

# Class 05

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## Using GGPLOT

The ggplot2 package needs to be installed as it doesn't come with R "out of the box".

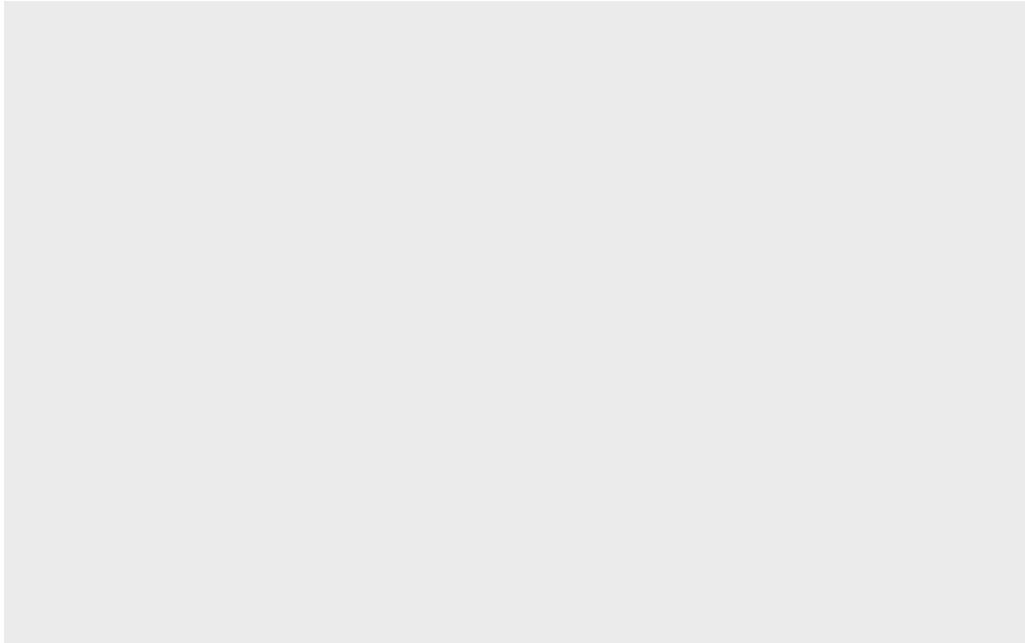
We use `install.packages()` function to do this.

```
head(cars)
```

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10

To use ggplot I need to load it up before I can call any of the functions in the package. I do this with the `library()` function.

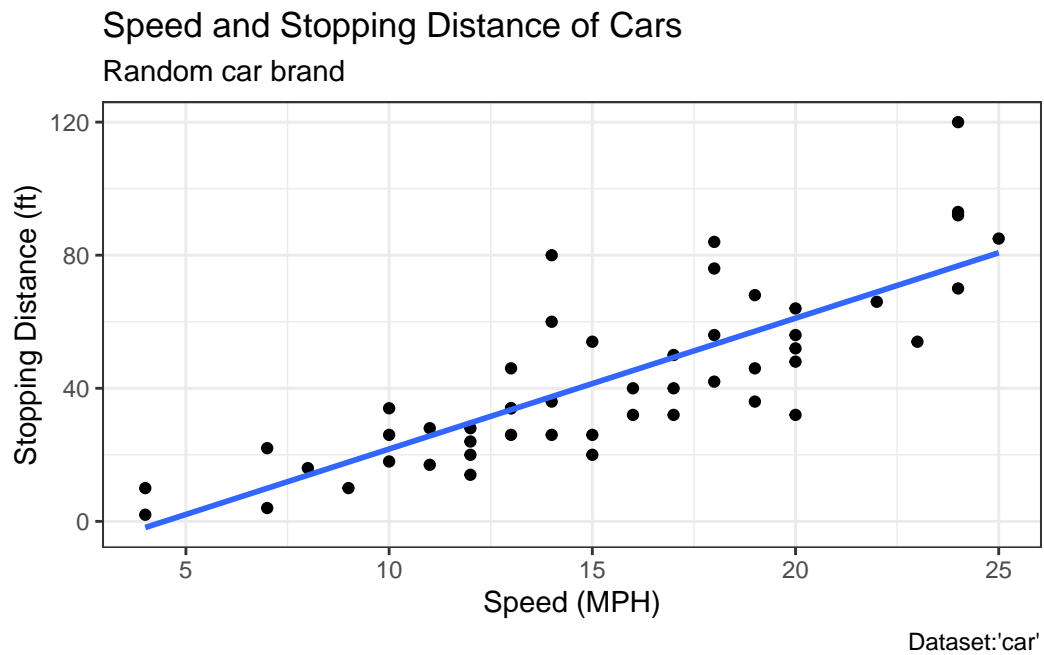
```
library(ggplot2)  
ggplot()
```



All ggplot figures have at least 3 things: - data (the stuff we want to plot) - aesthetic mapping (aes values) - geoms

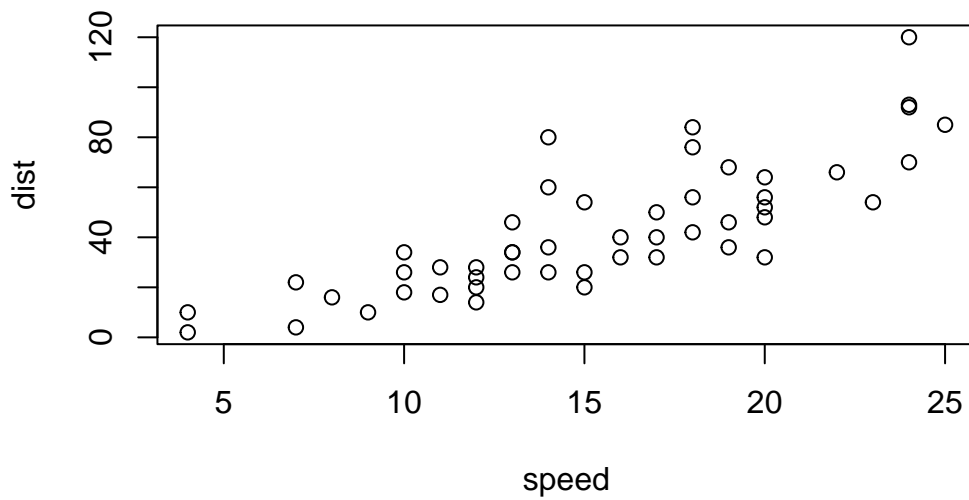
```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  labs(title= "Speed and Stopping Distance of Cars",  
        x="Speed (MPH)",  
        y = "Stopping Distance (ft)",  
        subtitle = "Random car brand",  
        caption = "Dataset: 'car'") +  
  geom_smooth(method = "lm", se=FALSE) +  
  theme_bw()
```

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



ggplot is not the only graphing system in R there are lots of others. There is even “base R” graphics.

```
plot(cars)
```



```
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

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

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

down	unchanging	up
72	4997	127

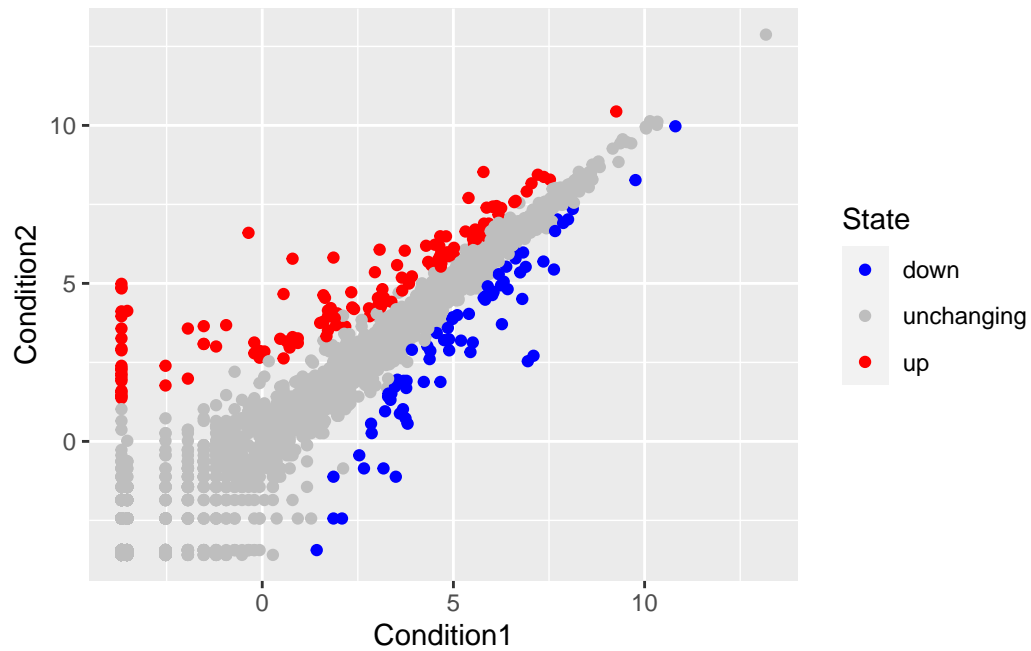
```
table(genes[, "State"])
```

down	unchanging	up
72	4997	127

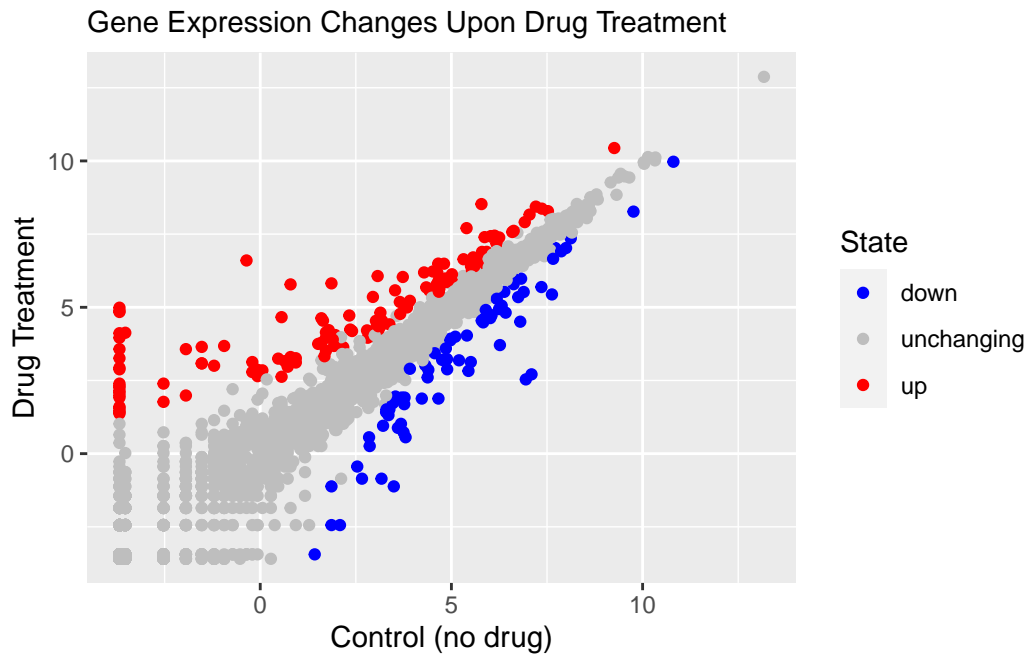
```
round( table(genes[, "State"]) / nrow(genes) *100, 2)
```

down	unchanging	up
1.39	96.17	2.44

```
p <- ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()  
p + scale_colour_manual( values=c("blue", "gray", "red") )
```



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



```
library(gapminder)
library(dplyr)
```

Attaching package: 'dplyr'

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

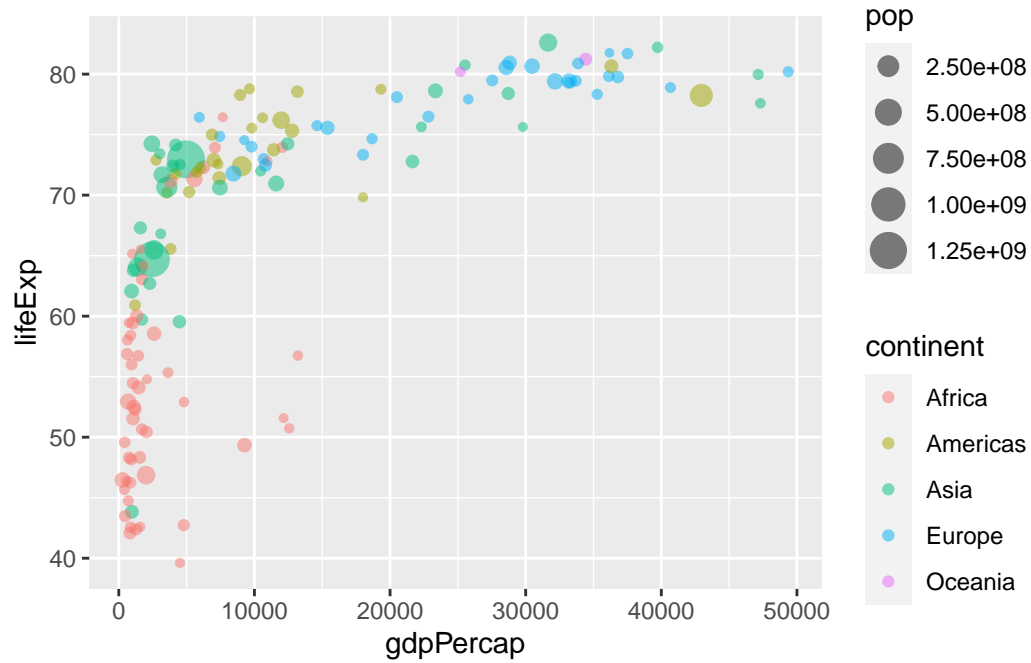
filter, lag

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

intersect, setdiff, setequal, union

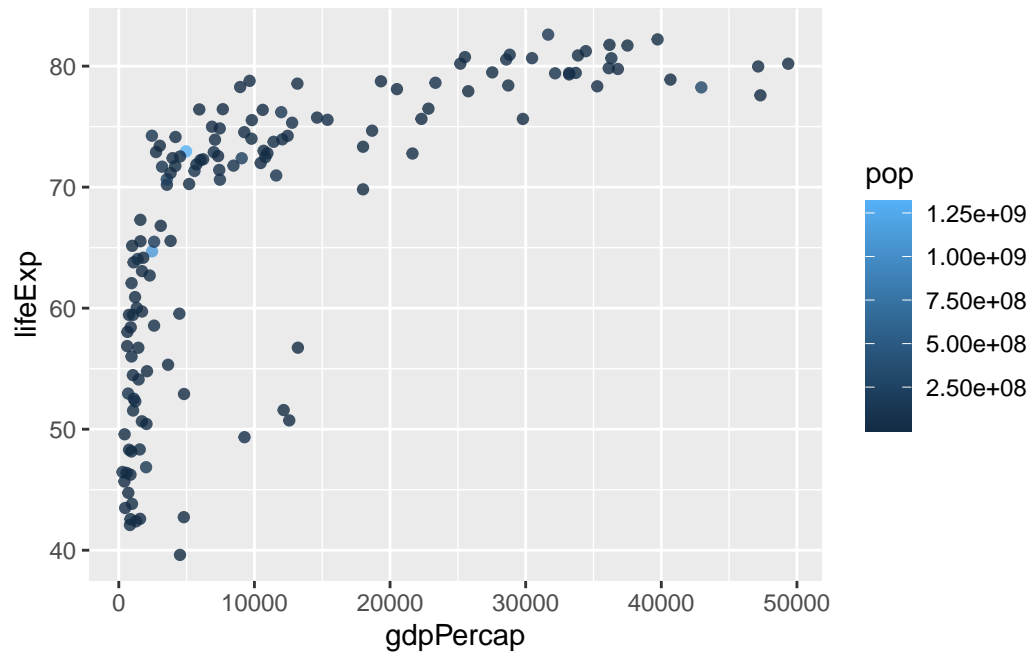
```
gapminder_2007 <- gapminder %>% filter(year==2007)

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

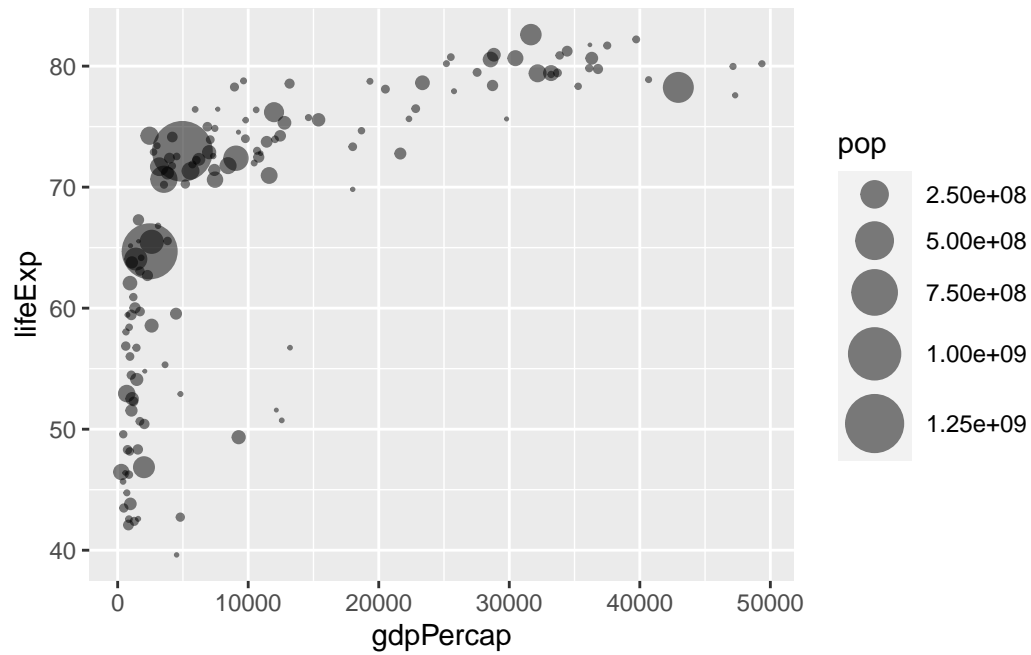


```
ggplot(gapminder_2007) +  
  aes(x = gdpPercap, y = lifeExp, color = pop) +  
  geom_point(alpha=0.8)
```



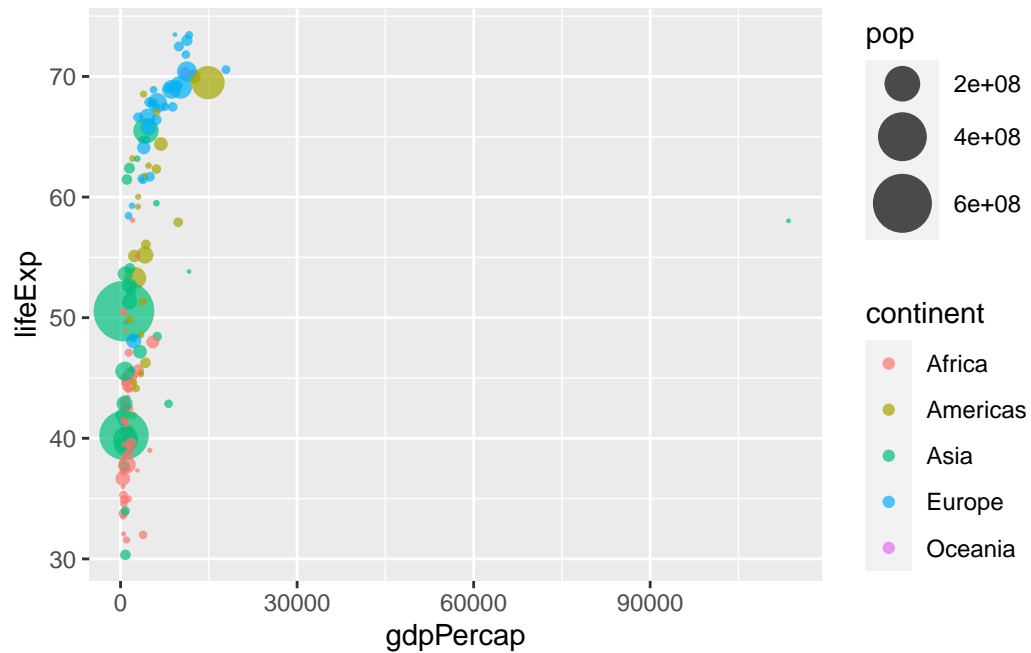


```
ggplot(gapminder_2007) +  
  aes(x = gdpPerCap, y = lifeExp, size = pop) +  
  geom_point(alpha=0.5) +  
  scale_size_area(max_size = 10)
```



```
gapminder_1957 <- gapminder %>% filter(year==1957)

ggplot(gapminder_1957) +
  aes(x = gdpPercap, y = lifeExp, color=continent,
      size = pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 10)
```



```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_1957) +
  aes(x = gdpPercap, y = lifeExp, size = pop,
      color = continent) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 10) +
  facet_wrap(~year)
```

