class05

Amit Subramanian

Quarto

Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see https://quarto.org.

Running Code

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
1 + 1
```

```
[1] 2
```

You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).

Insalling packages

install.packages("ggplot2")

Adding Library

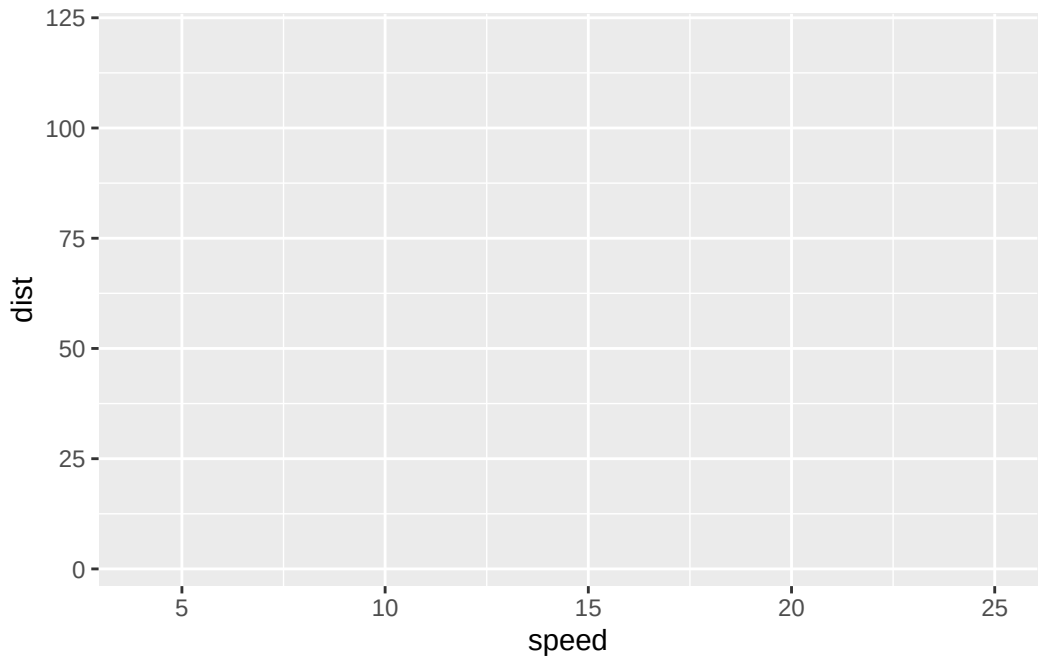
```
library(ggplot2)
```

Cars Data

#View(cars) #plot(cars)

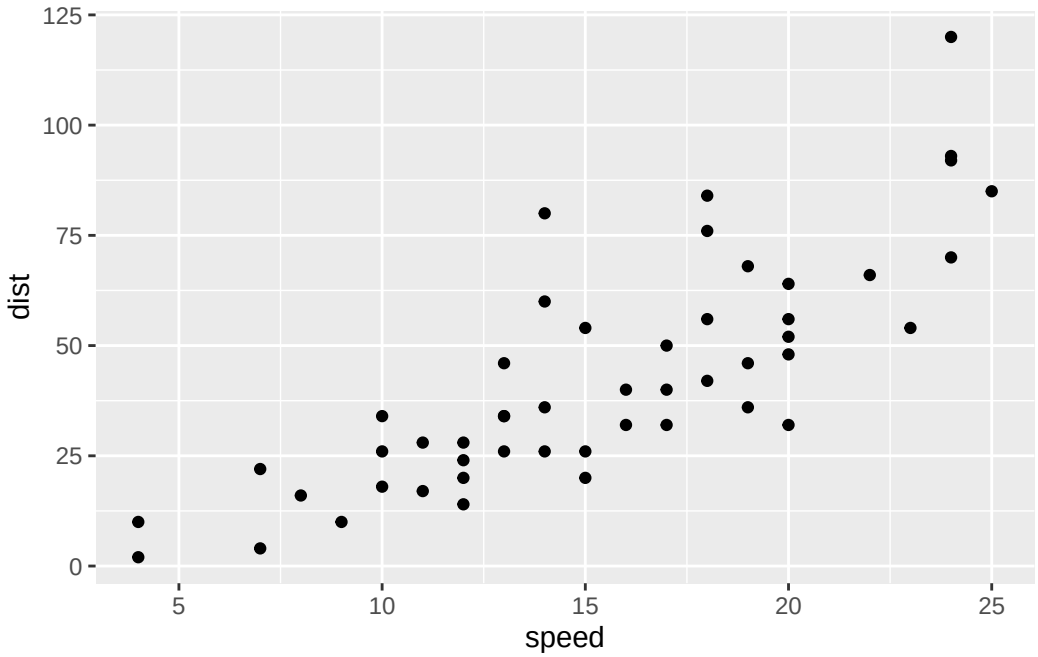
Making scatterplot for cars

```
ggplot(cars) +
  aes(x=speed, y=dist)
```



Adding axis

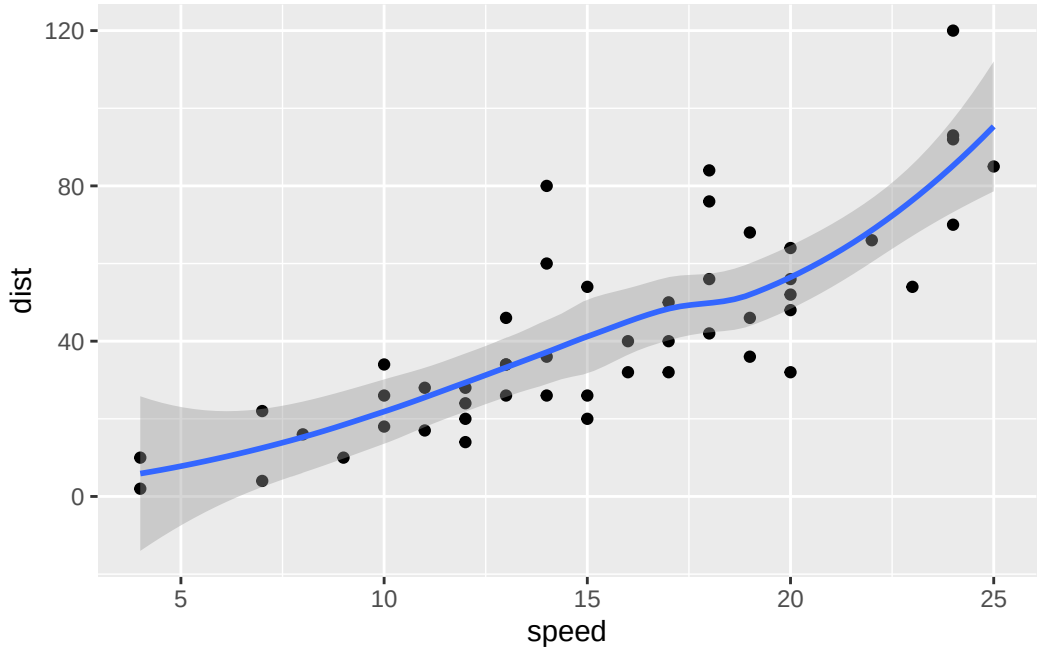
```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



Adding trendline

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth()
```

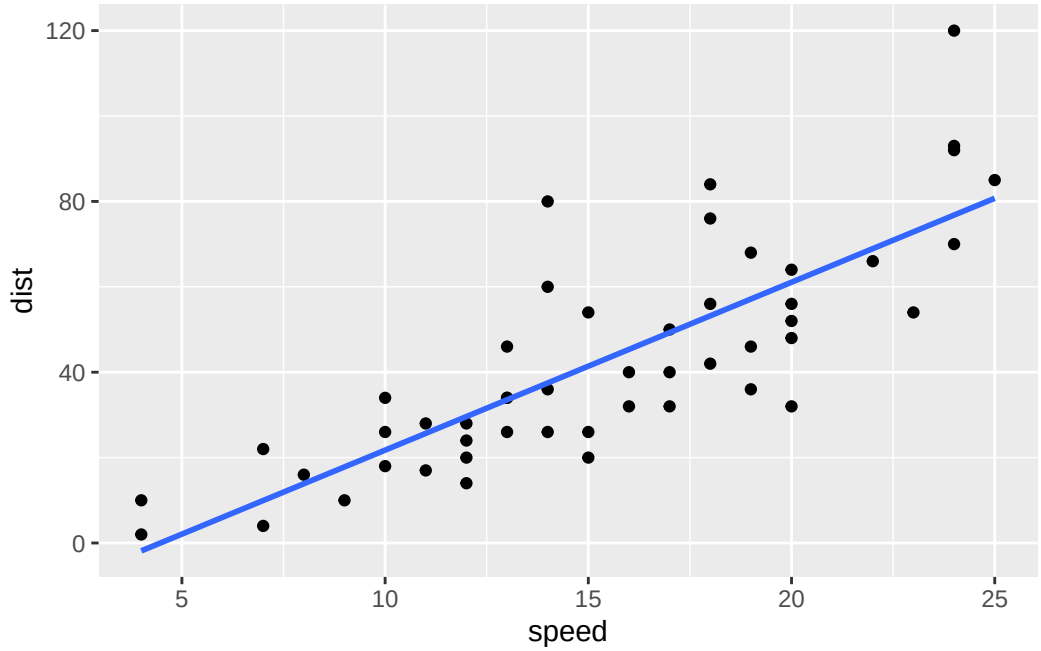
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



Adding false function

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE)
```

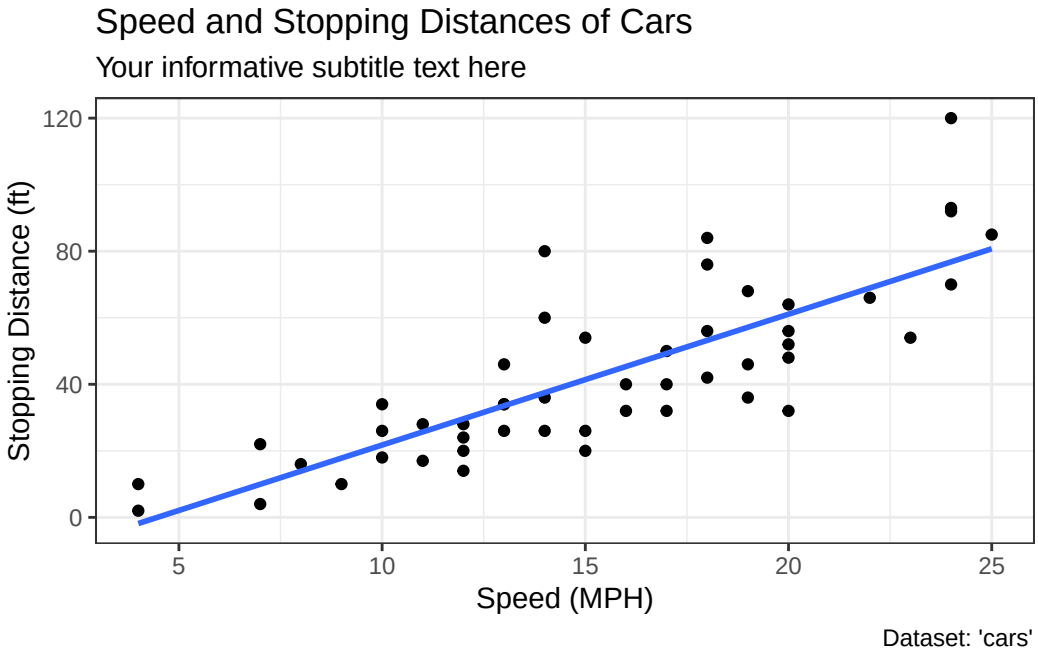
```
`geom_smooth()` using formula = 'y ~ x'
```



Finalizing graph

```
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'
```



Drug Expression Data

```
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
```

#Pulling Data

nrow(genes)

colnames(genes)

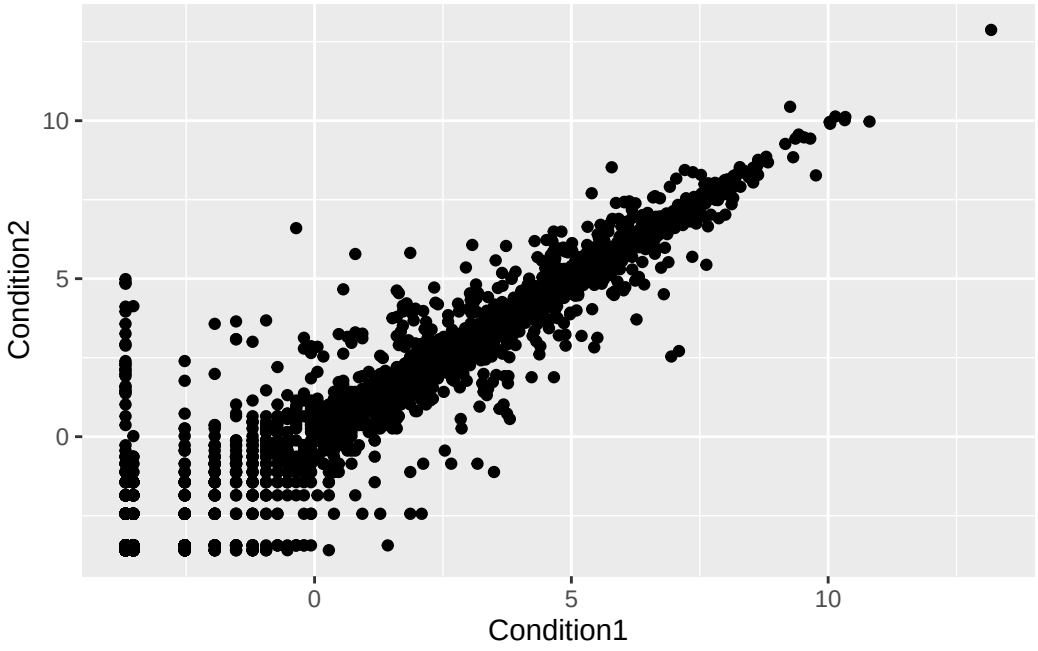
ncol(genes)

table(genes$State)

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

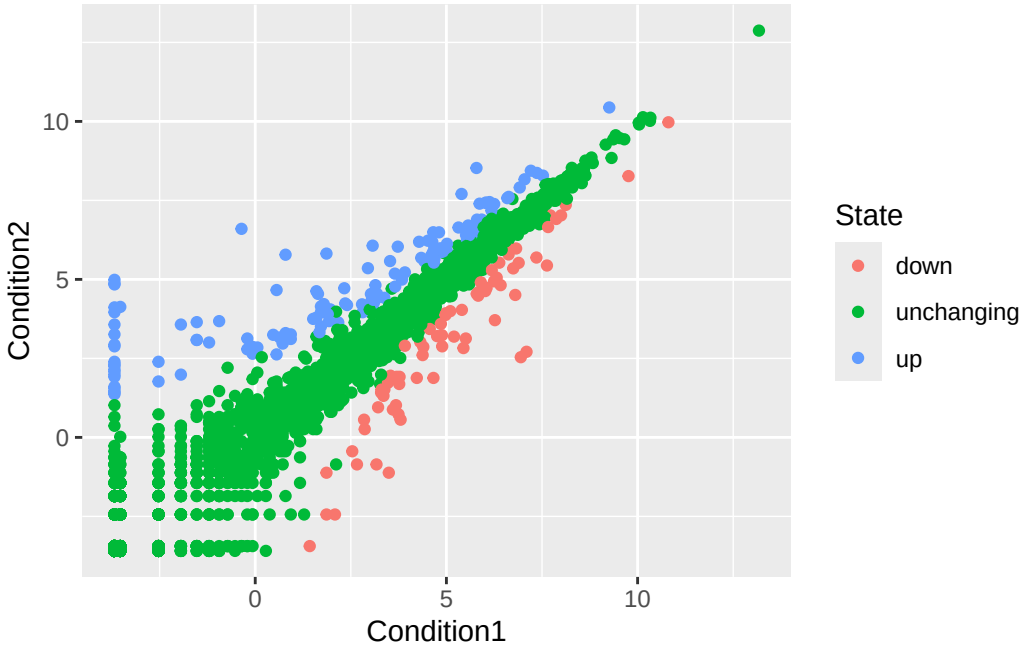
Creating new scatterplot

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



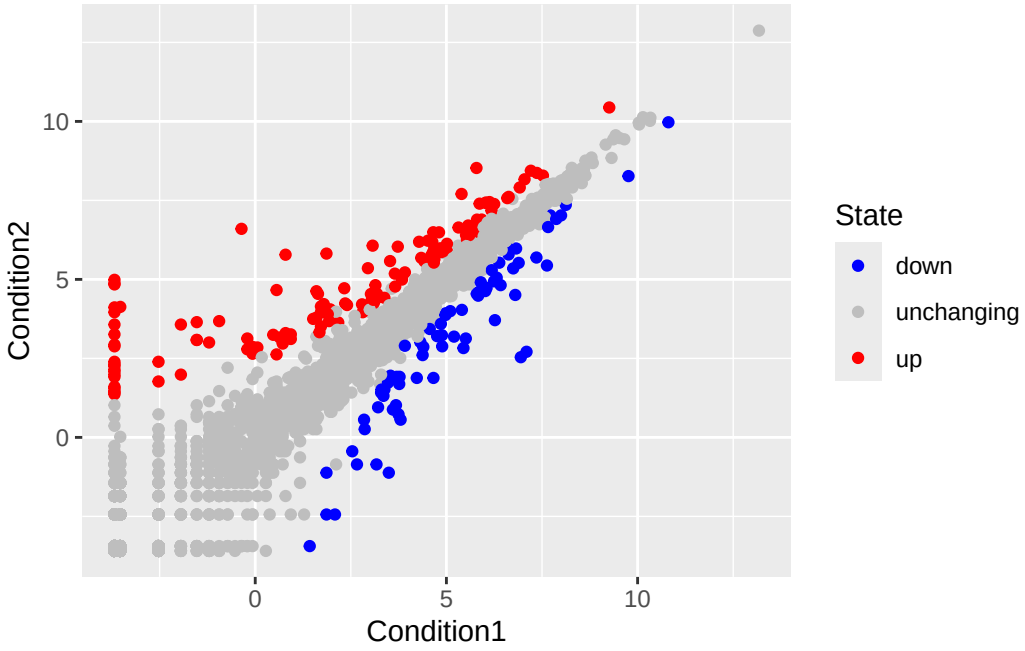
Adding aesthetics and trendline

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



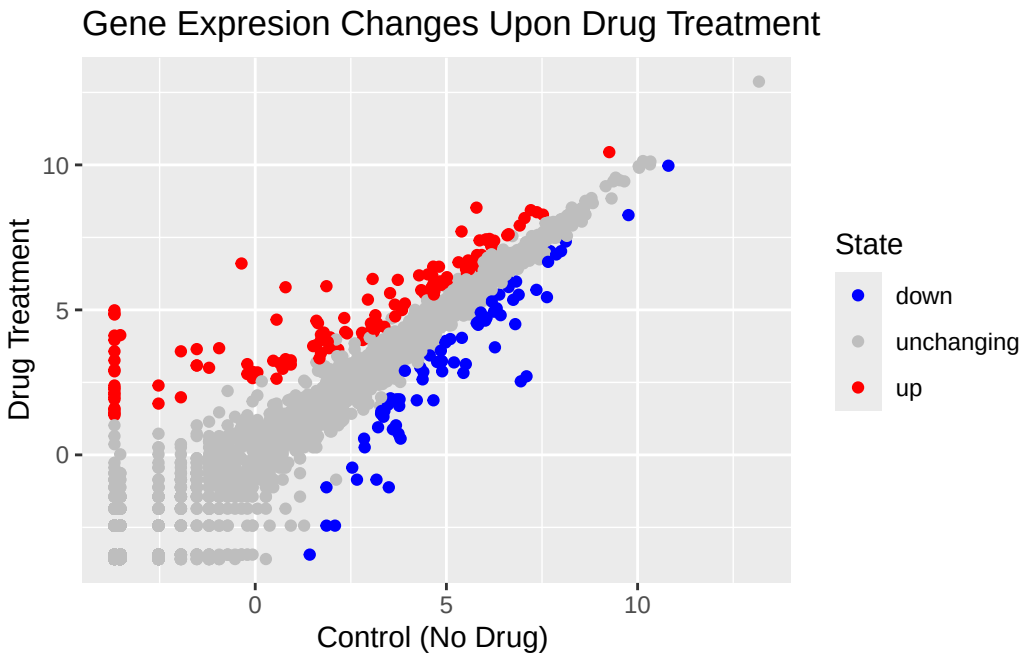
Changing color

```
p + scale_colour_manual( values=c("blue","gray","red") )
```



Changing axis names

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



Info

```
sessionInfo()
```

```
R version 4.3.3 (2024-02-29)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Sonoma 14.1.2

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/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

time zone: America/Los_Angeles
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base
```

```
other attached packages:
[1] ggplot2_3.5.0

loaded via a namespace (and not attached):
 [1] vctrs_0.6.5       nlme_3.1-164      cli_3.6.2         knitr_1.45
 [5] rlang_1.1.3       xfun_0.43         generics_0.1.3    jsonlite_1.8.8
 [9] labeling_0.4.3    glue_1.7.0        colorspace_2.1-0  htmltools_0.5.8.1
[13] scales_1.3.0      fansi_1.0.6       rmarkdown_2.26    grid_4.3.3
[17] evaluate_0.23     munsell_0.5.1     tibble_3.2.1      fastmap_1.1.1
[21] yaml_2.3.8        lifecycle_1.0.4   compiler_4.3.3    dplyr_1.1.4
[25] pkgconfig_2.0.3   mgcv_1.9-1        rstudioapi_0.16.0 lattice_0.22-6
[29] farver_2.1.1      digest_0.6.35     R6_2.5.1          tidyselect_1.2.1
[33] utf8_1.2.4        splines_4.3.3     pillar_1.9.0      magrittr_2.0.3
[37] Matrix_1.6-5      withr_3.0.0       tools_4.3.3       gtable_0.3.4
```