class05

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
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
```

## Including Plots

You can also embed plots, for example:
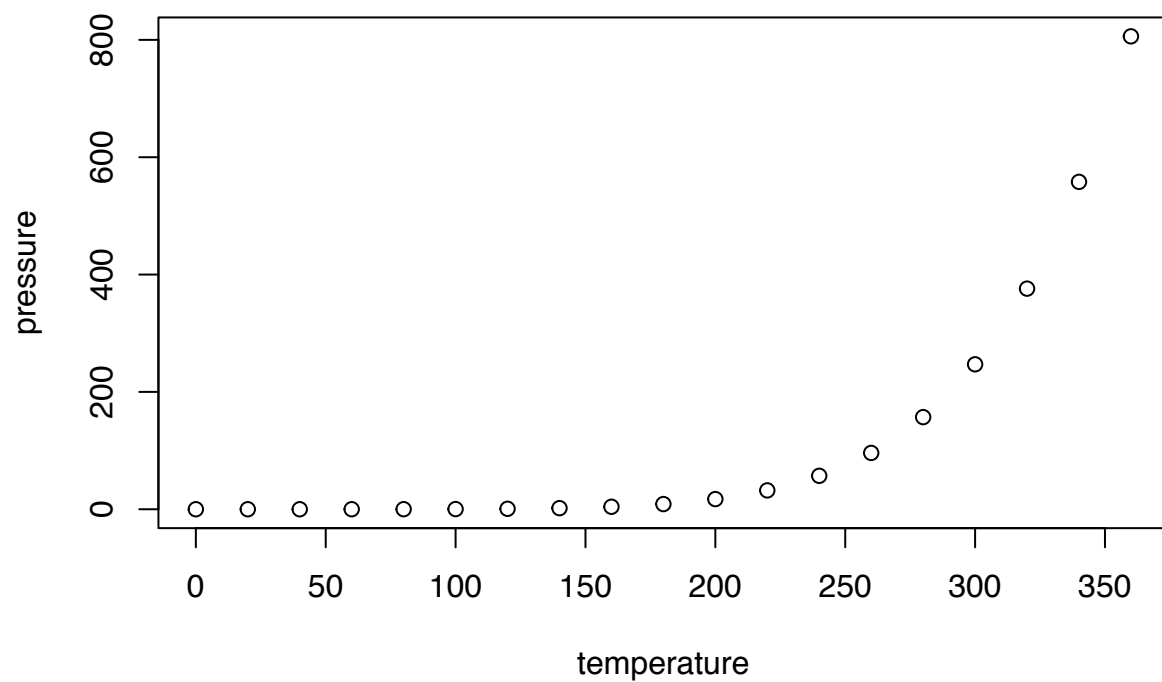
Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

All ggplot figures need at least 3 things:

-data (this is the data.frame with our numbers) -aesthetics("aes", how our data maps to the plot) geoms (do want lines, points, columns, etc...)

```r
library(ggplot2)
ggplot(data=cars) +
aes(x=speed, y=dist)+
  geom_point()
```
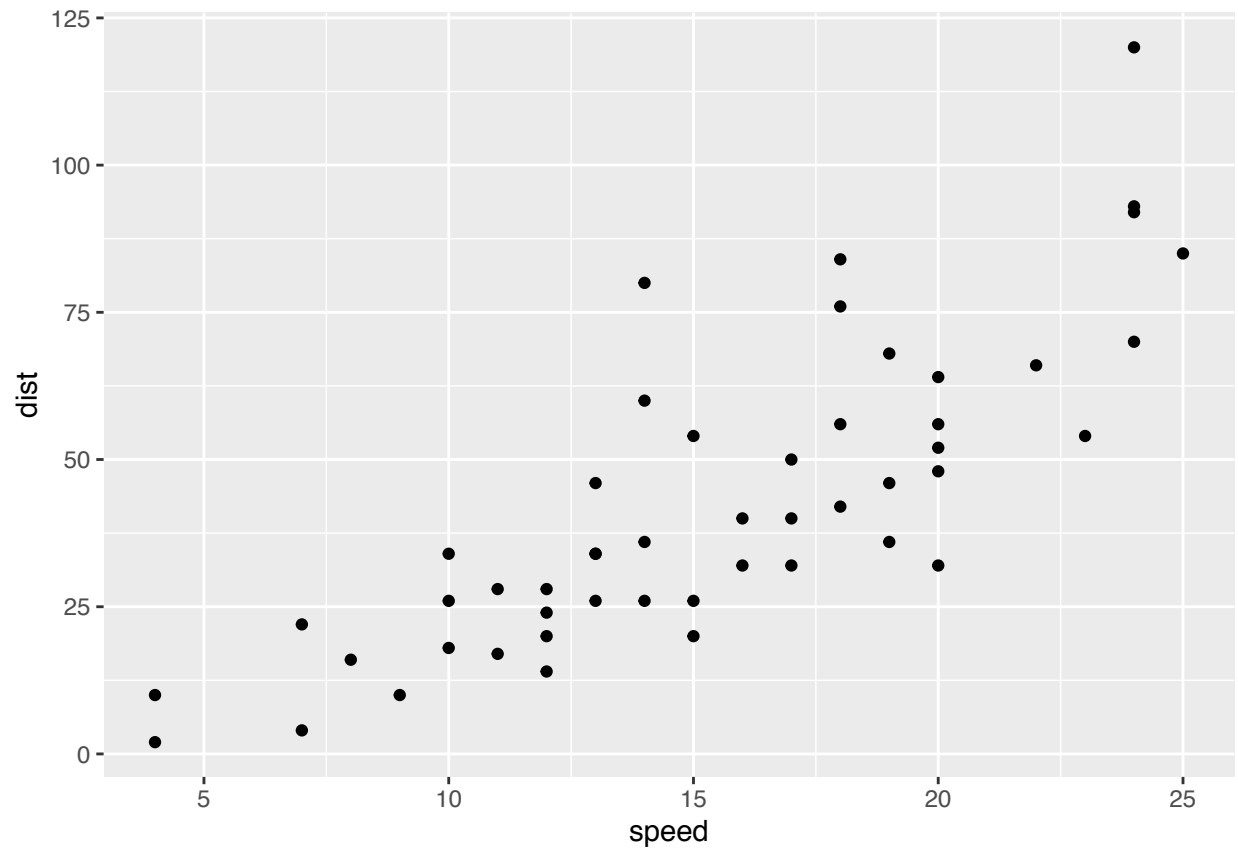
I want a trend line to show the relationship between the speed and stopping distance
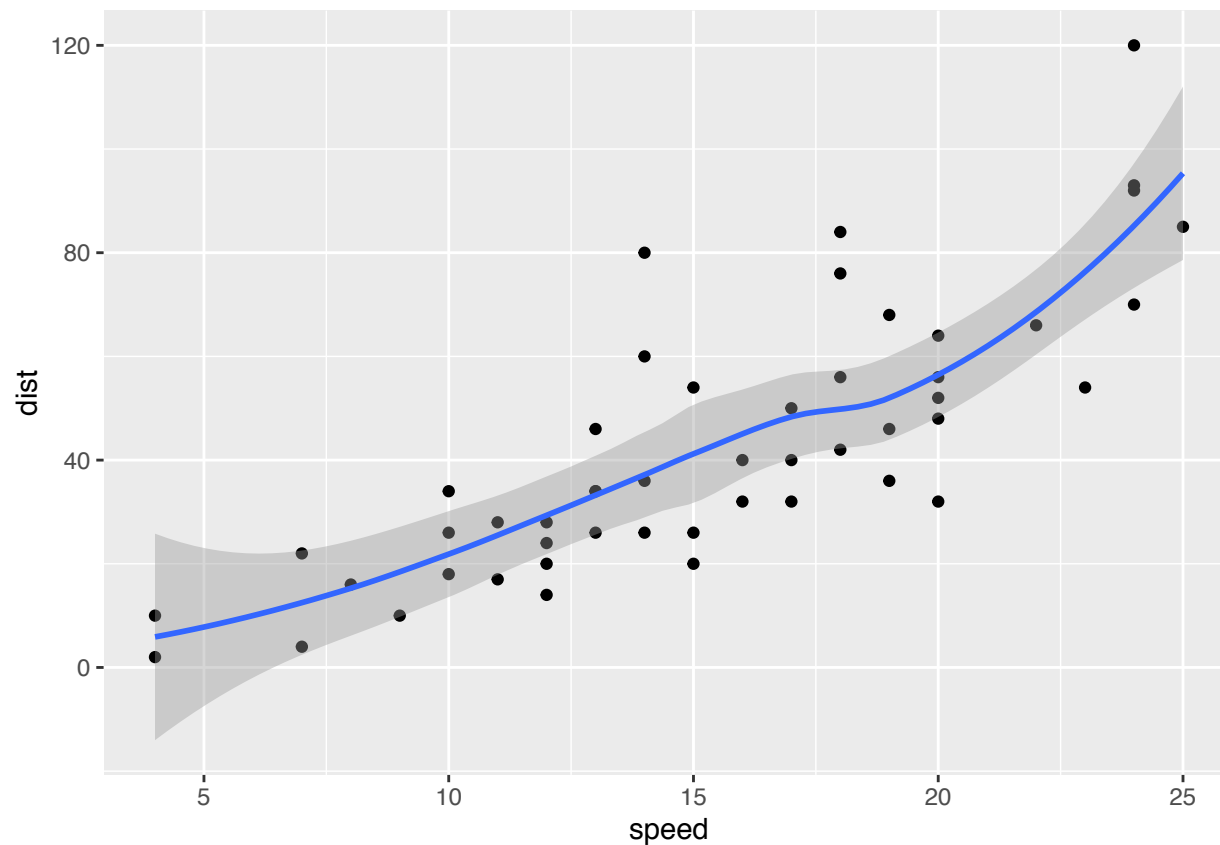
```
library(ggplot2)
ggplot(data=cars) +
aes(x=speed, y=dist)+
  geom_point()+
  geom_line()
```
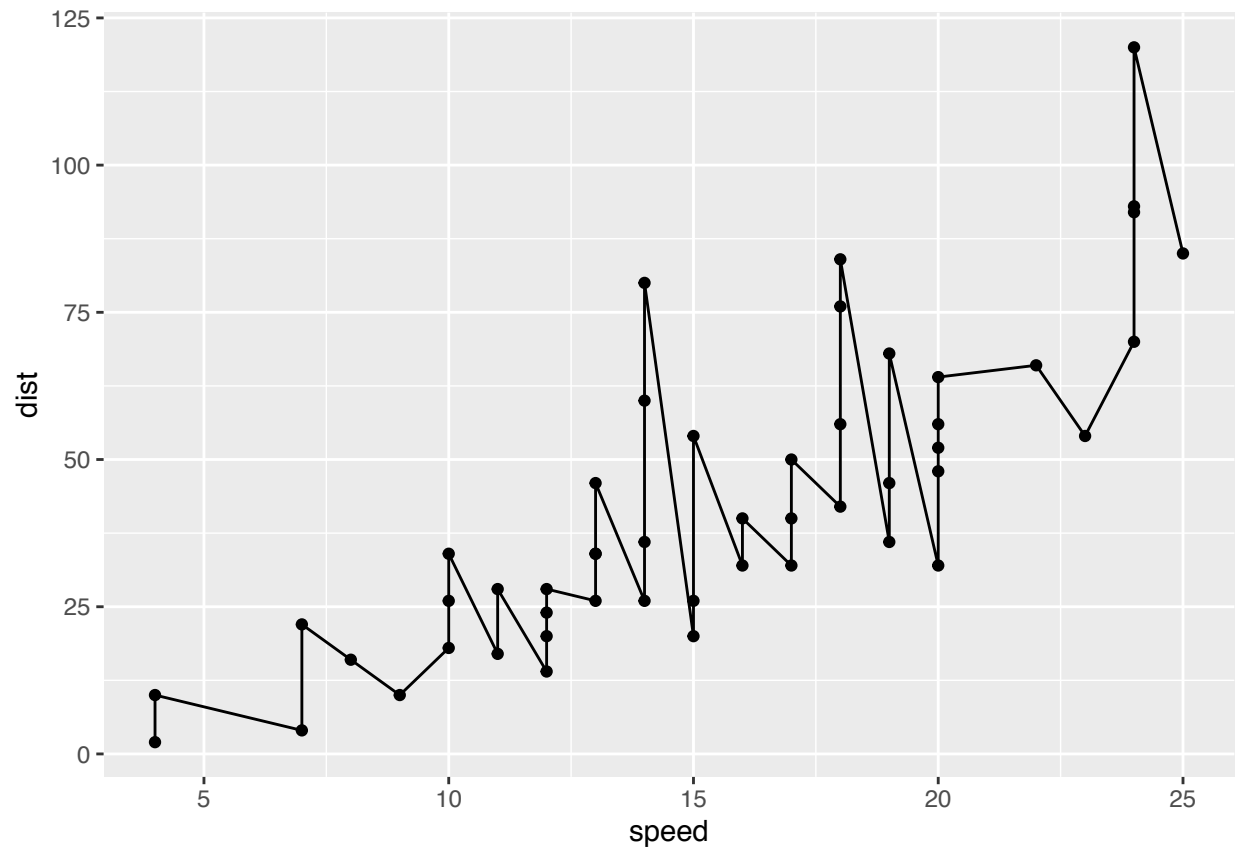
That is not what we want

```
library(ggplot2)
ggplot(data=cars) +
aes(x=speed, y=dist)+
  geom_point()+
  geom_smooth()
```

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

Gene expression Example

```
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
```

the 'head()' function will print out just the first few rows (6 by default)

```
nrow(genes)
```

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

```
colnames(genes)
```

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

```
ncol(genes)
```

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

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

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

```
ggplot(genes)+
  aes(Condition1,Condition2,color=State)+
  geom_point()+
  labs(title="Some Plot",subtitle="With a subtitle")
```

Some Plot
With a subtitle