Week 3: Data visualization Lab
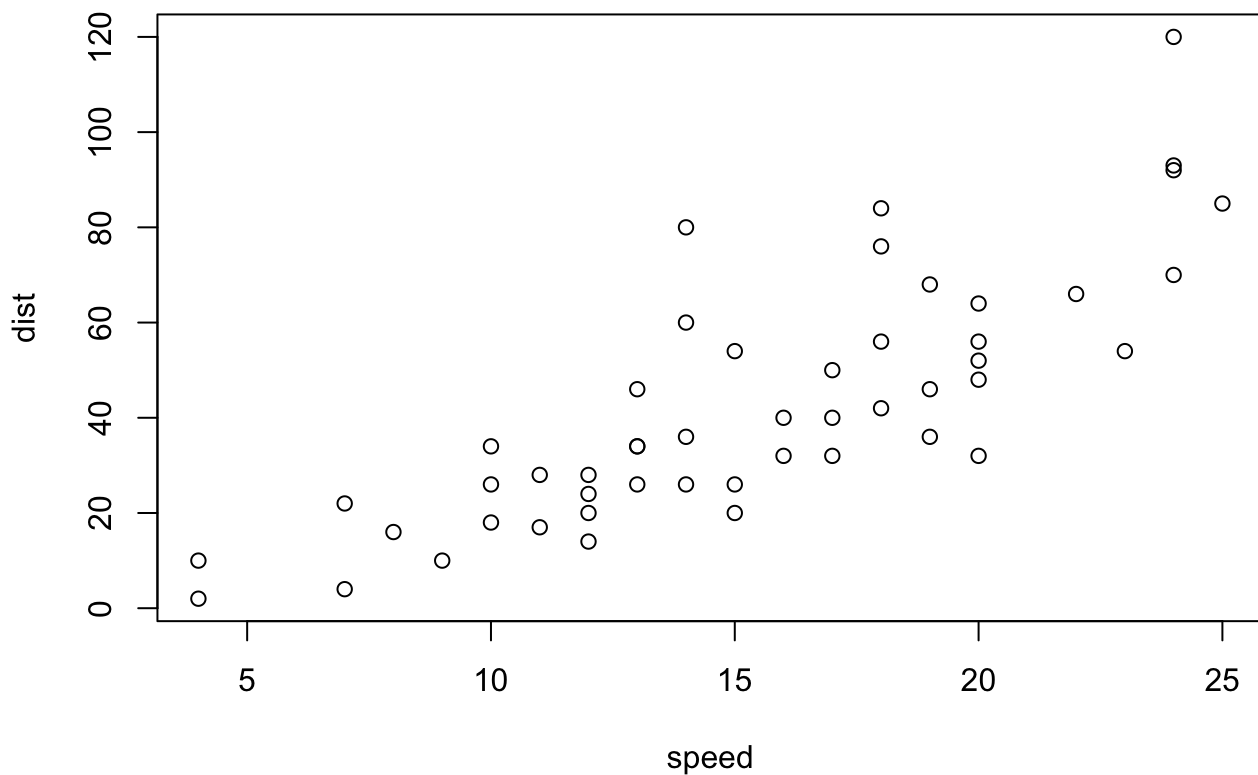
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```
# Week 3 Data visualization Lab

# Install the package ggplot2

#Any time I want to use this package I need to load it
library("ggplot2")

View(cars)

# A quick base R plot- this is not ggplot
plot(cars)
```
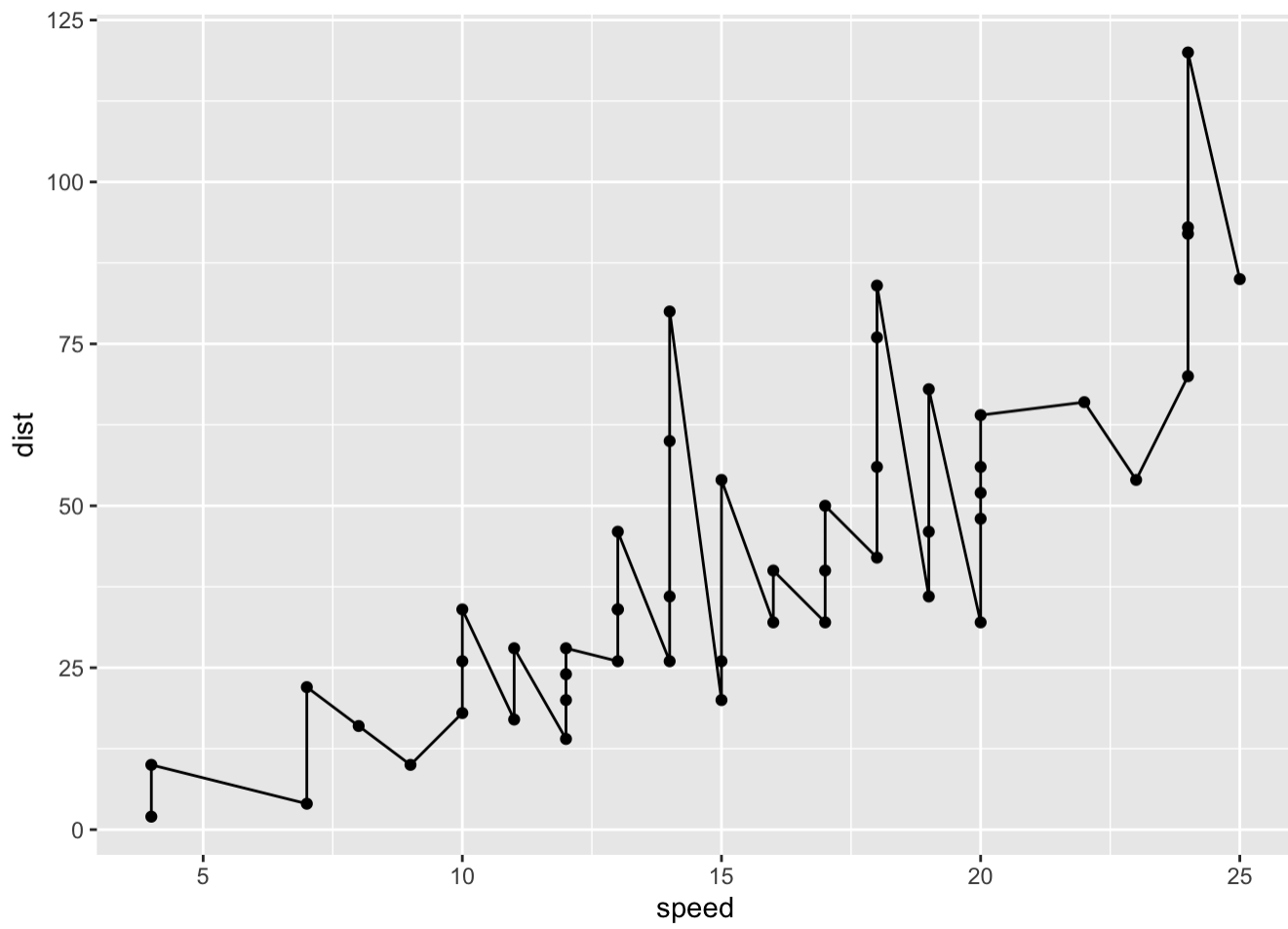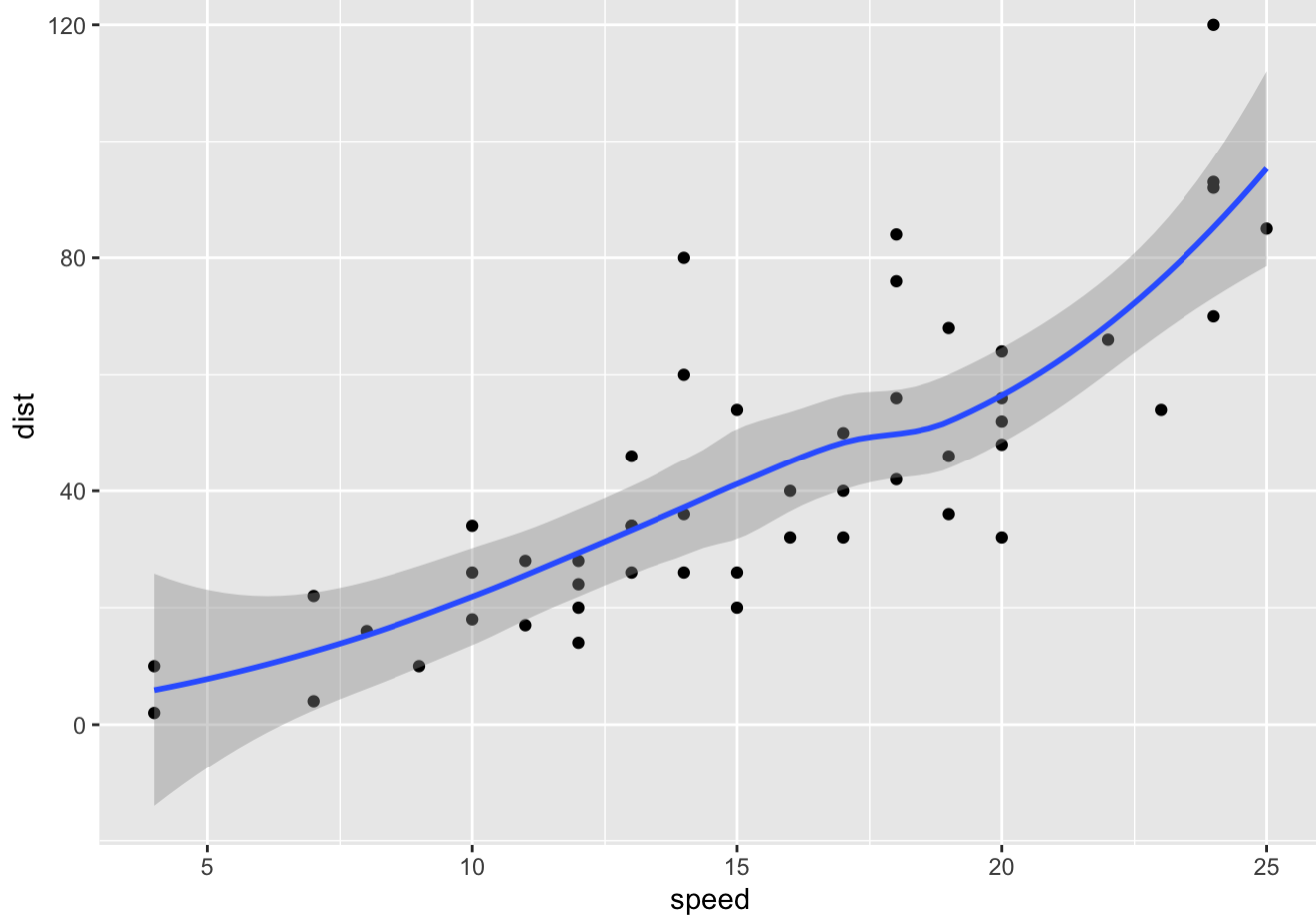


```
# Our first ggplot
# we need data + aes + geom
p <- ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point()

# Add a line geom with geom_line()
p + geom_line()
```
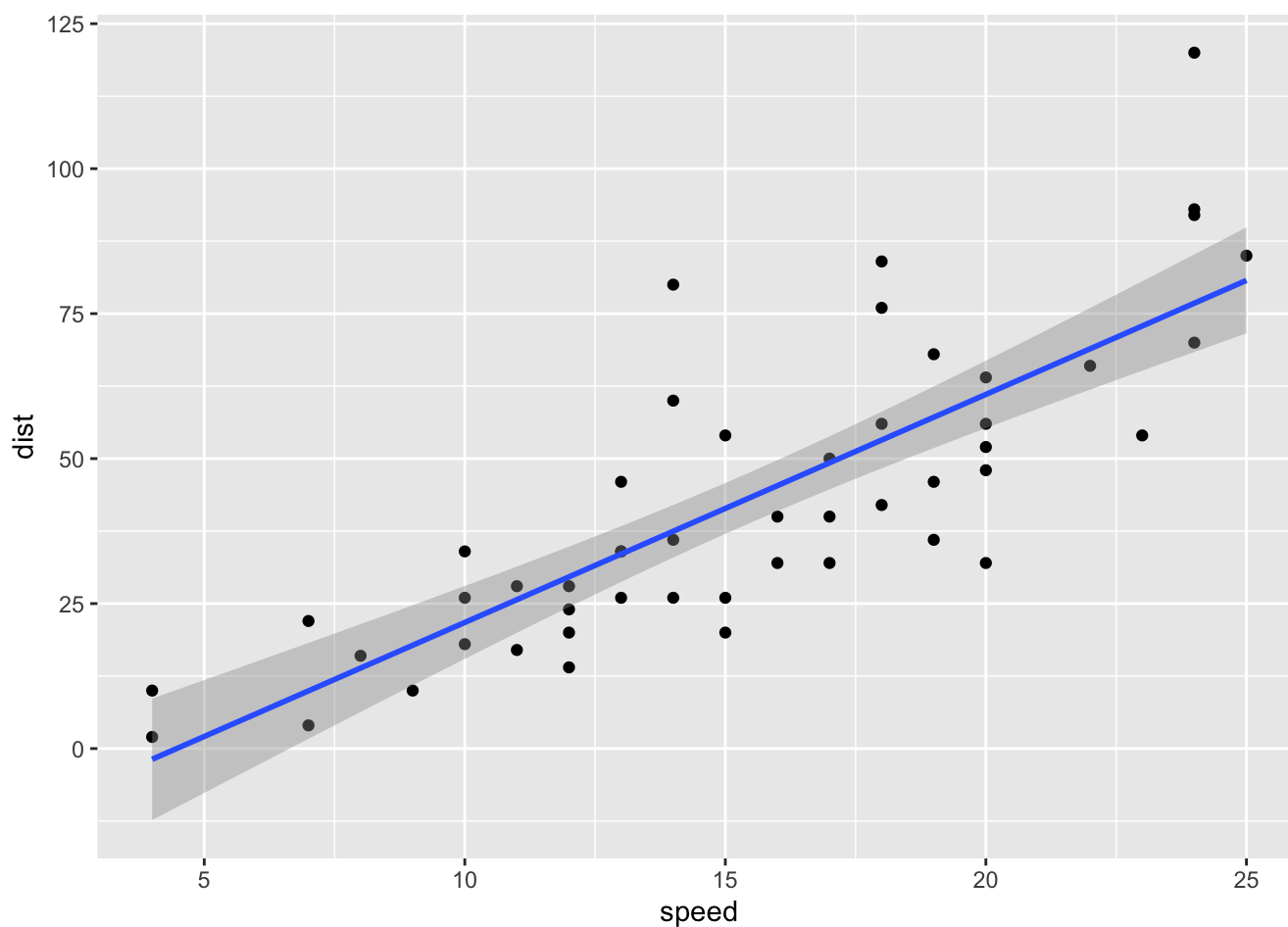
```
# Add a trend line close to the data
p + geom_smooth()
```

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

```
p + geom_smooth(method="lm")
```

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

```
# Read in our 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
```

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

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

```
# Q. How many 'up' regulated genes
table(genes$State)
```

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

```r
# Q. What fraction of total genes is up-regulated
round((table(genes$State) / nrow(genes)) * 100)
```

```
##
##       down unchanging         up
##          1         96          2
```

```r
# Let's make a first plot attempt
g <- ggplot(data=genes) +
aes(x=Condition1,y=Condition2, col=State) + geom_point()

# Remember to run g!!
g
```

```r
# Add some color
g + scale_color_manual(values=c("blue", "grey", "red")) +
  labs (title= "Gene expression changes", x="control (no drug)", y="experiment (with drug)") +
  theme_bw()
```