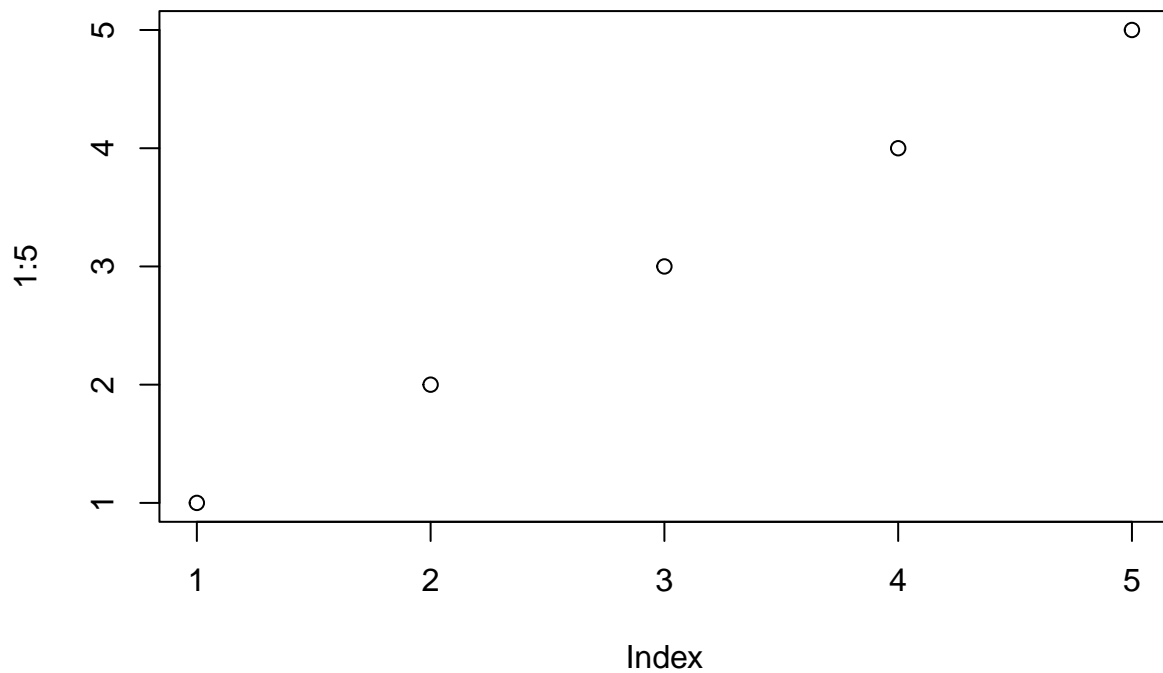


# class05.R

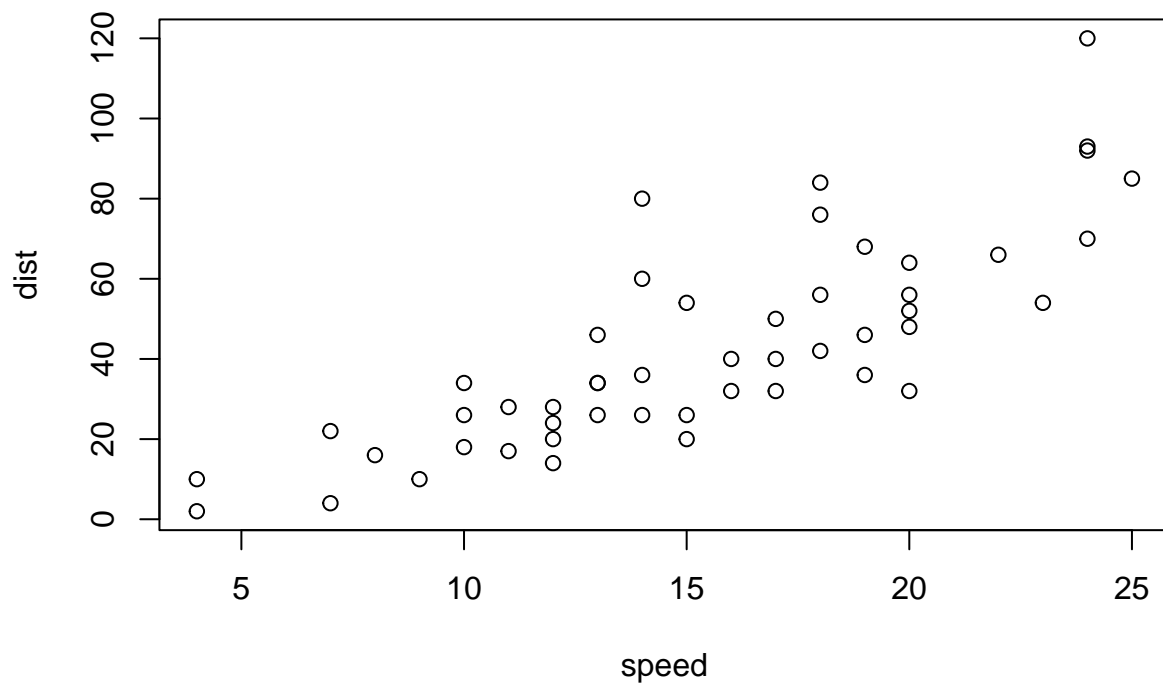
Michelle

2022-02-02

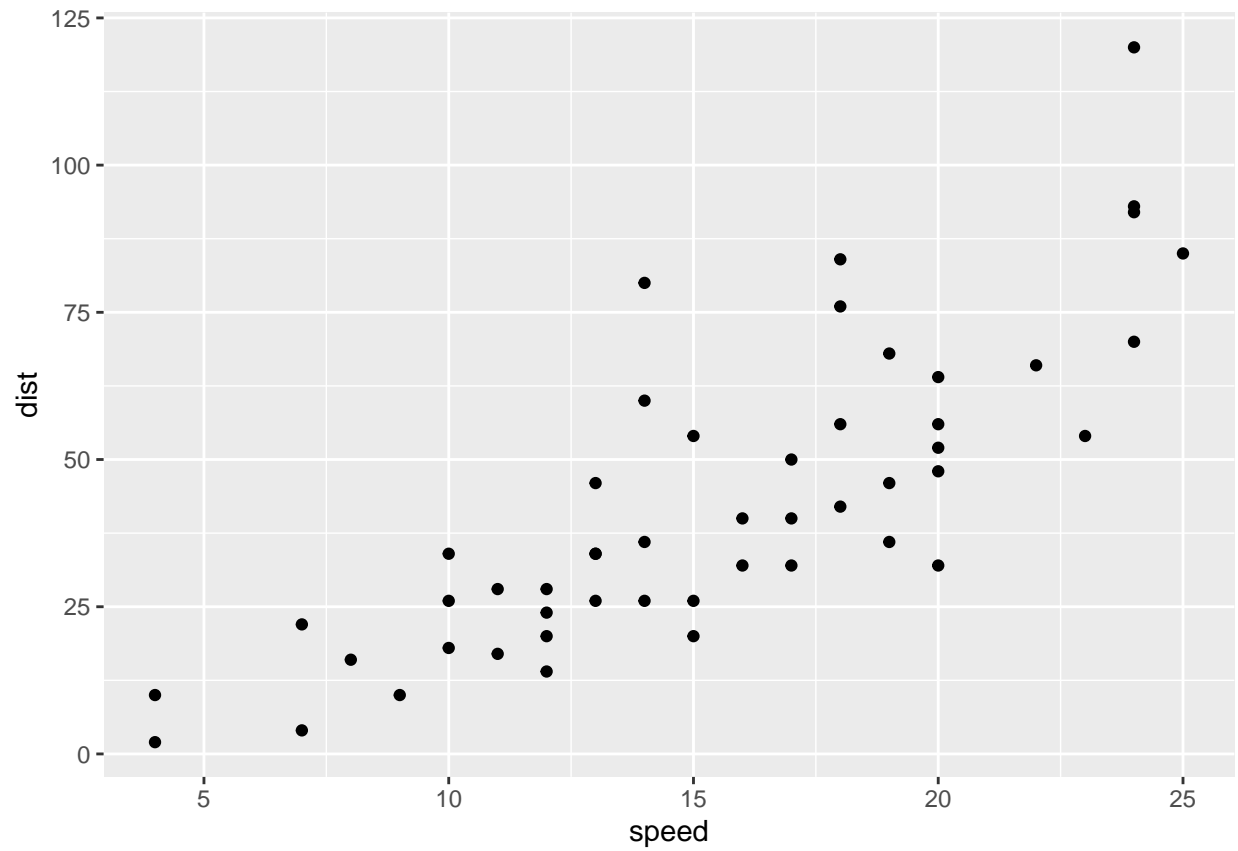
```
# Class 5 Data visualization  
plot(1:5)  
  
# install.packages("ggplot2")  
  
# Before I can use this package, I need to load it  
library(ggplot2)
```



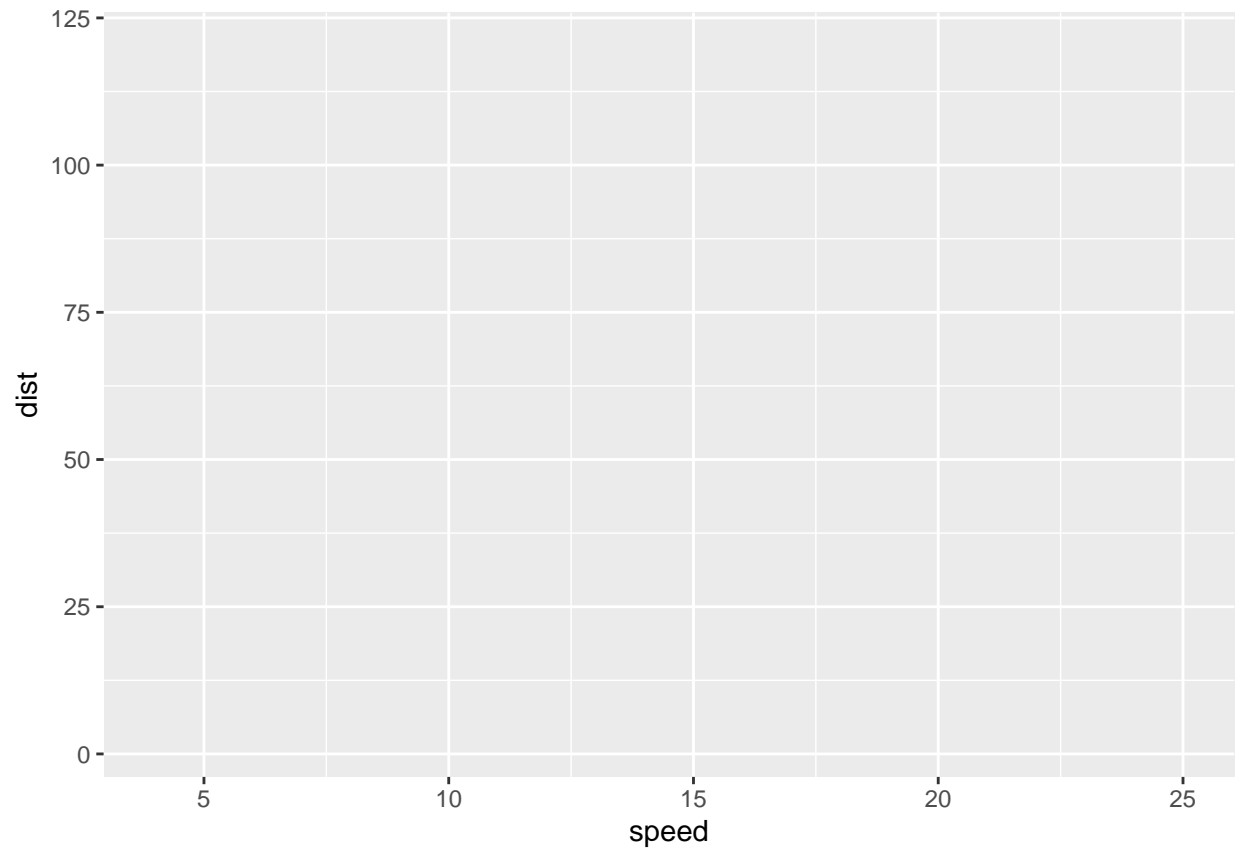
```
# View(cars) # Opens a table with cars data  
  
plot(cars)
```



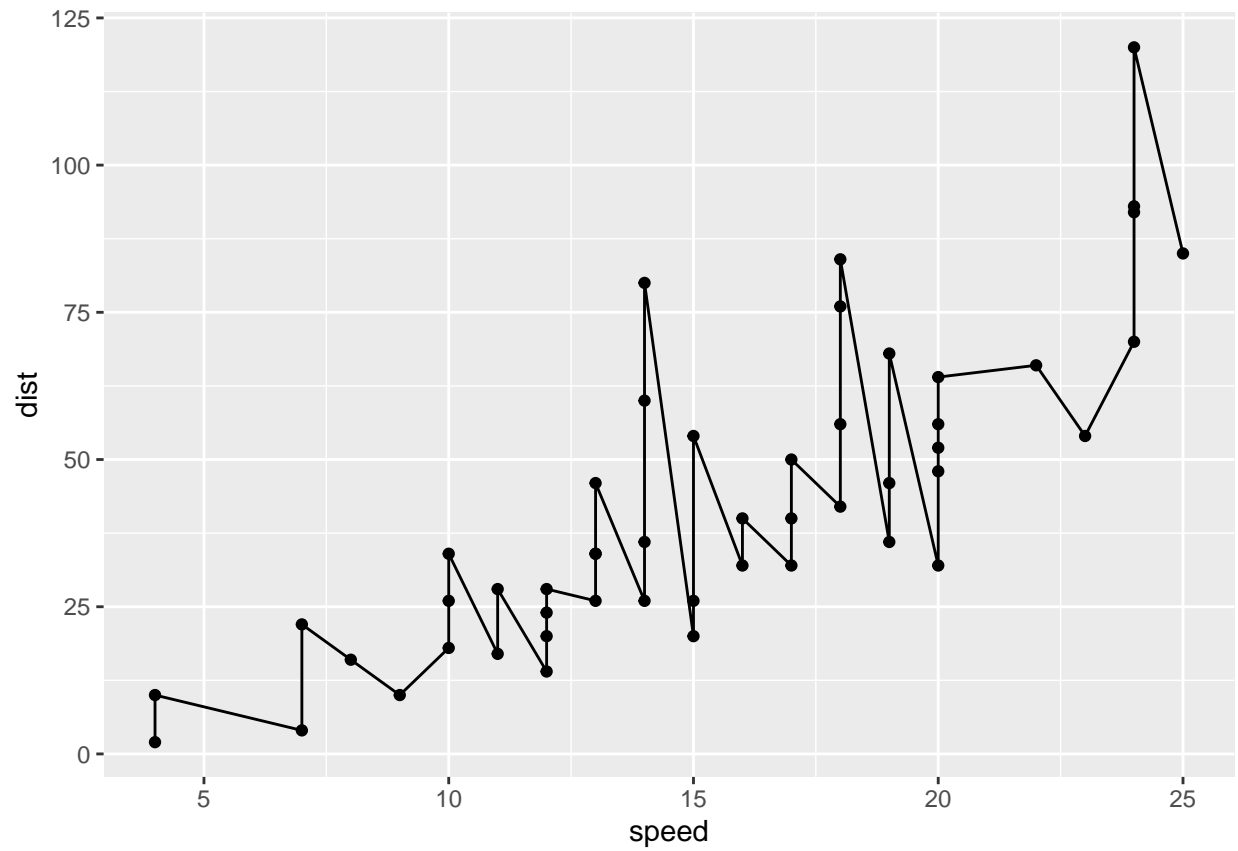
```
# Plot cars with ggplot  
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```



```
# Other way  
ggplot(cars, aes(speed, dist), geom_point)
```

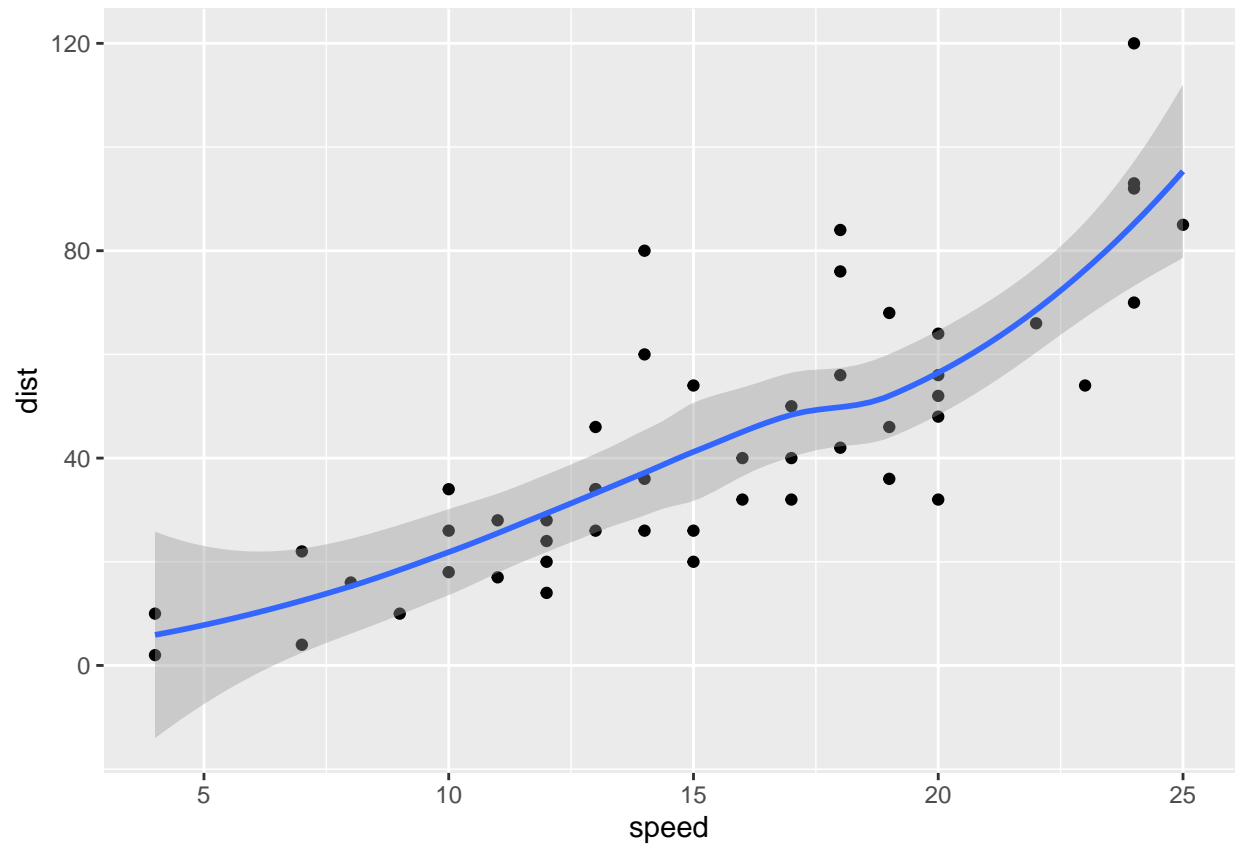


```
# You can save it in a variable  
p <- ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()  
  
p + geom_line() #Add lines connecting the points
```

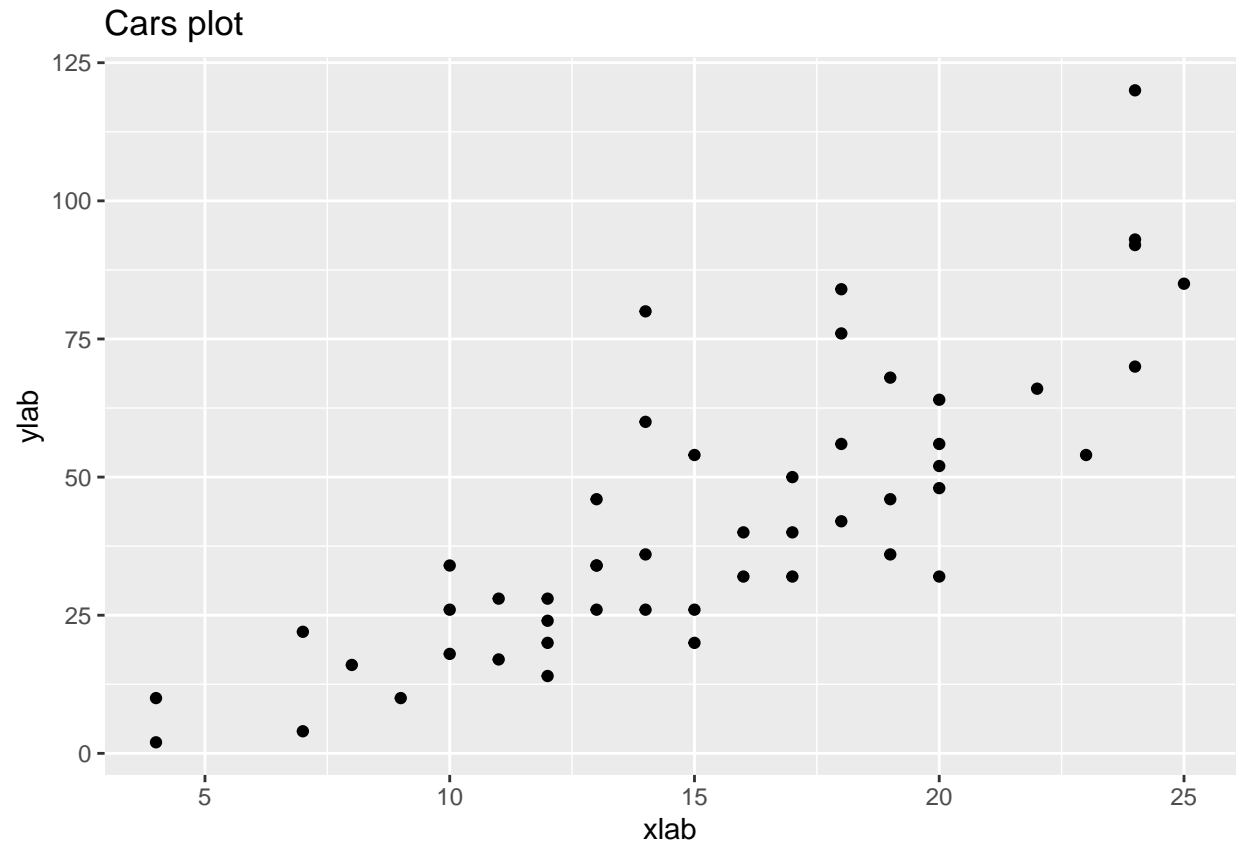


```
p + geom_smooth() #
```

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



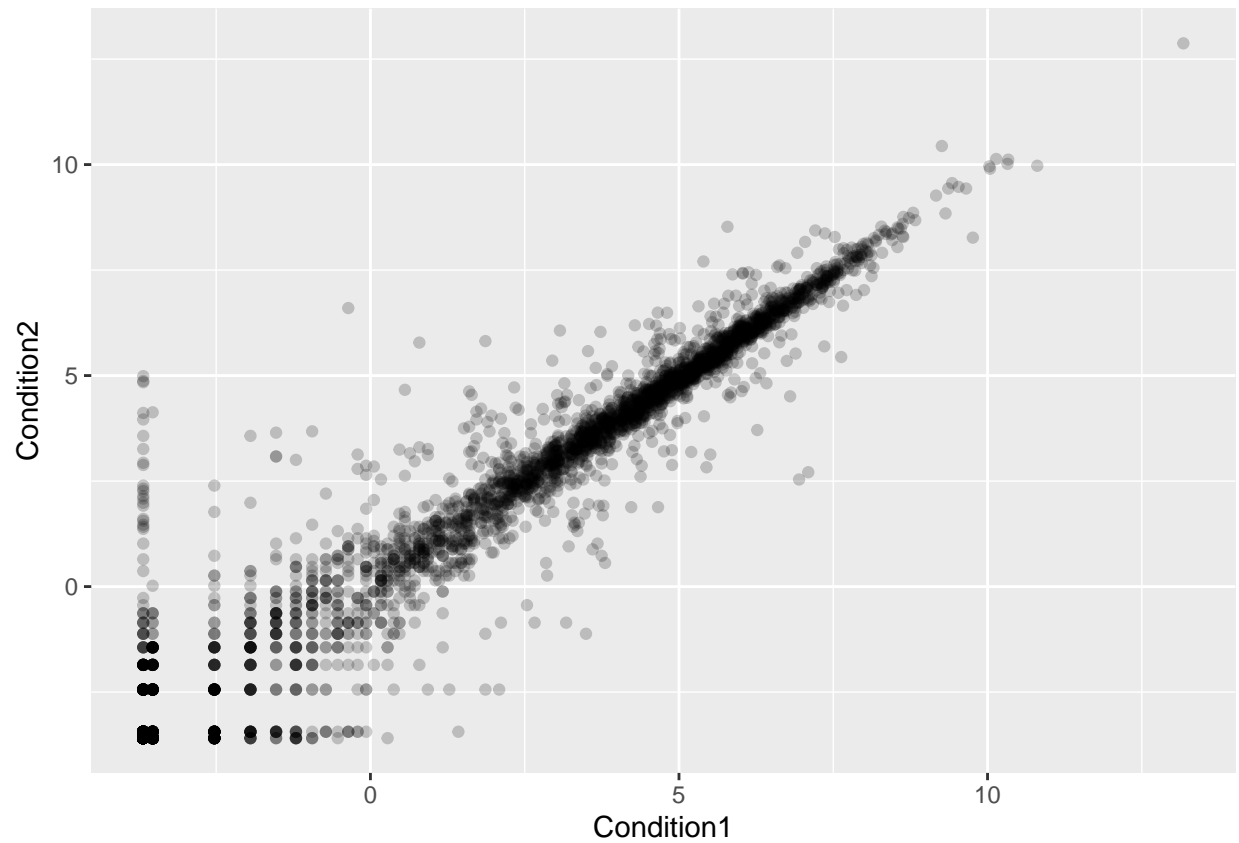
```
p + labs(title="Cars plot")+ xlab("xlab") + ylab("ylab")
```



```
# RNA-Seq plot
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
```

```
# Make a scatter plot with genes data
ggplot(data=genes) +
  aes(x=Condition1, y=Condition2) +
  geom_point(alpha=0.2)
```



```
# Install packages for making PDFs  
# install.packages("tinytex")  
  
library(tinytex)  
install_tinytex()
```