Fitted Regression Model Lines

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```r
library(ggplot2)

#install.packages("alr3")
library(alr3)

#load Pearson-Lee data: collection of data, heights in inches of mothers
#and their daughters, on over 1100 families in England in the period 1893
#to 1898
ht <- heights
head(ht)
```

```
##   Mheight Dheight
## 1    59.7    55.1
## 2    58.2    56.5
## 3    60.6    56.0
## 4    60.7    56.8
## 5    61.8    56.0
## 6    55.5    57.9
```

```r
#adding fitted regression model lines
#base plot with 95% confidence region
sp <- ggplot(ht, aes(x=Mheight, y=Dheight))
sp + geom_point() + stat_smooth(method=lm, level=0.95)
```
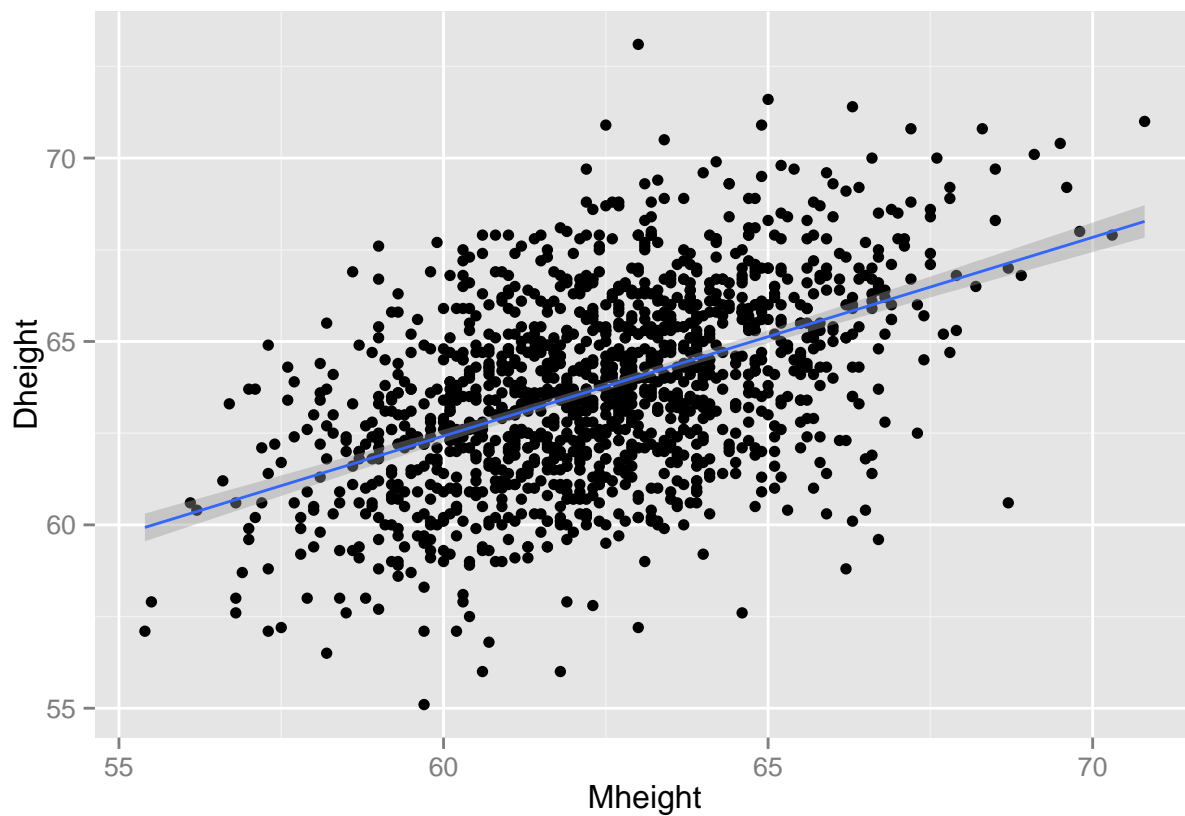
```
#fit logistic regression line
library(MASS) #for data
b <- biopsy
head(b)
```

```
##         ID V1 V2 V3 V4 V5 V6 V7 V8 V9    class
## 1 1000025  5  1  1  1  2  1  3  1  1   benign
## 2 1002945  5  4  4  5  7 10  3  2  1   benign
## 3 1015425  3  1  1  1  2  2  3  1  1   benign
## 4 1016277  6  8  8  1  3  4  3  7  1   benign
## 5 1017023  4  1  1  3  2  1  3  1  1   benign
## 6 1017122  8 10 10  8  7 10  9  7  1 malignant
```

```
b$classn[b$class=="benign"] <- 0
b$classn[b$class=="malignant"] <- 1
head(b)
```

```
##         ID V1 V2 V3 V4 V5 V6 V7 V8 V9    class classn
## 1 1000025  5  1  1  1  2  1  3  1  1   benign      0
## 2 1002945  5  4  4  5  7 10  3  2  1   benign      0
## 3 1015425  3  1  1  1  2  2  3  1  1   benign      0
## 4 1016277  6  8  8  1  3  4  3  7  1   benign      0
## 5 1017023  4  1  1  3  2  1  3  1  1   benign      0
## 6 1017122  8 10 10  8  7 10  9  7  1 malignant      1
```

```
#use smoothing method glm with binomial formula
ggplot(b, aes(x=V1, y=classn)) +
  geom_point(position=position_jitter(width=0.3, height=0.06), alpha=0.4,
             shape=21, size=1.5) +
  stat_smooth(method=glm, family=binomial)
```
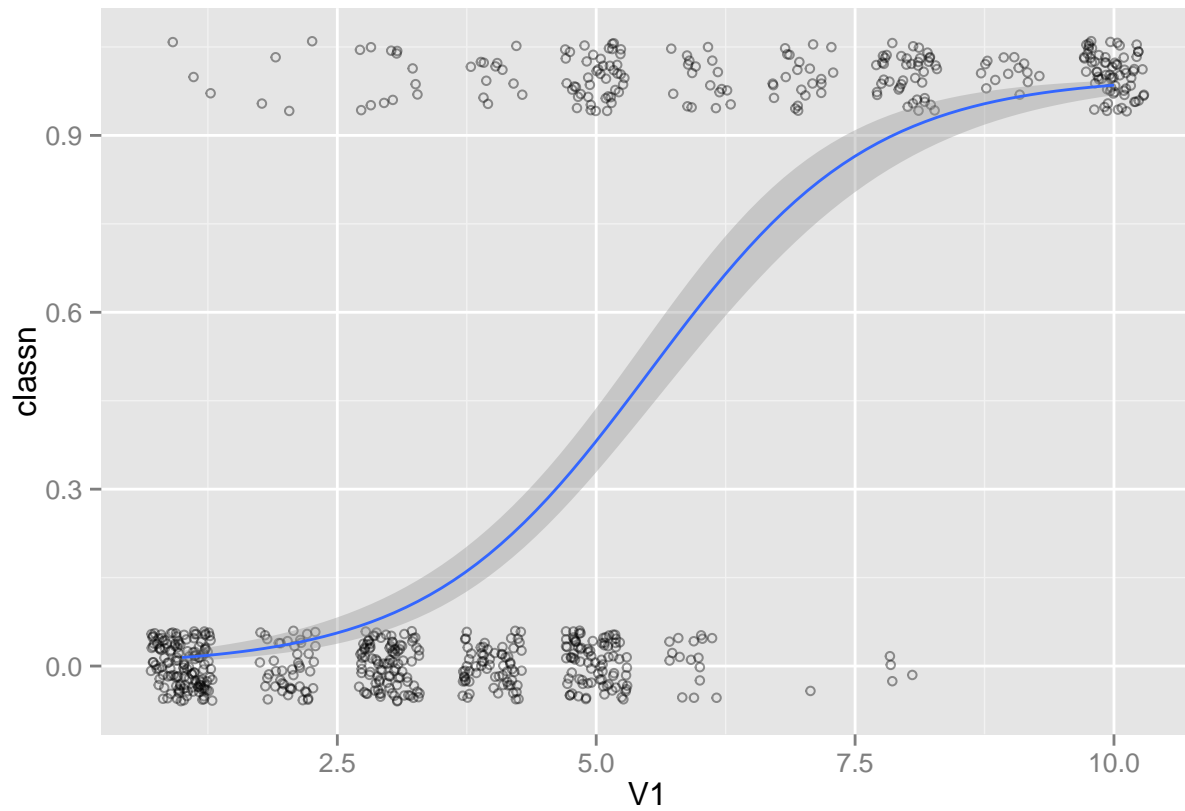


```
#use the stat_smooth() loess (locally weighted polynomial) curve method
    sp + geom_point(colour="gray") + stat_smooth(method=loess)
```