Class 5: Data Visualization with ggplot

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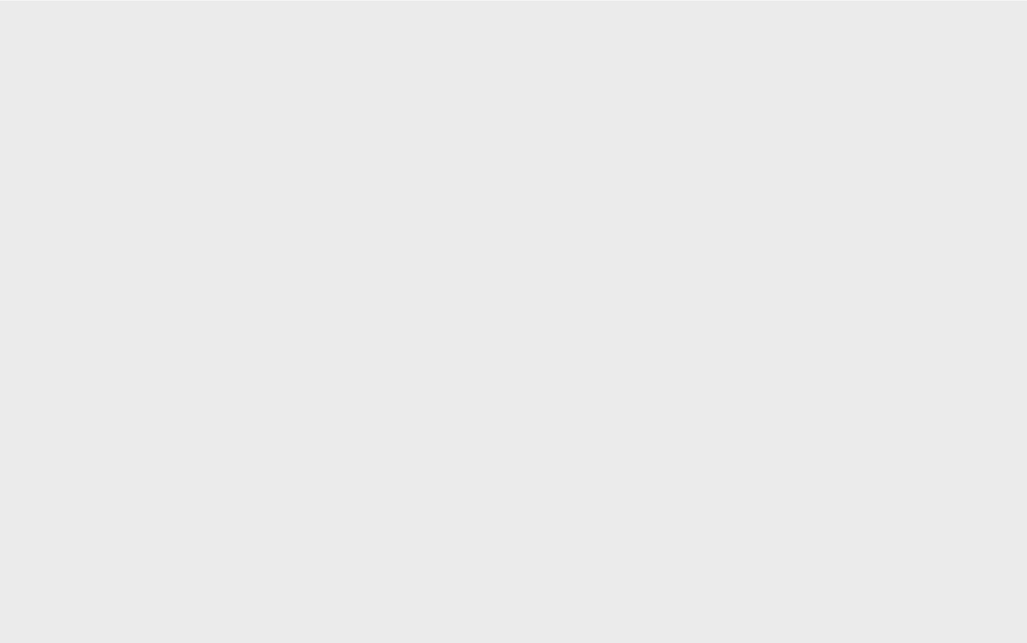
##Using GGPLOT

To use ggplot2 we first need to install it on our computers. To do this we will use the function `install.packages()`.

Before I use any package functions I have to load them up with a `library()` call, like so:

```r
library(ggplot2)
ggplot(cars)
```

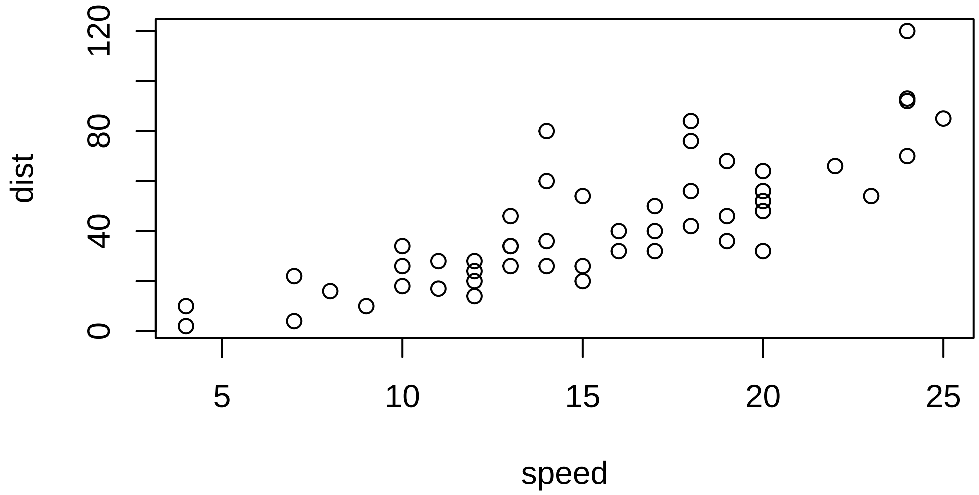


```r
head(cars)
```

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

There is always the “base R” graphics system, i.e. `plot()`

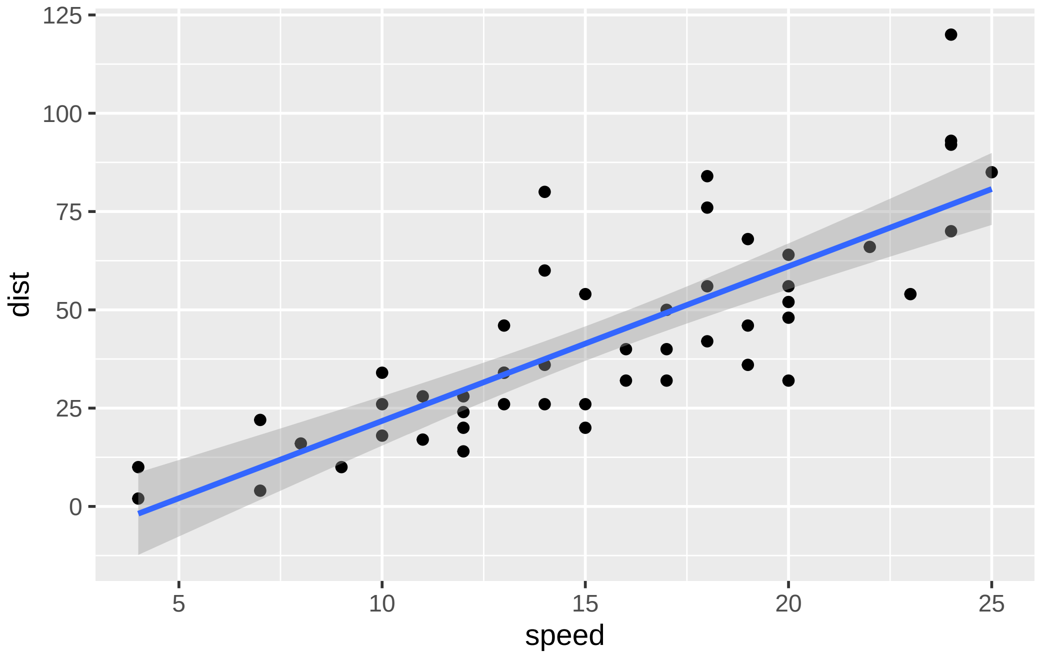
```
plot(cars)
```



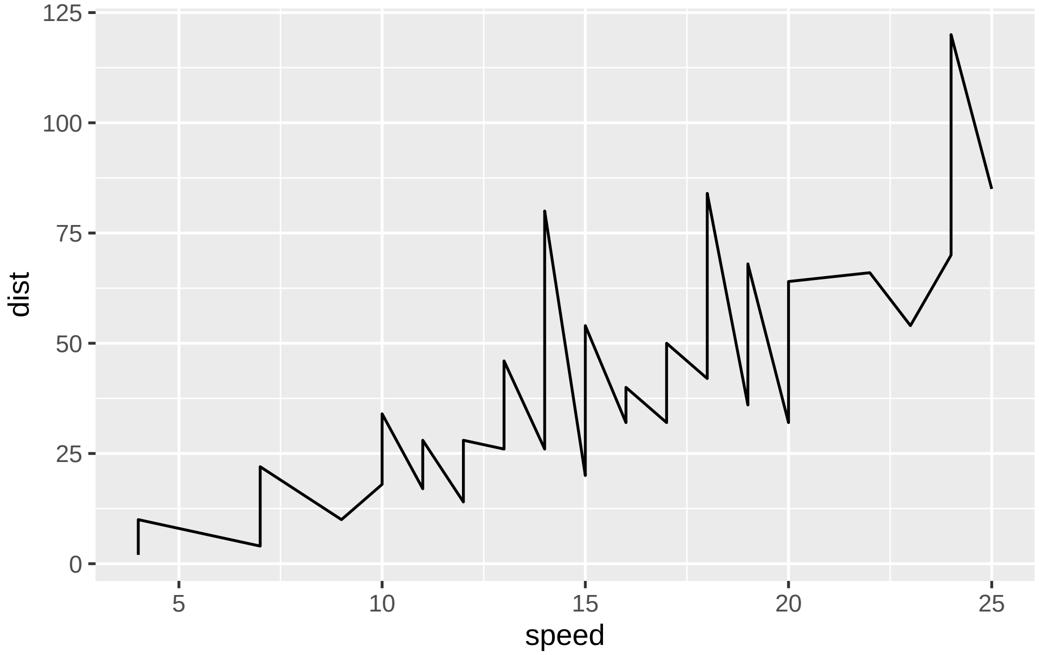
To use ggplot I need to spell out at least 3 things: -data (the stuff I want to plot as a data.frame) -aesthetics(aes()values - how the data map to the plot). -geoms (how I want things drawn)

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

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

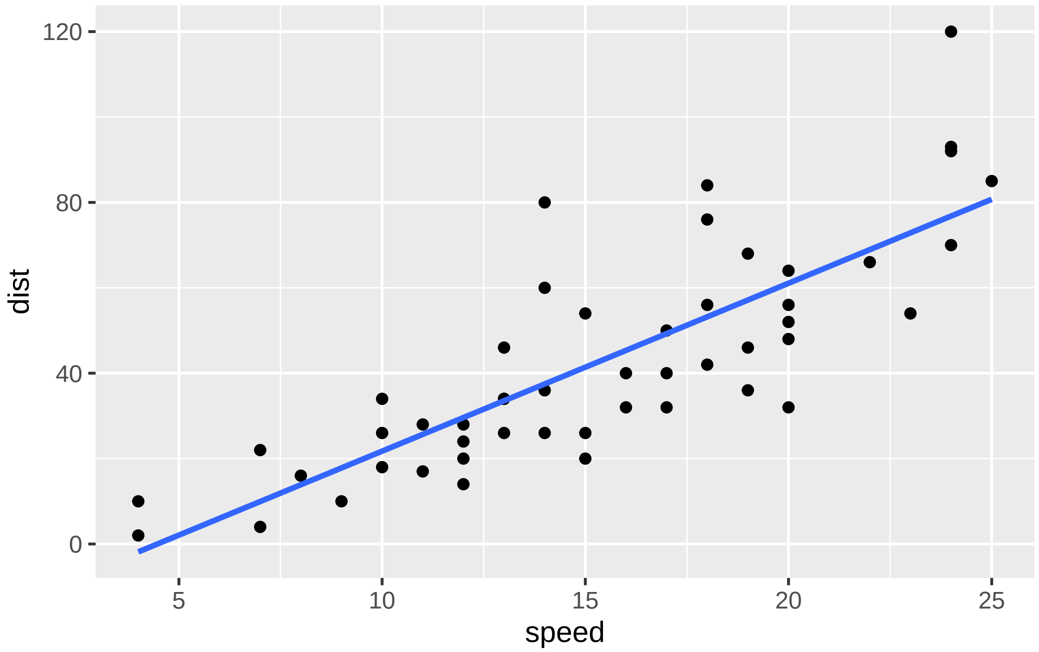


```
ggplot(cars)+
  aes(x=speed, y=dist)+
  geom_line()
```



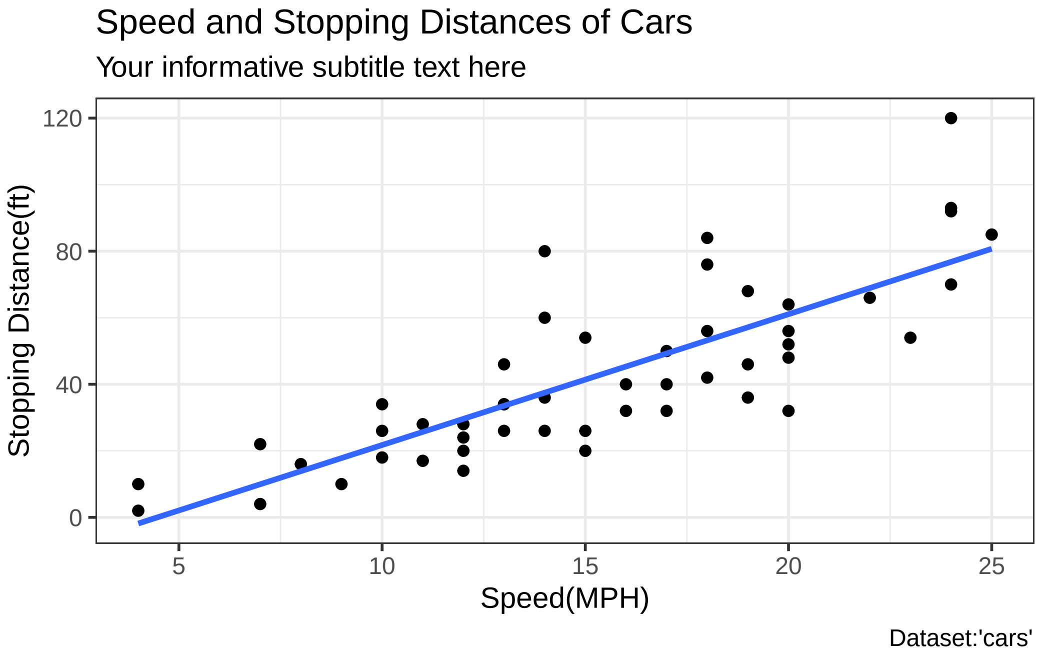
```
ggplot(cars)+
  aes(x=speed, y=dist)+
  geom_point()+
  geom_smooth(method="lm", se=FALSE)
```

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



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

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


Speed and Stopping Distances of Cars

Your informative subtitle text here

Dataset:'cars'

```r
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
```

The number of genes in this dataset is:

```r
nrow(genes)
```

```
[1] 5196
```

The column names are:

```
colnames(genes)
```

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

The number of columns is:

```
ncol(genes)
```

```
[1] 4
```

The number of 'up'regulated genes is:

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

```

      down unchanging         up 
        72       4997        127 
```

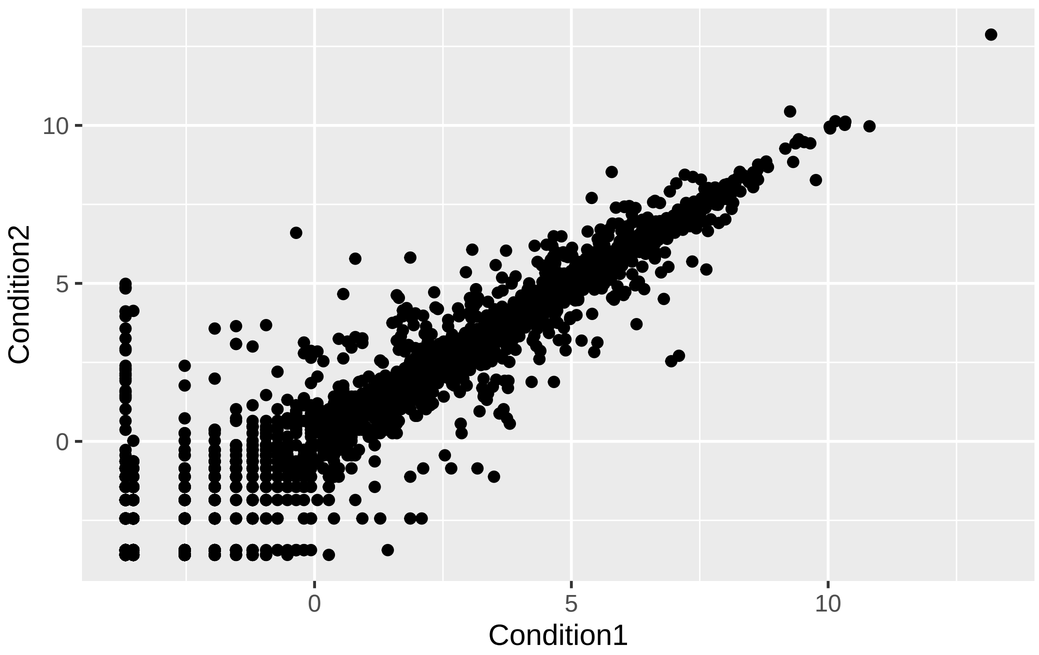
There are 127 "UP" regulated genes in this dataset

The fraction of total genes that is up-regulated in this dataset:

```
127/(72+4997+127)
```

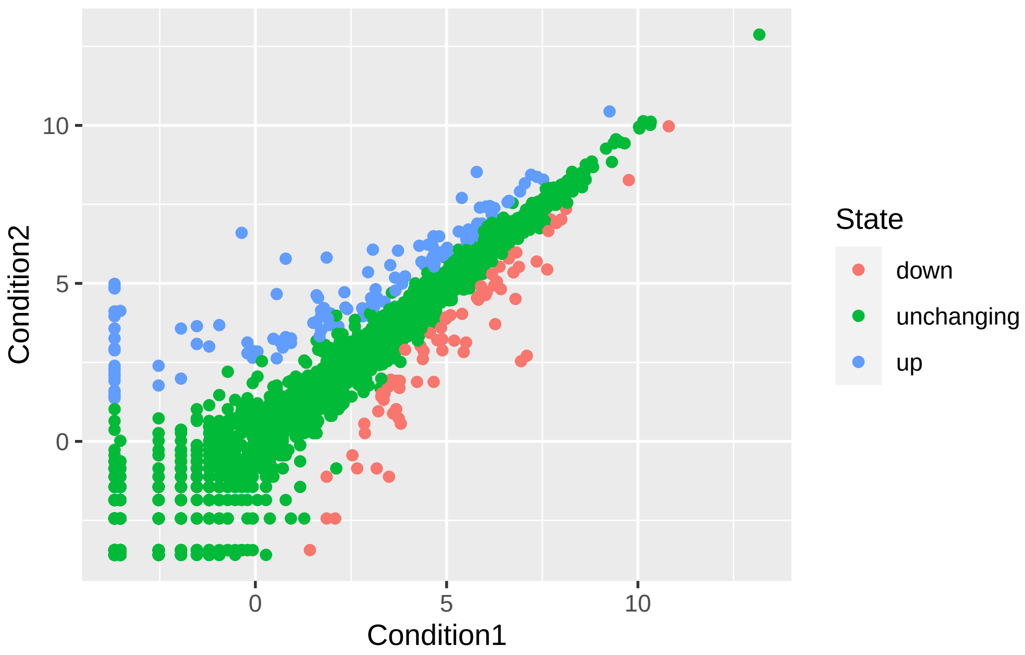
```
[1] 0.02444188
```

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

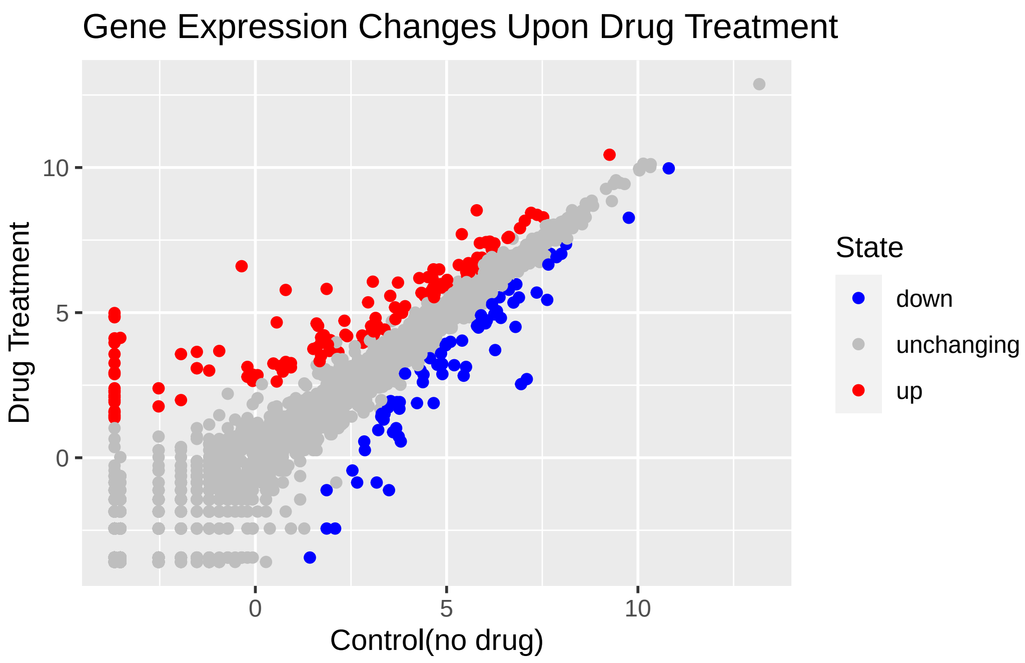


```
p <- ggplot(genes)+
  aes(x=Condition1, y=Condition2, col=State)+
  geom_point()
```

```
p
```



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



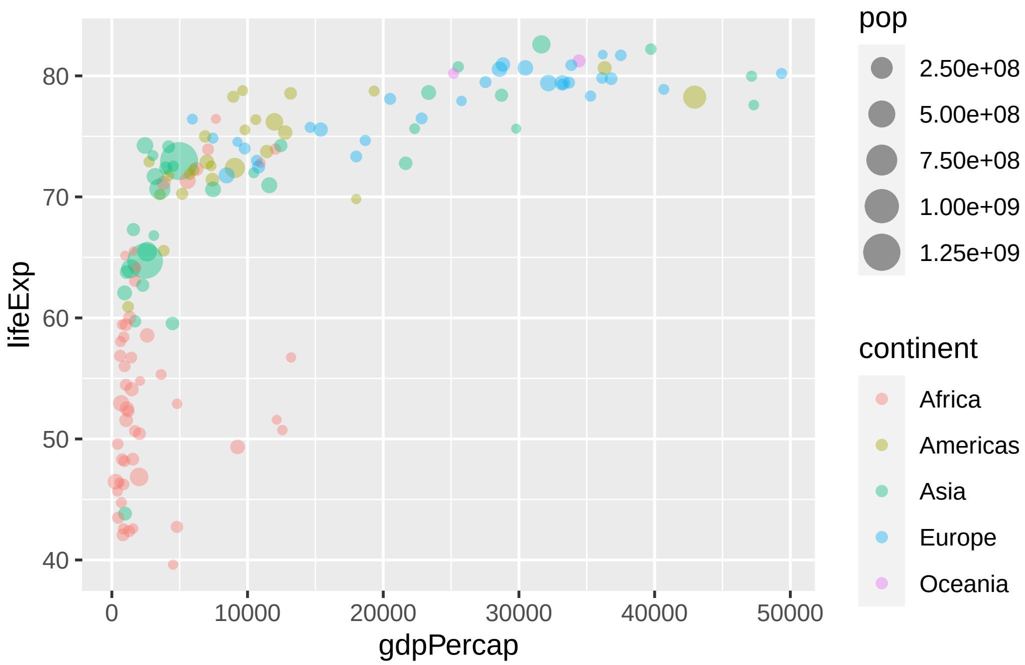
```
library(gapminder)
```

```
library(dplyr)
```

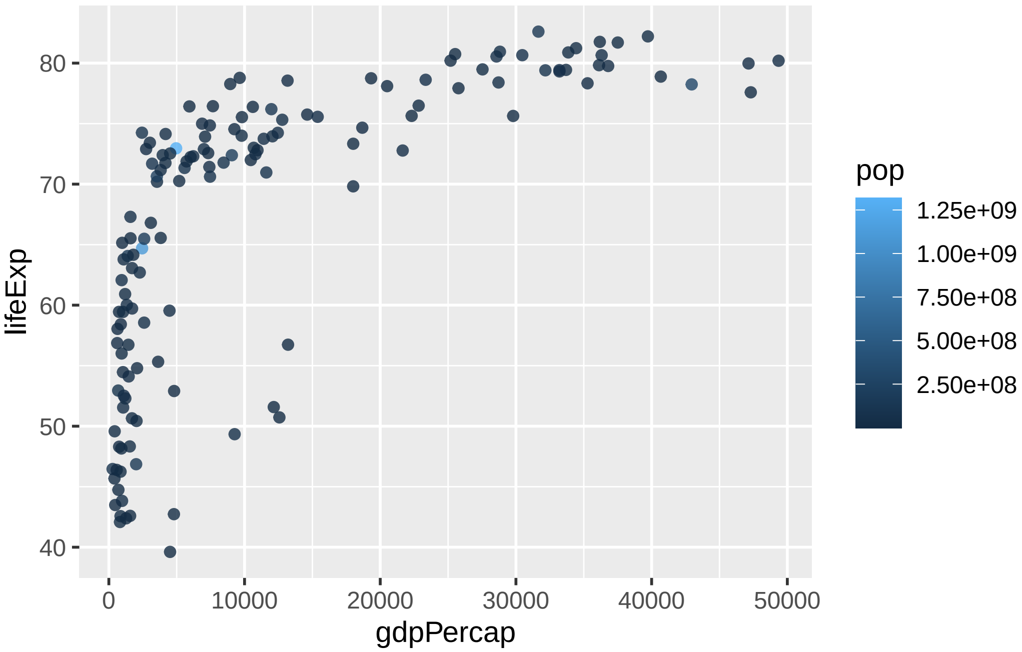
```

 '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)
```

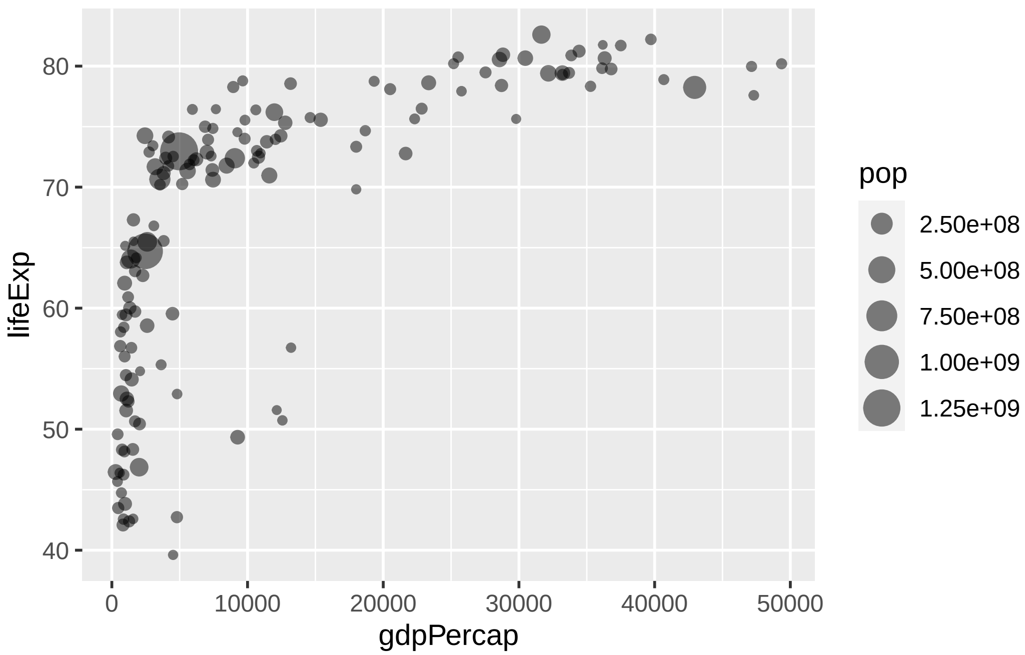
```
ggplot(gapminder_2007)+
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.4)
```



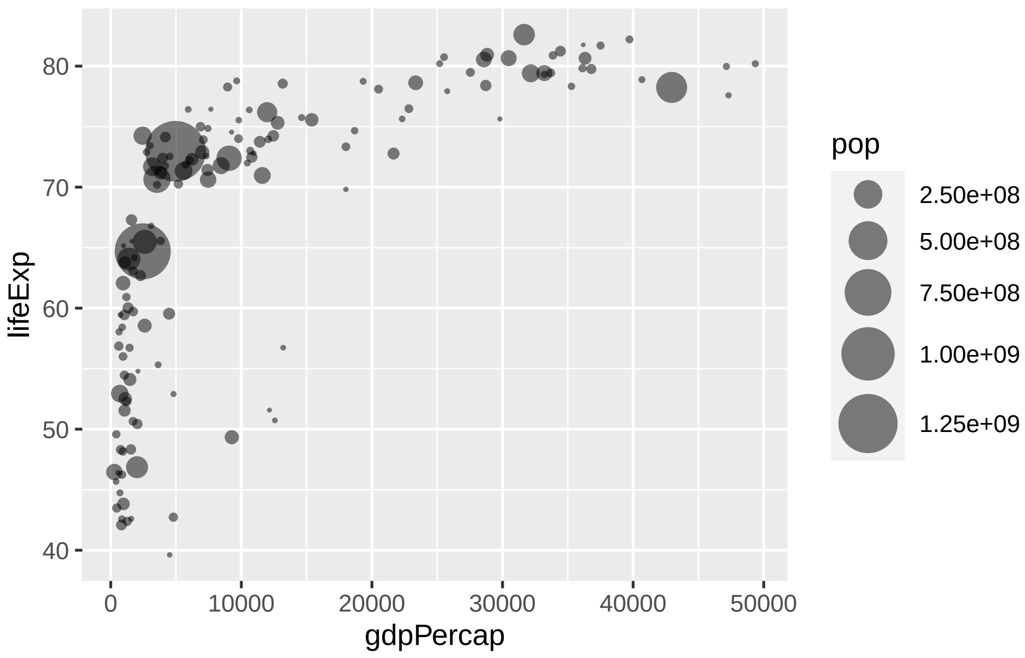
```
ggplot(gapminder_2007)+
  aes(x=gdpPercap, y=lifeExp, color=pop)+
  geom_point(alpha=0.8)
```



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

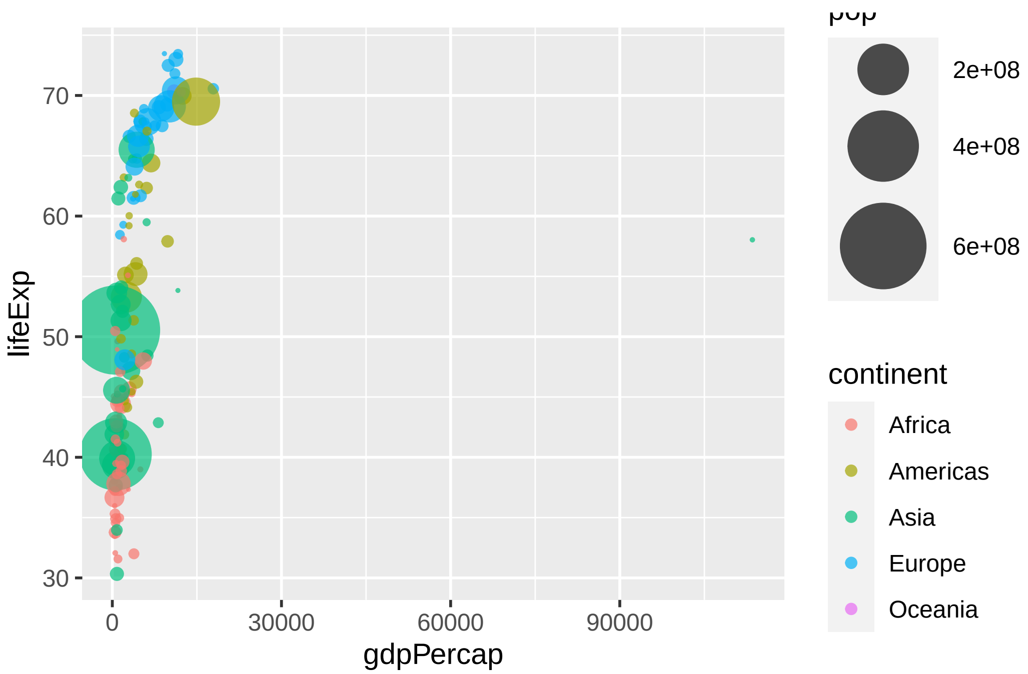


```
ggplot(gapminder_2007)+
  geom_point(aes(x=gdpPercap, y=lifeExp, size=pop), alpha=0.5) +
  scale_size_area(max_size=10)
```



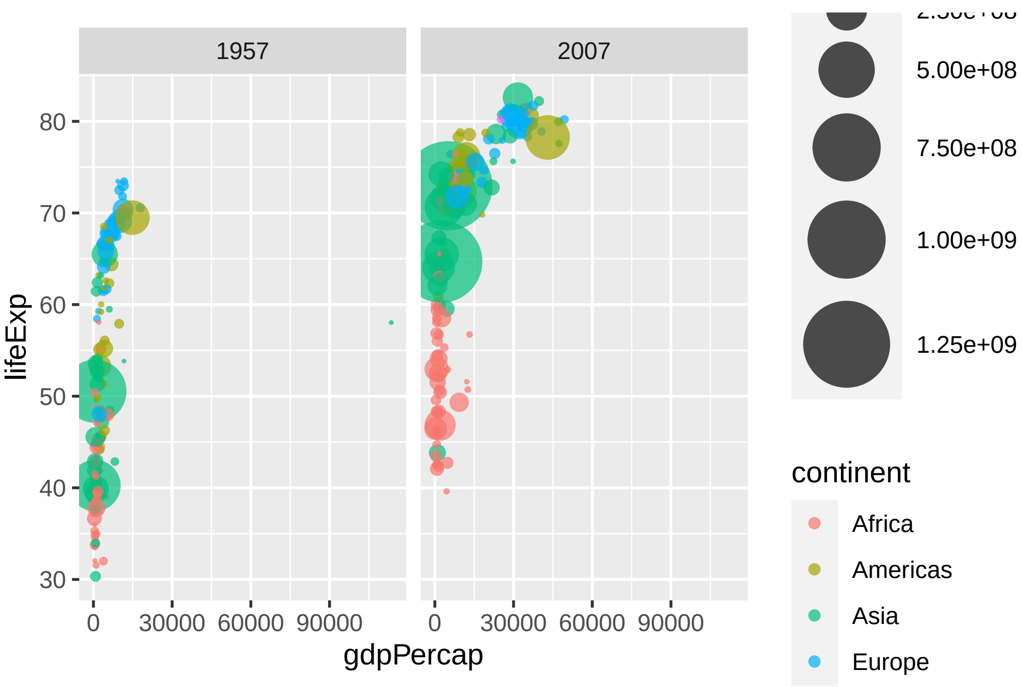
```
gapminder_1957 <- gapminder %>% filter(year==1957)
```

```
ggplot(gapminder_1957)+
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.7)+
  scale_size_area(max_size=15)
```



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

```
ggplot(gapminder_1957)+
  geom_point(aes(x=gdpPercap, y=lifeExp, color=continent, size=pop),alpha=0.7)+
  scale_size_area(max_size=15)+
  facet_wrap(~year)
```


1957
2007
lifeExp
80
70
60
50
40
30
0
30000
60000
90000
0
30000
60000
90000
gdpPercap
2.50e+08
5.00e+08
7.50e+08
1.00e+09
1.25e+09
continent
Africa
Americas
Asia
Europe