

# class05

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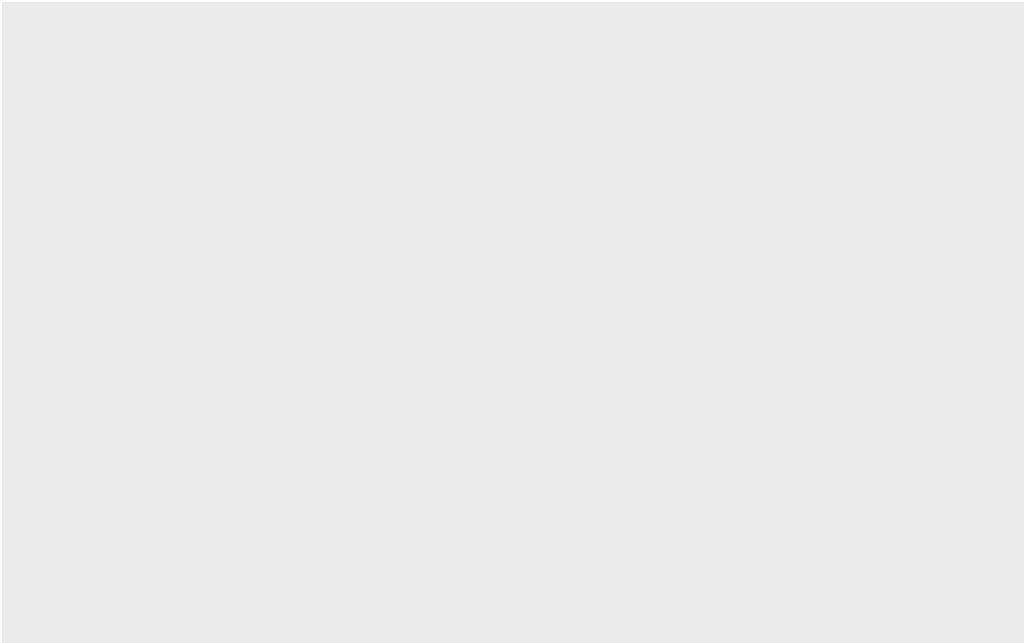
## Our first ggplot

To use the ggplot2 package I first need to have it installed on my computer.

To install my package we use the `install.packages()` command.

Now can I use it?

```
library(ggplot2)  
ggplot()
```



mpg

# A tibble: 234 x 11

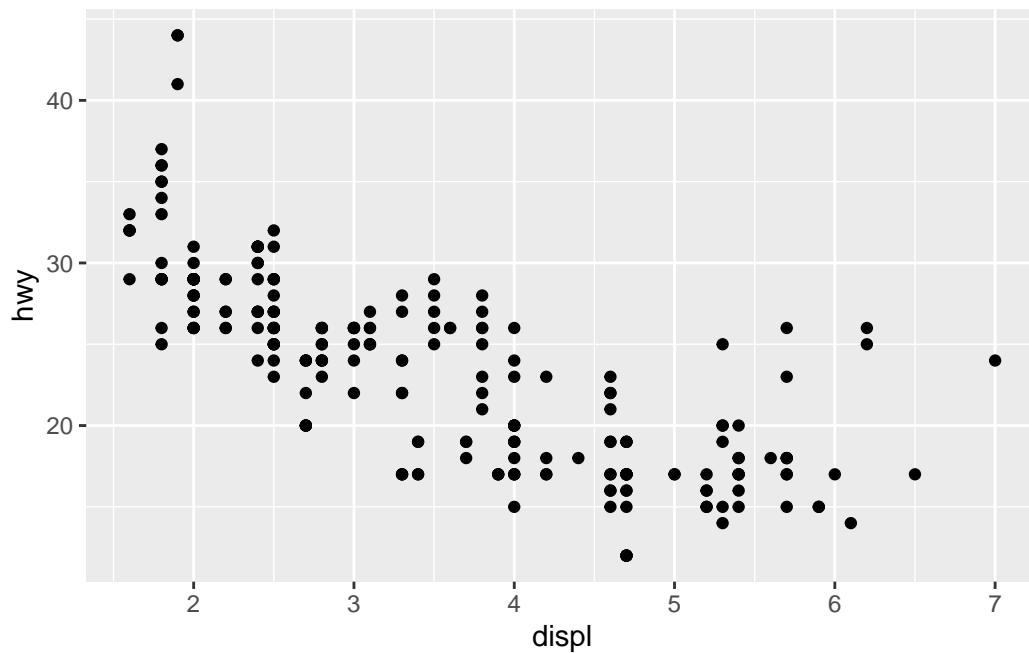
	manufacturer	model	displ	year	cyl	trans	drv	cty	hwy	fl	class
	<chr>	<chr>	<dbl>	<int>	<int>	<chr>	<chr>	<int>	<int>	<chr>	<chr>
1	audi	a4	1.8	1999	4	auto~	f	18	29	p	comp~
2	audi	a4	1.8	1999	4	manu~	f	21	29	p	comp~
3	audi	a4	2	2008	4	manu~	f	20	31	p	comp~
4	audi	a4	2	2008	4	auto~	f	21	30	p	comp~
5	audi	a4	2.8	1999	6	auto~	f	16	26	p	comp~
6	audi	a4	2.8	1999	6	manu~	f	18	26	p	comp~
7	audi	a4	3.1	2008	6	auto~	f	18	27	p	comp~
8	audi	a4 quattro	1.8	1999	4	manu~	4	18	26	p	comp~
9	audi	a4 quattro	1.8	1999	4	auto~	4	16	25	p	comp~
10	audi	a4 quattro	2	2008	4	manu~	4	20	28	p	comp~

# ... with 224 more rows

Our first plot of displ vs hwy All ggplot() graphs are made in the same way:

-data+aes+geoms

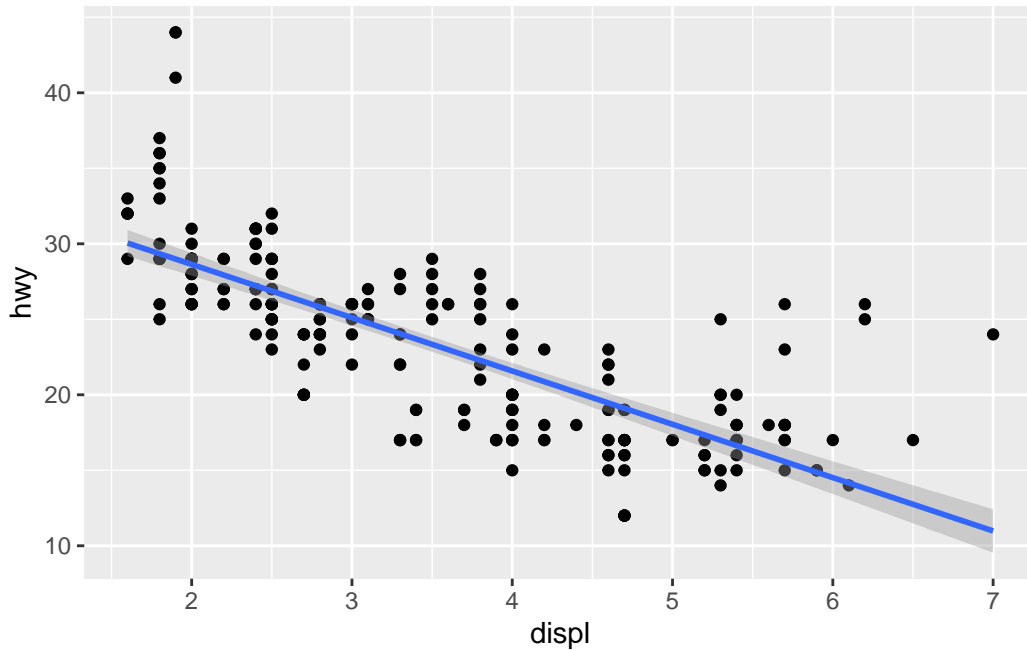
```
ggplot(mpg)+aes(displ,hwy)+geom_point()
```



I can add more layers:

```
ggplot(mpg)+aes(displ,hwy)+geom_point()+geom_smooth(method=lm, se=TRUE)
```

`geom\_smooth()` using formula 'y ~ x'



## Plot of gene expression 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)
```

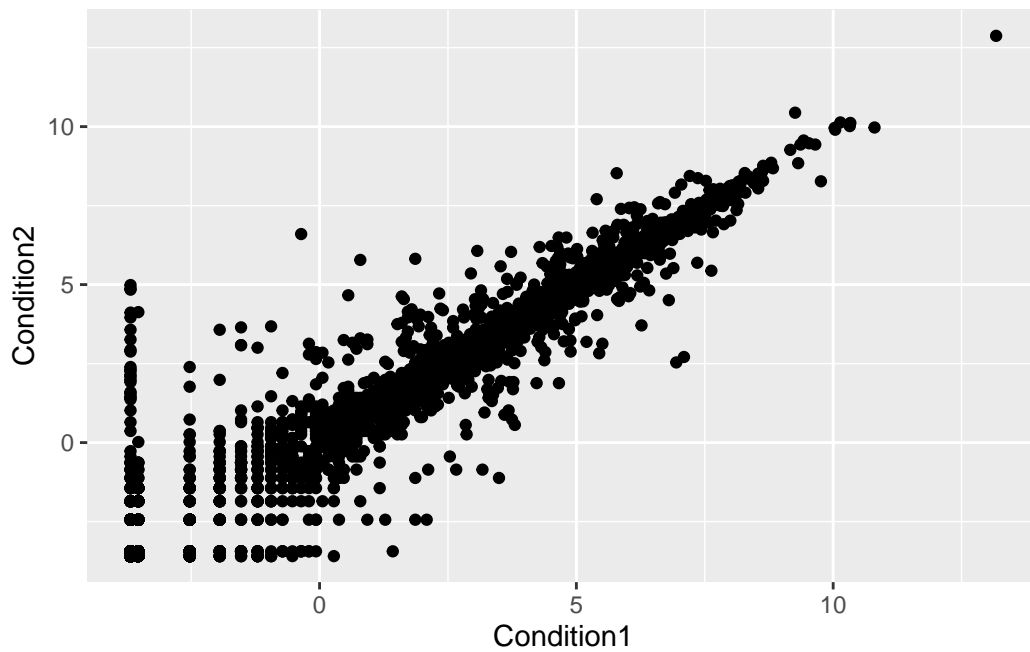
```
[1] 5196
```

What are the colnames?

```
colnames(genes)
```

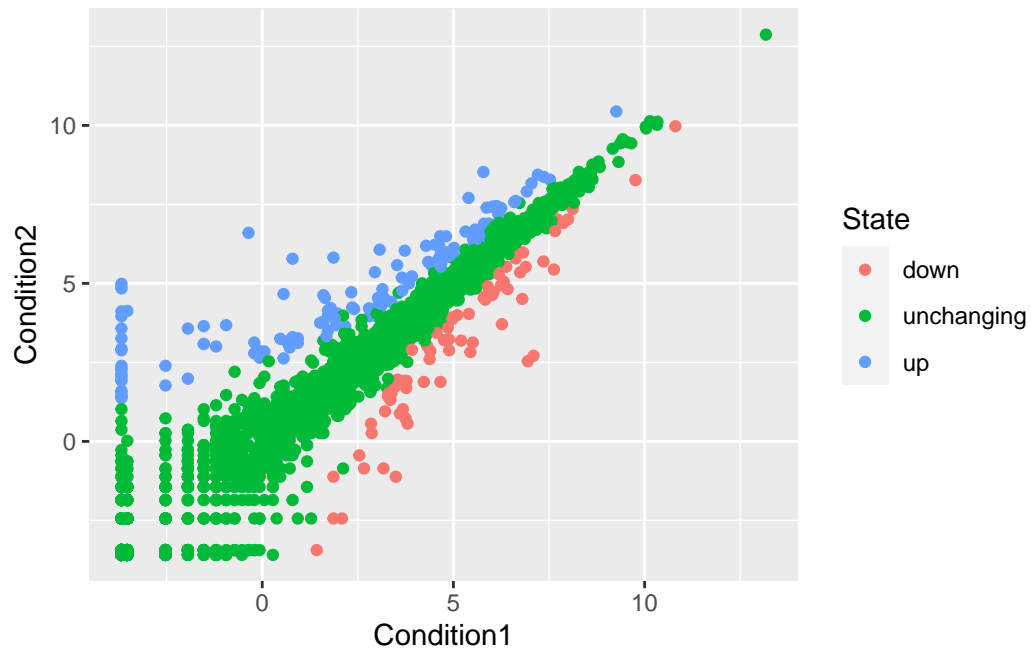
```
[1] "Gene"          "Condition1" "Condition2" "State"
```

```
ggplot(genes,aes(Condition1,Condition2))+geom_point()
```



Let's add some color. To do this we can add another `aes()` mapping of color to the `State` column in our data'

```
ggplot(genes,aes(Condition1,Condition2,color=State))+geom_point()
```



Q how many genes are upregulated and downregulated

```
head(genes)
```

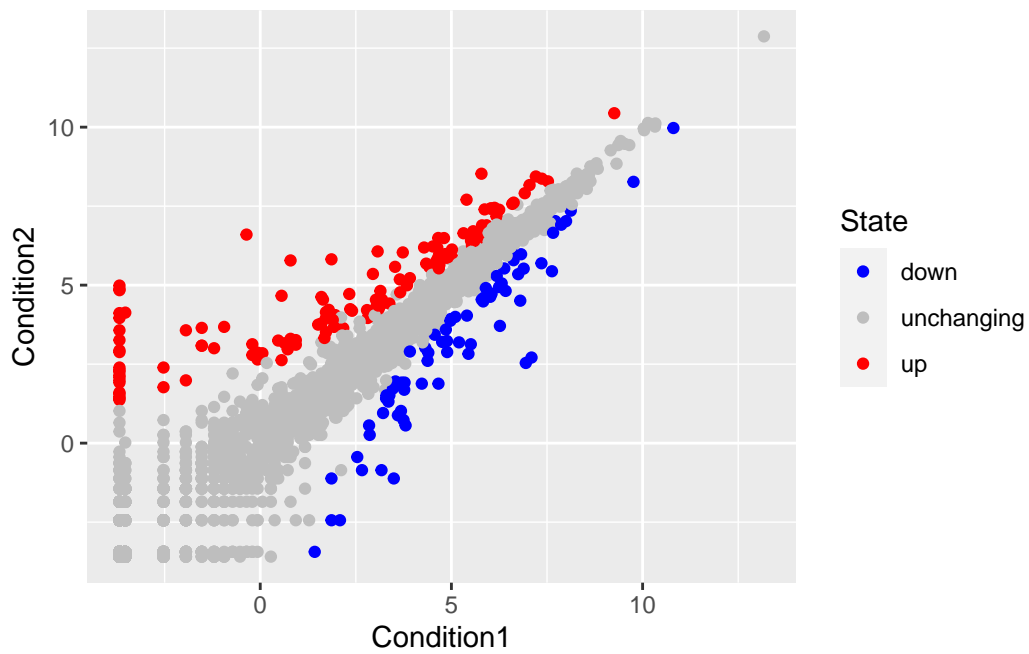
	Gene	Condition1	Condition2	State
1	A4GNT	-3.6808610	-3.4401355	unchanging
2	AAAS	4.5479580	4.3864126	unchanging
3	AASDH	3.7190695	3.4787276	unchanging
4	AATF	5.0784720	5.0151916	unchanging
5	AATK	0.4711421	0.5598642	unchanging
6	AB015752.4	-3.6808610	-3.5921390	unchanging

To get at just the State column

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

down	unchanging	up
72	4997	127

```
ggplot(genes,aes(Condition1,Condition2,color=State))+geom_point()+scale_colour_manual( val
```

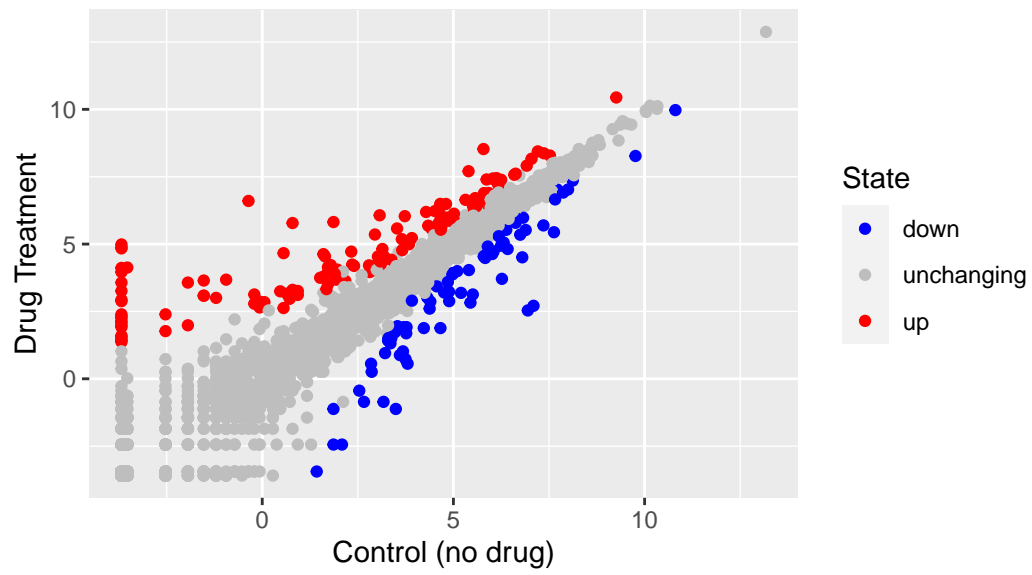


```
p<-ggplot(genes,aes(Condition1,Condition2,color=State))+geom_point()+scale_colour_manual(
```

Adding anotations

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

## Gene Expression Changes Upon Drug Treatment



Made by me