class05.R

belia

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```
# Week5 Data Visualization
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#Creating ScatterPlots
library(ggplot2)
ggplot(cars)
```
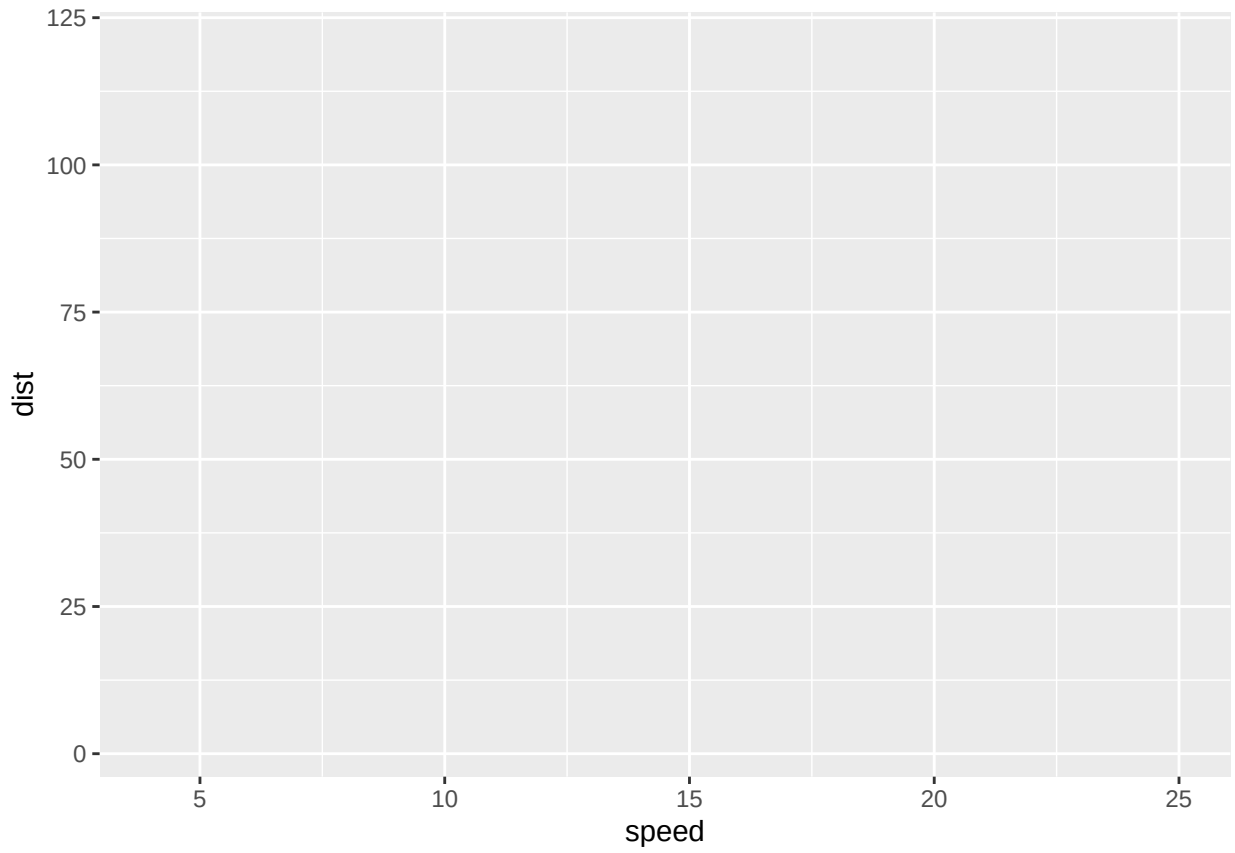
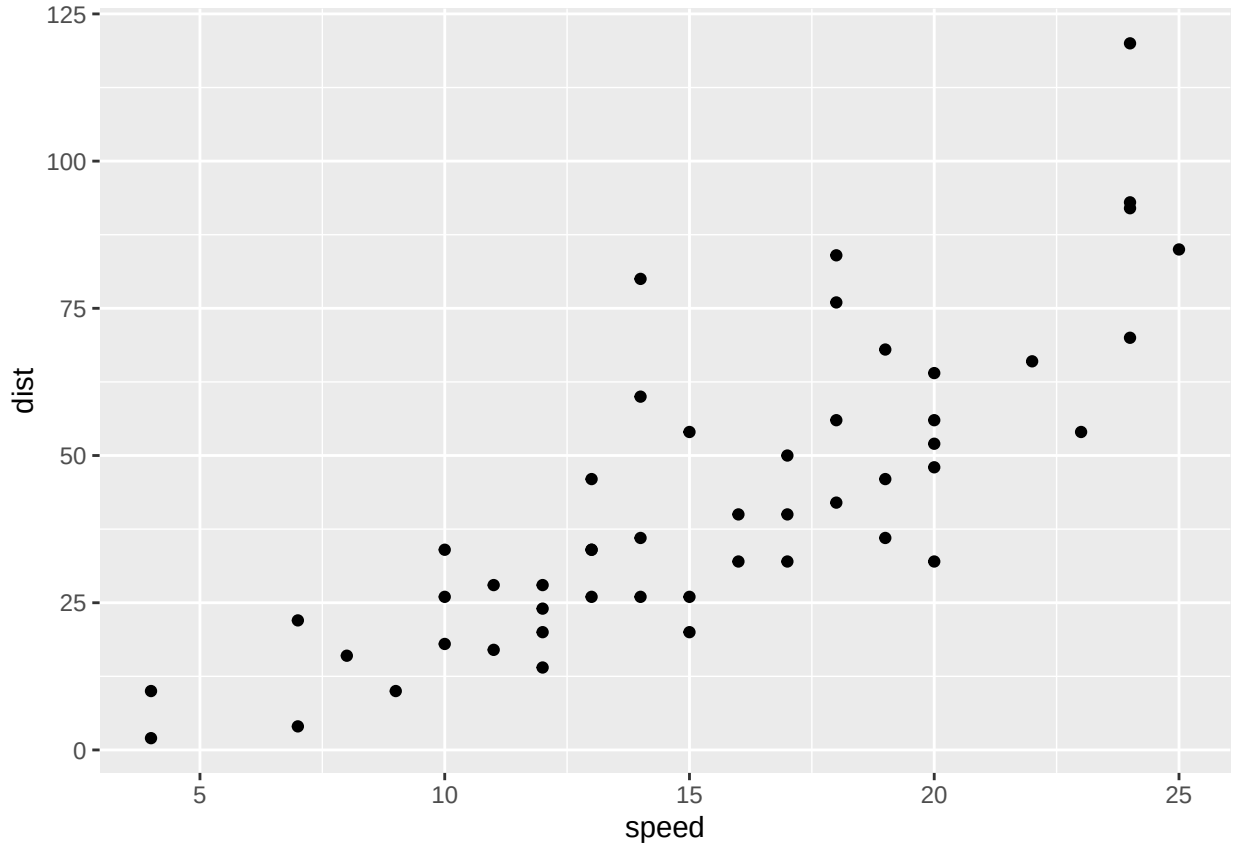

```
ggplot(cars) + aes(x=speed,y=dist)
```

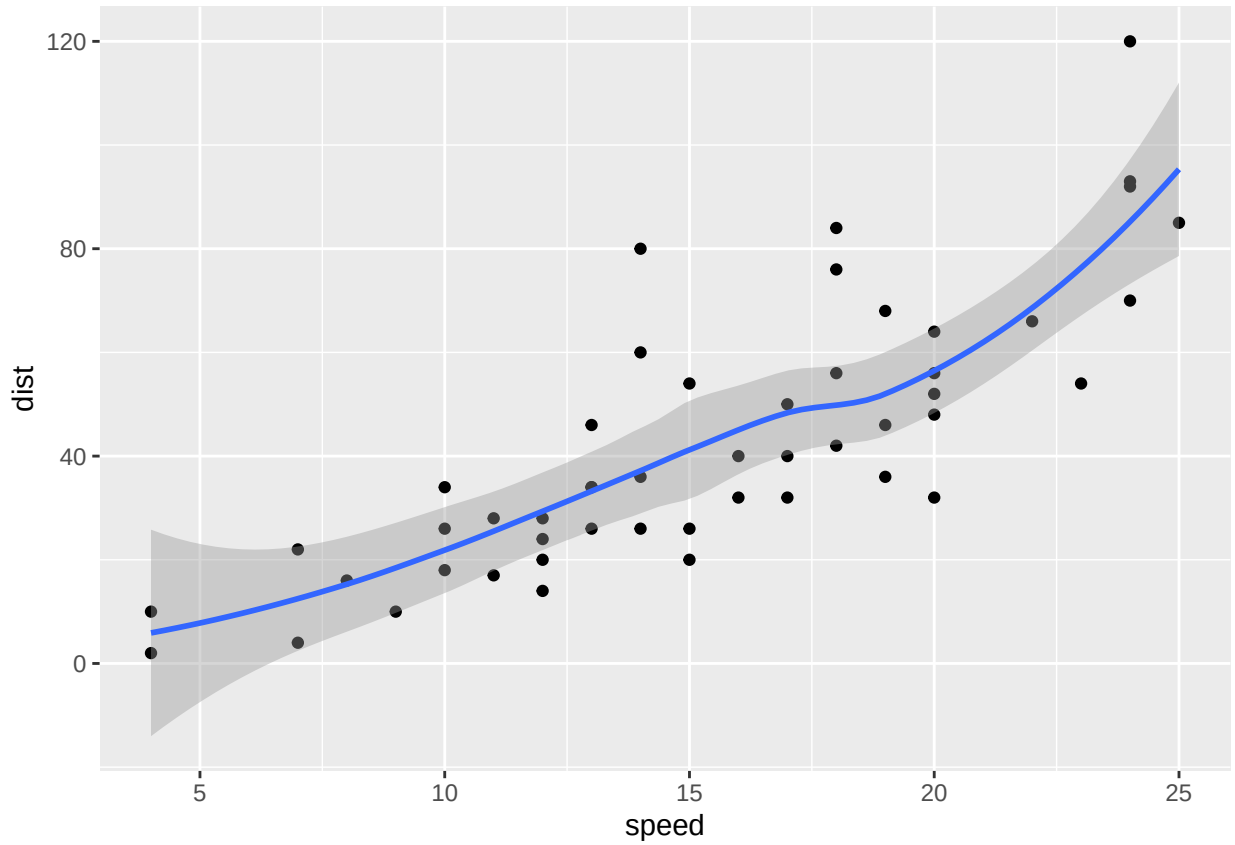



```
ggplot(cars) + aes(x=speed,y=dist) + geom_point()
```



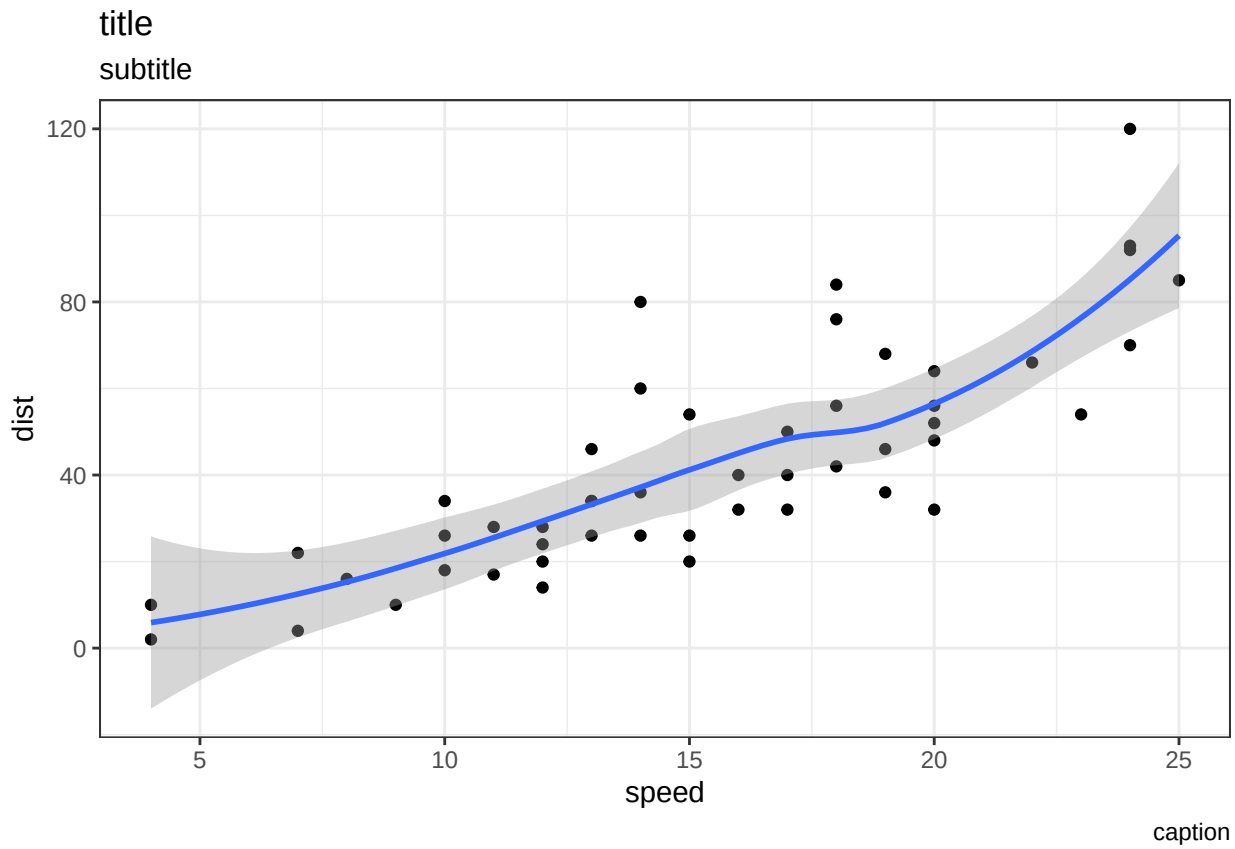

```
ggplot(cars) + aes(x=speed,y=dist) + geom_point() +geom_smooth()
```

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




```
ggplot(cars) + aes(x=speed,y=dist) + geom_point() +geom_smooth() + theme_bw() + labs(title = "title", ca
```

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




```
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
```

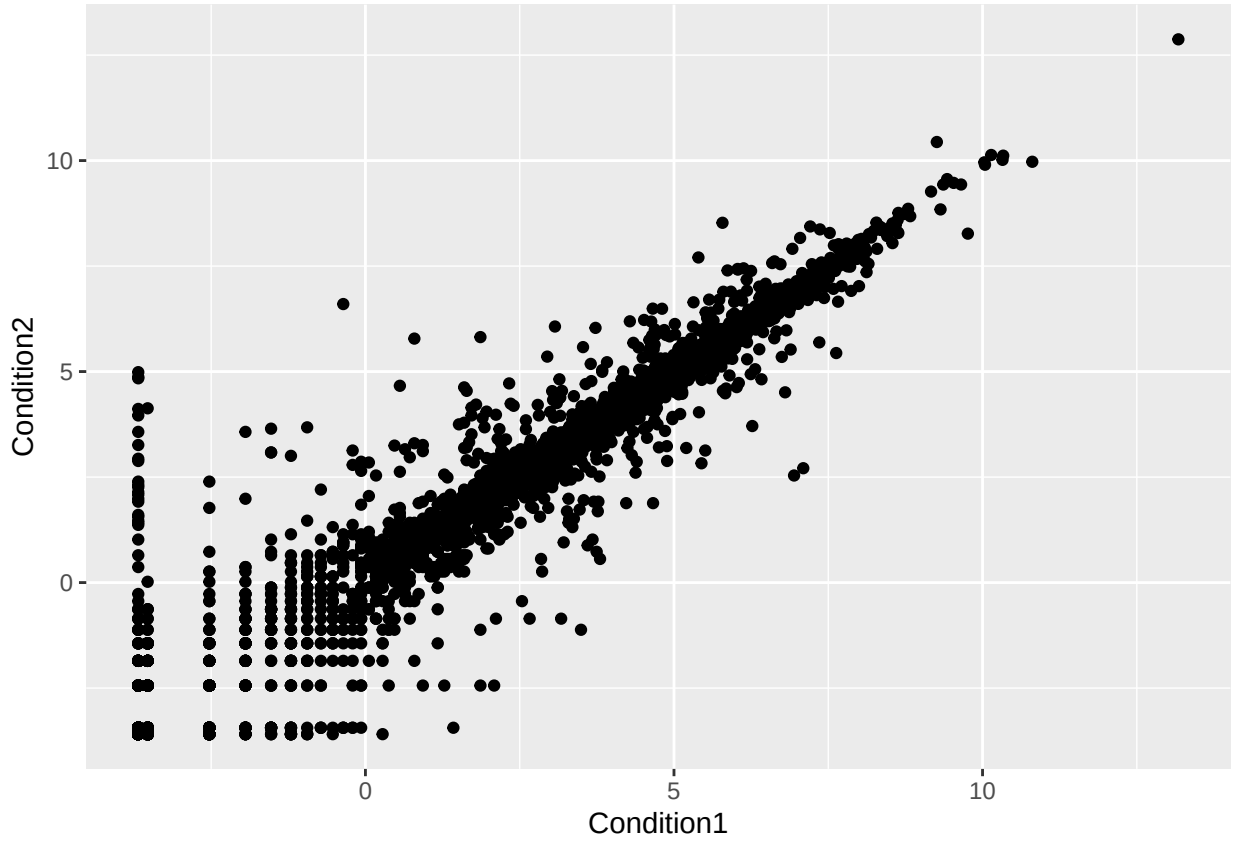
```
round(table(genes$State)/nrow(genes) *100,2)
```

```
##
##       down unchanging         up
##       1.39      96.17       2.44
```

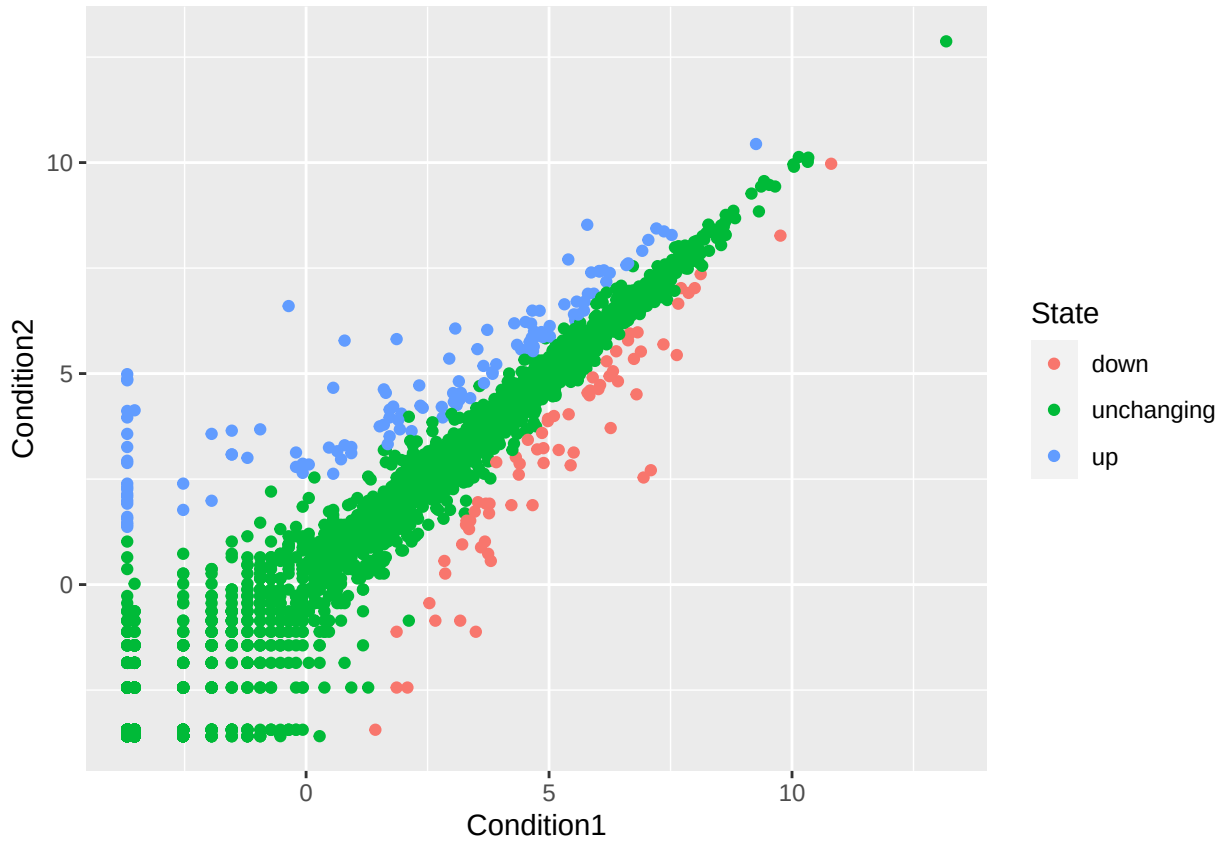
```
ggplot(genes)
```



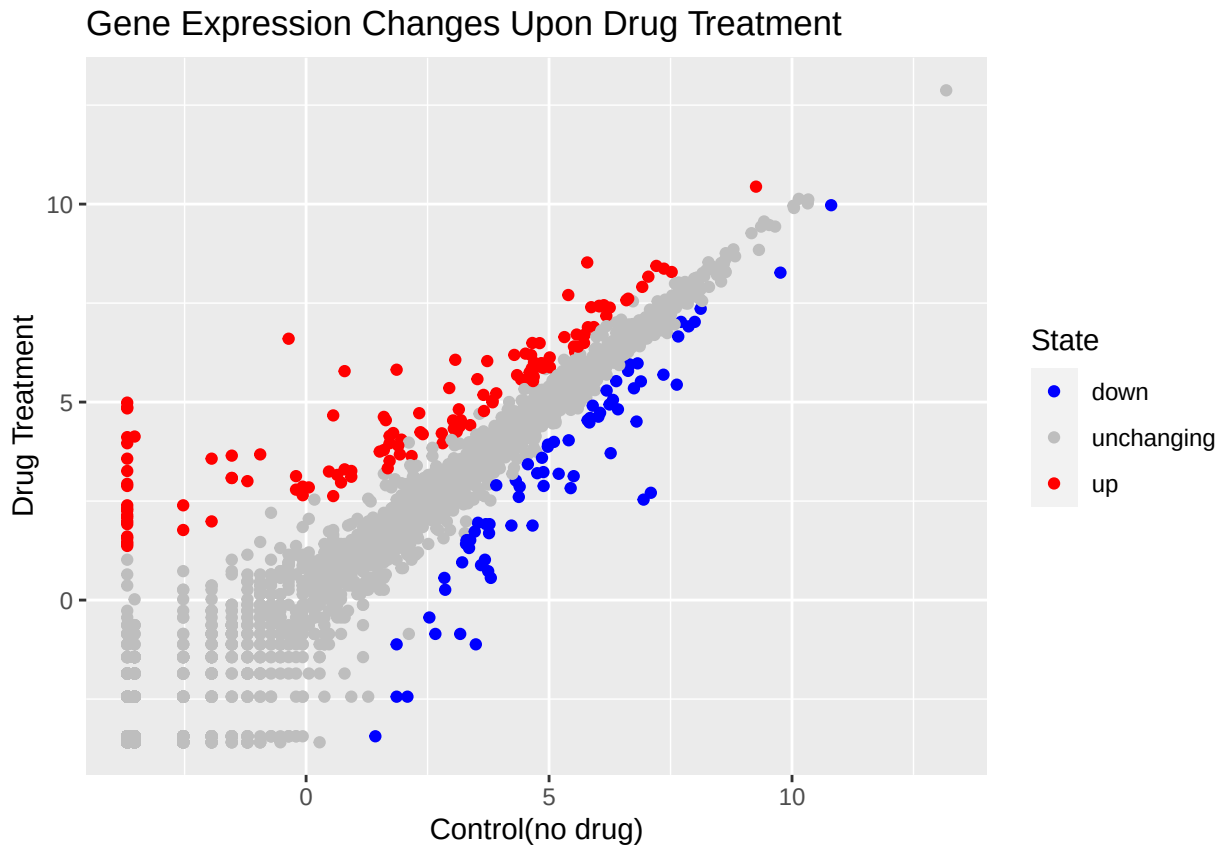
```
ggplot(genes) + aes(x=Condition1, y=Condition2) +geom_point()
```




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



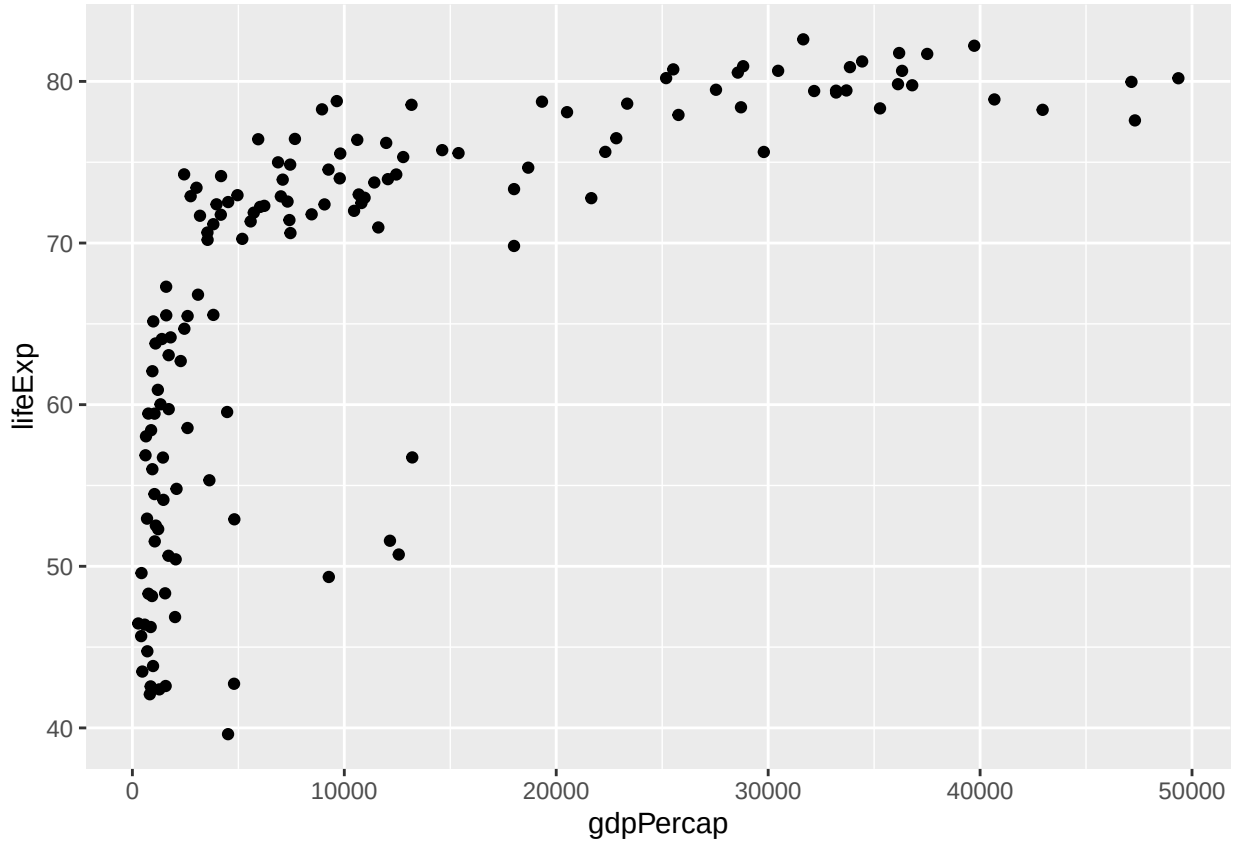

```
p <- ggplot(genes) + aes(x=Condition1, y=Condition2, col= State) +geom_point()
q <- p + scale_colour_manual(values=c("blue","gray", "red"))
q + labs(title = "Gene Expression Changes Upon Drug Treatment",x="Control(no drug)", y= "Drug Treatment
```



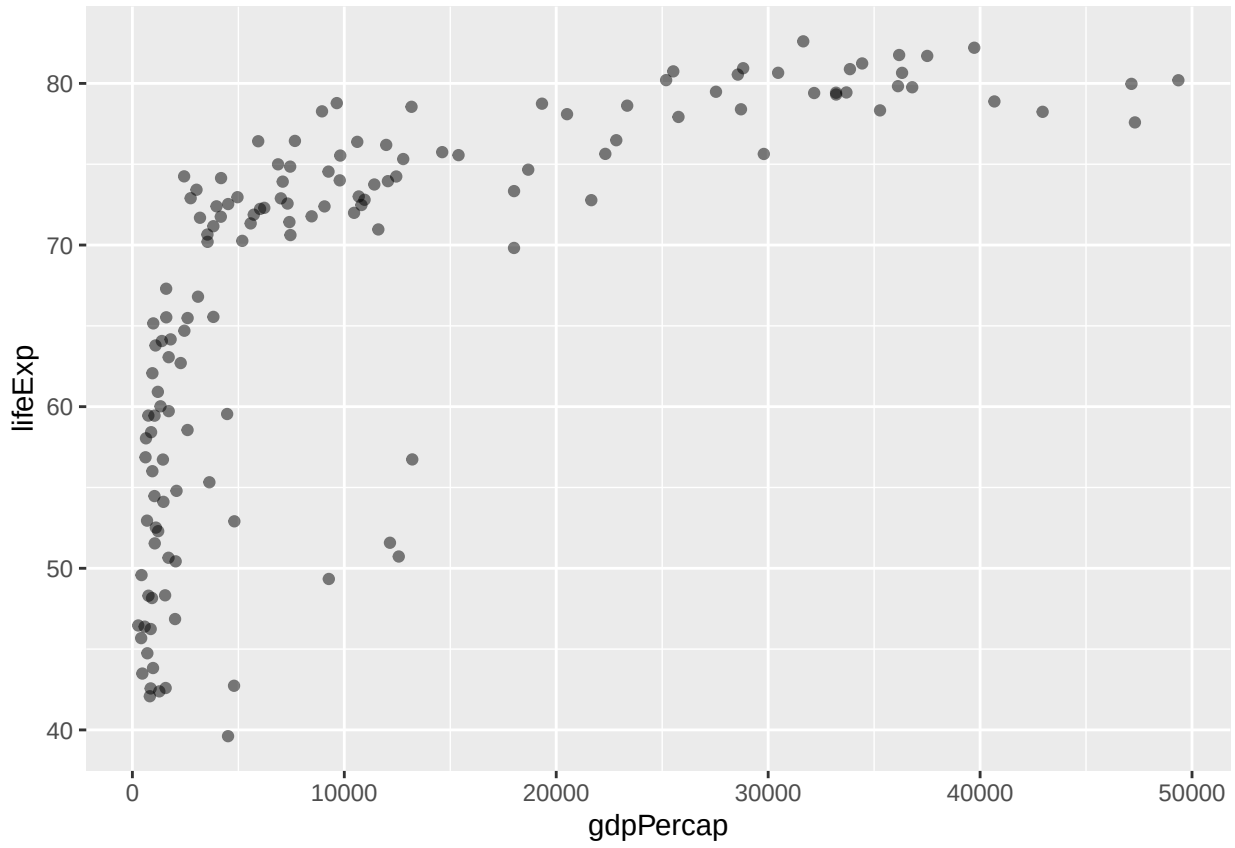

```
#6 Optional/Going Further
library(gapminder)
library(dplyr)
```

```
##
## 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
```

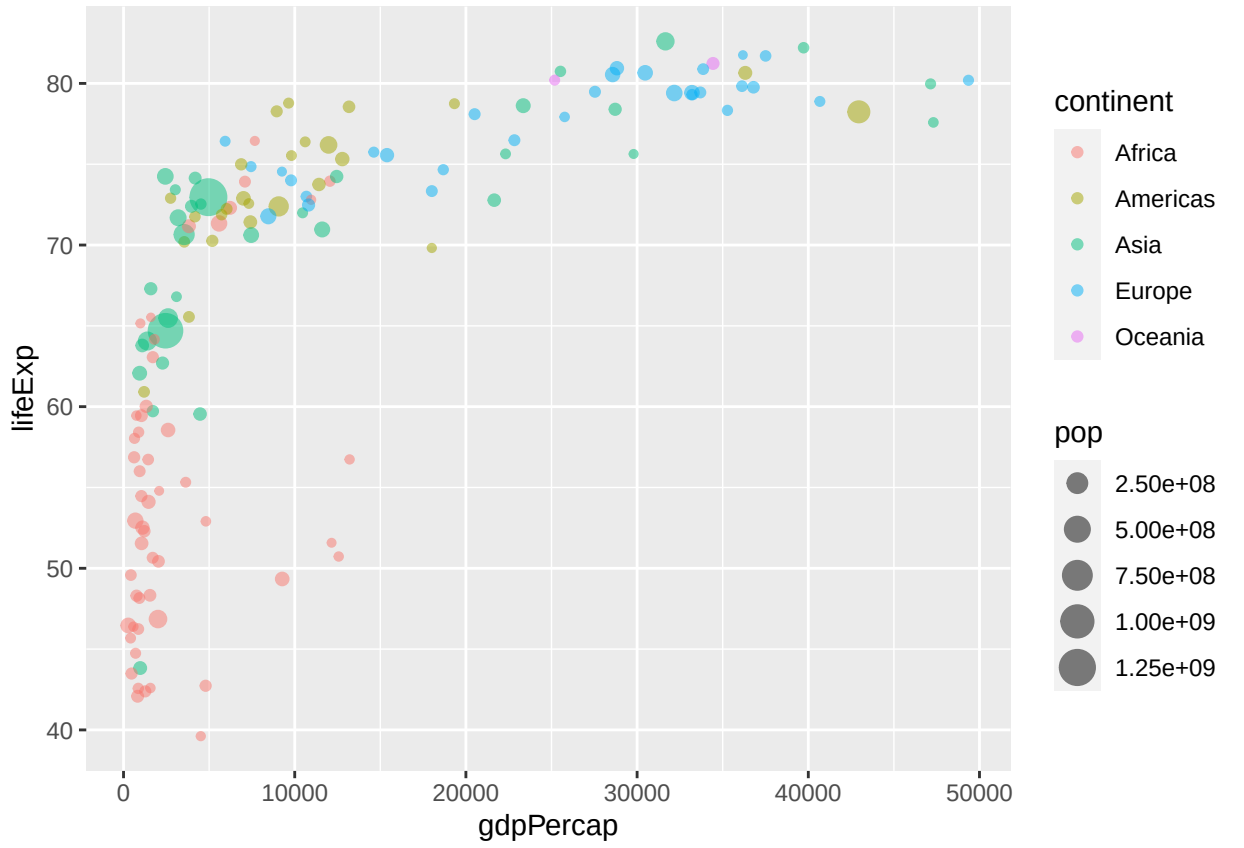
```
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) + aes(x=gdpPercap, y= lifeExp) + geom_point()
```



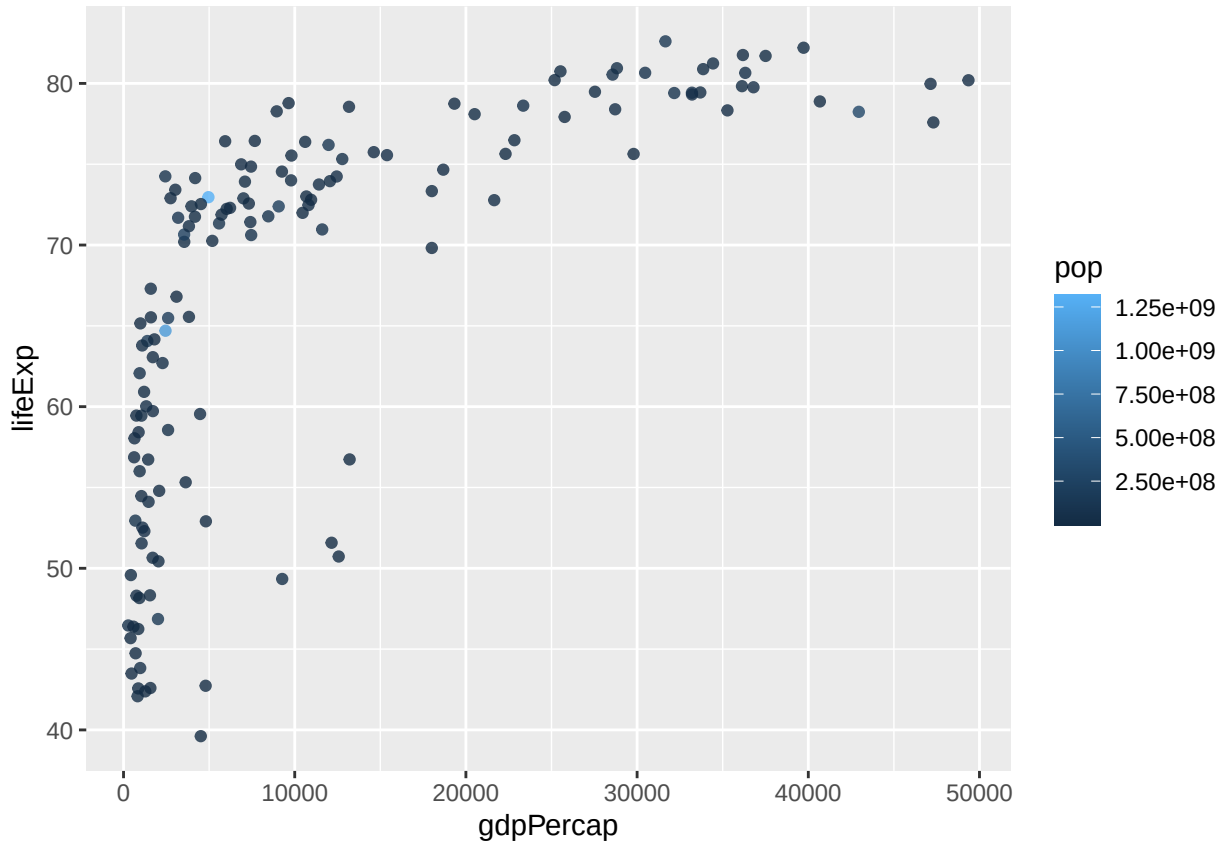

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y= lifeExp) + geom_point(alpha=0.5)
```



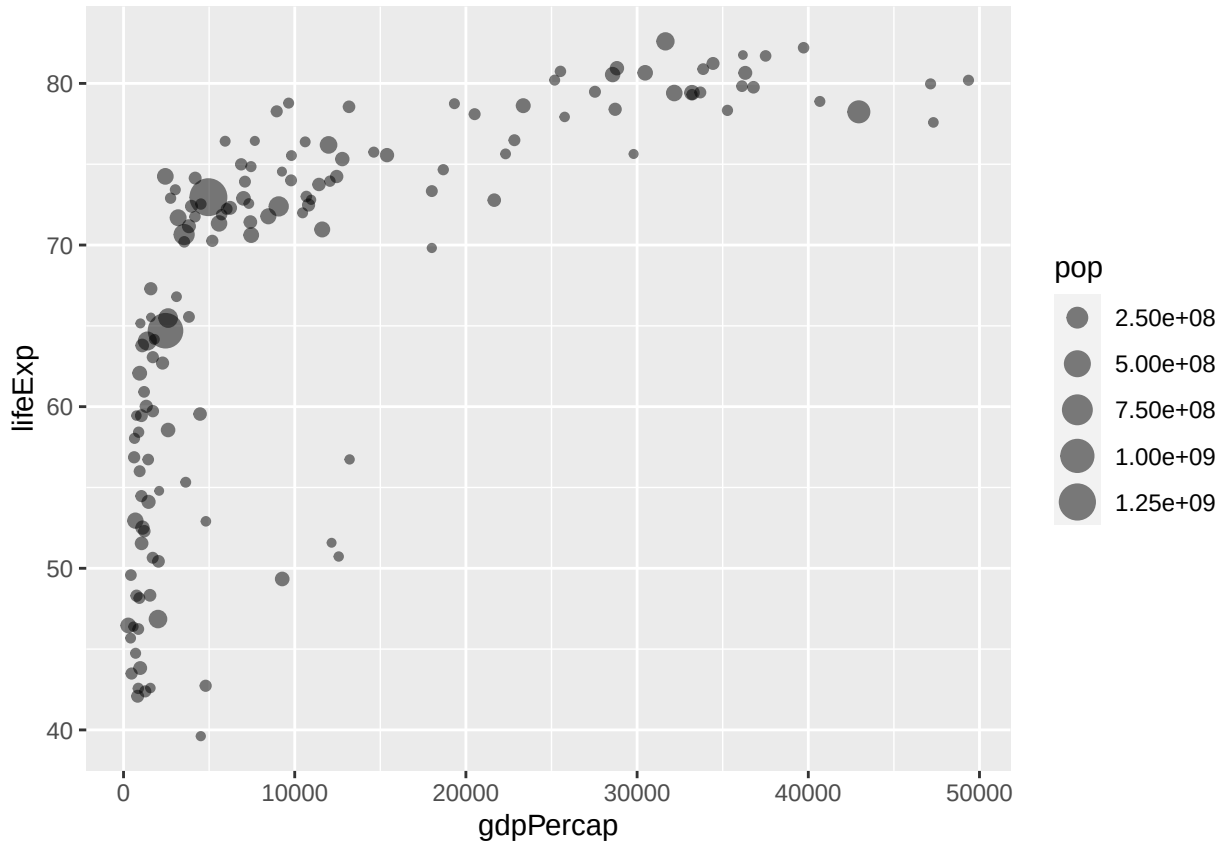

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y= lifeExp, color=continent, size=pop) + geom_point(alpha=0.5)
```



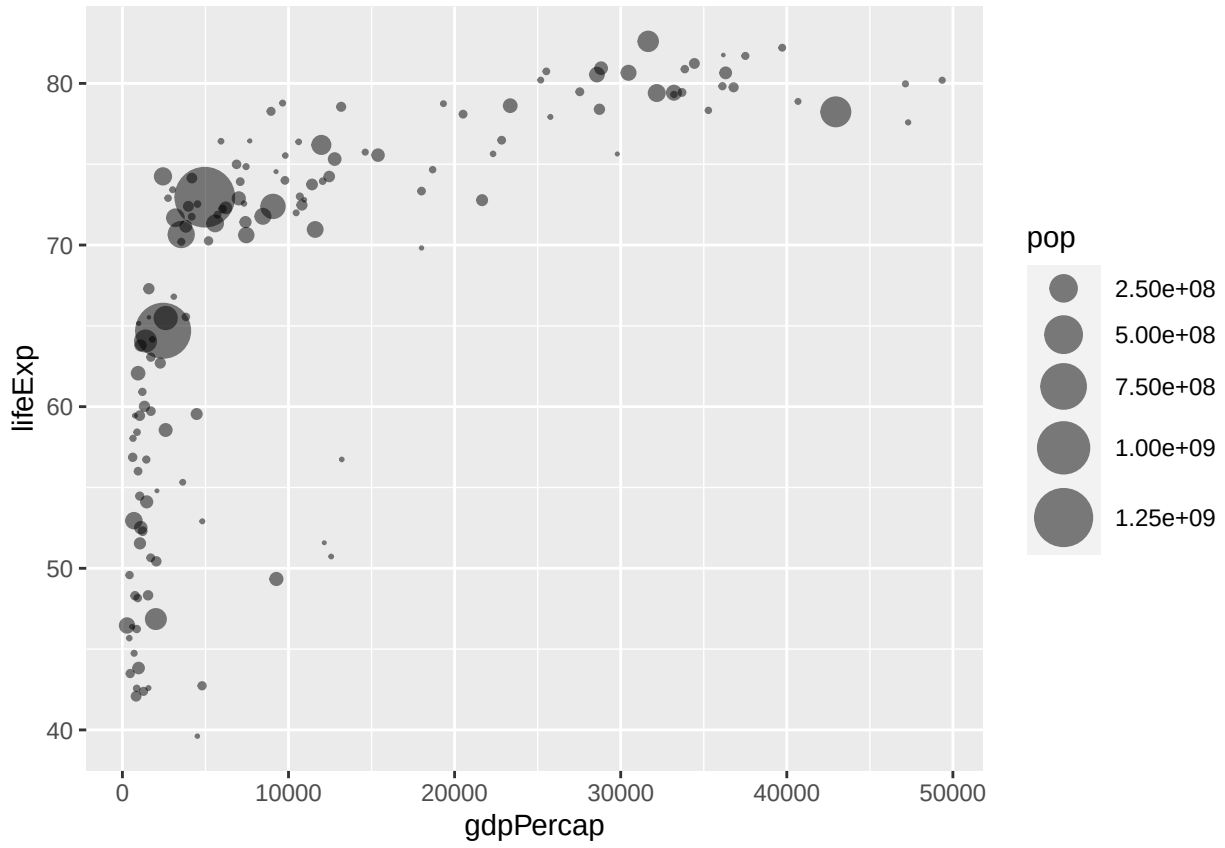

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y= lifeExp, color=pop) + geom_point(alpha=0.8)
```



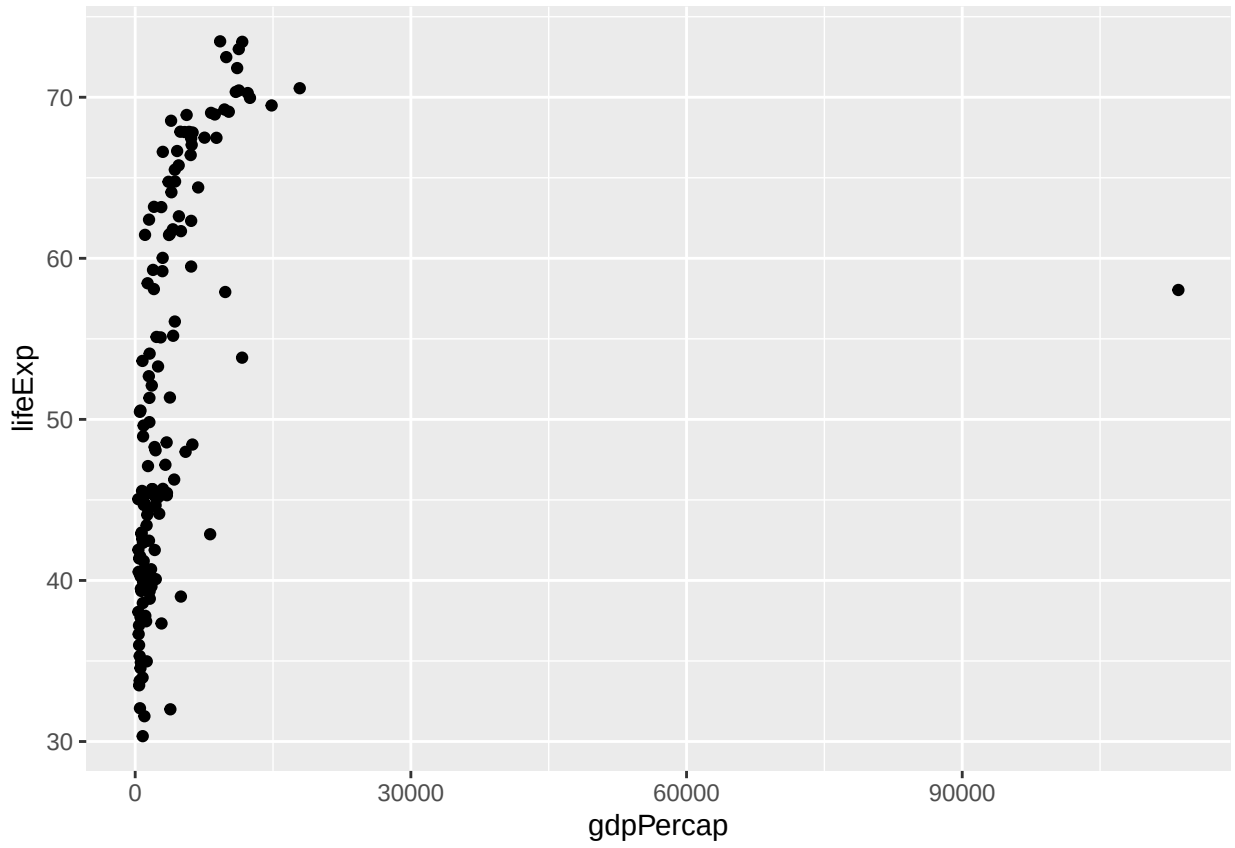

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y= lifeExp, size=pop) + geom_point(alpha=0.5)
```



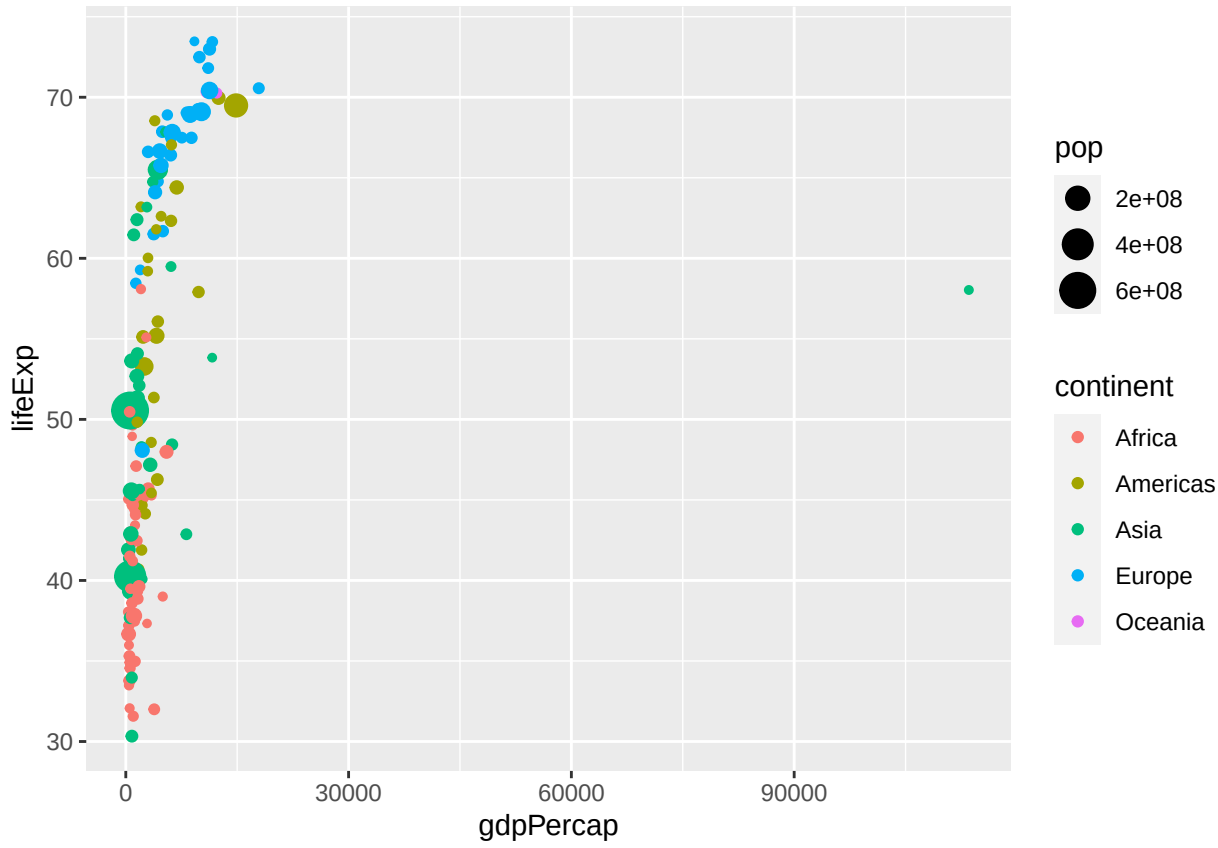

```
ggplot(gapminder_2007) + aes(x=gdpPercap, y= lifeExp, size=pop) + geom_point(alpha=0.5) + scale_size_ar
```



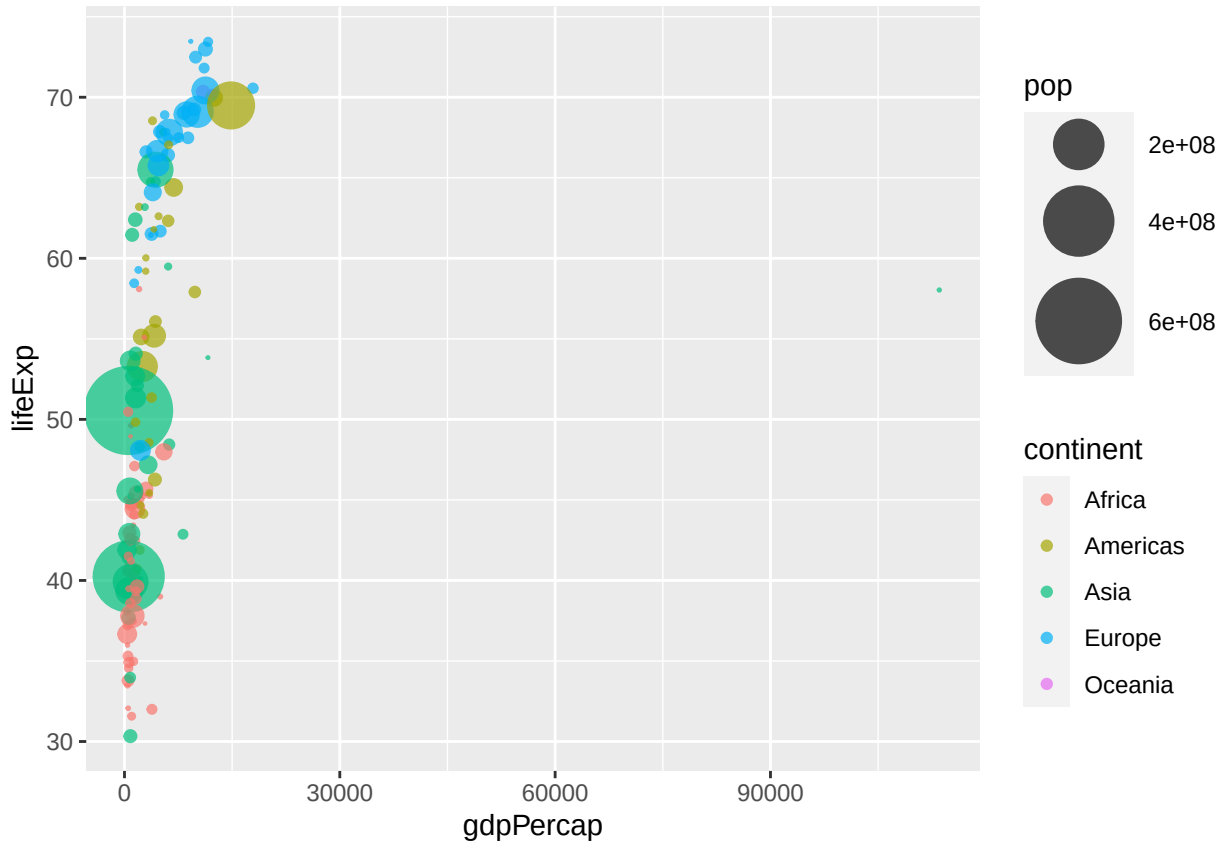

```
gapminder_1957 <- gapminder %>% filter(year==1957)
ggplot(gapminder_1957)+ aes(x=gdpPercap, y=lifeExp) + geom_point()
```




```
ggplot(gapminder_1957)+ aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) + geom_point()
```




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




```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)
ggplot(gapminder_1957)+ aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) + geom_point(alpha=0.7) +
```

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