# class05.R

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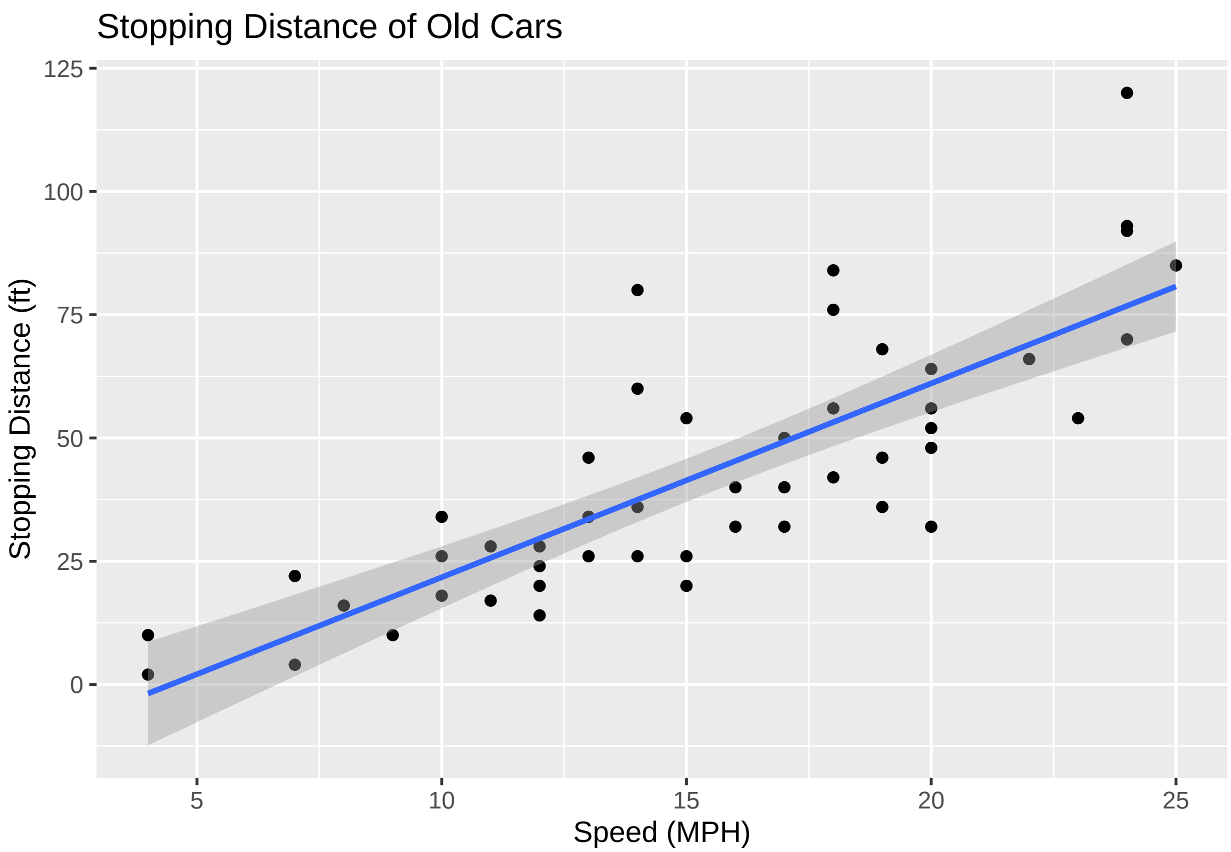
2021-10-13

```
# Class 05: Data Visualization

# Today we are going to use ggplot2 package

# First we need to load the package!
# install.packages("ggplot2")
library(ggplot2)

# we will use this inbuilt "cars" dataset first
head(cars)
```

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

```
# All ggplots have at least 3 layers,
# data + aes + geoms
ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm") +
  labs(title="Stopping Distance of Old Cars",
       x="Speed (MPH)",
       y="Stopping Distance (ft)")
```

```
## ‘geom_smooth()‘ using formula ’y ~ x’
```



```
# Side-note: ggplot is not the only graphics system
# a very popular one is good old "base" R graphics

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
```

```
# Q. How many genes are in the dataset?
nrow(genes)
```

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

```
# Q. How many columns are in the dataset?
colnames(genes)
```

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

```
ncol(genes)
```

```
## [1] 4
```

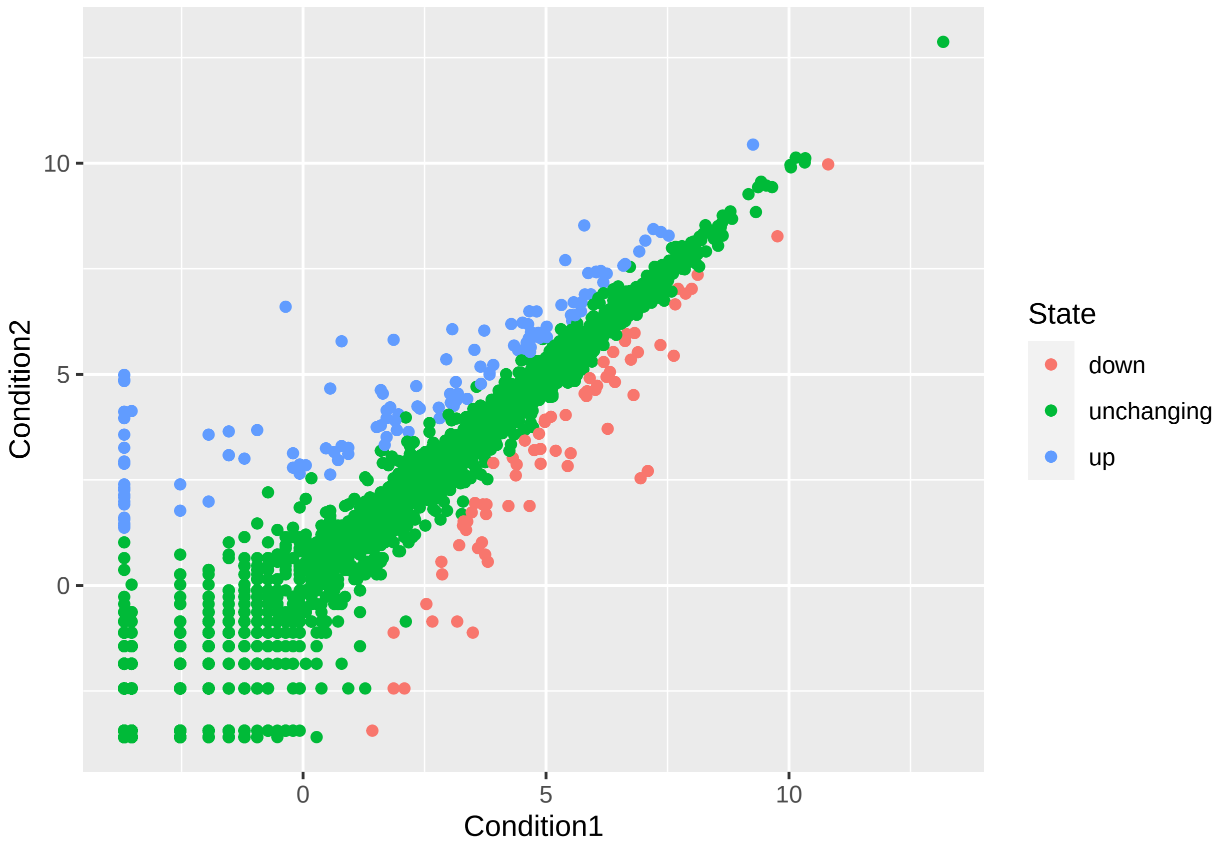
```
# Q. How many genes are "up"?
table(genes$State)
```

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

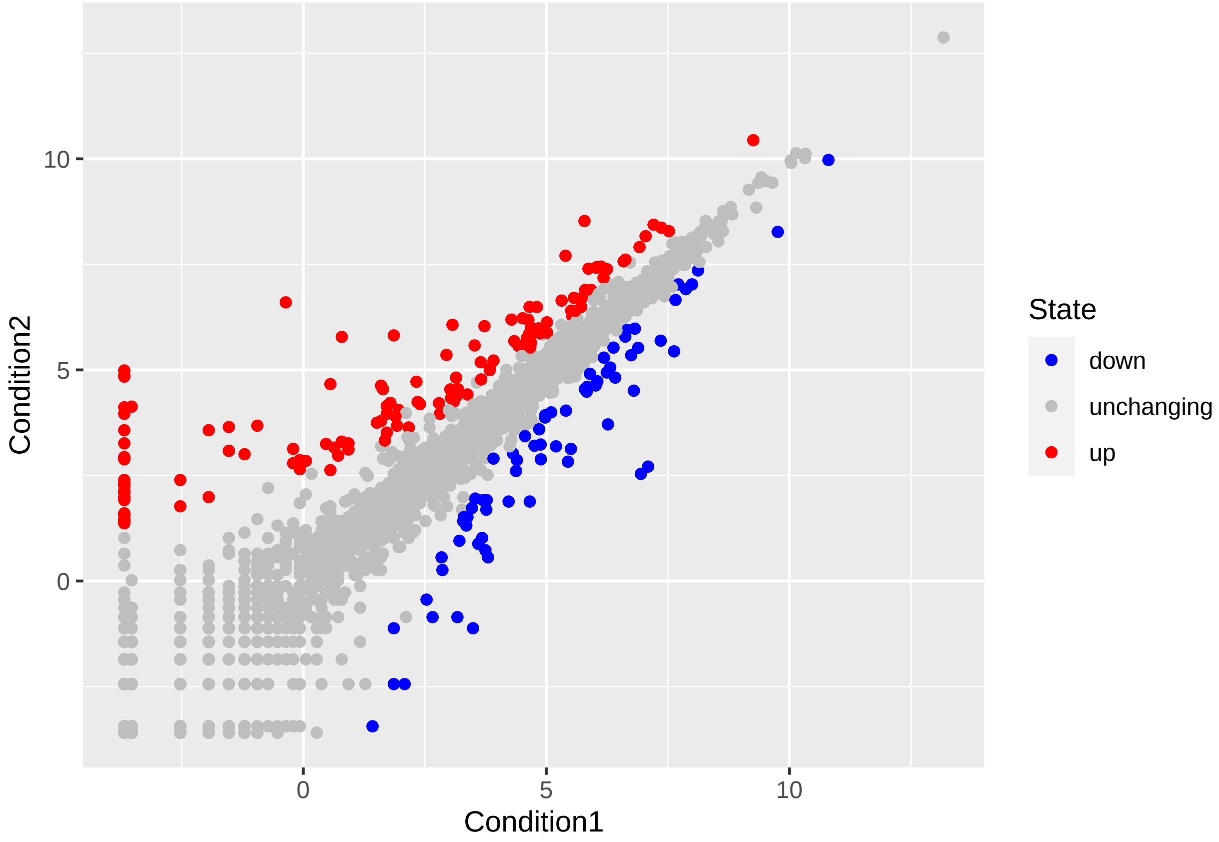
```
# Q. What % are up?
round(table(genes$State)/nrow(genes)*100, 2)
```

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

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



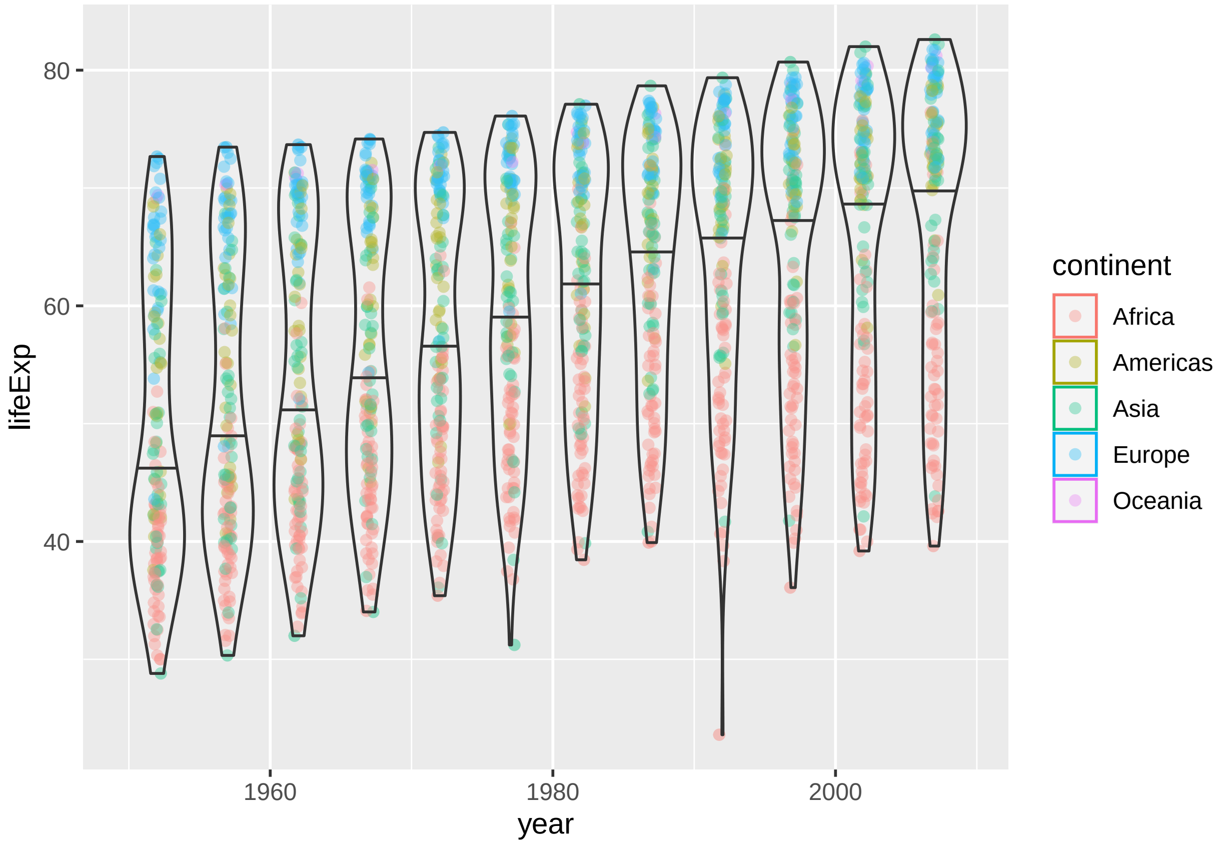
```
# I like it but not the default colors, lets change them
p + scale_colour_manual(values=c("blue","gray","red"))
```



```
# I will give a title to the plot,
# and change the names of x-axis and y-axis
p <- p +
  labs(title="Gene Expression Changes Upon Drug Treatment",
       x="Control (no drug)",
       y="Drug Treatment")

# Lets explore the gapminder dataset
# 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.
```

```
# Lets make a new plot of year vs lifeExp
ggplot(gapminder) +
  aes(x=year, y=lifeExp, col=continent) +
  geom_jitter(width=0.3, alpha=0.4) +
  geom_violin(aes(group=year), alpha=0.2,
              draw_quantiles = 0.5)
```



```
# Install the plotly
# install.packages("plotly")
# library(plotly)
# ggplotly()
```