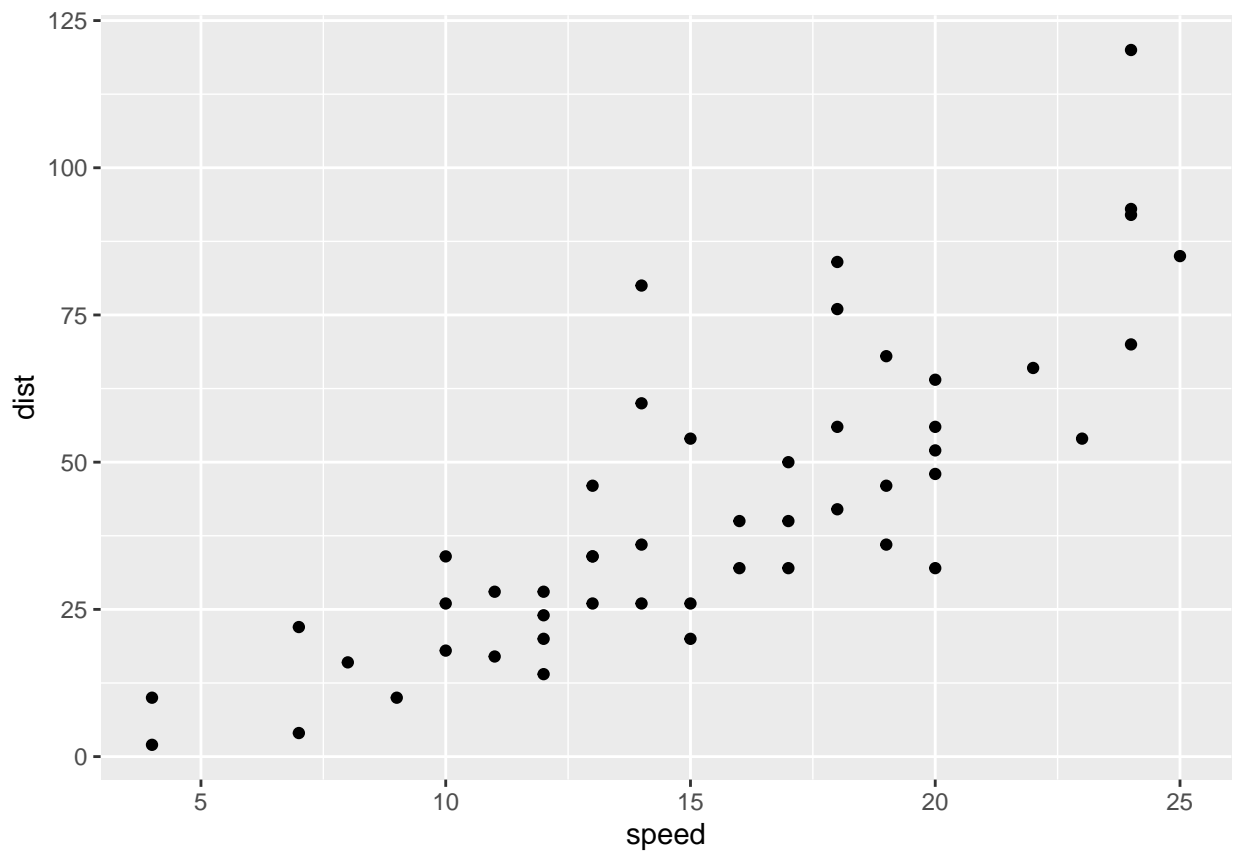


# Wk 5 Class 5 Data Visualization lab

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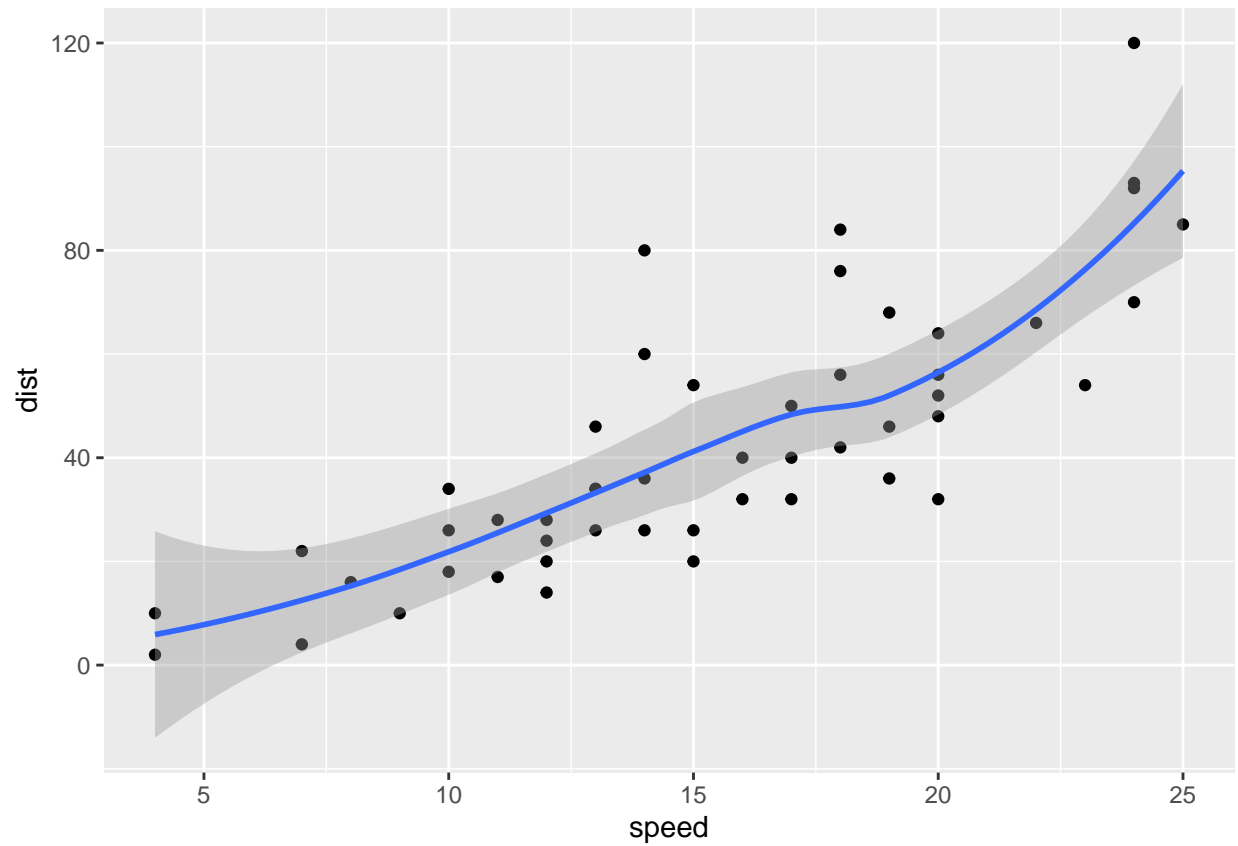
2022-02-07

```
# Week 5 Class 5 Data Visualization lab  
#One time only install  
# install.packages("ggplot2")  
#Load this every time a new session is started and ggplot is needed  
library(ggplot2)  
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'
```

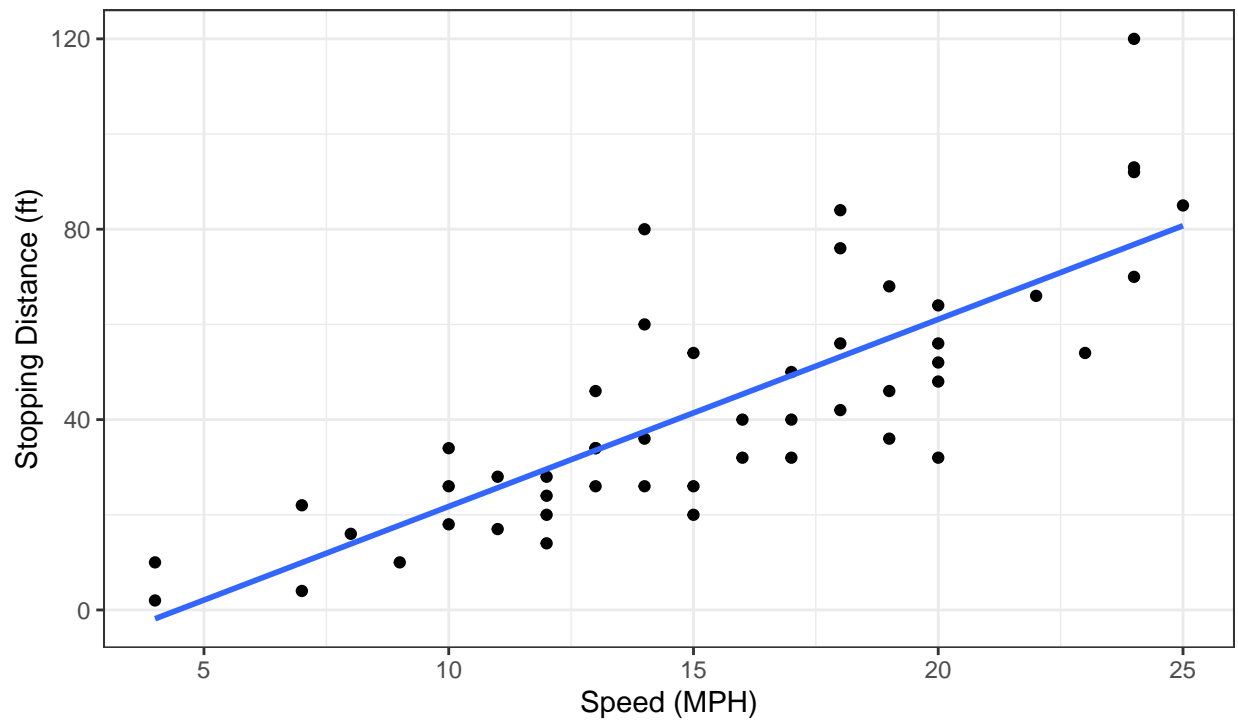


```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  labs(title="Speed and Stopping Distances of Cars",  
        x="Speed (MPH)",  
        y="Stopping Distance (ft)",  
        subtitle = "Your informative subtitle text here",  
        caption="Dataset: 'cars'") +  
  geom_smooth(method="lm", se=FALSE) +  
  theme_bw()
```

```
## '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)
```

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

```
colnames(genes)
```

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

```
ncol(genes)
```

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

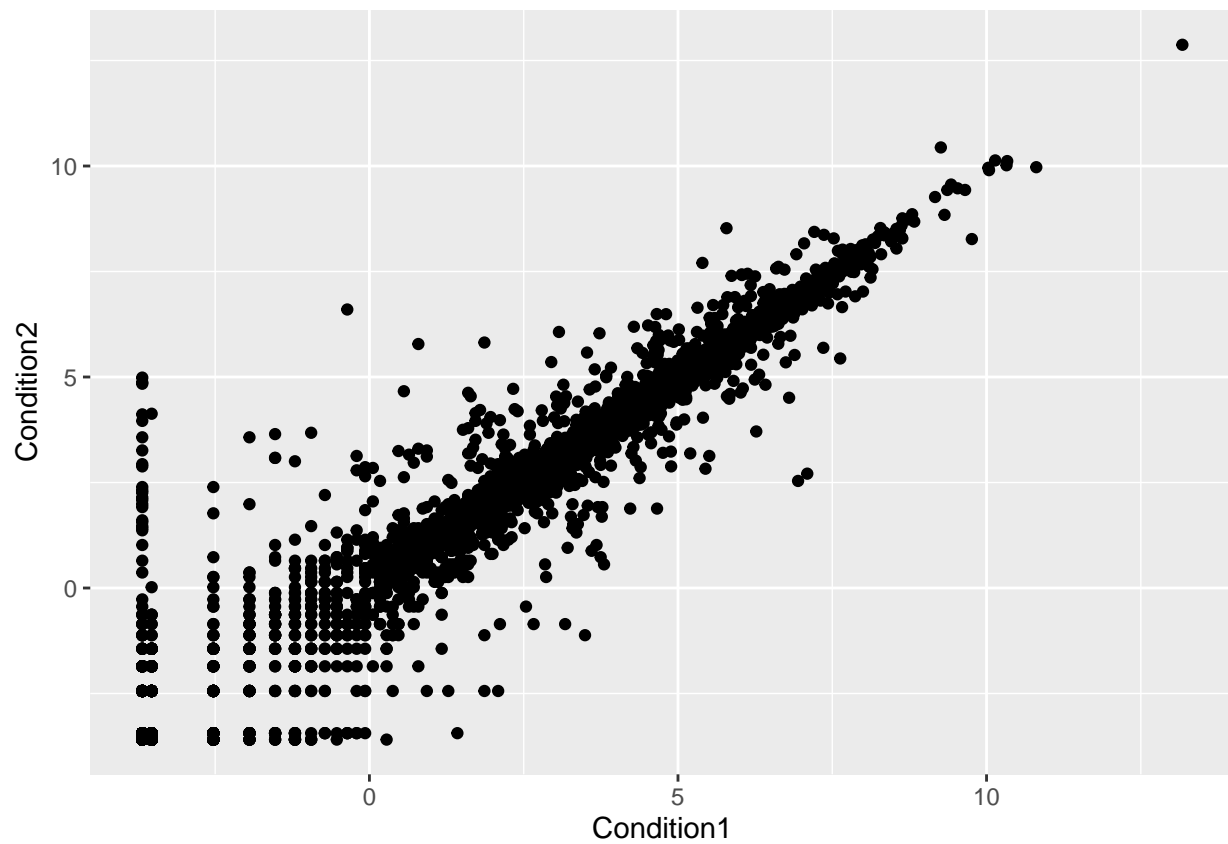
```
table(genes$State)
```

```
##  
##      down  unchanged      up  
##      72      4997      127
```

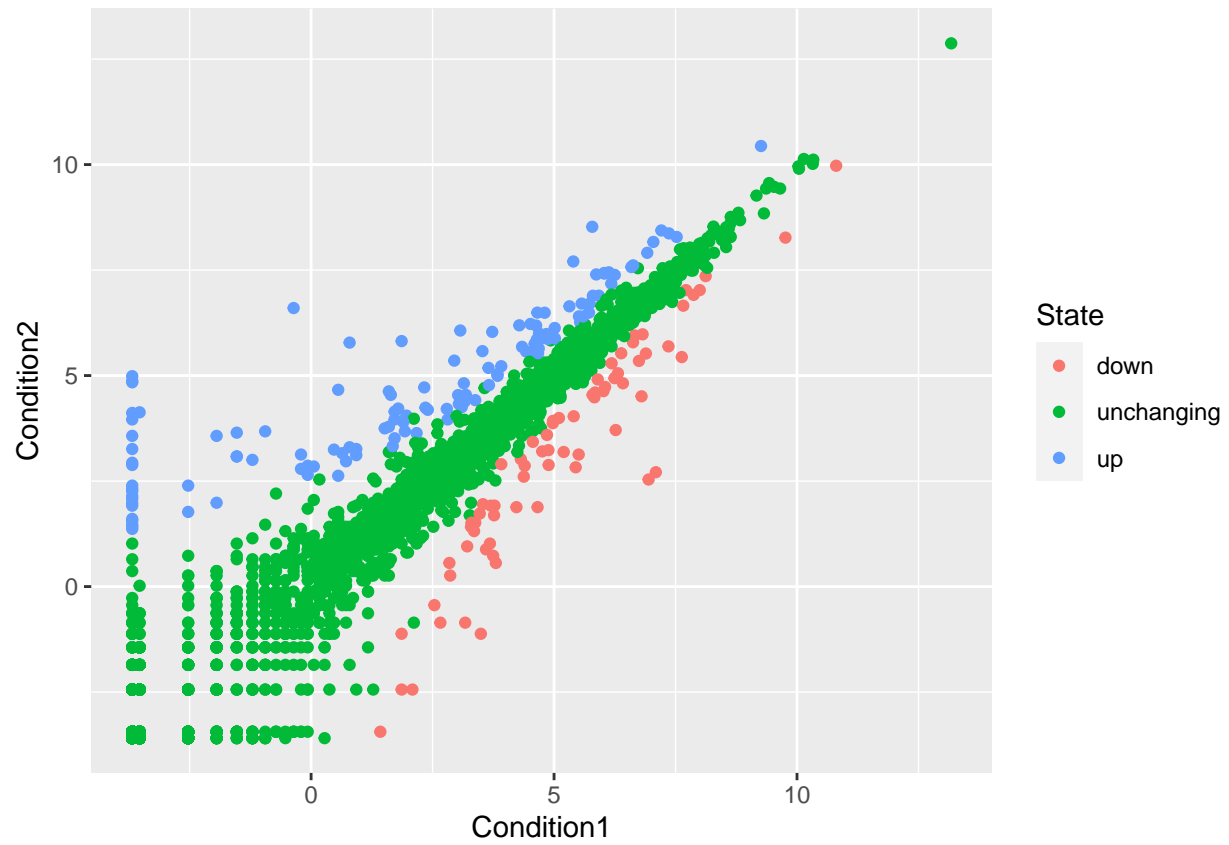
```
round( table(genes$State)/nrow(genes)*100, 2 )
```

```
##  
##      down  unchanged      up  
##      1.39      96.17      2.44
```

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

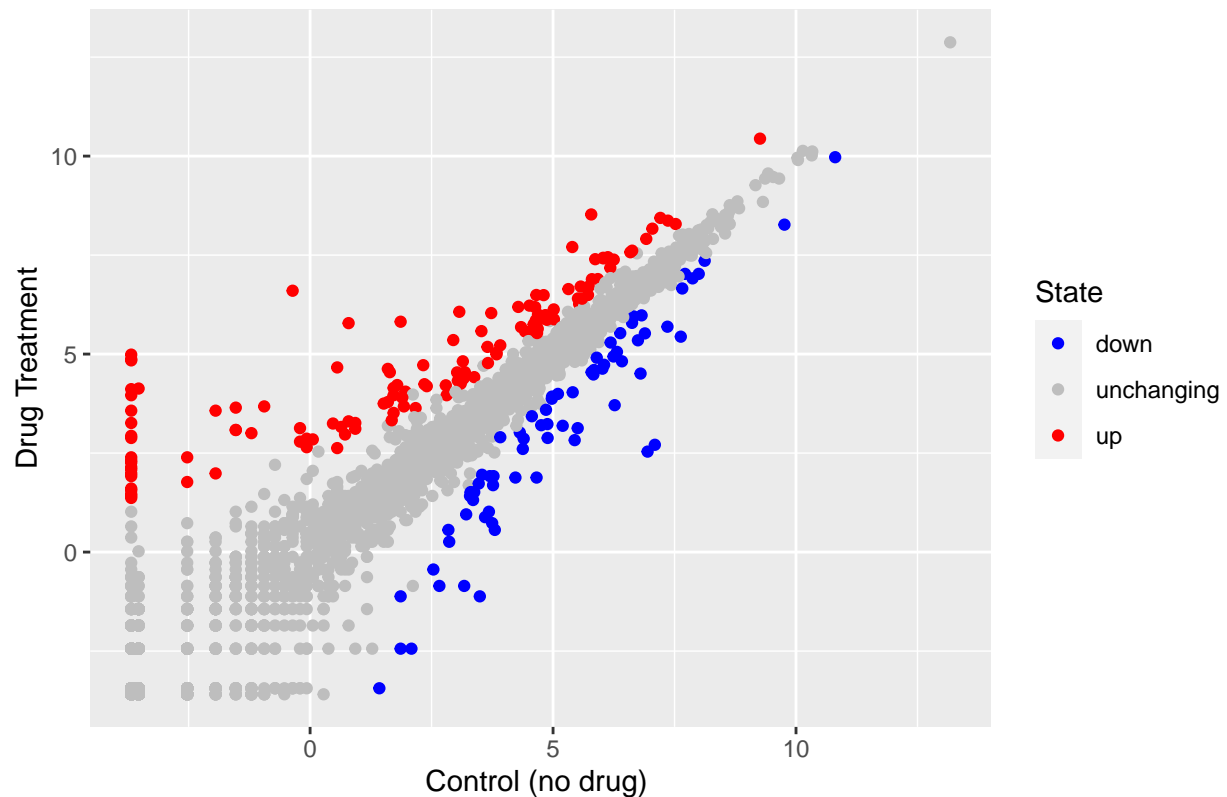


```
p<- ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point()  
p
```



```
p + scale_colour_manual(values=c("blue","gray","red"))+
  labs(title="Gene Expression Changes Upon Drug Treatment",
        x="Control (no drug) ",
        y="Drug Treatment")
```

## Gene Expression Changes Upon Drug Treatment



```
r = getOption("repos")
r["CRAN"] = "http://cran.us.r-project.org"
options(repos = r)
```

```
sessionInfo()
```

```
## R version 4.1.2 (2021-11-01)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] ggplot2_3.3.5
##
## loaded via a namespace (and not attached):
## [1] pillar_1.7.0    compiler_4.1.2  highr_0.9       tools_4.1.2
## [5] digest_0.6.29   evaluate_0.14   lifecycle_1.0.1 tibble_3.1.6
```

```
## [9] gtable_0.3.0      nlme_3.1-153      lattice_0.20-45   mgcv_1.8-38
## [13] pkgconfig_2.0.3   rlang_1.0.1       Matrix_1.3-4      cli_3.1.1
## [17] yaml_2.2.2        xfun_0.29         fastmap_1.1.0     withr_2.4.3
## [21] stringr_1.4.0     knitr_1.37        vctrs_0.3.8       grid_4.1.2
## [25] glue_1.6.1        R6_2.5.1          fansi_1.0.2       rmarkdown_2.11
## [29] farver_2.1.0      magrittr_2.0.2    scales_1.1.1      ellipsis_0.3.2
## [33] htmltools_0.5.2   splines_4.1.2     colorspace_2.0-2  labeling_0.4.2
## [37] utf8_1.2.2        stringi_1.7.6     munsell_0.5.0     crayon_1.4.2
```