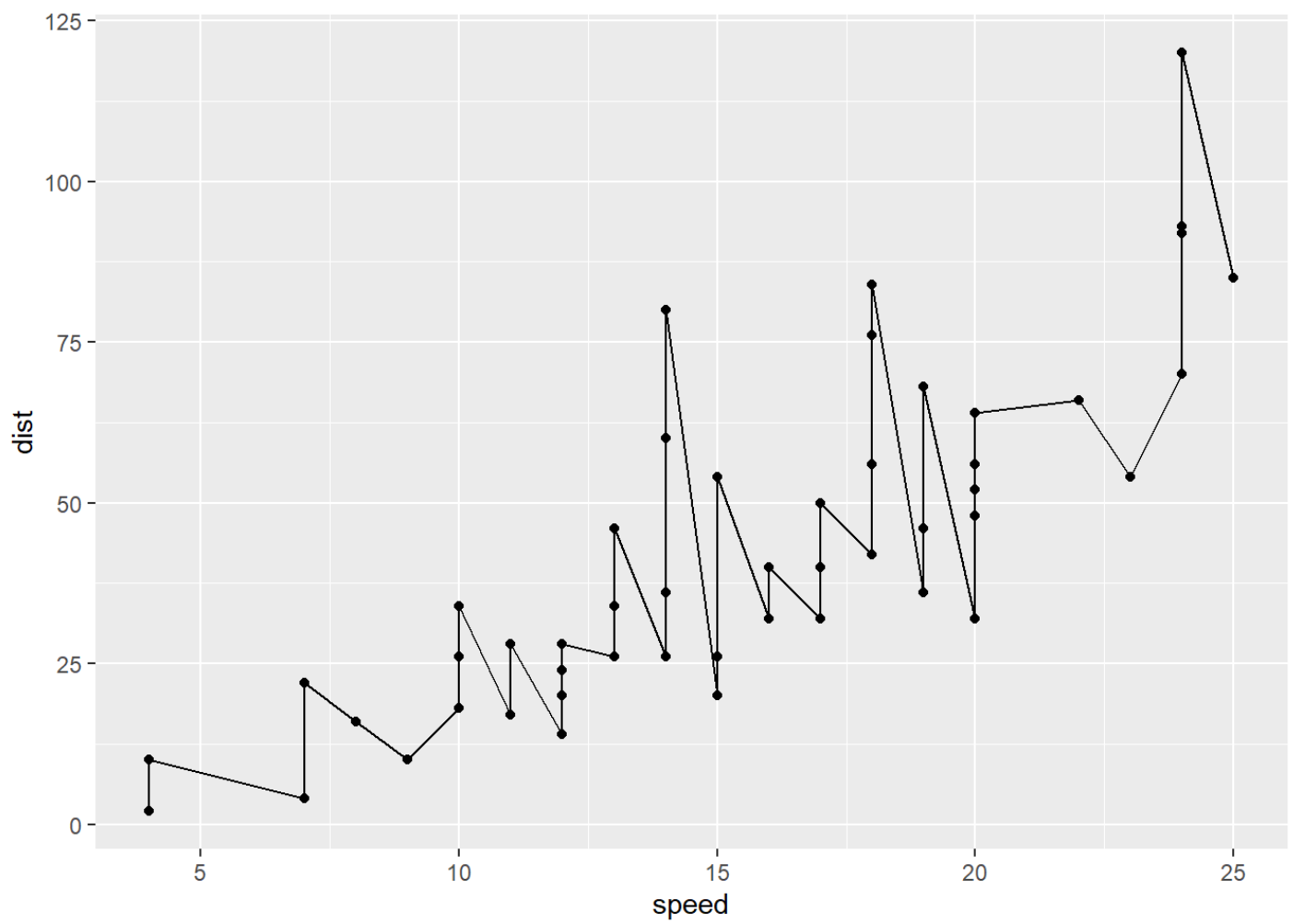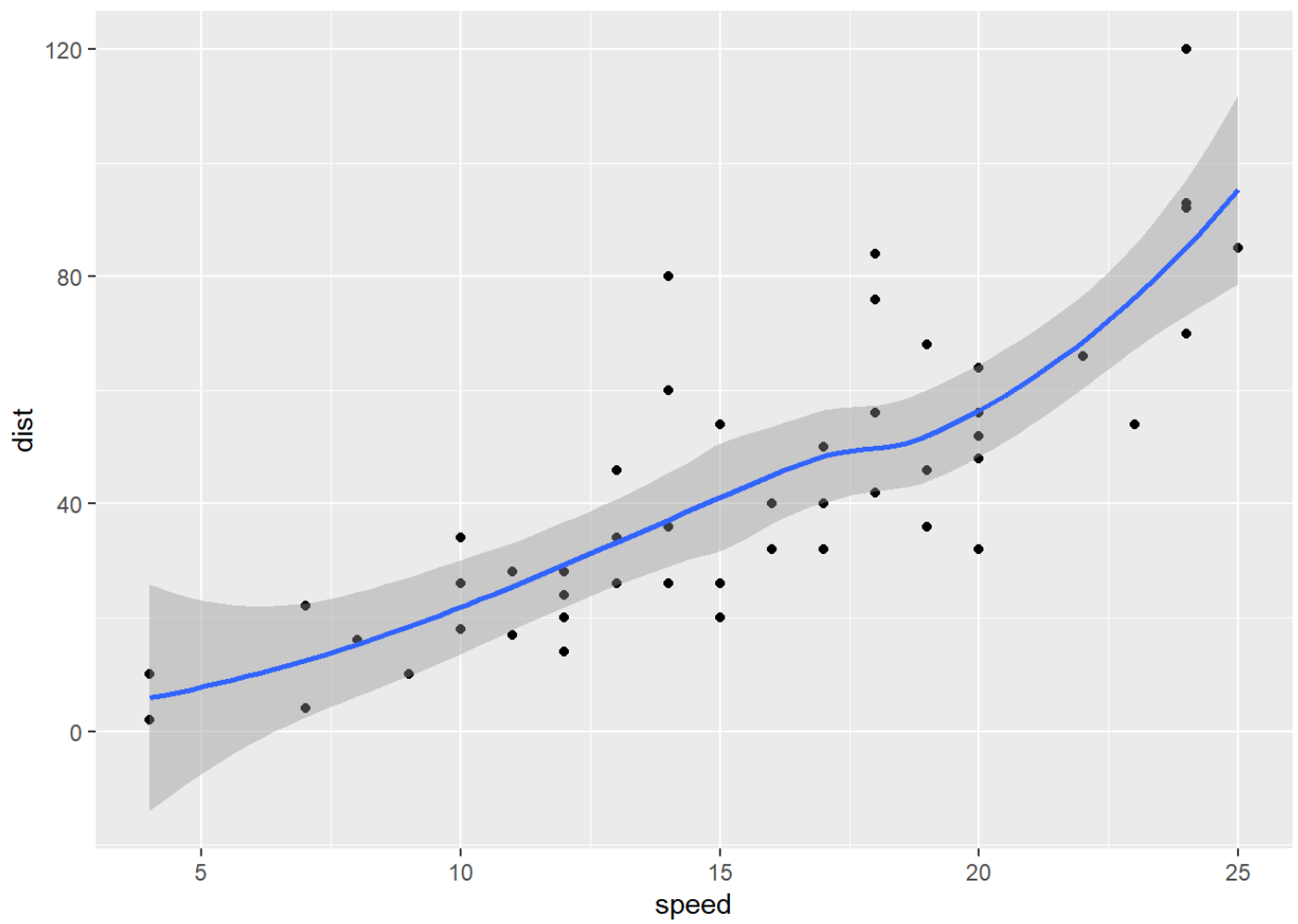# Class05

Norman Lee

10/21/2025

```r
##install the package ggplot
#install.package("ggplot2")

#load package
library(ggplot2)


#View(cars)
##quick plot but not actual ggplot
#plot(cars)

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

##Add a line
p + geom_line()
```
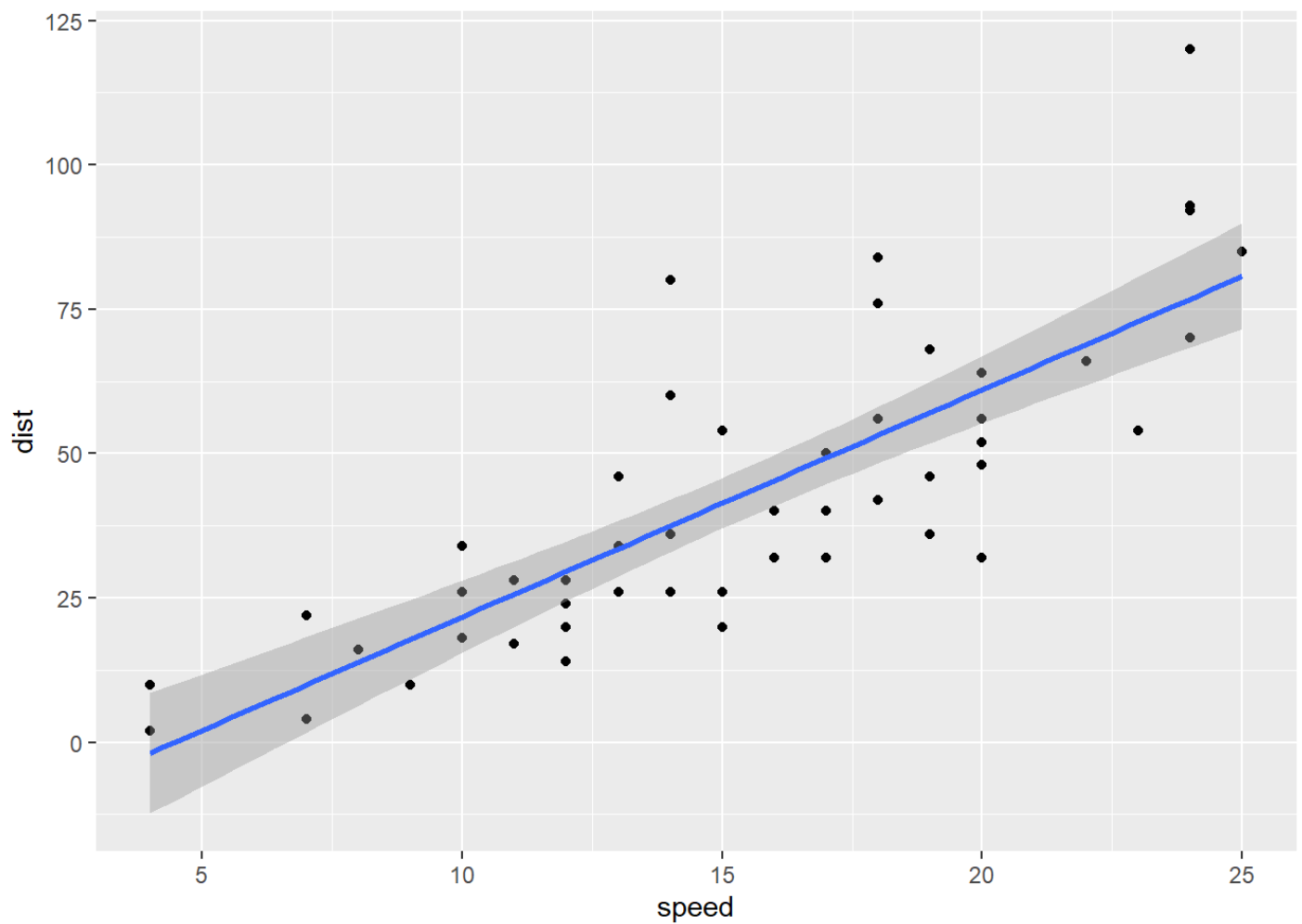
```
##line with best fit or trendline
p+ geom_smooth()
```

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

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

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

```
#-------#
#read in  drug expression

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
```

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

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

#add color
g + scale_colour_manual( values=c("blue","gray","red") )+
   labs(title="Gene Expresion Changes Upon Drug Treatment",
        x="Control (no drug) ",
        y="Drug Treatment")+
   theme_bw()
```


Gene Expresion Changes Upon Drug Treatment