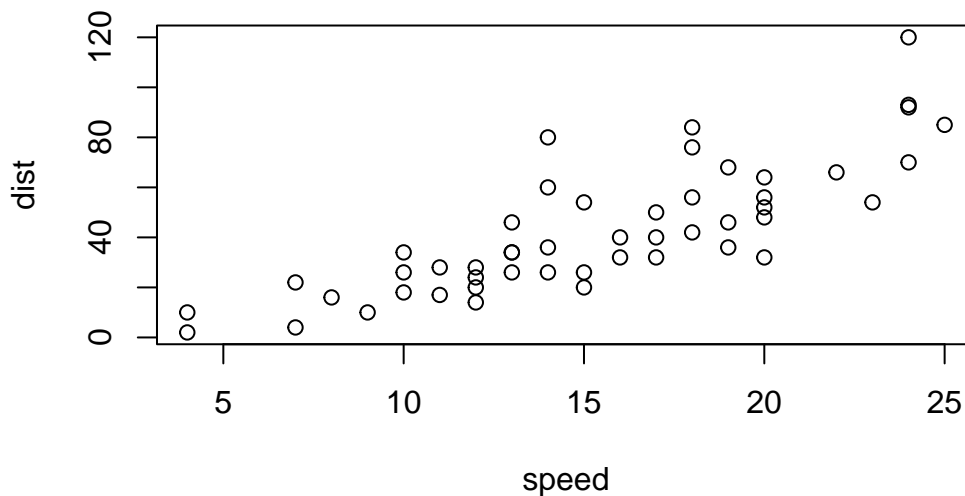


# Class 5: Data Viz with ggplot

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R has a lot of ways to make figures and graphs. In particular, one that comes with R out of the box is called “**base**” **R** - the `plot()` function.

```
plot(cars)
```



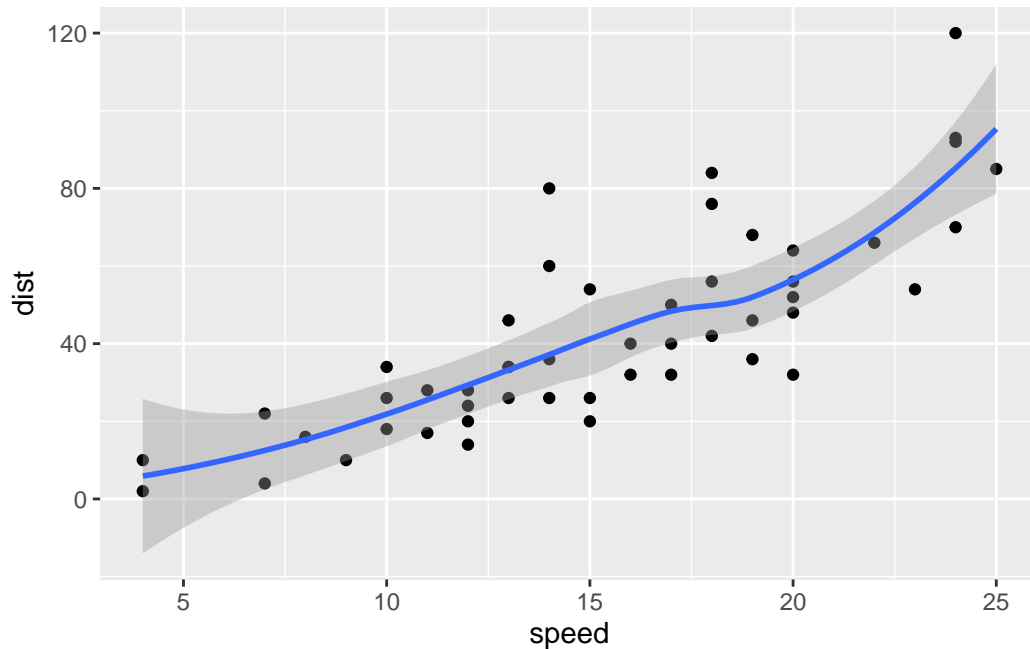
A very popular package is called **ggplot2**

Before I can use any add-on package like this one I must install it. We can use the `install.packages("ggplot2")` command. Install the add-on on the console.

Before using, I need to call it with `library()`

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

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



Remember that ggplot works in layers. You need to add them in order to get the data displayed. Every ggplot has at least 3 layers:

- **data** (the number or stuff you want to plot –usually a data frame `data.frame`–)
- **aesthetics** (mapping of your columns in the data frame to your plot –position x,y; size, line type, line width, color, shape)
- **geoms** (there are tones of these; basics are `geom_point()`, `geom_line()`, `geom_col()`)

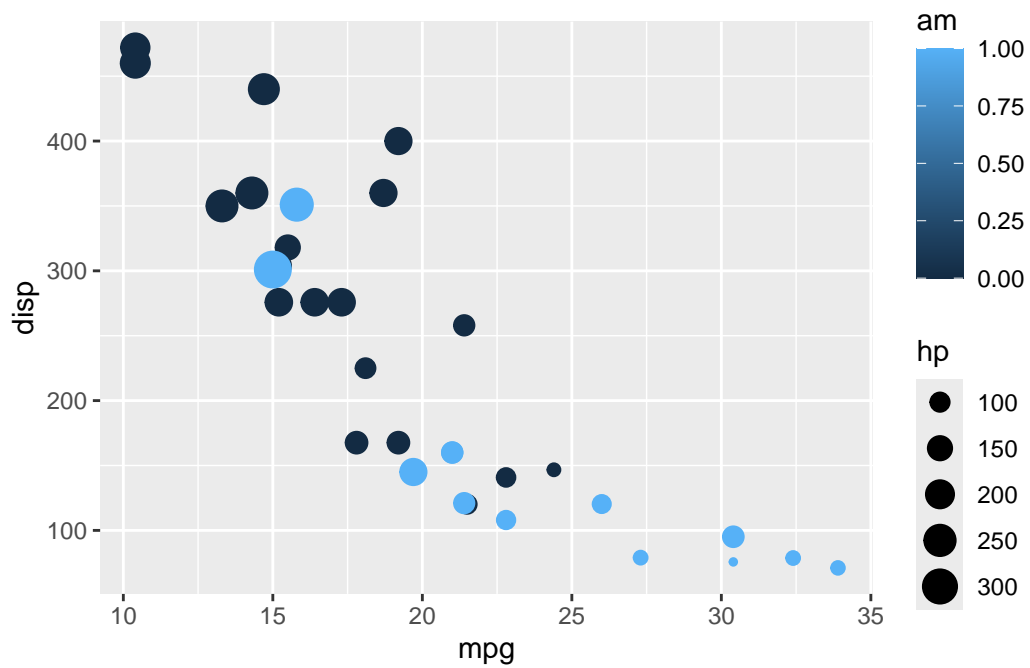
`mtcars`

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160.0	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160.0	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1

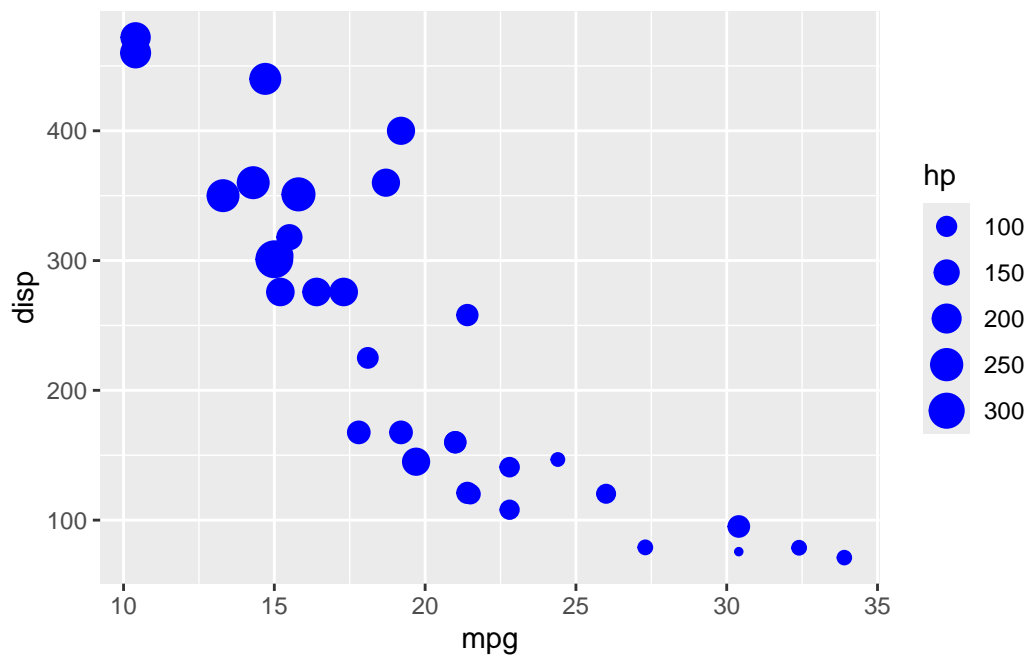
Hornet 4 Drive	21.4	6	258.0	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360.0	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225.0	105	2.76	3.460	20.22	1	0	3	1
Duster 360	14.3	8	360.0	245	3.21	3.570	15.84	0	0	3	4
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Merc 280	19.2	6	167.6	123	3.92	3.440	18.30	1	0	4	4
Merc 280C	17.8	6	167.6	123	3.92	3.440	18.90	1	0	4	4
Merc 450SE	16.4	8	275.8	180	3.07	4.070	17.40	0	0	3	3
Merc 450SL	17.3	8	275.8	180	3.07	3.730	17.60	0	0	3	3
Merc 450SLC	15.2	8	275.8	180	3.07	3.780	18.00	0	0	3	3
Cadillac Fleetwood	10.4	8	472.0	205	2.93	5.250	17.98	0	0	3	4
Lincoln Continental	10.4	8	460.0	215	3.00	5.424	17.82	0	0	3	4
Chrysler Imperial	14.7	8	440.0	230	3.23	5.345	17.42	0	0	3	4
Fiat 128	32.4	4	78.7	66	4.08	2.200	19.47	1	1	4	1
Honda Civic	30.4	4	75.7	52	4.93	1.615	18.52	1	1	4	2
Toyota Corolla	33.9	4	71.1	65	4.22	1.835	19.90	1	1	4	1
Toyota Corona	21.5	4	120.1	97	3.70	2.465	20.01	1	0	3	1
Dodge Challenger	15.5	8	318.0	150	2.76	3.520	16.87	0	0	3	2
AMC Javelin	15.2	8	304.0	150	3.15	3.435	17.30	0	0	3	2
Camaro Z28	13.3	8	350.0	245	3.73	3.840	15.41	0	0	3	4
Pontiac Firebird	19.2	8	400.0	175	3.08	3.845	17.05	0	0	3	2
Fiat X1-9	27.3	4	79.0	66	4.08	1.935	18.90	1	1	4	1
Porsche 914-2	26.0	4	120.3	91	4.43	2.140	16.70	0	1	5	2
Lotus Europa	30.4	4	95.1	113	3.77	1.513	16.90	1	1	5	2
Ford Pantera L	15.8	8	351.0	264	4.22	3.170	14.50	0	1	5	4
Ferrari Dino	19.7	6	145.0	175	3.62	2.770	15.50	0	1	5	6
Maserati Bora	15.0	8	301.0	335	3.54	3.570	14.60	0	1	5	8
Volvo 142E	21.4	4	121.0	109	4.11	2.780	18.60	1	1	4	2

Make a ggplot of `mtcars` data set using `mpg` vs `disp`. Set the size of the points to the `hp`. Also, set the color to `am`.

```
ggplot(mtcars) +
  aes(x=mpg, y=disp, size=hp, color=am) +
  geom_point()
```

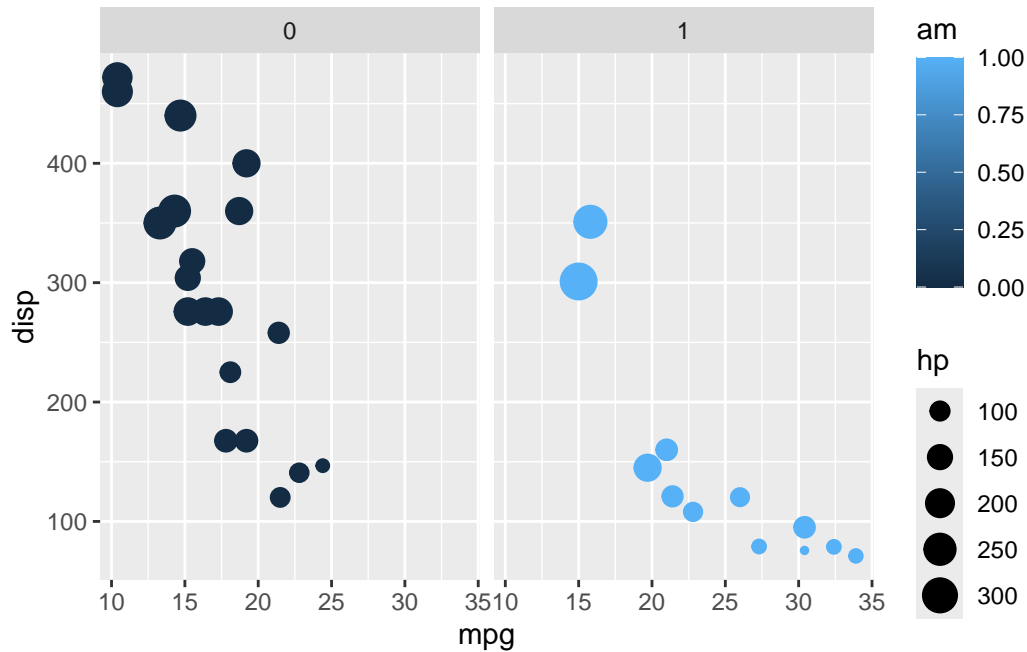


```
ggplot(mtcars) +
  aes(x=mpg, y=dis, size=hp) +
  geom_point(col="blue")
```



You can plot subgraph with the facet layer

```
ggplot(mtcars) +  
  aes(x=mpg, y=disp, size=hp, col=am) +  
  geom_point() +  
  facet_wrap(~am)
```

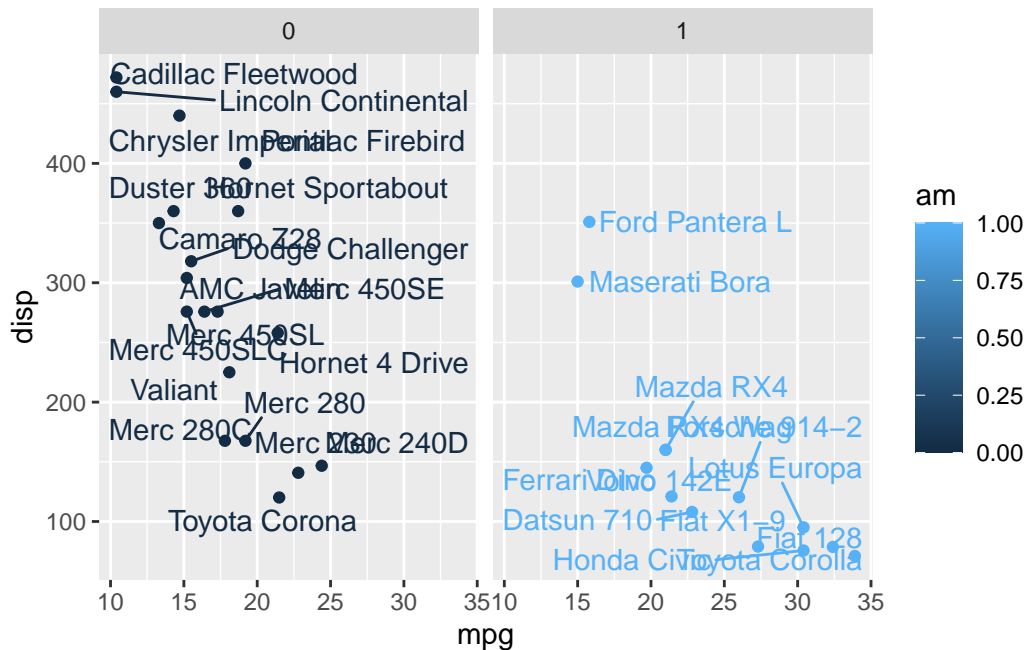


How can we identify what data is each point? But we need to install ggrepel

```
rownames(mtcars)
```

[1] "Mazda RX4"	"Mazda RX4 Wag"	"Datsun 710"
[4] "Hornet 4 Drive"	"Hornet Sportabout"	"Valiant"
[7] "Duster 360"	"Merc 240D"	"Merc 230"
[10] "Merc 280"	"Merc 280C"	"Merc 450SE"
[13] "Merc 450SL"	"Merc 450SLC"	"Cadillac Fleetwood"
[16] "Lincoln Continental"	"Chrysler Imperial"	"Fiat 128"
[19] "Honda Civic"	"Toyota Corolla"	"Toyota Corona"
[22] "Dodge Challenger"	"AMC Javelin"	"Camaro Z28"
[25] "Pontiac Firebird"	"Fiat X1-9"	"Porsche 914-2"
[28] "Lotus Europa"	"Ford Pantera L"	"Ferrari Dino"
[31] "Maserati Bora"	"Volvo 142E"	

```
library(ggrepel)
ggplot(mtcars) +
  aes(x=mpg, y=disp, col=am, label=rownames(mtcars)) +
  geom_point() +
  facet_wrap(~am) +
  geom_text_repel()
```



Now section 7. Going further.

```
library(gapminder)
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"
gapminder <- read.delim(url)
```

```
library(dplyr)
```

Attaching package: 'dplyr'

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

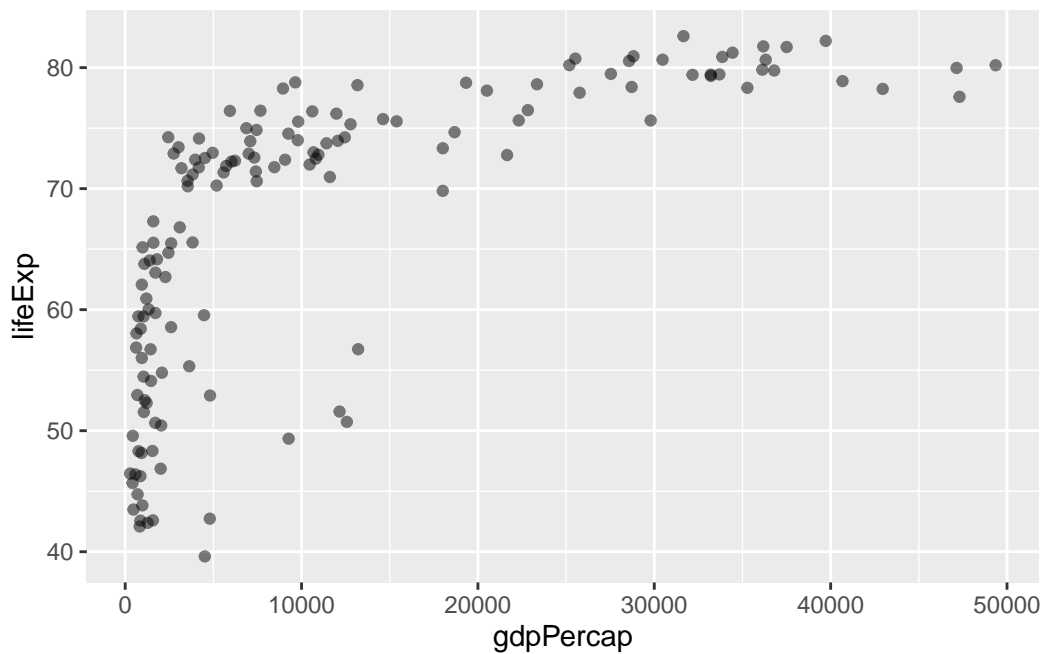
filter, lag

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

intersect, setdiff, setequal, union

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

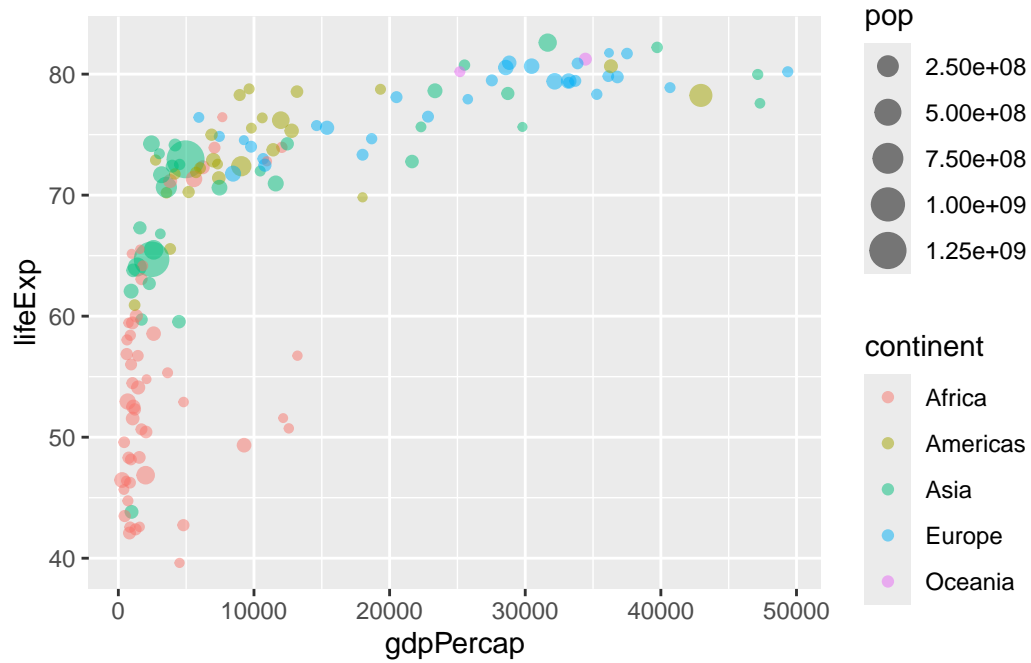
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.5)
```



Now we are adding more variables to the aesthetic layer:

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

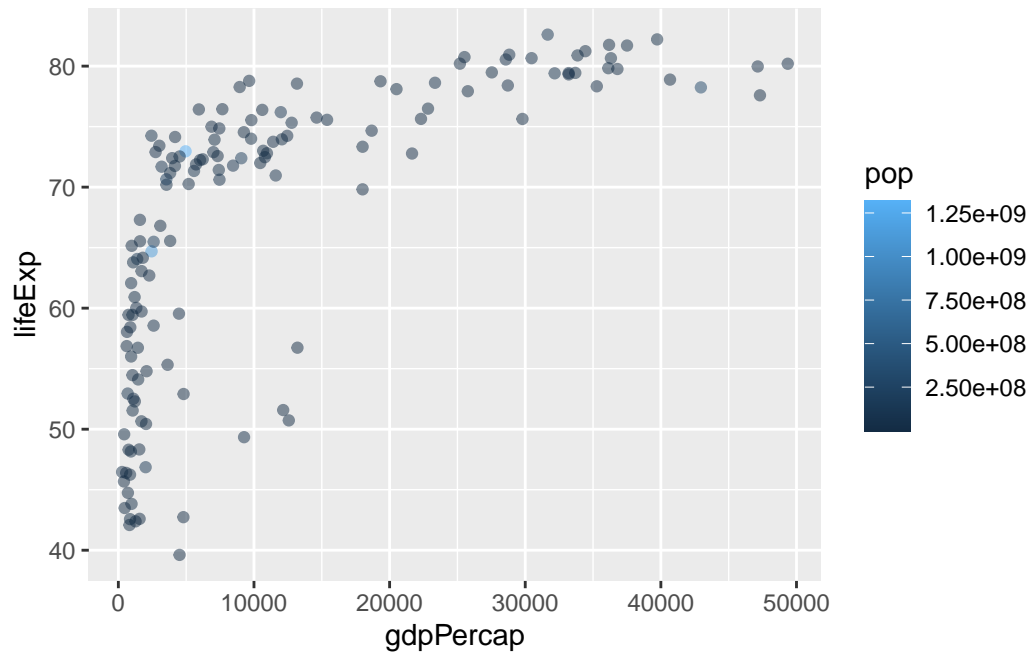
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



Coloring by population

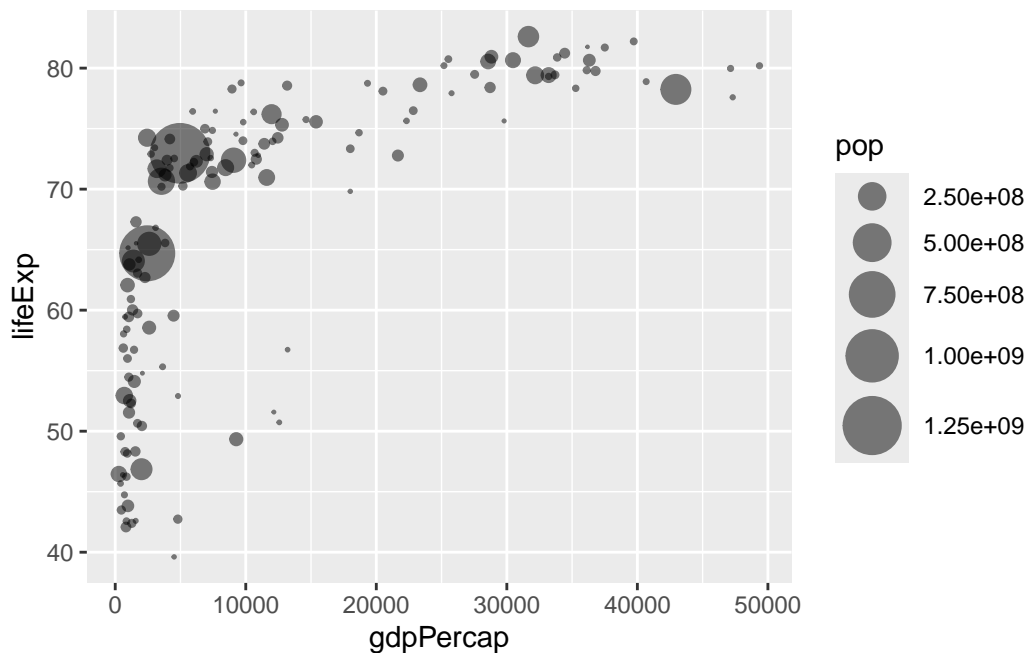
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=pop) +
  geom_point(alpha=0.5)
```





Another way to write this code:

```
ggplot(gapminder_2007) +  
  geom_point(aes(x = gdpPercap, y = lifeExp,  
                 size = pop), alpha=0.5) +  
  scale_size_area(max_size = 10)
```



NOW LETS GO BACK TO THE 6TH PART...

```
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

There are `n nrow(genes)` genes in this data set.

Functions such as `nrow()`, `ncol()`, and `table()` are useful and important.

```
nrow(genes)
```

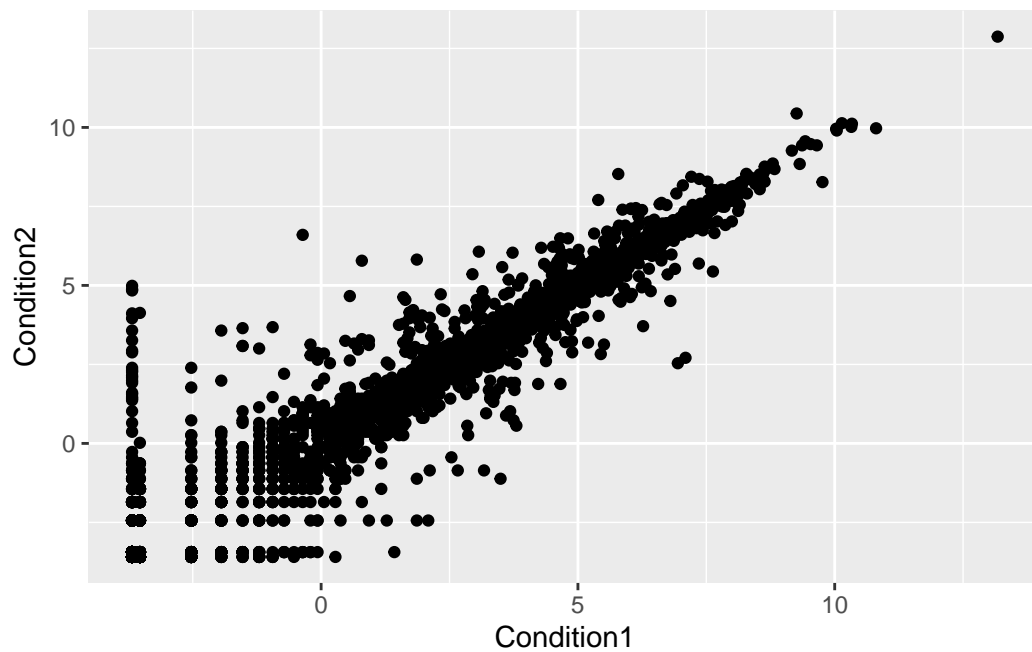
```
[1] 5196
```

```
unique(genes$State)
```

```
[1] "unchanging" "up"          "down"
```

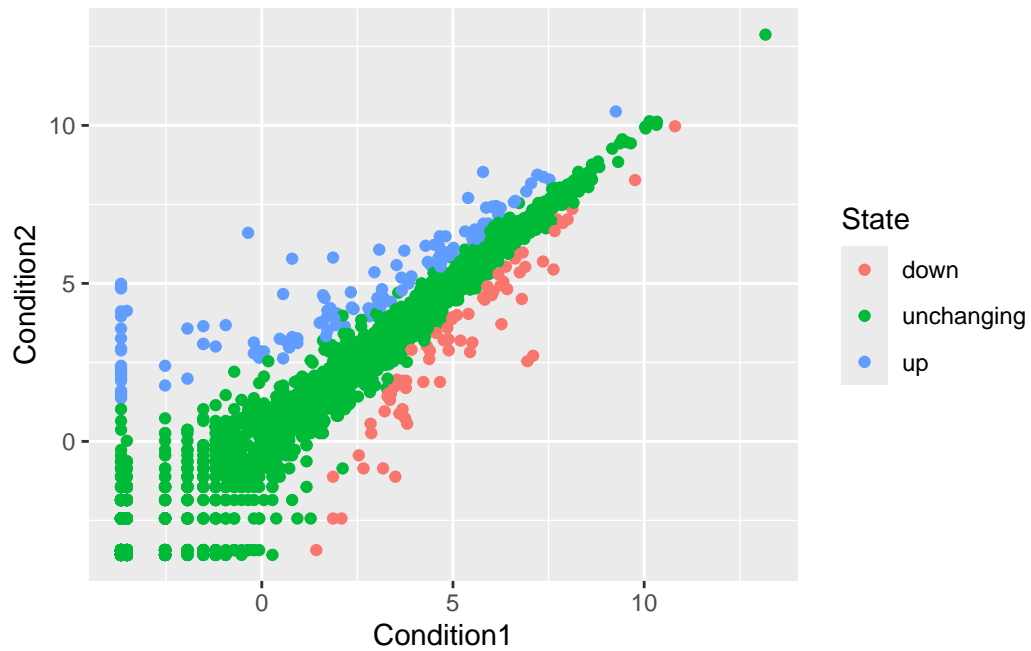
Now we need to compare the two conditions

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



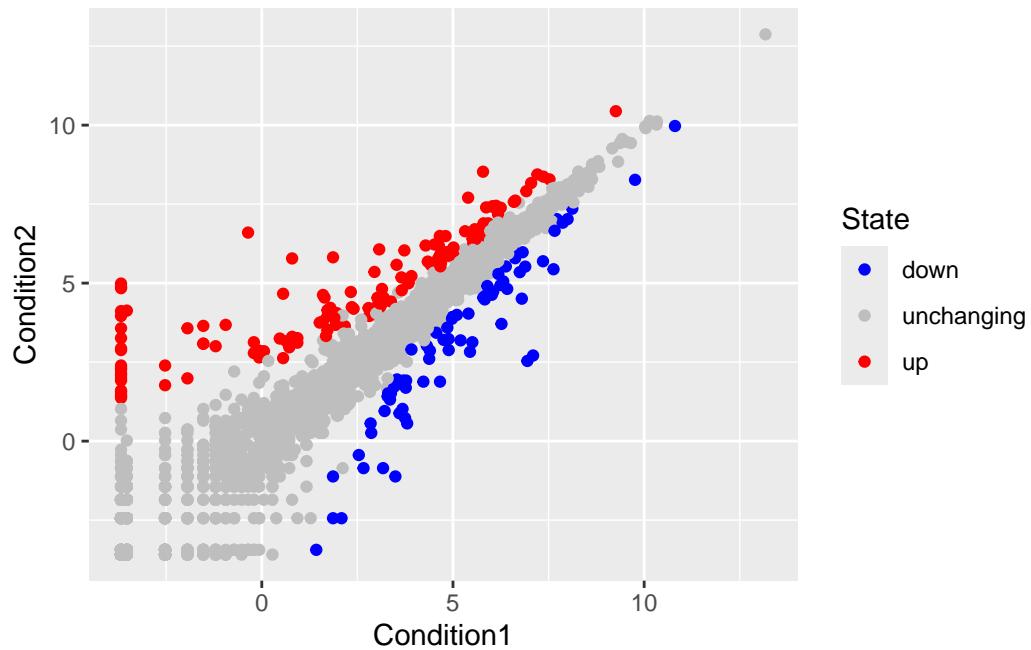
With colors and saving it as a vector

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



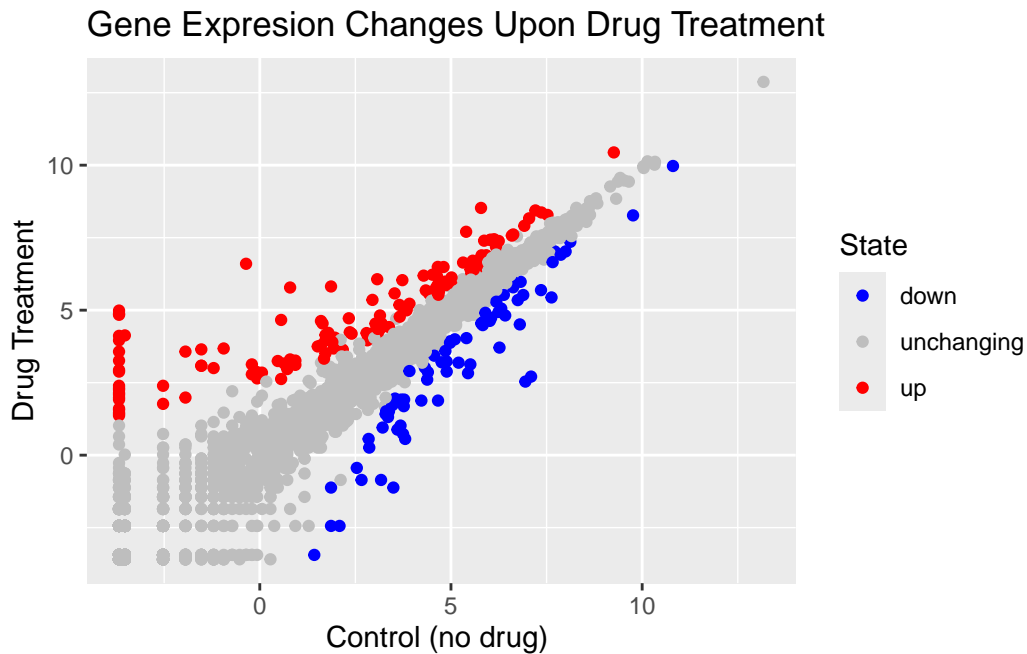
Then, we wanna change the colors to common used ones in gene expression profiling.

```
p + scale_colour_manual( values=c("blue","gray","red") )
```



If we want to add labels, we can use the function `labs()`. For this, let define x as control treatment and y as drug treatment.

```
p + scale_colour_manual( values=c("blue","gray","red") ) +  
  labs(title="Gene Expression Changes Upon Drug Treatment",  
        x="Control (no drug) ",  
        y="Drug Treatment")
```



Key points from the lesson: Saving plots with `ggsave()` Different plot “types” with different `geoms_**()` Faceting with `facet_wrap()` Multi-plot layout with the **patchwork** package.