Skin Cancer

Tarek El-Hajjaoui

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Loading the dataset

file_path = '/Users/Tarek/Documents/UCI_MDS_Coding/Stats210P/R_Statistical_Modeling/SkinCancer/skincanc
Skincancer = read.table(file_path, header=TRUE, sep="", dec=".")

summary(Skincancer)

##	State	Lat	Mort	Ocean
##	Length:49	Min. :28.00	Min. : 86.0	Min. :0.000
##	Class :character	1st Qu.:36.00	1st Qu.:128.0	1st Qu.:0.000
##	Mode :character	Median :39.50	Median :147.0	Median :0.000
##		Mean :39.53	Mean :152.9	Mean :0.449
##		3rd Qu.:43.00	3rd Qu.:178.0	3rd Qu.:1.000
##		Max. :47.50	Max. :229.0	Max. :1.000
##	Long			
##	Min. : 69.00			
##	1st Qu.: 78.50			
##	Median : 89.50			
##	Mean : 90.94			
##	3rd Qu.:100.00			
##	Max. :121.00			

Creating a Linear Model where latitude (X) is predictive of mortality rate (Y) due to skin cancer.

```
model <- lm(Mort ~ Lat, data=Skincancer)</pre>
summary(model)
##
## Call:
## lm(formula = Mort ~ Lat, data = Skincancer)
##
## Residuals:
##
      Min
               1Q Median
                               ЗQ
                                      Max
                    0.972 12.006 43.938
## -38.972 -13.185
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 389.1894
                          23.8123
                                    16.34 < 2e-16 ***
                                    -9.99 3.31e-13 ***
## Lat
               -5.9776
                           0.5984
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 19.12 on 47 degrees of freedom
## Multiple R-squared: 0.6798, Adjusted R-squared: 0.673
## F-statistic: 99.8 on 1 and 47 DF, p-value: 3.309e-13
```

Find and interpret a 99% confidence interval for the mean mortality rate when Lat=40.

```
predict(model, list(Lat=40), level = 0.99, interval= "c")

## fit lwr upr
## 1 150.0839 142.7148 157.453
```

Find and interpret a 99% prediction interval for the individual mortality rate when Lat=40.

```
predict(model, list(Lat=40), level = 0.99, interval= "p")
## fit lwr upr
## 1 150.0839 98.24214 201.9257
```

Plotting 99% confidence and prediction intervals:

```
predictions <- predict(model, level = 0.99, interval="prediction")
new_df <- cbind(Skincancer, predictions)

ggplot(new_df, aes(x=Lat, y=Mort))+
    geom_point() +
    geom_line(aes(y=lwr), color = "red", linetype = "dashed")+
    geom_line(aes(y=upr), color = "red", linetype = "dashed")+
    geom_smooth(method=lm, se=TRUE)</pre>
```

