

# class05

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## Our first ggplot

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

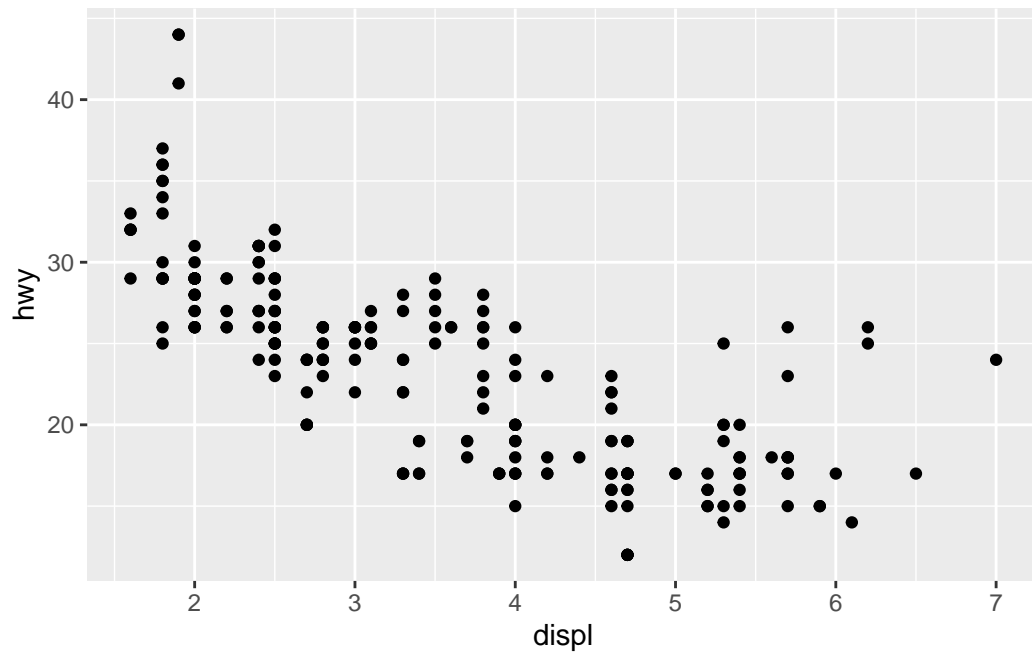
1. use the `'install.packages()'` command.

ggplot is not loaded by default to save disk space. To manually load the package,

2. use `'library(ggplot2)'` to load the ggplot2 package

```
library(ggplot2)
```

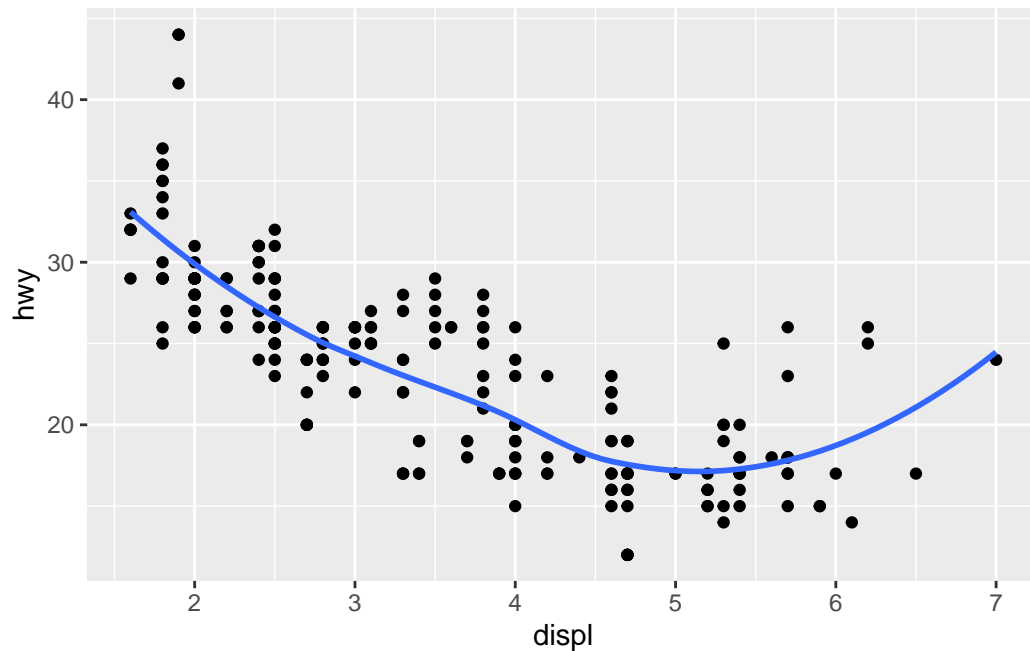
```
ggplot(mpg) +  
  aes(displ, hwy) +  
  geom_point()
```



I can add more layers:

```
ggplot(mpg) +  
  aes(displ, hwy) +  
  geom_point() +  
  geom_smooth(se=0)
```

`geom\_smooth()` using method = 'loess' and formula 'y ~ x'



## Plot of gene expression data

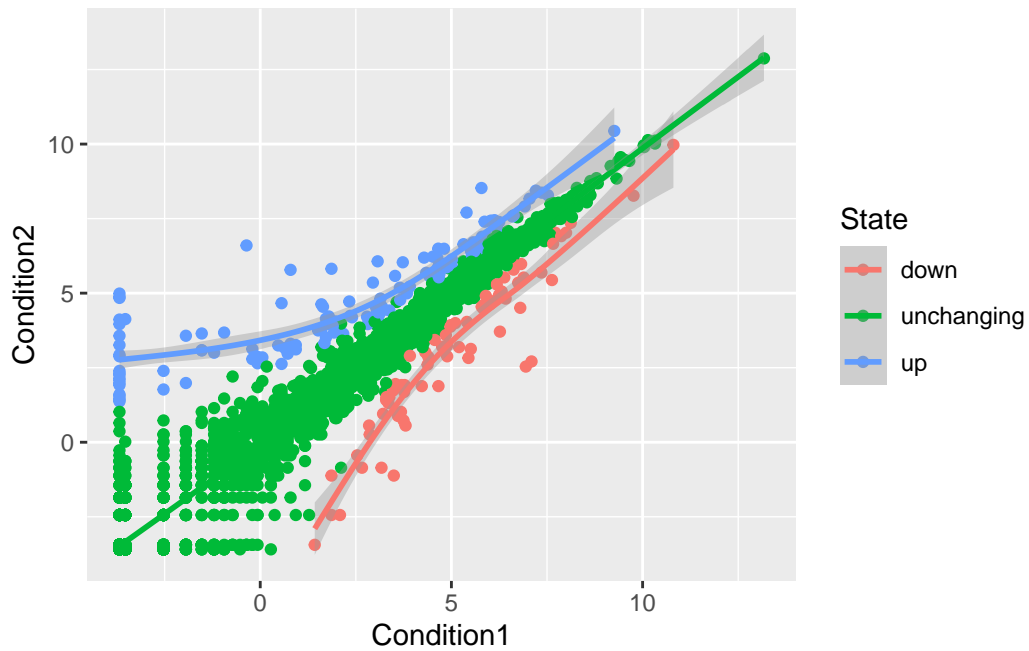
First read the data from online.

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

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

p

``geom_smooth()`` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'



Q: How many genes are in the dataset

```
nrow(genes)
```

```
[1] 5196
```

Q: How many genes are up/downregulated or unchanged?

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

```

down  unchanging      up
  72      4997      127

```

Q: Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset?

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

down	unchanging	up
1.39	96.17	2.44

## Further implementation to ggplot

```
p <- ggplot(genes) +
  aes(Condition1, Condition2, color=State) +
  geom_point(alpha=.3) +
  scale_color_manual(values=c("blue","gray","red")) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
        subtitle="Condition 1 VS. Condition 2",
        caption="By Runqi Zhang")
```

p

Gene Expression Changes Upon Drug Treatment  
Condition 1 VS. Condition 2

