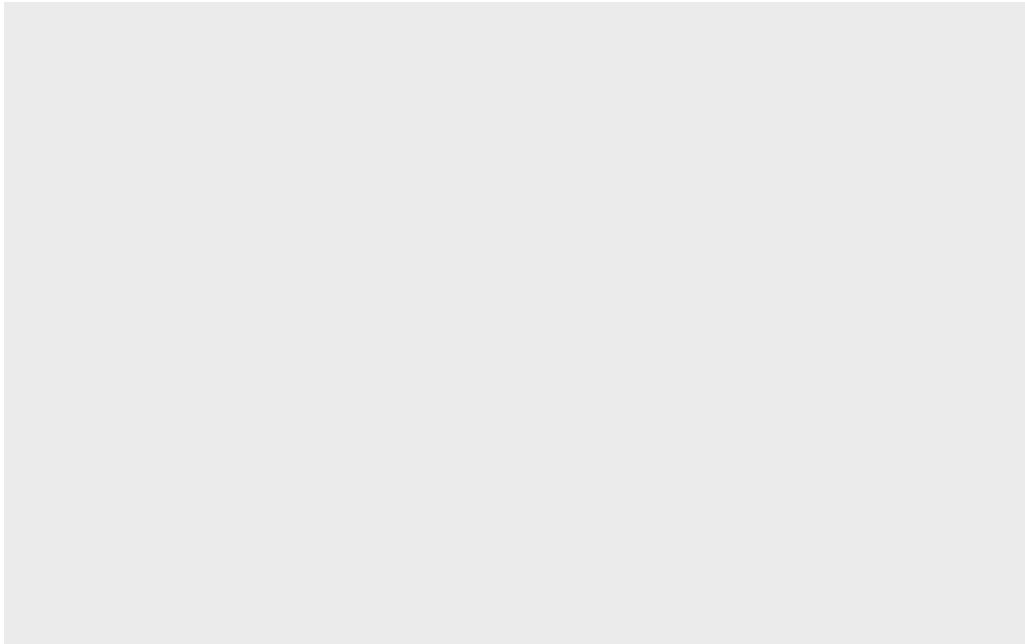
This is an add package – i.e. we need to install it. I install it (like I install any package) with the `install.packages()` function.

```
plot(cars)
```



Before I can use the functions from a package I have to look up the package from my “library”. We use the `library(ggplot2)` command to load it up.

```
#install.packages(ggplot2)
library("ggplot2")
ggplot(cars)
```



Every ggplot is made up of at least 3 things: - data (the numbers etc. that will go into your plot) - aes (how the columns of data map to the plot aesthetics) - geoms (how the plot actually looks, points, bars, lines, ect.)

```
ggplot(cars) + aes(x=speed, y=dist) + geom_point()
```



For simple plots ggplot is more verbose - it takes more code - than base R plot.

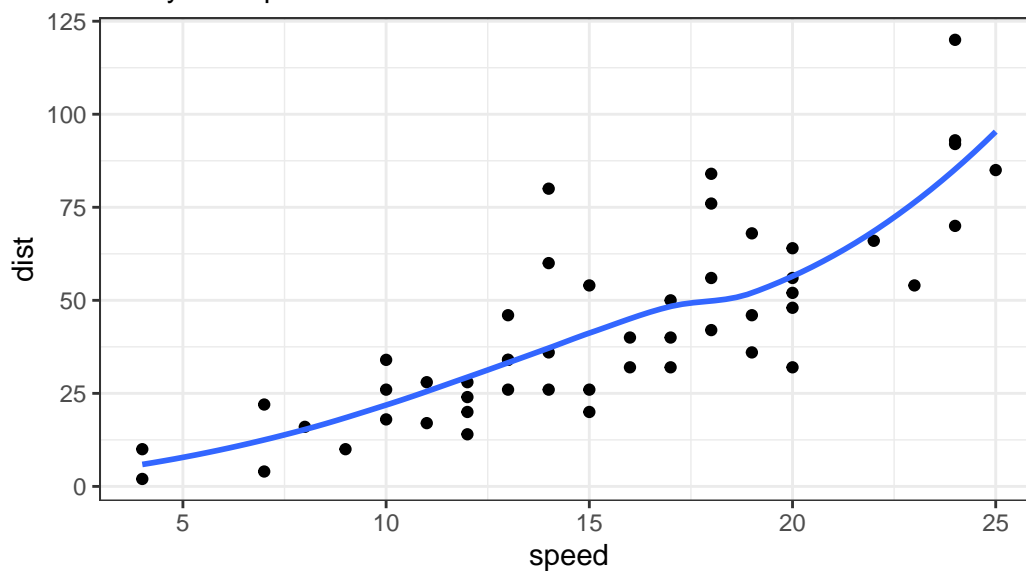
Add some more layers to our ggplot:

```
ggplot(cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth(se=F) + labs(title="Stopping Distance vs Speed")
```

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

Stopping Distance of Old Cars

A Silly Example Plot



Calling up **Gene Data Set** from class hand-out

```
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

Getting information from data set

```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

```
colnames(genes)
```

```
[1] "Gene"          "Condition1" "Condition2" "State"
```

```
num_upreg<-sum(genes$State == "up")  
num_upreg
```

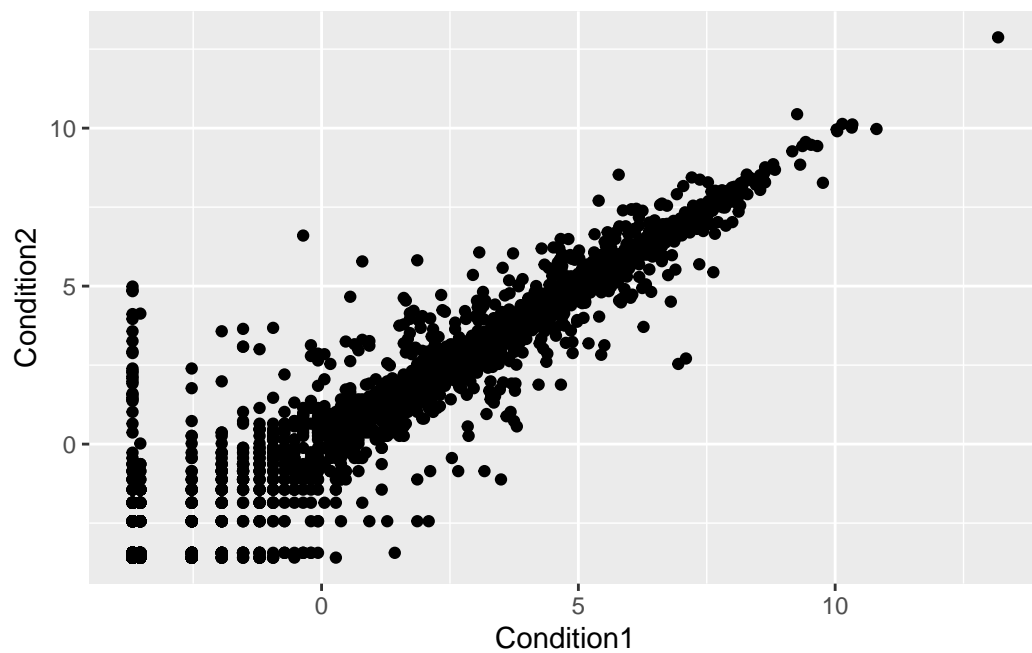
```
[1] 127
```

```
(num_upreg) / (nrow(genes)) * 100
```

```
[1] 2.444188
```

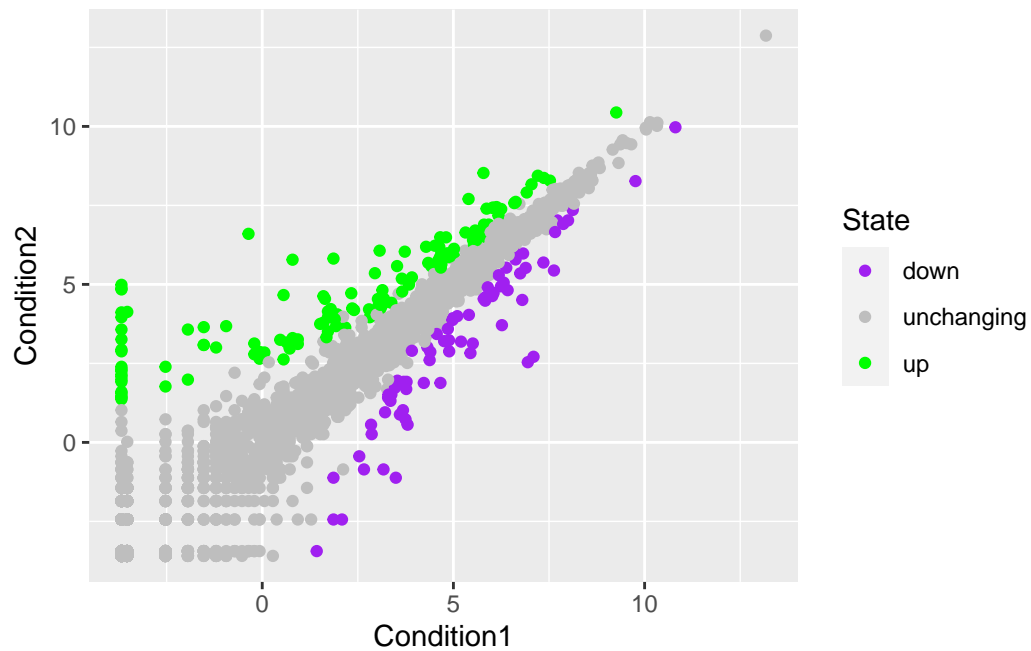
Making a simple plot of “Genes”

```
ggplot(genes) + aes(x=Condition1, y=Condition2) + geom_point()
```



Adding some complexities to the plot

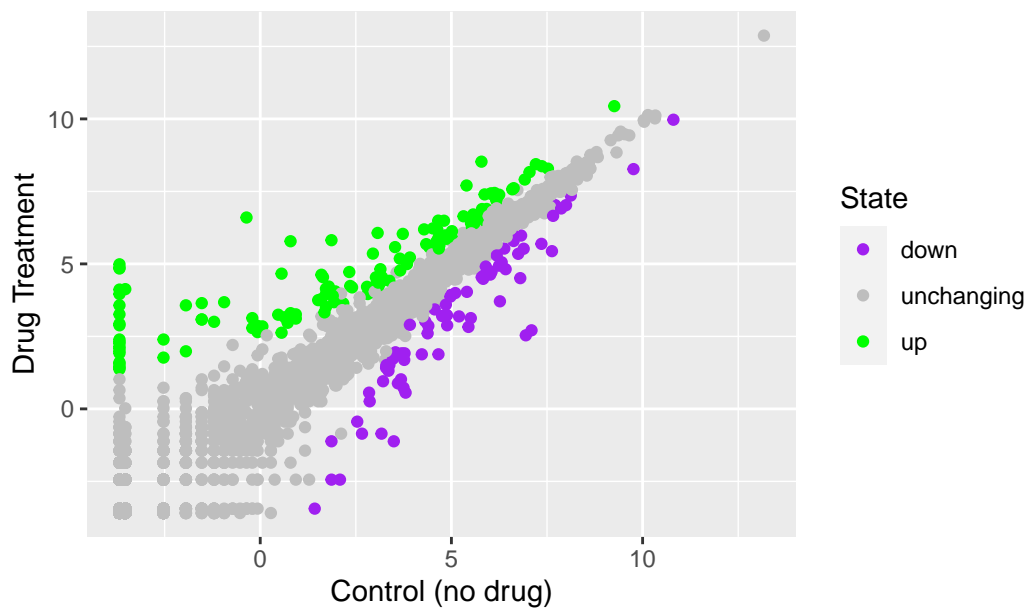
```
gene_plot<-ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()  
gene_plot + scale_colour_manual( values=c("purple", "gray", "green") )
```



Adding Labels to graph

```
gene_plot + labs(title="Gene Expression Changes Upon Drug Treatment", x="Control (no drug)")
```

Gene Expression Changes Upon Drug Treatment



Installed gapminder and dplyr packages

```
# install.packages(gapminder)
# install.packages(dplyr)
library(gapminder)
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

Loading in **Gapminder Data Set**

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

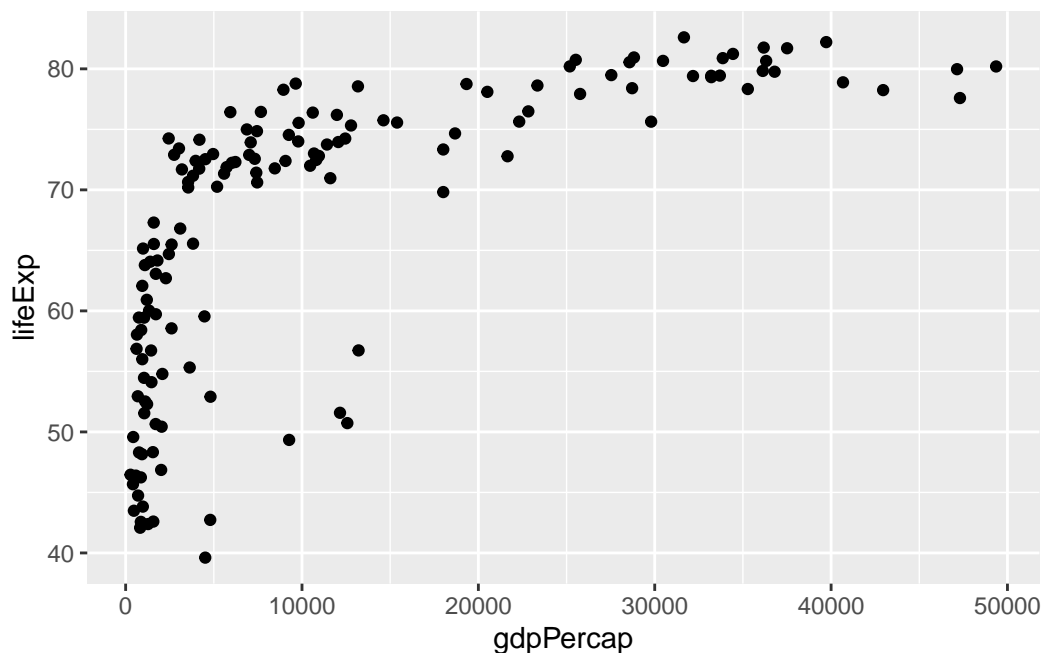
A tibble: 142 x 6

	country	continent	year	lifeExp	pop	gdpPercap
	<fct>	<fct>	<int>	<dbl>	<int>	<dbl>
1	Afghanistan	Asia	2007	43.8	31889923	975.
2	Albania	Europe	2007	76.4	3600523	5937.
3	Algeria	Africa	2007	72.3	33333216	6223.
4	Angola	Africa	2007	42.7	12420476	4797.
5	Argentina	Americas	2007	75.3	40301927	12779.
6	Australia	Oceania	2007	81.2	20434176	34435.
7	Austria	Europe	2007	79.8	8199783	36126.
8	Bahrain	Asia	2007	75.6	708573	29796.
9	Bangladesh	Asia	2007	64.1	150448339	1391.
10	Belgium	Europe	2007	79.4	10392226	33693.

i 132 more rows

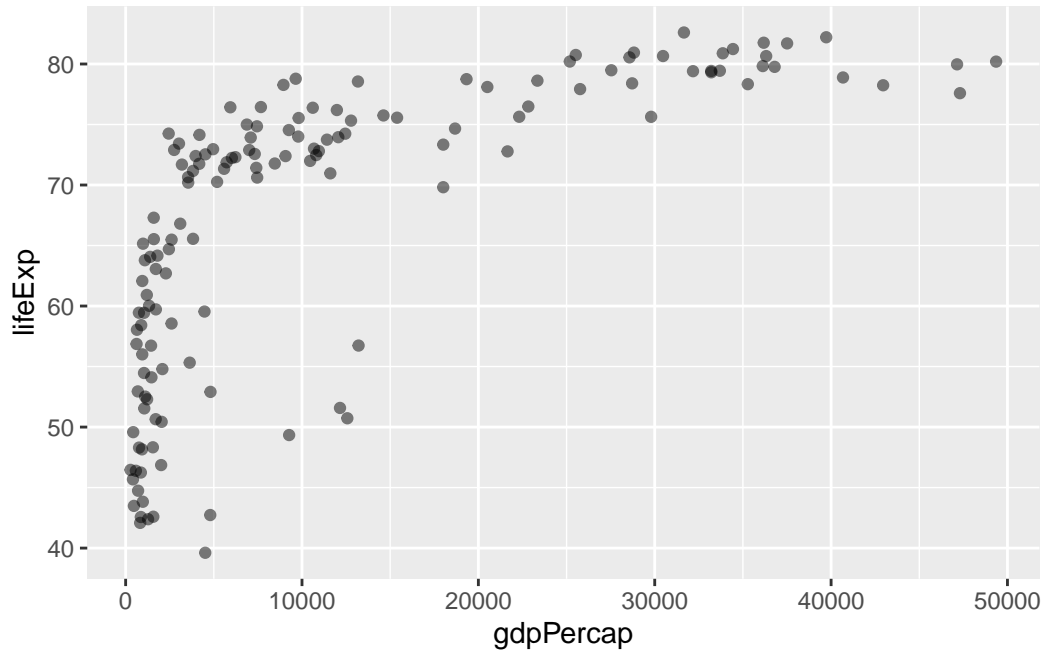
Making a basic scatter plot with data

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp) + geom_point()
```



Making points slightly transparent because many of them are overlapping

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp) + geom_point(alpha=0.5)
```



Adding more variables

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp, col=continent, size=pop) + geom_point
```

