

Class 5: Data Viz with ggplot

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#Intro to ggplot

There are many graphic systems in R(ways to make plots and figures). These include “base” R plots. Today we will focus on the **ggplot2** package.

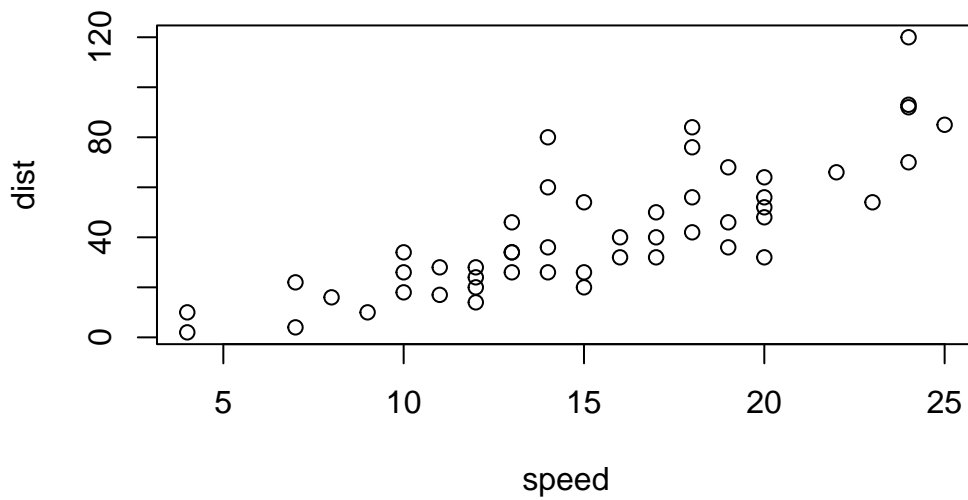
Let’s start with a plot of a simple in-built dataset called **cars**

`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

```
plot(cars)
```

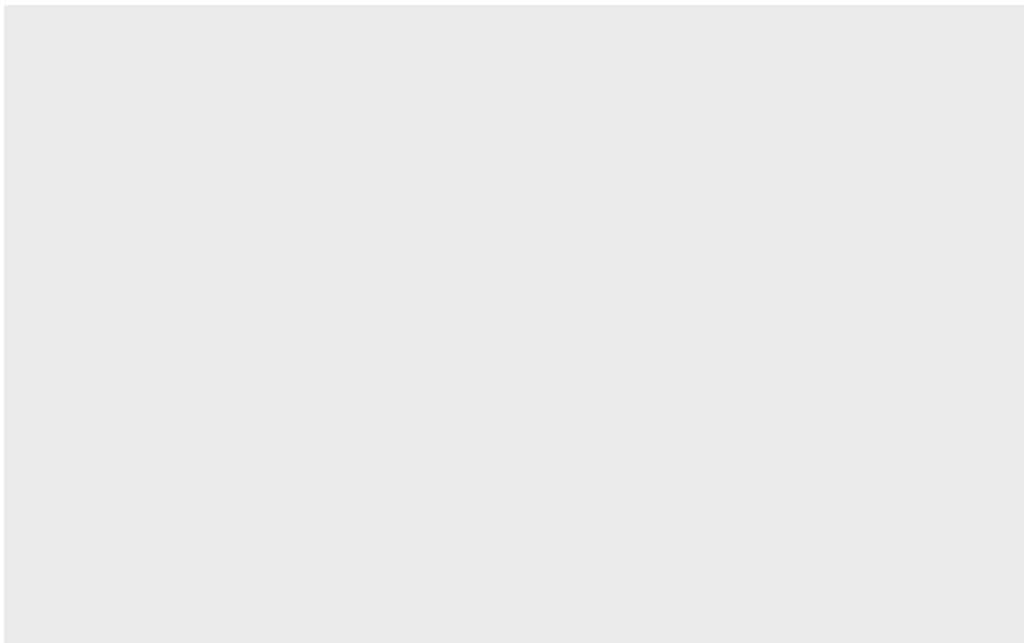


Let's see how we can make this figure using **ggplot**. First I need to install this package on my computer. To install any R package, I use the function `install.packages()`

I will run `'install.packages("ggplot2")` in my R console not this quarto document!

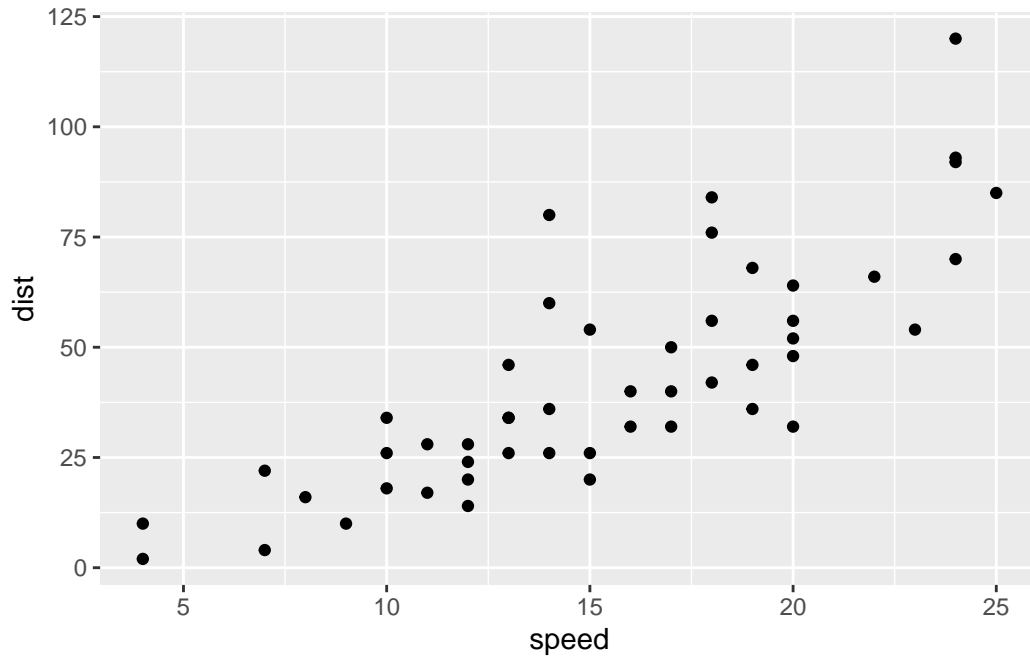
Before I can use any functions from add on packages I need to load the package from my "library()" with the `library(ggplot2)` call.

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



All ggplot figures have at least 3 things (called layers). These include: - **data** (the input dataset I want to plot from) - **aes** (aesthetic mapping of data to my plot) - **geom**(the `geom_point()`, `geom_line()`, etc that I want to draw)

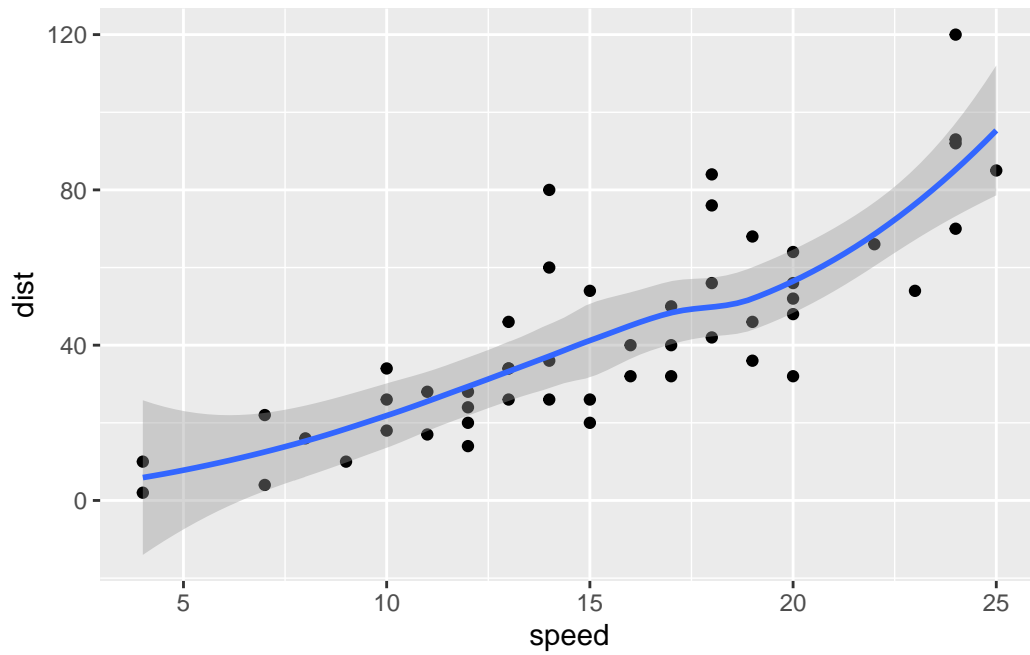
```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



Let's add a line to show the relationship here:

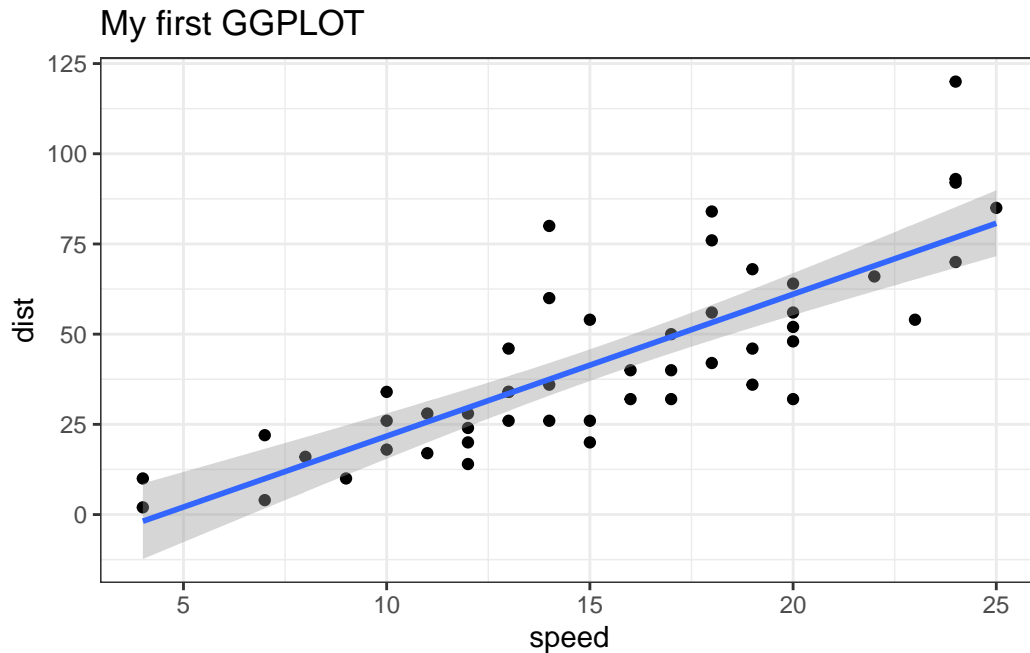
```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point()+  
  geom_smooth()
```

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



```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point()+  
  geom_smooth(method="lm")+  
  theme_bw()+  
  labs(title="My first GGPlot")
```

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



Q1. Which geometric layer should be used to create scatter plots in ggplot2?

`geom_point()`

Part 2: Adding more plot aesthetics through `aes()`

The code to read the dataset

```
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

Q2. How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

5196 genes in the data set

Q3. Use the `colnames()` function and the `ncol()` function on the `genes` data frame to find out what the column names are (we will need these later) and how many columns there are. How many columns did you find?

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

4 columns

Q4. Use the `table()` function on the `State` column of this `data.frame` to find out how many 'up' regulated genes there are. What is your answer?

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

down	unchanging	up
72	4997	127

127 upregulated genes

Q5. 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),4)
```

down	unchanging	up
0.0139	0.9617	0.0244

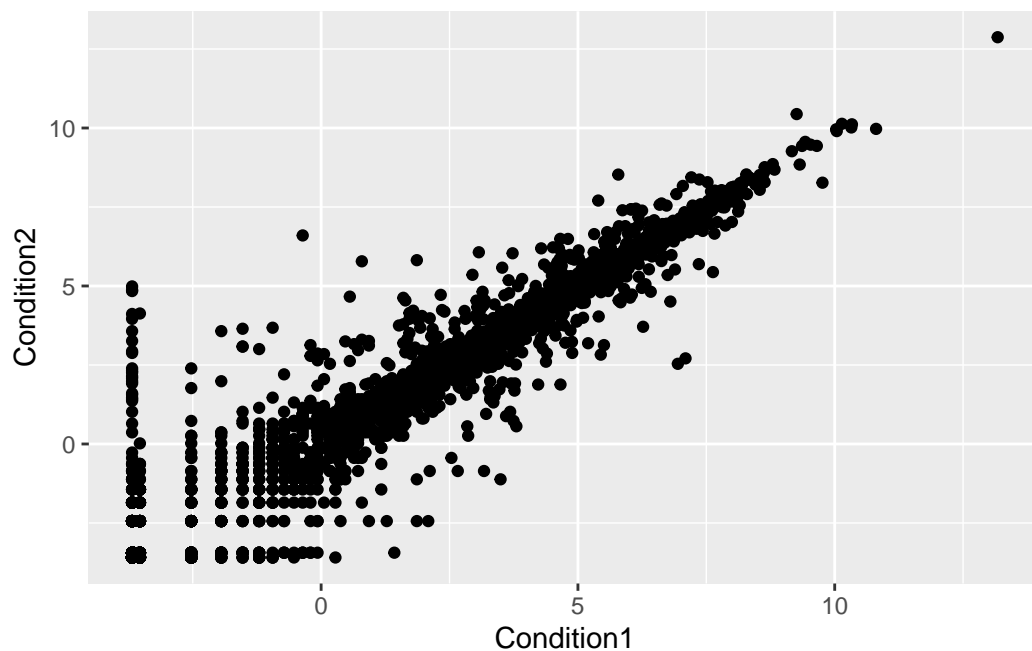

```
n.tot <- nrow(genes)
vals <- table(genes$State)

vals.percent <- vals/n.tot * 100
round(vals.percent, 2)
```

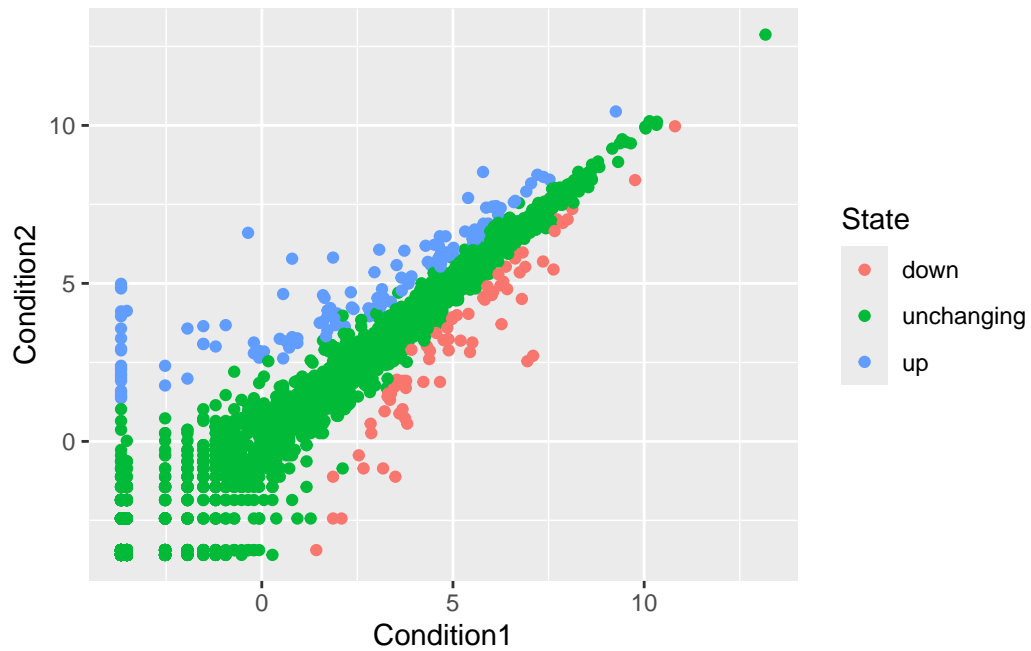
down	unchanging	up
1.39	96.17	2.44

2.44% of genes are upregulated

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

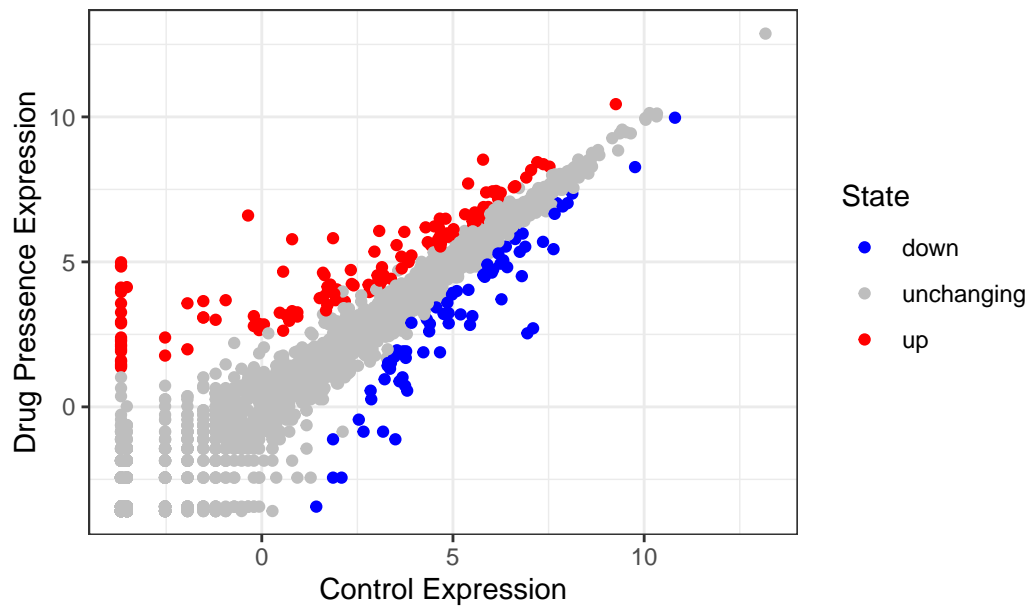


```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
```



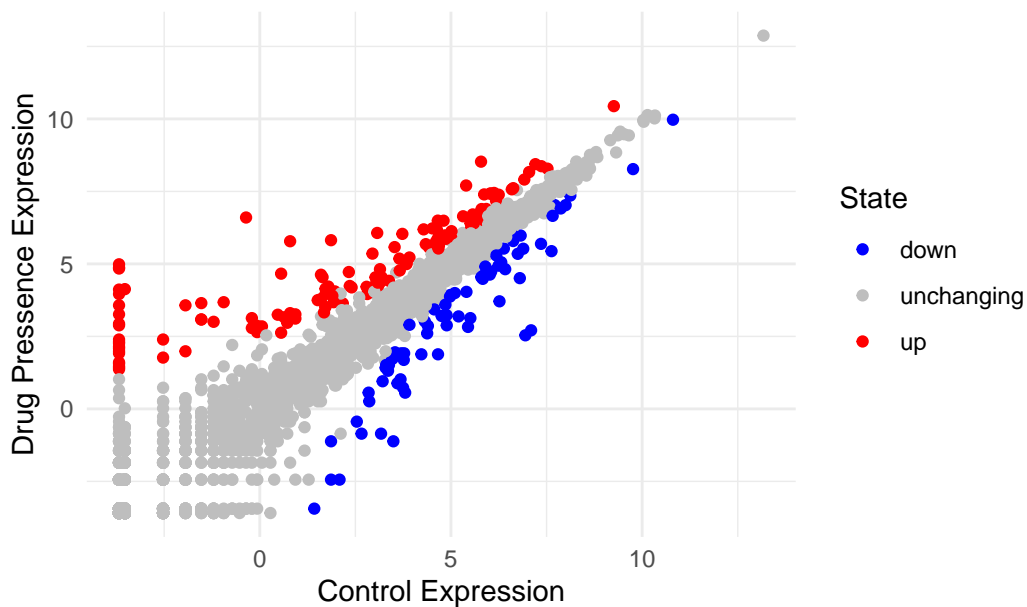
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()+
  theme_bw()+
  labs(title="Gene Expression changes upon drug treatment", x="Control Expression", y="Drug Expression") +
  scale_color_manual(values=c("blue","grey","red"))
```

Gene Expression changes upon drug treatment



```
p <-ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()+  
  theme_bw()+  
  labs(title="Gene Expression changes upon drug treatment", x="Control Expression", y="Drug Presence Expression") +  
  scale_color_manual(values=c("blue","grey","red"))  
  
p + theme_minimal()
```

Gene Expression changes upon drug treatment



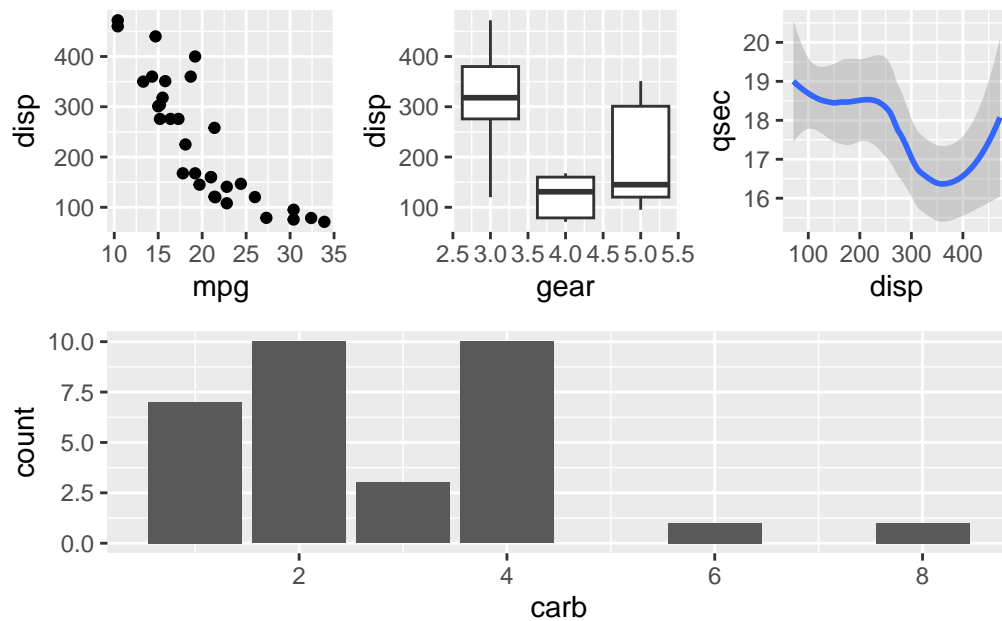
Part 3:Combining plots

```
#install.packages("patchwork")
library(patchwork)

# Setup some example plots
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(disp, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))

# Use patchwork to combine them here:
(p1 | p2 | p3) /
  p4
```

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



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

gapminder <- read.delim(url)
#install.packages("dplyr")
library(dplyr)
```

Attaching package: 'dplyr'

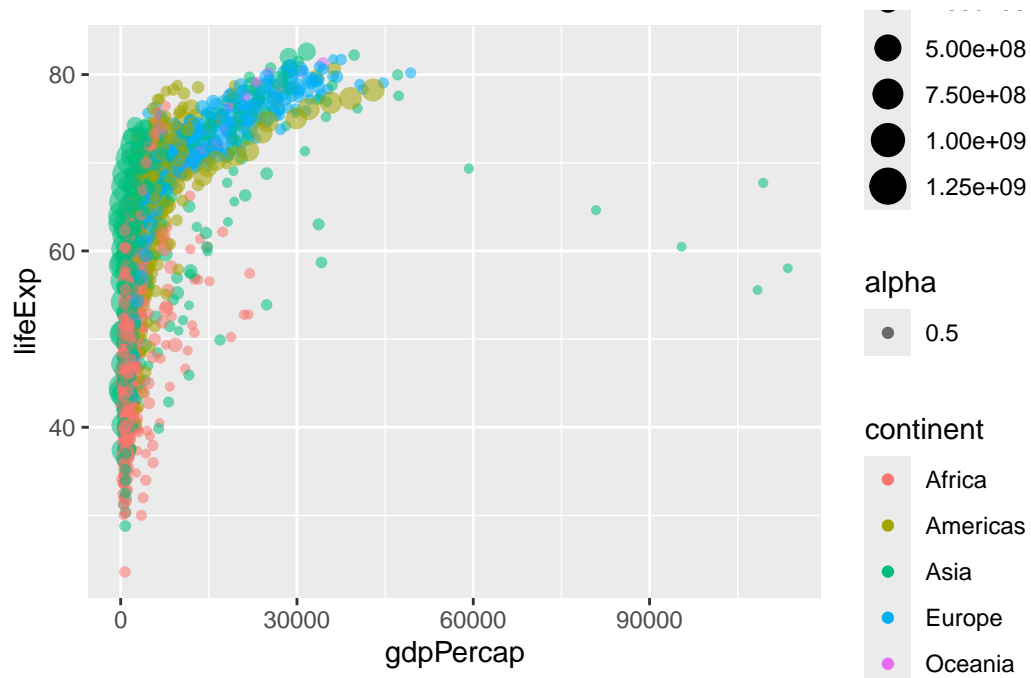
The following objects are masked from 'package:stats':

filter, lag

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

intersect, setdiff, setequal, union

```
ggplot(gapminder)+
  geom_point()+
  aes(x = gdpPercap, y = lifeExp, color=continent, size = pop, alpha=0.5)
```



```
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  geom_point()+
  aes(x = gdpPerCap, y = lifeExp, color= continent, size = pop, alpha=0.5) +
  scale_size_area(max_size = 10)
```

