Wk 5 Class 5 Data Visualization lab

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```r
# Week 5 Class 5 Data Visualization lab
r = getOption("repos")
r["CRAN"] = "http://cran.us.r-project.org"
options(repos = r)
#One time only install
install.packages("ggplot2")
```

```
##
## The downloaded binary packages are in
##  /var/folders/9r/2f14lwsd285gxhxcsztcvzp40000gn/T//RtmpwY9NXT/downloaded_packages
```

```r
#Load this every time a new session is started and ggplot is needed
library(ggplot2)
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
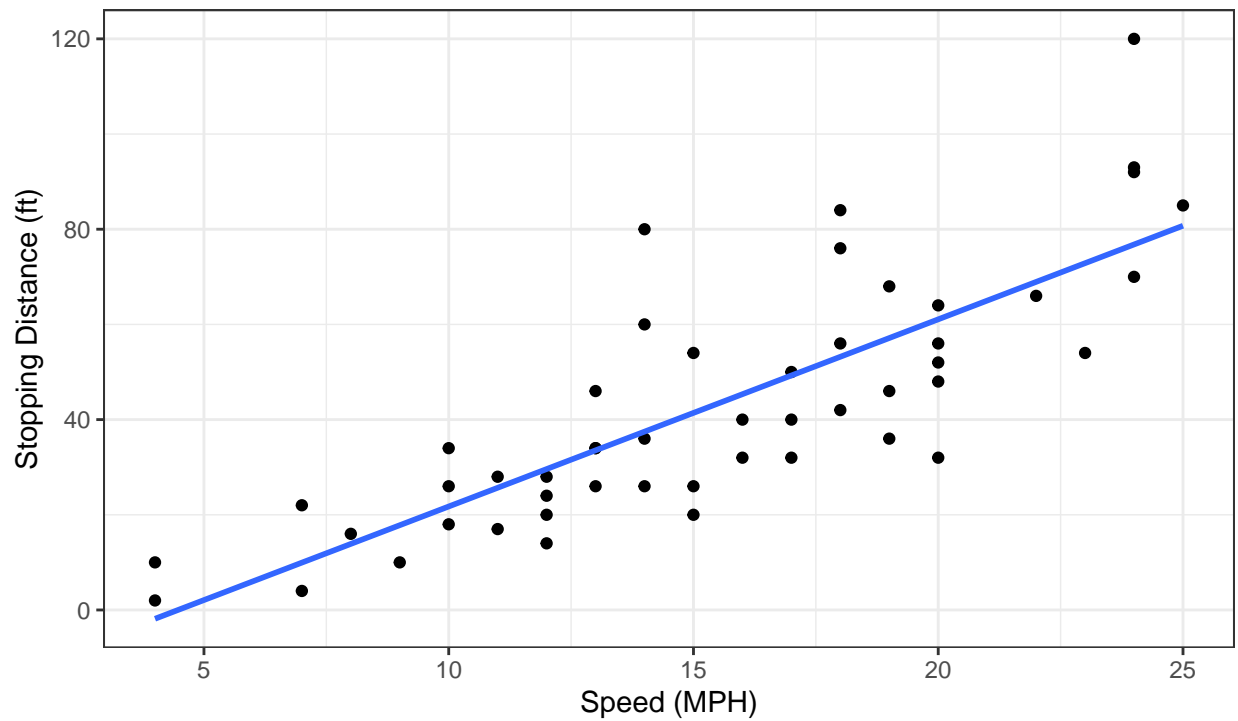
Dataset: 'cars'

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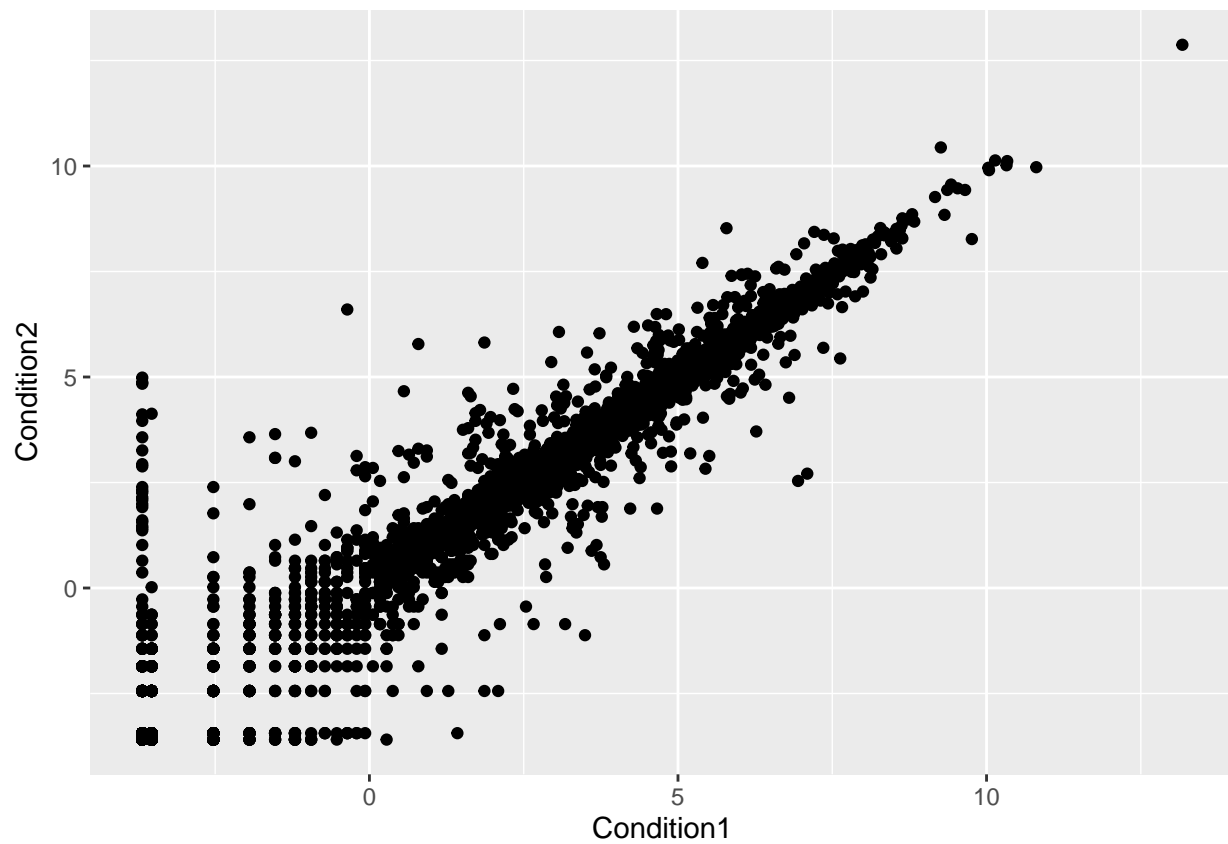
```
## [1] 4
```

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

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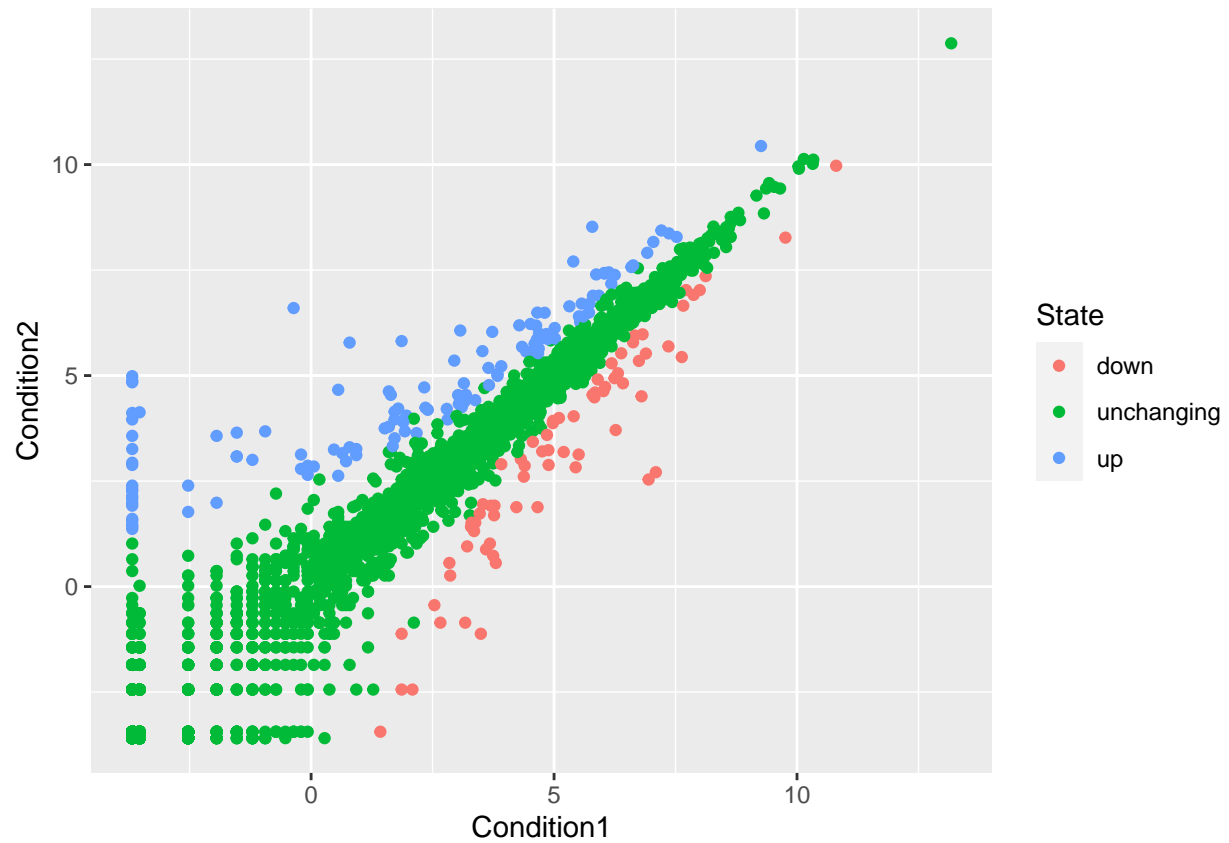
```
round( table(genes$State)/nrow(genes)*100, 2 )
```

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

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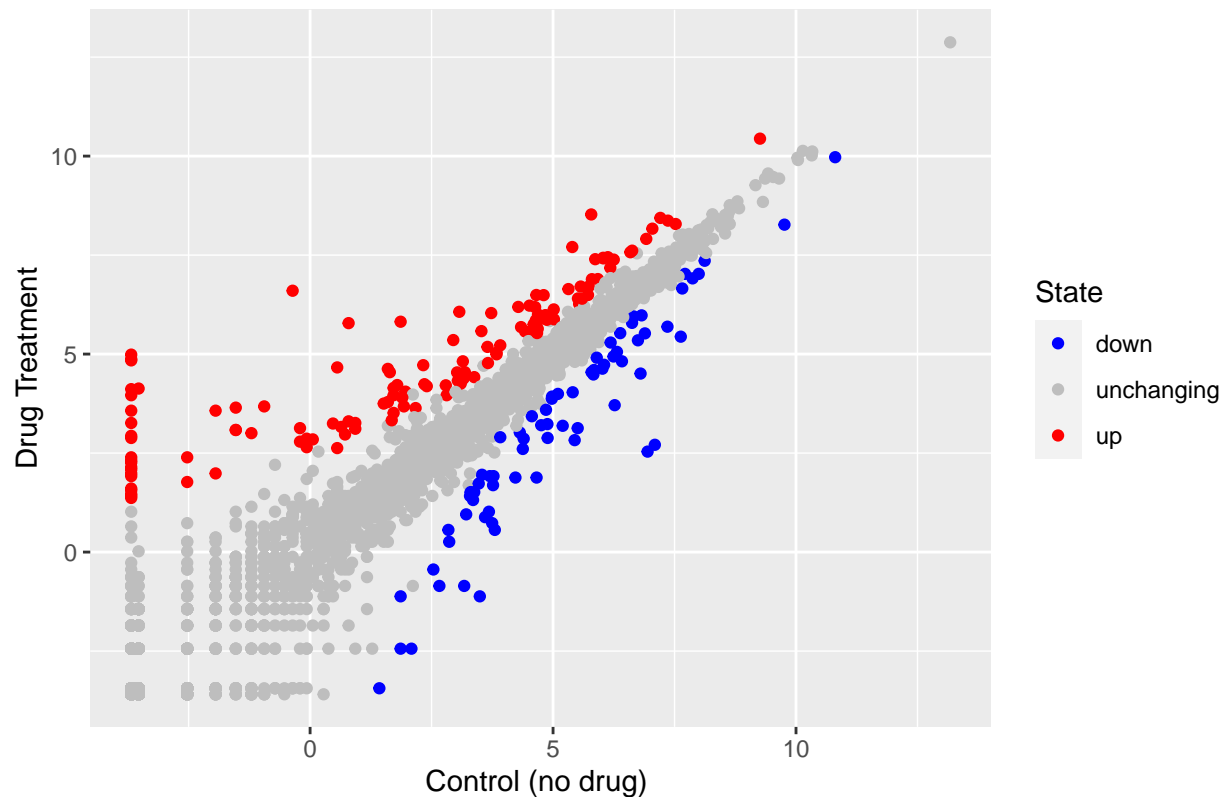


```
p<- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p
```

```
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


```
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
```