

# class05.R

ziyuanhan

2021-10-13

```
#Class 05: Data visualization
```

```
#load the package
```

```
library(ggplot2)
```

```
ggplot(cars)
```

```
head(cars)
```

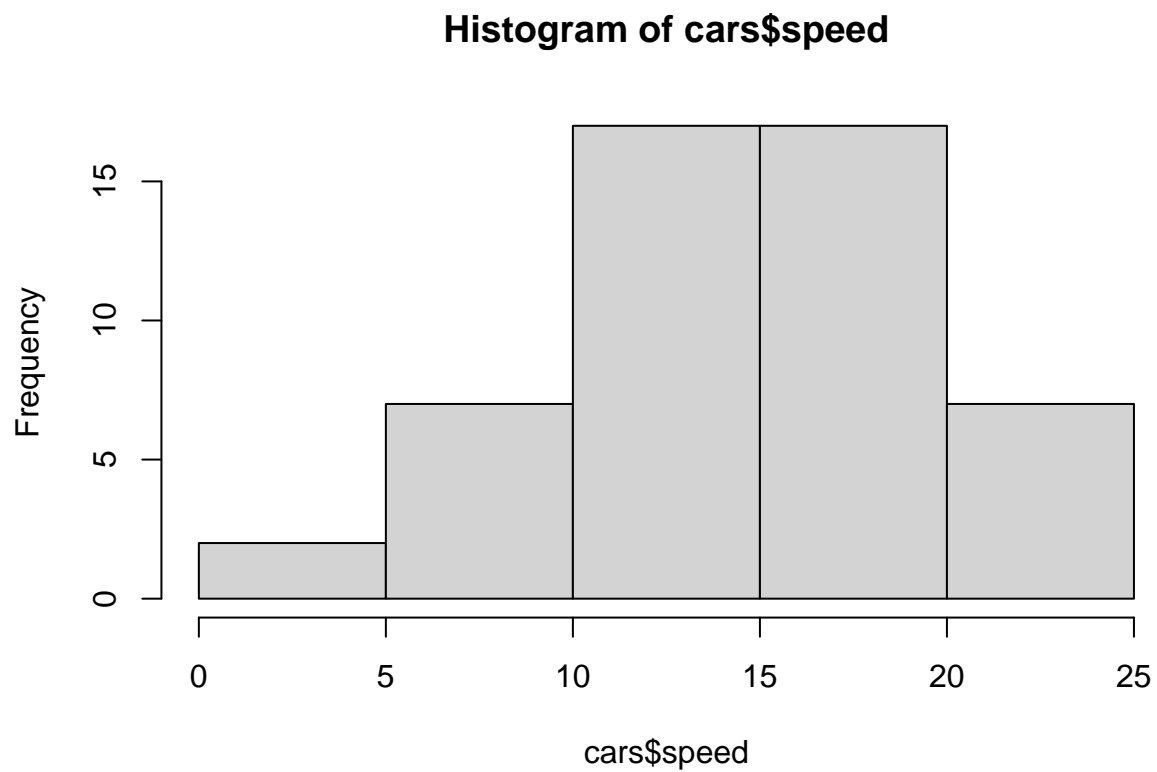
```
##   speed dist
## 1     4    2
## 2     4   10
## 3     7    4
## 4     7   22
```

```
## 5      8    16
## 6      9    10
```

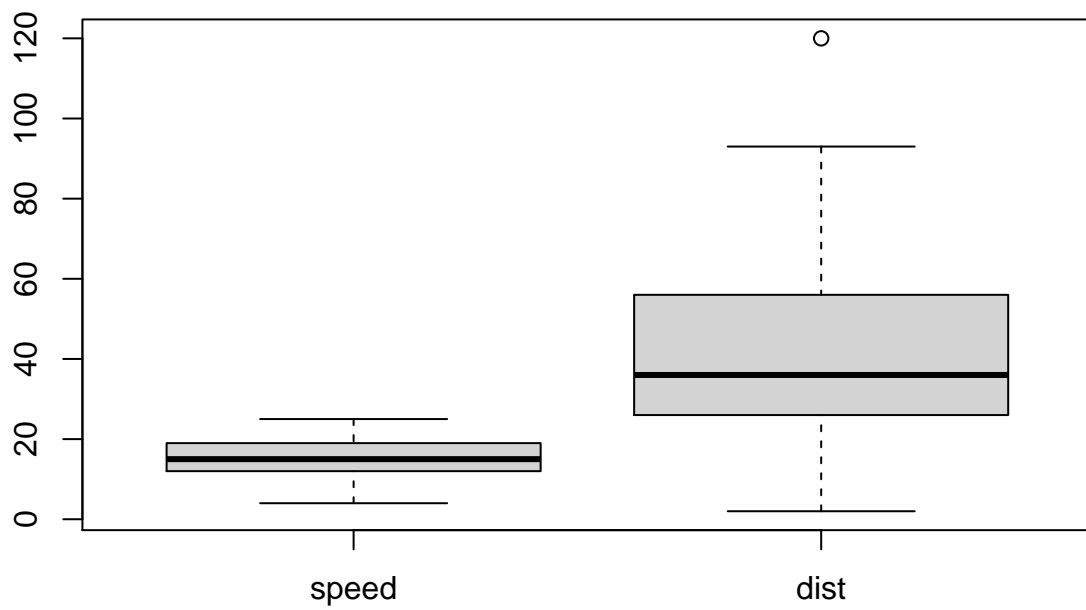
```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0    Min.   :  2.00
## 1st Qu.:12.0    1st Qu.: 26.00
##  Median :15.0    Median : 36.00
##   Mean  :15.4    Mean   : 42.98
## 3rd Qu.:19.0    3rd Qu.: 56.00
##   Max.  :25.0    Max.    :120.00
```

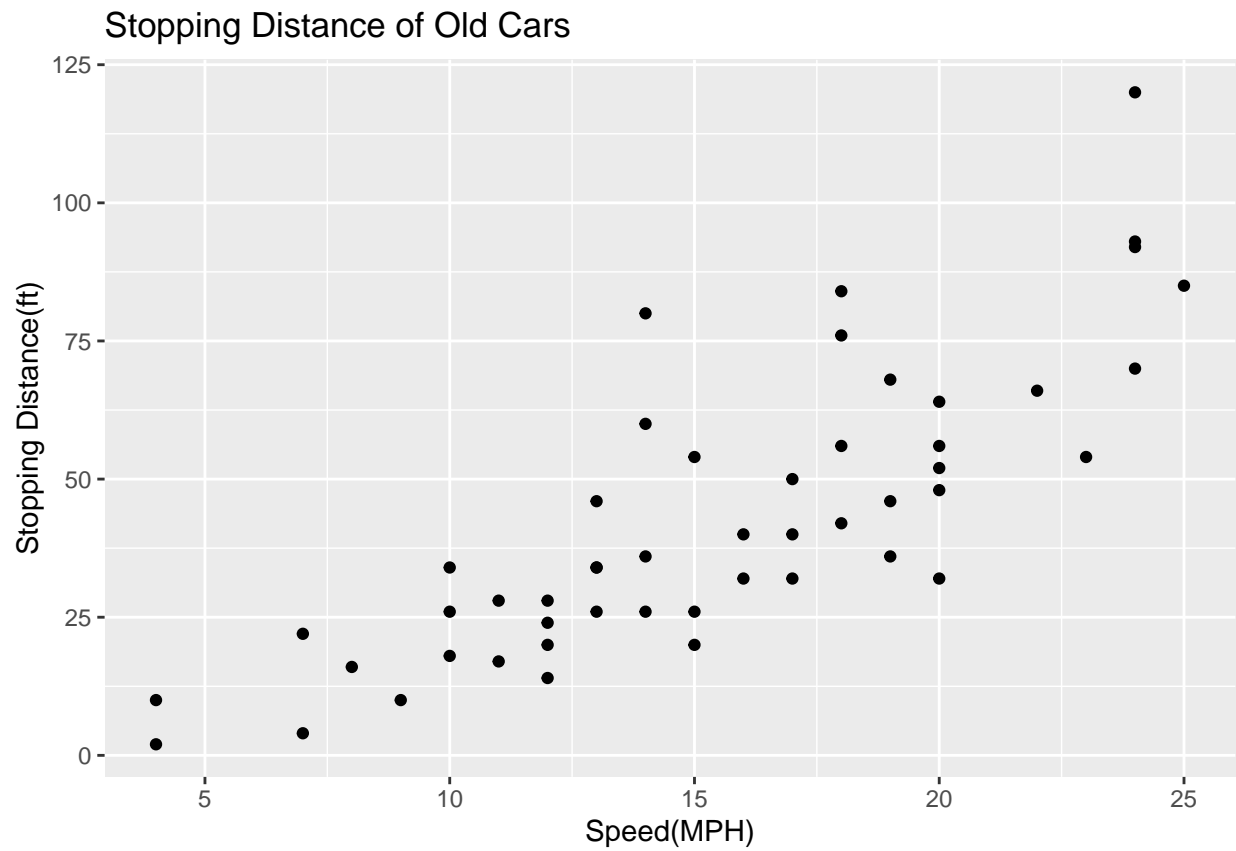
```
hist(cars$speed)
```



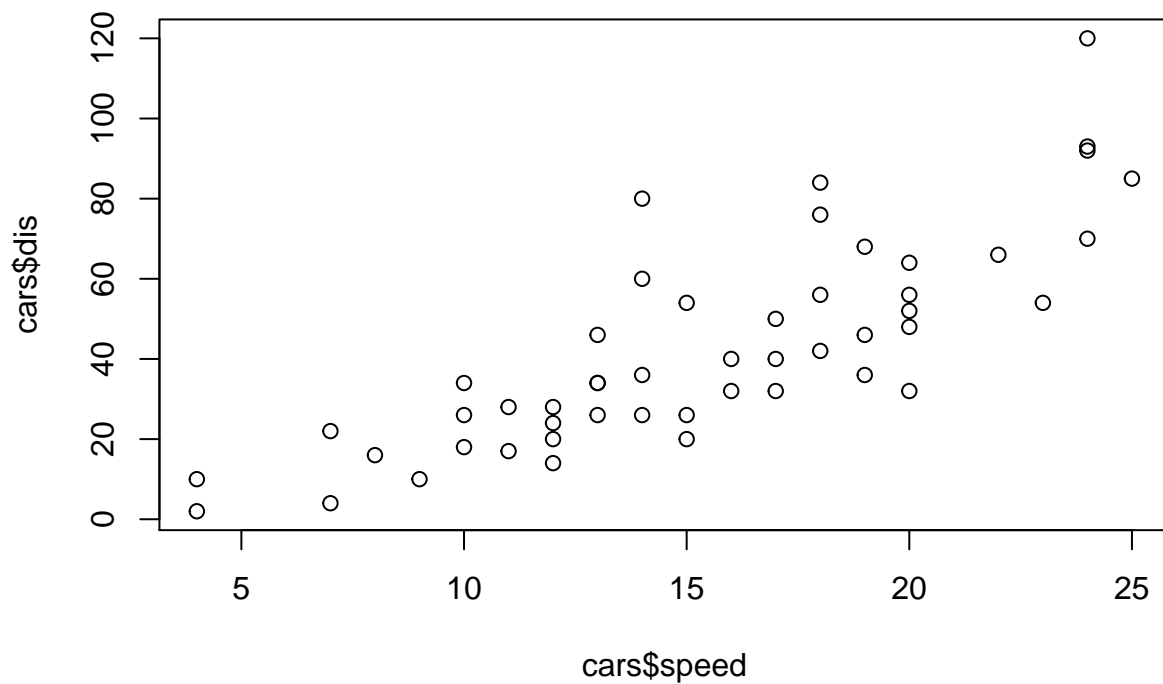
```
boxplot(cars)
```



```
ggplot(data=cars) +  
  aes(x=speed, y=dist)+  
  geom_point() +  
  labs(title="Stopping Distance of Old Cars",  
        x="Speed(MPH)",y="Stopping Distance(ft)")
```



*#side-note:ggplot is not the only graphics system*  
`plot(cars$speed,cars$dis)`



```
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"
```

```
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
```

```
#How many genes
nrow(genes)
```

```
## [1] 5196
```

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

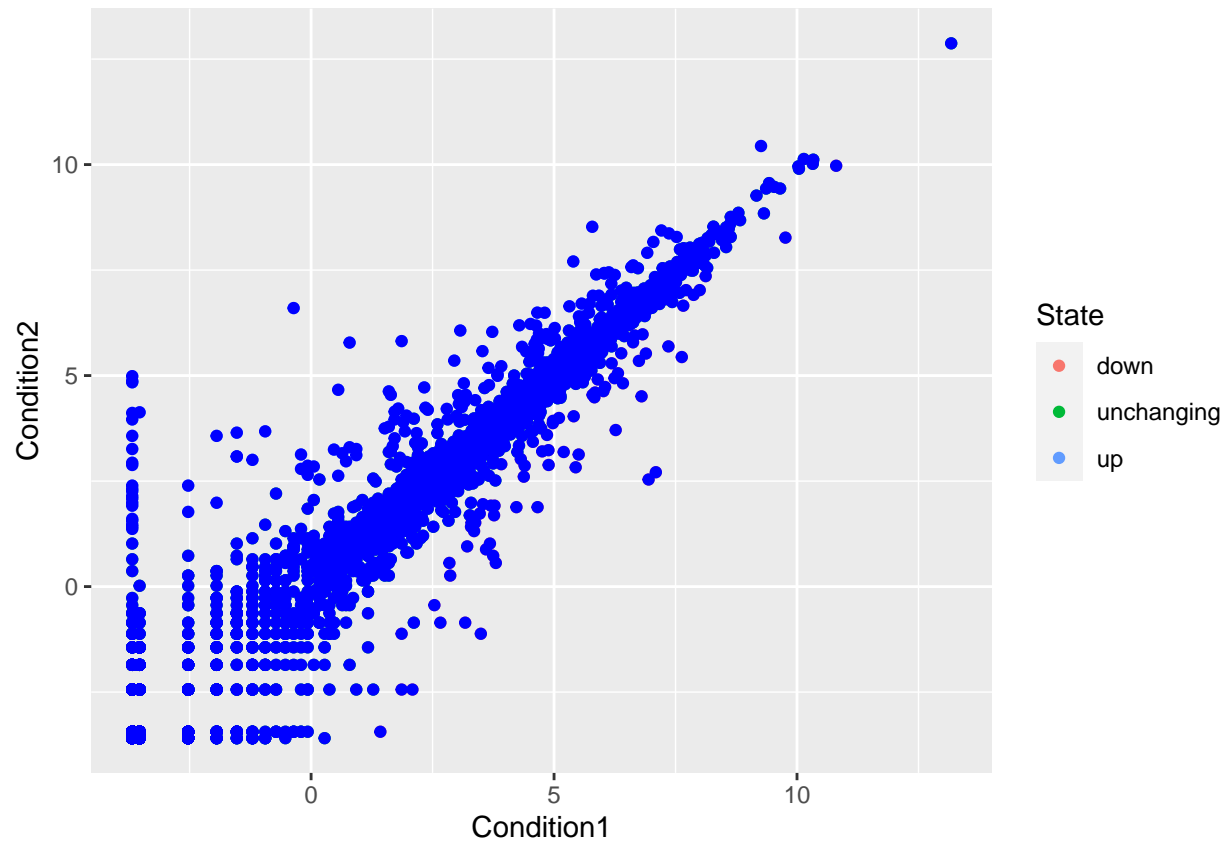
```
##
##      down unchanging      up
##       72      4997      127
```

```
round(table(genes$State)/nrow(genes) * 100,3)
```

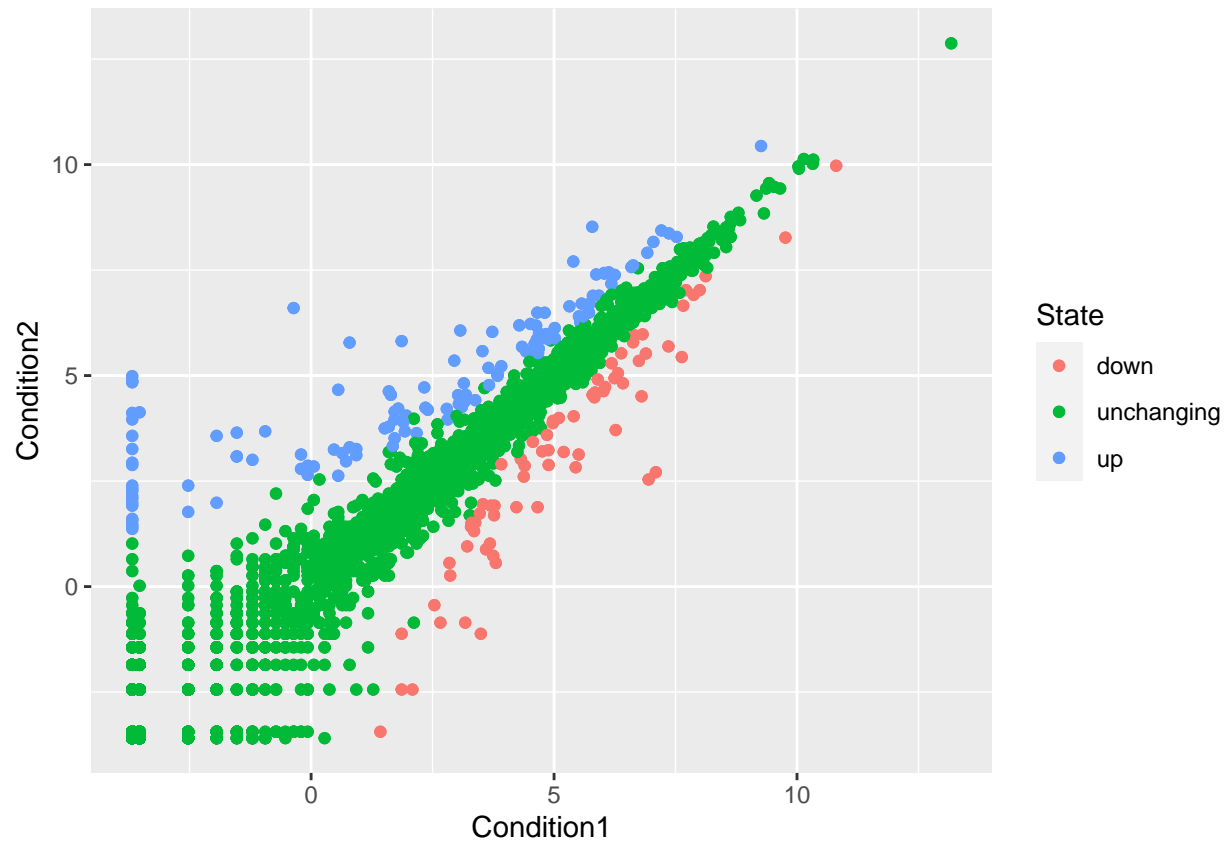
```
##
##      down unchanging      up
##    1.386    96.170    2.444
```

```
#let's make a figure
p<-ggplot(genes)+
  aes(x=Condition1,y=Condition2,col=State)+
  geom_point()

p+ geom_point(col="blue")
```

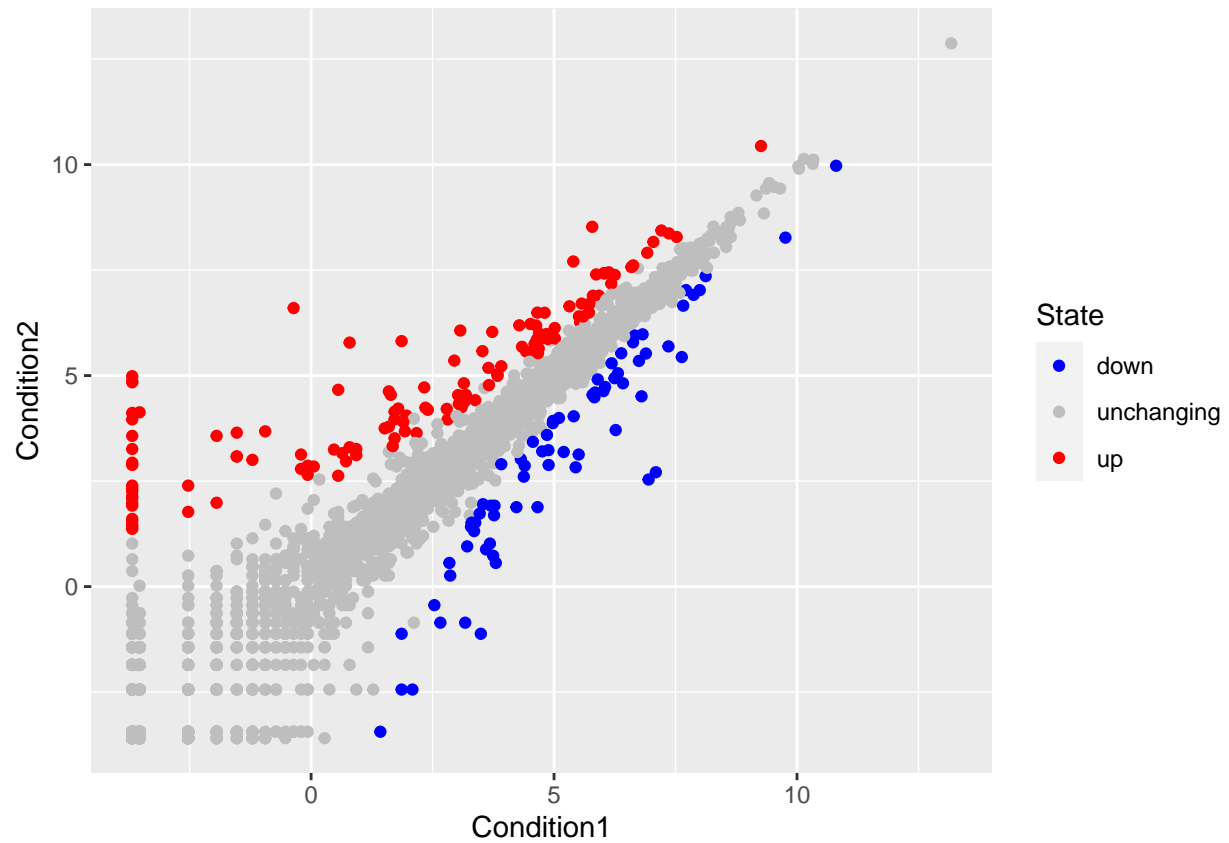


```
p+aes(col=State) + geom_point()
```



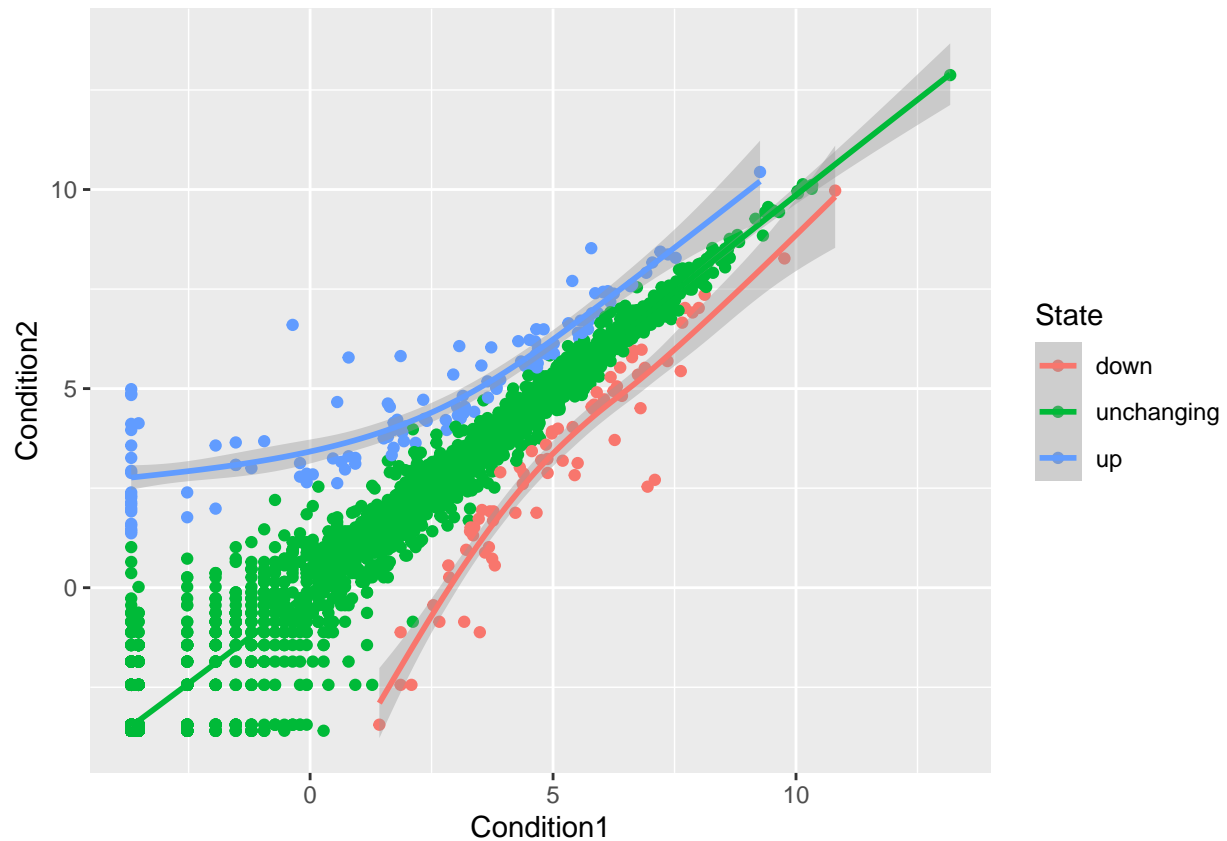
```
#changing color of the dots  
p+scale_color_manual(values=c("blue","gray","red"))
```





```
p+geom_smooth()
```

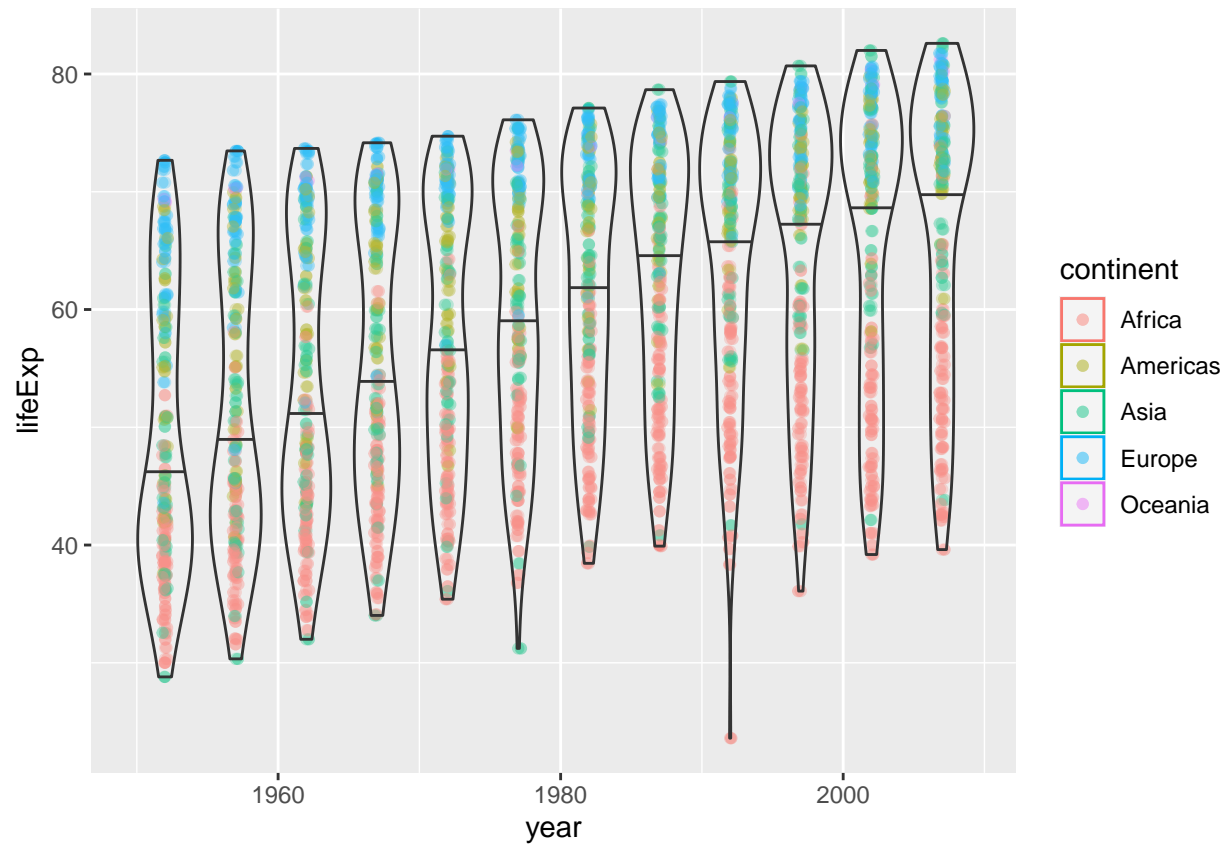
```
## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```



```
#install gapminder
#install.packages("gapminder")
library(gapminder)
head(gapminder)
```

```
## # A tibble: 6 x 6
##   country    continent  year lifeExp      pop gdpPercap
##   <fct>      <fct>    <int>  <dbl>   <int>   <dbl>
## 1 Afghanistan Asia      1952   28.8  8425333    779.
## 2 Afghanistan Asia      1957   30.3  9240934    821.
## 3 Afghanistan Asia      1962   32.0 10267083    853.
## 4 Afghanistan Asia      1967   34.0 11537966    836.
## 5 Afghanistan Asia      1972   36.1 13079460    740.
## 6 Afghanistan Asia      1977   38.4 14880372    786.
```

```
#visualizing gapminder
ggplot(gapminder) +
  aes(x=year,y=lifeExp,col=continent)+
  geom_point(alpha=0.3)+
  geom_jitter(width=0.2,alpha=0.4)+
  # geom_boxplot(aes(group=year),alpha=0.2)+
  geom_violin(aes(group=year),alpha=0.2,draw_quantiles = 0.5)
```



```
#install the plotly
#install.packages("plotly")
# library(plotly)
# ggplotly()
#install.packages("tinytex")
#tinytex::install_tinytex()
```