class05: Data Visualization with GGPLOT

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Quarto

Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see https://quarto.org.

Running Code

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:
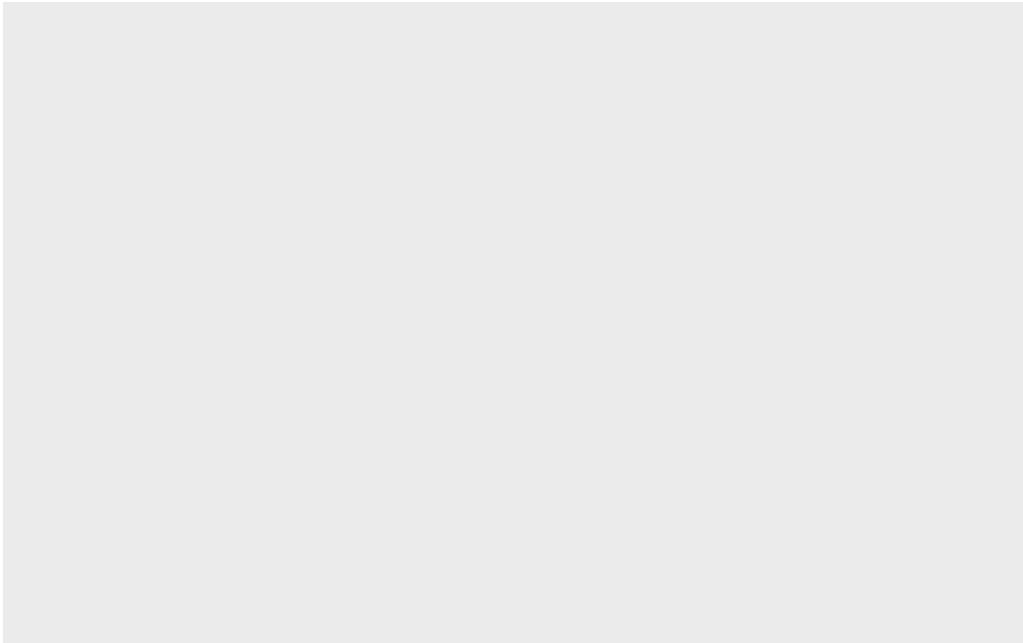
```
1 + 1
```

```
[1] 2
```

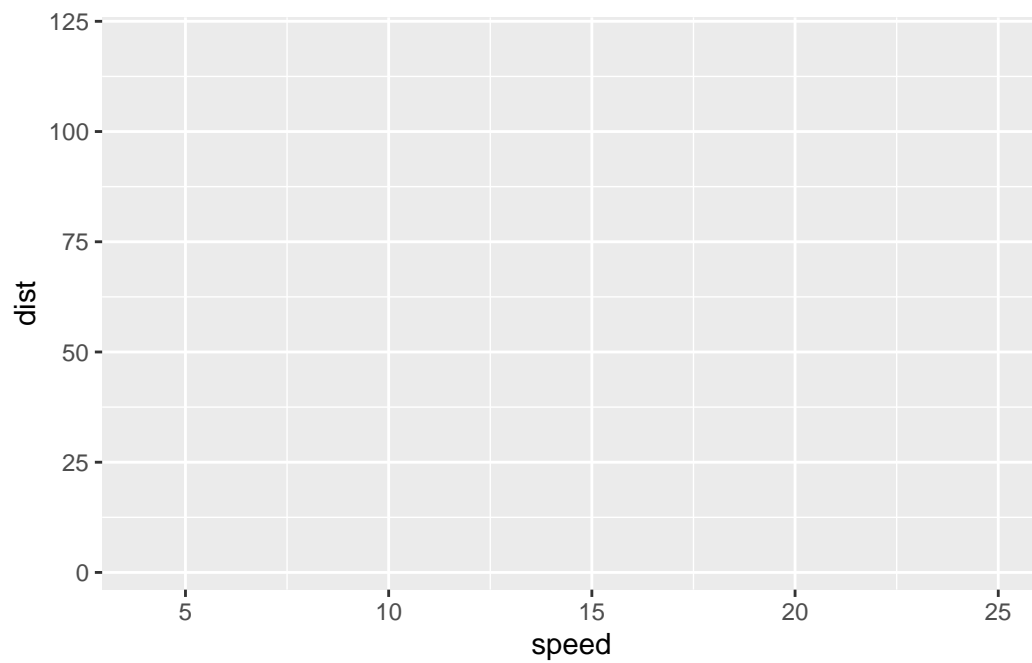You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).
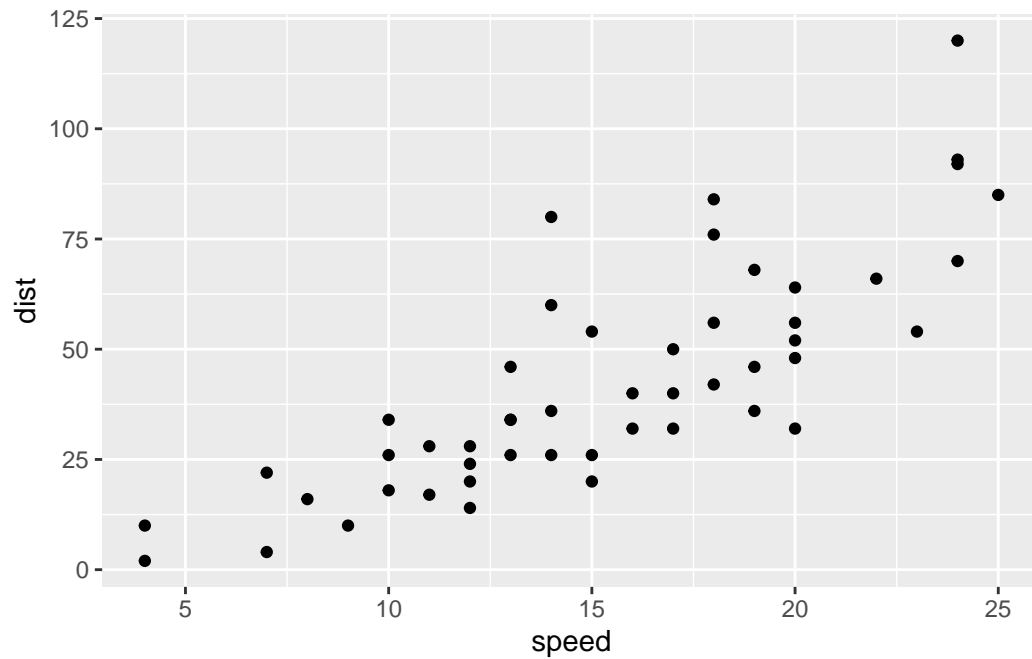
```
library(ggplot2)
ggplot(cars)
```

```
library(ggplot2)

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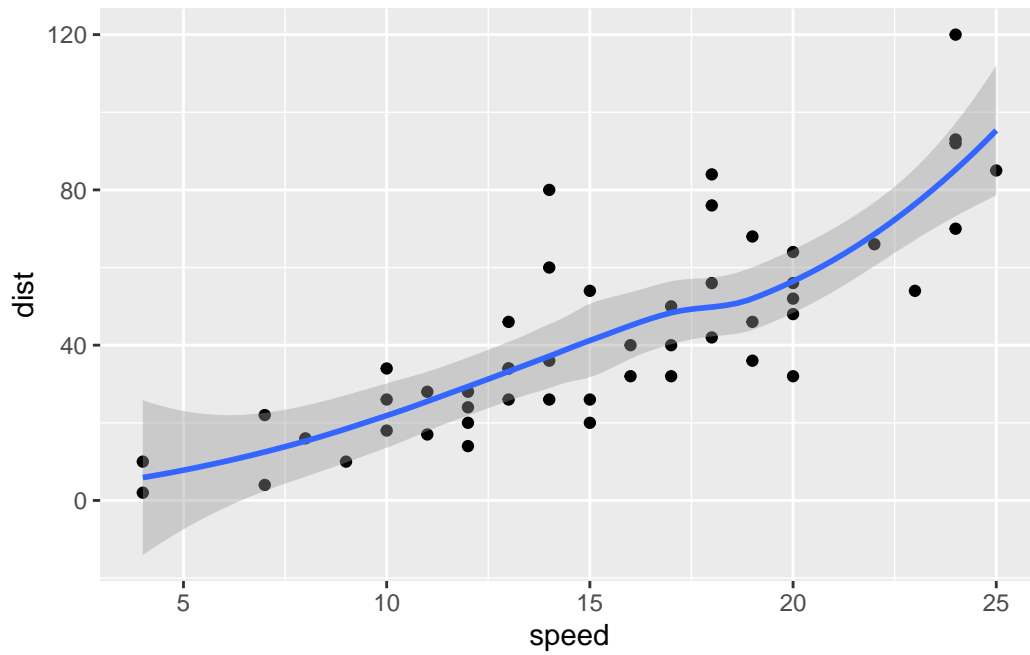
```
library(ggplot2)

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



```
library(ggplot2)

ggplot(cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth()
```
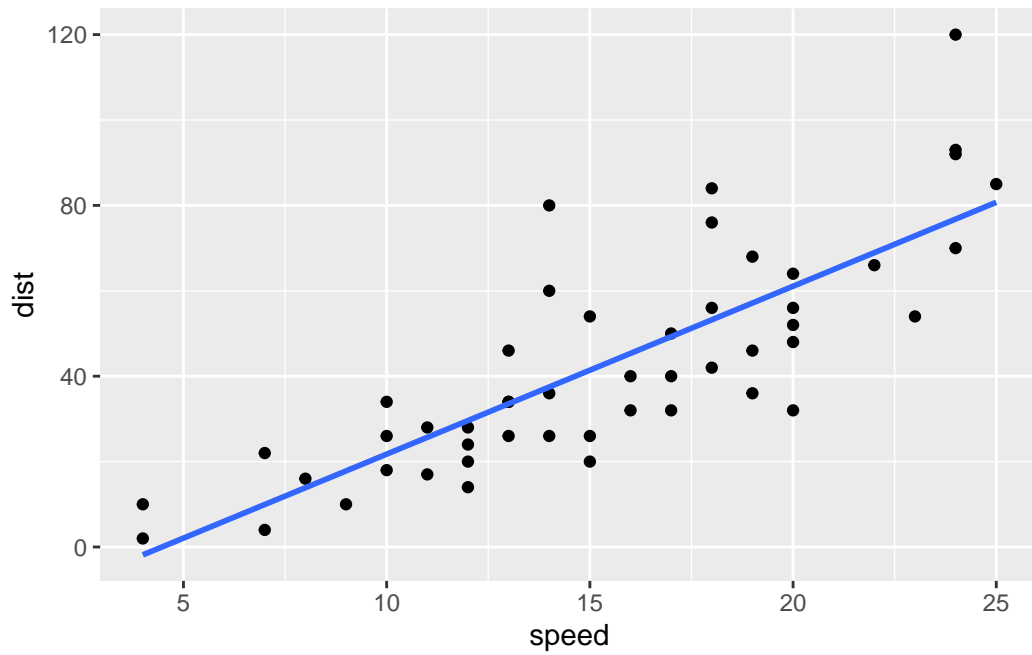
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'

```
library(ggplot2)

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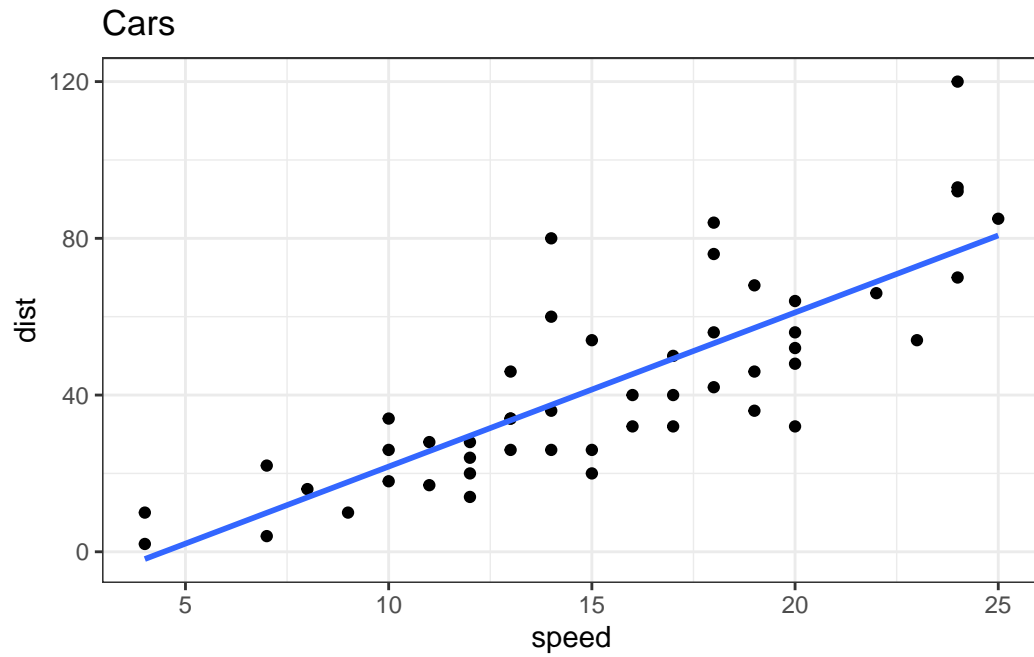
`geom_smooth()` using formula = 'y ~ x'

```
library(ggplot2)

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

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

Cars

```
library(ggplot2)

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

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

Speed and Stopping Distances of Cars
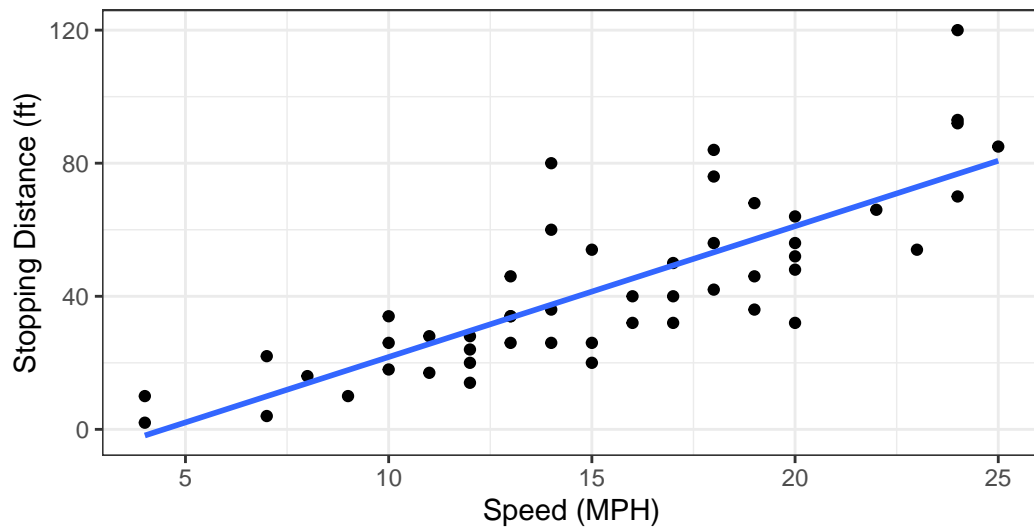Your informative subtitle text here

Dataset: '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[,2])
```

NULL

NULL

NULL

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

```
[1] "Gene"       "Condition1" "Condition2" "State"
```
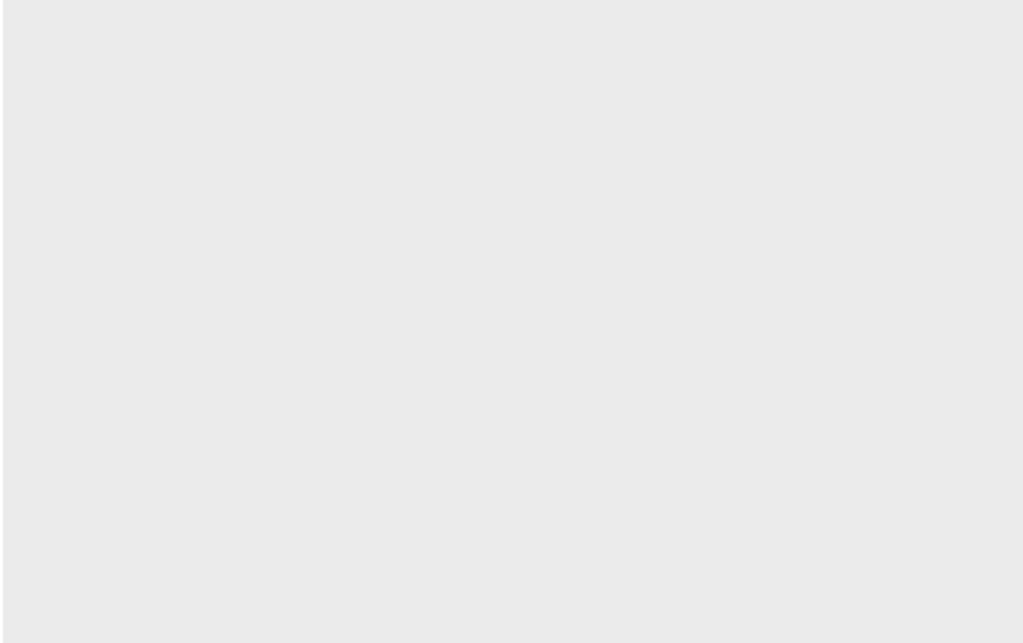
```
ncol(genes)
```

```
[1] 4
```

```
table(genes[,4])
```

```
      down unchanging         up
        72       4997        127
```
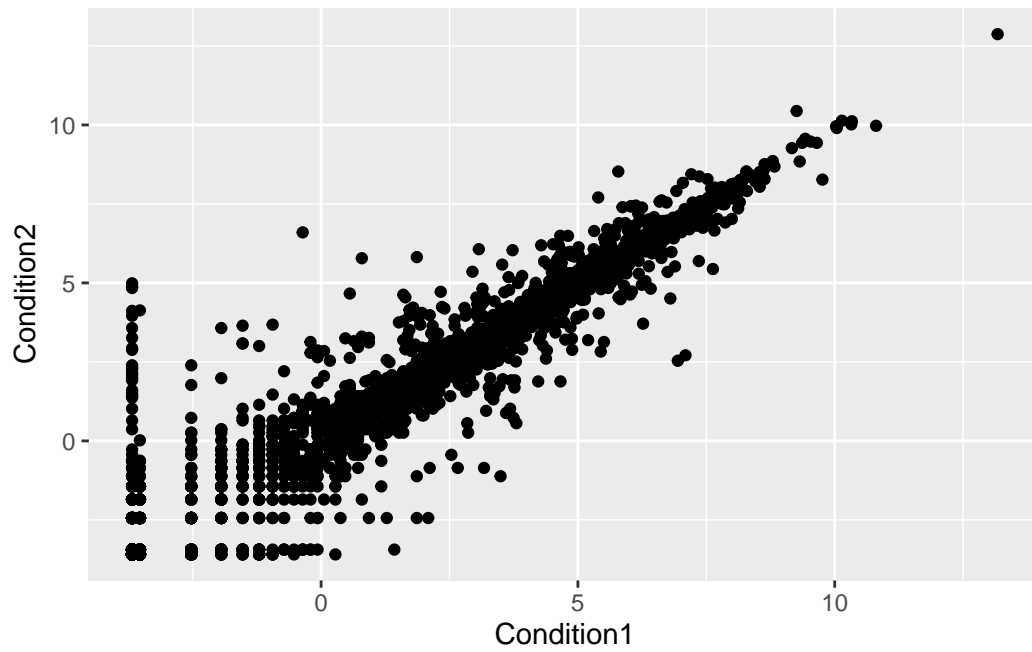
```
round(table(genes$State)/nrow(genes) * 100, 2)
```

```
      down unchanging         up
      1.39      96.17       2.44
```
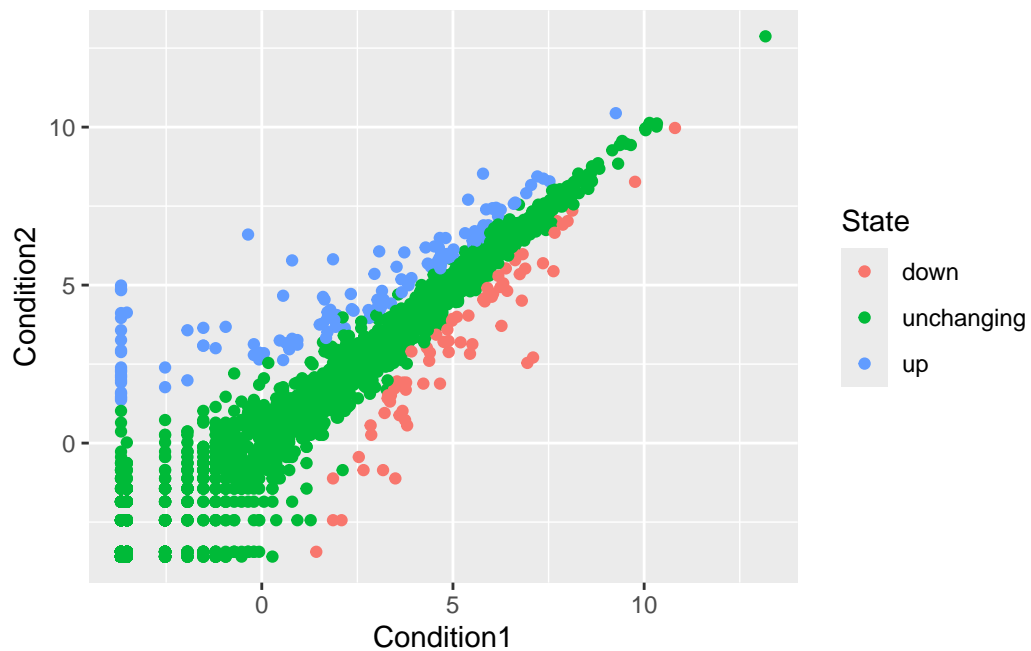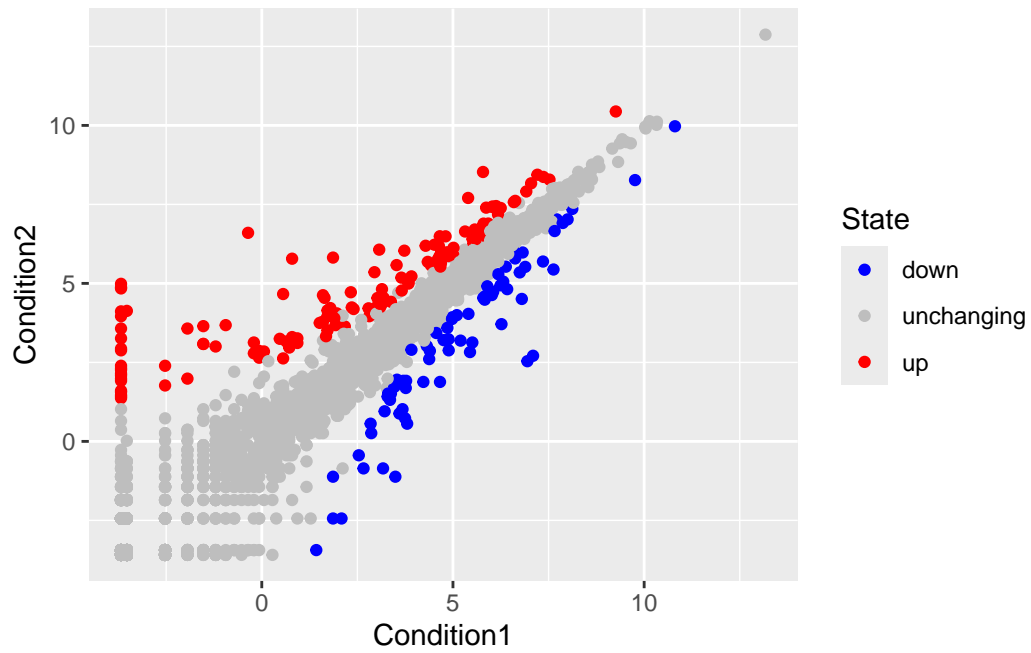
```
ggplot(genes)
```

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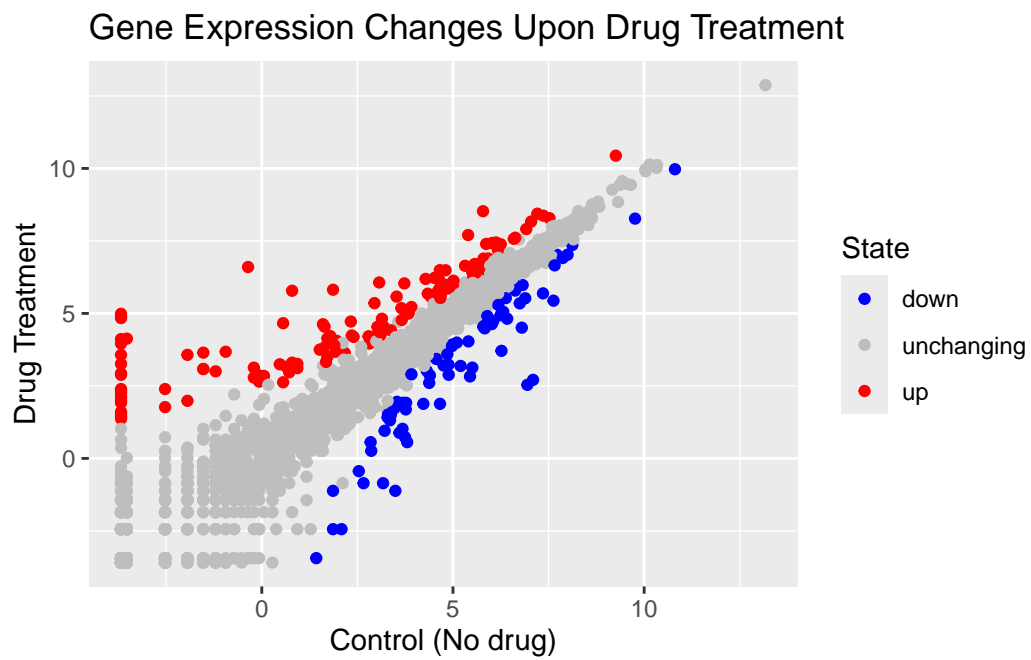

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```
ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
```



```
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(title="Gene Expression Changes
```

Gene Expression Changes Upon Drug Treatment

```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts
gapminder <- read.delim(url)

library(dplyr)
```

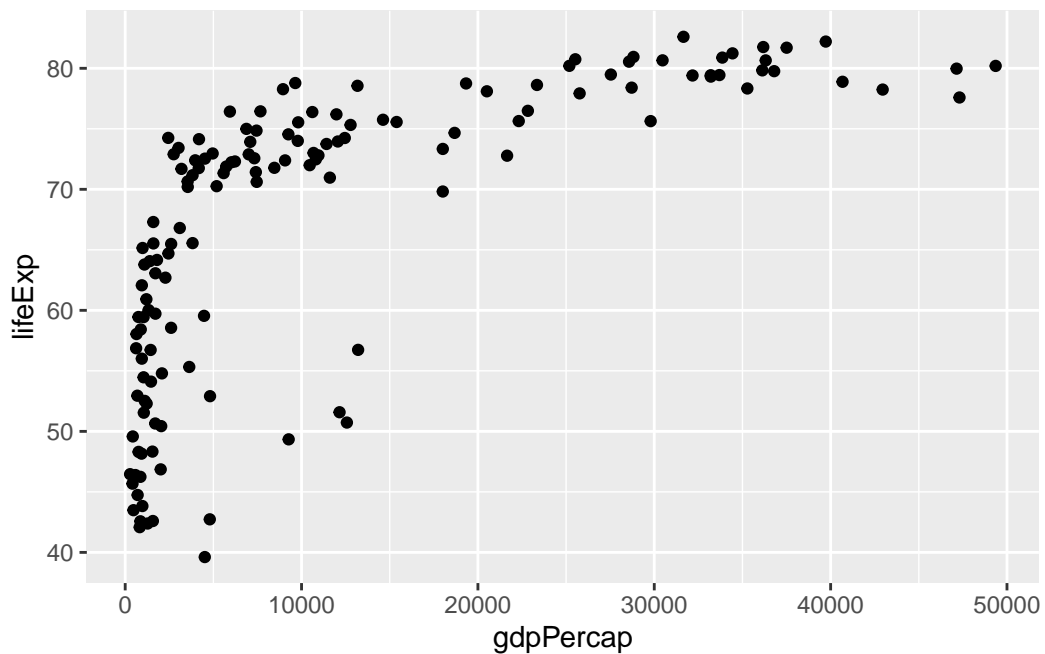```
Attaching package: 'dplyr'

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

    filter, lag

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

    intersect, setdiff, setequal, union
```
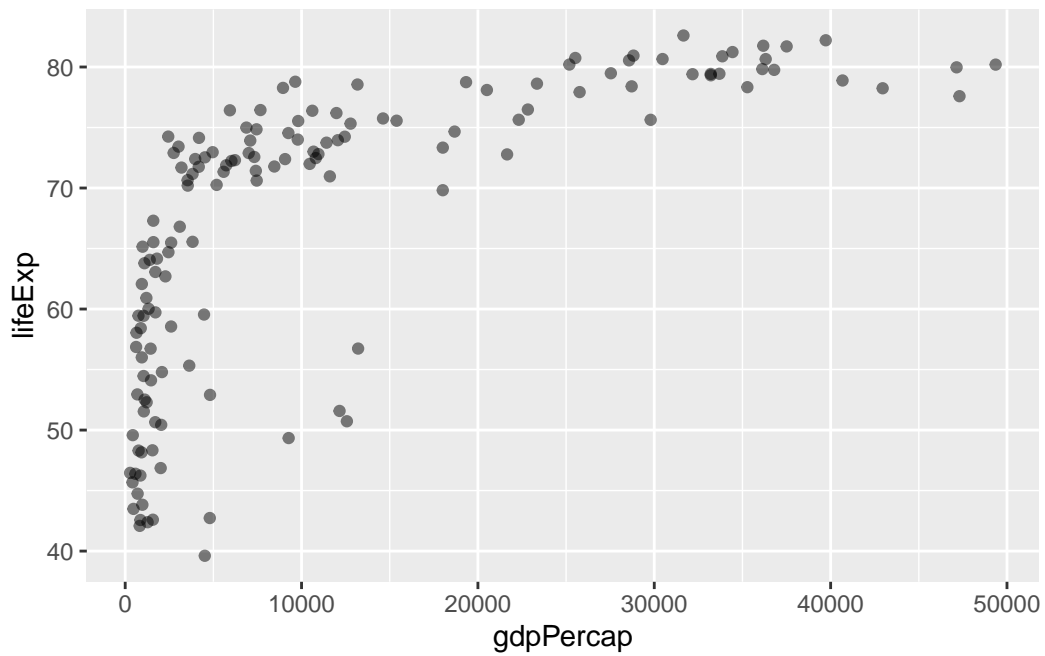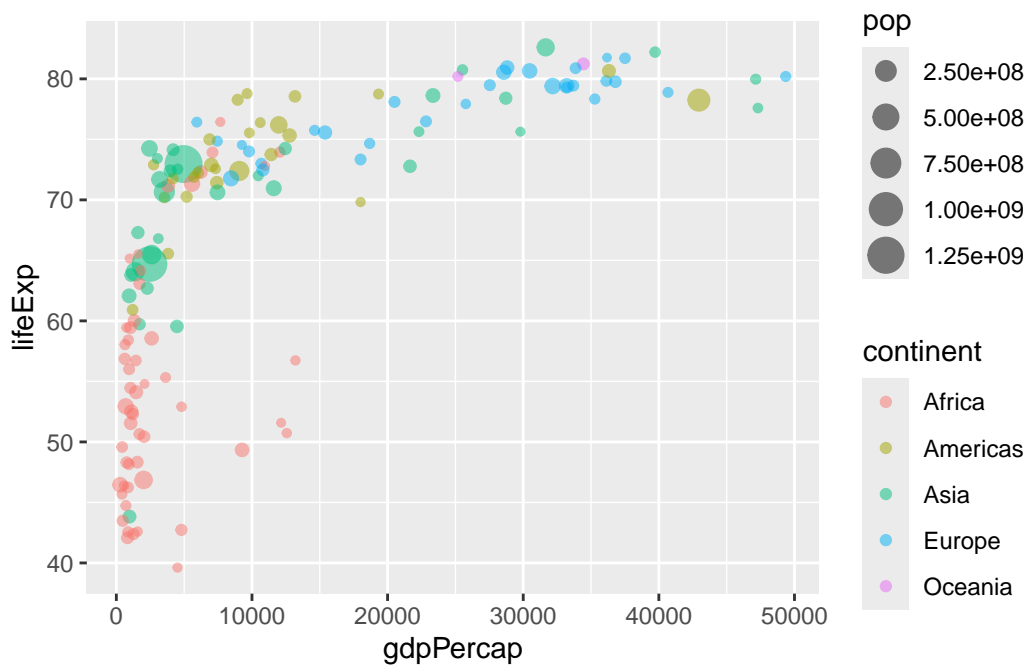
```
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp) + geom_point()
```
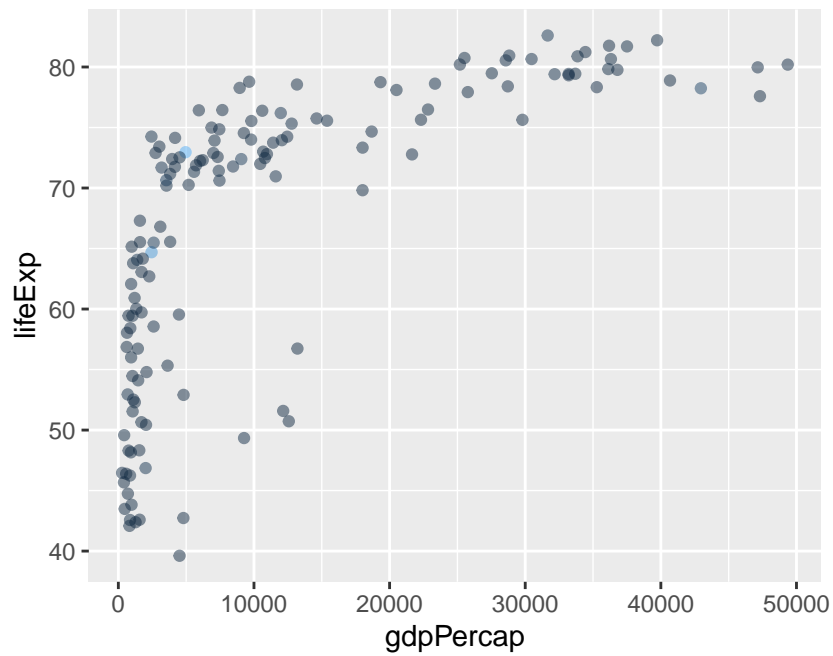
```
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp) + geom_point(alpha=0.5)
```
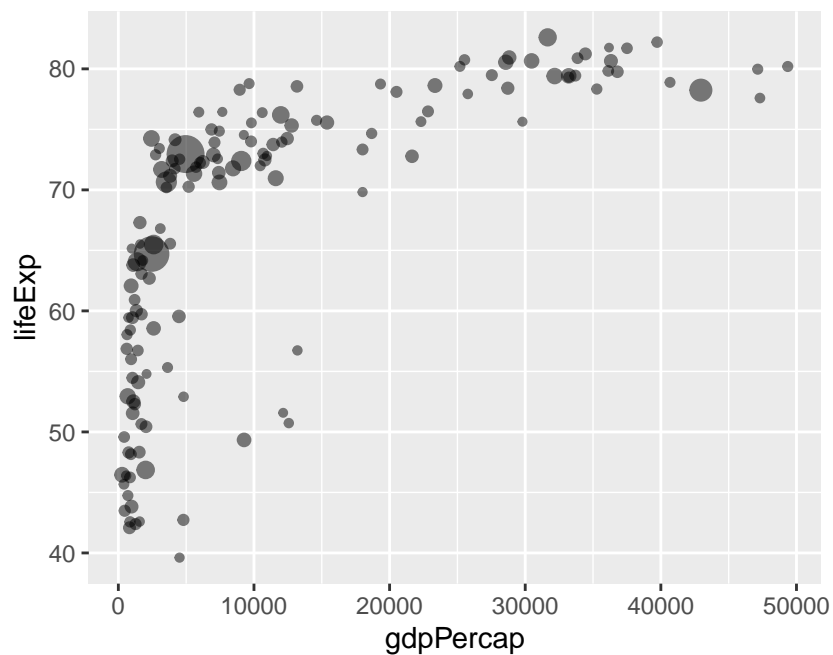


```
ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) + geom_point
```
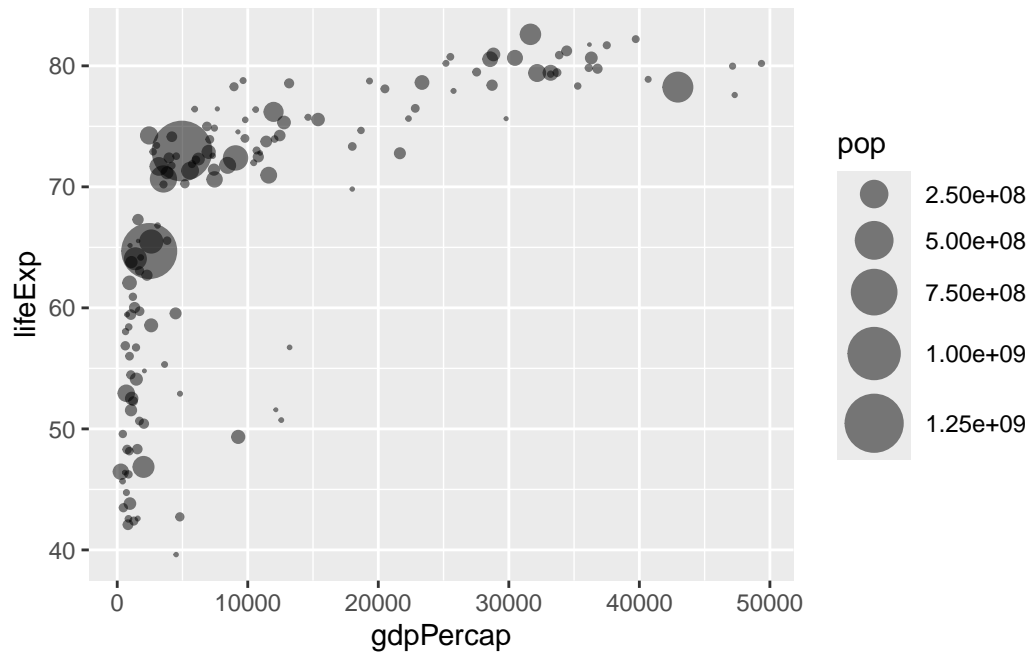
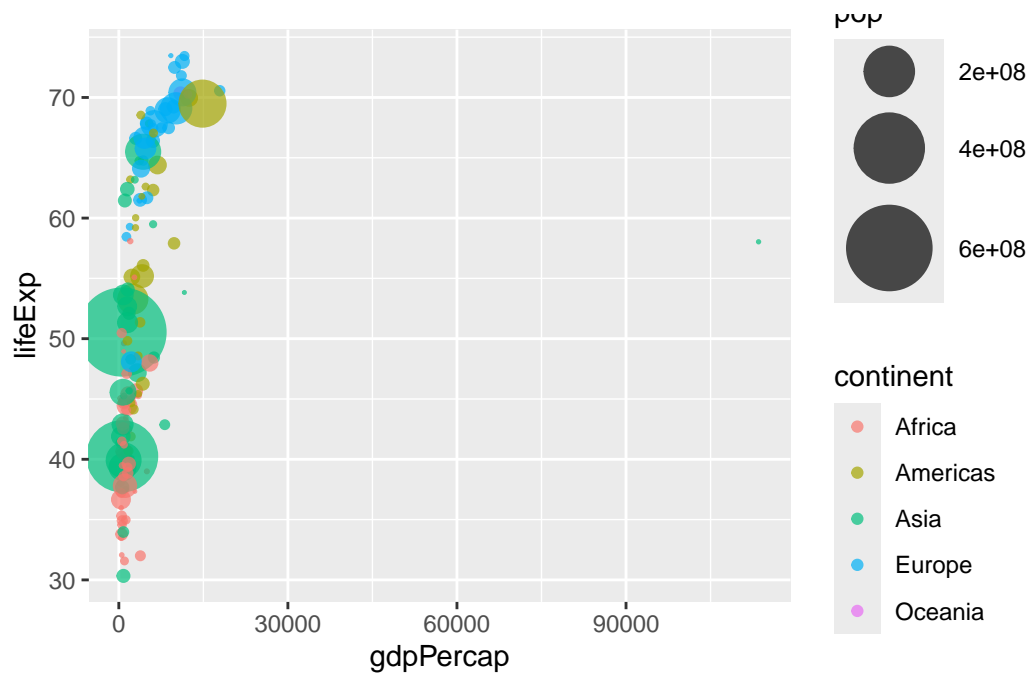`ggplot(gapminder_2007) + aes(x=gdpPercap, y=lifeExp, color=pop) + geom_point(alpha=0.5)`



`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) + scal
```



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


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