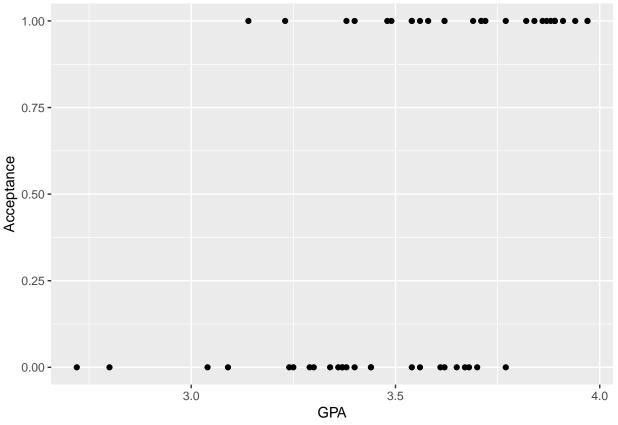
Stats_Term_Project

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```
library(ggplot2)
library(Stat2Data)
library(broom)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
#Load the MedGPA data from the Stats2Data library
data("MedGPA")
#Select the GPA and the Acceptance
head(MedGPA%>%select(GPA,Acceptance))
##
      GPA Acceptance
## 1 3.62
## 2 3.84
## 3 3.23
                   1
## 4 3.69
## 5 3.38
                   1
## 6 3.72
                   1
#Visualize the data using a scatter plot
data_points<-ggplot(data = MedGPA, aes(y = Acceptance, x = GPA))+geom_point()</pre>
data_points
```



#Fit the logistic model using the glm function
mod<-glm(Acceptance-GPA, data =MedGPA, family = binomial)
summary(mod)</pre>

```
##
## Call:
## glm(formula = Acceptance ~ GPA, family = binomial, data = MedGPA)
##
## Deviance Residuals:
##
      Min
                1Q
                     Median
                                  3Q
                                          Max
## -1.7805 -0.8522
                     0.4407
                              0.7819
                                       2.0967
##
## Coefficients:
              Estimate Std. Error z value Pr(>|z|)
##
## (Intercept) -19.207
                            5.629 -3.412 0.000644 ***
                                   3.454 0.000553 ***
## GPA
                 5.454
                            1.579
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
      Null deviance: 75.791 on 54 degrees of freedom
## Residual deviance: 56.839 on 53 degrees of freedom
## AIC: 60.839
##
## Number of Fisher Scoring iterations: 4
```

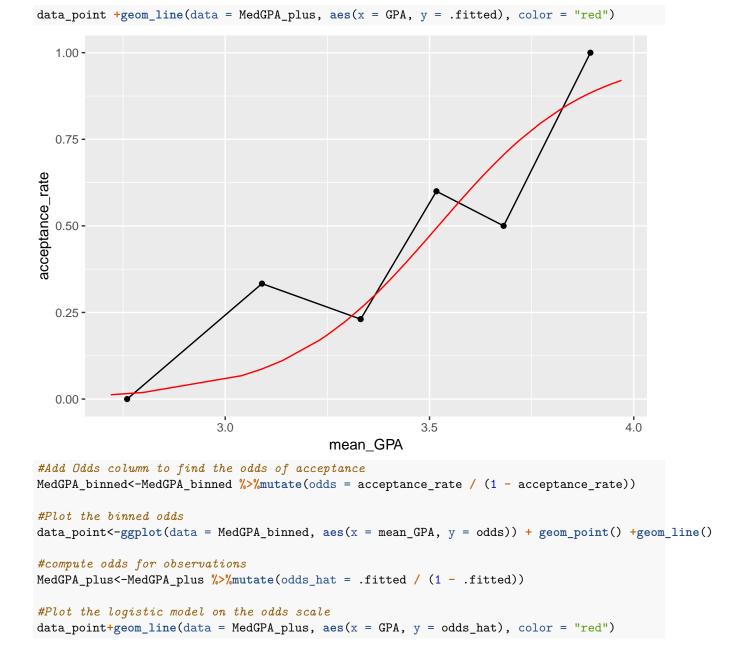
#Bin the GPA column and find the average GPA and Acceptance Rate for each bin

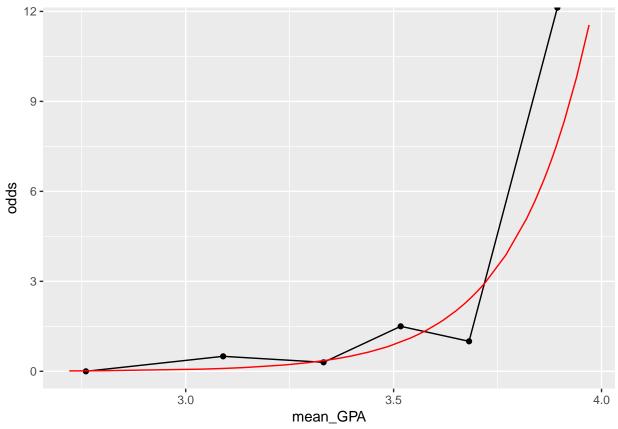
MedGPA_binned<-MedGPA%>%mutate(Bins = cut(GPA, breaks=seq(0, 4, by=.20)))%>%group_by(Bins)%>%summarize()

MedGPA_binned

GPA

```
## # A tibble: 6 x 3
##
    Bins
               mean_GPA acceptance_rate
     <fct>
##
                  <dbl>
                                   <dbl>
## 1 (2.6,2.8]
                   2.76
                                   0.333
## 2 (3,3.2]
                   3.09
                                   0.231
## 3 (3.2,3.4]
                   3.33
## 4 (3.4,3.6]
                   3.52
                                   0.6
## 5 (3.6,3.8]
                   3.68
                                   0.5
## 6 (3.8,4]
                   3.89
                                   1
#Plot the binned Mean GPA
data_point<-ggplot(data = MedGPA_binned, aes(x = mean_GPA, y = acceptance_rate)) +</pre>
 geom_point() + geom_line()
#Augment the model, type.predict argument has been set to "response" to ensure fitted values are on the
MedGPA_plus<-mod%>%augment(type.predict = "response")
#plot logistic model on probability scale
```





```
#Compute the log of the odds of acceptance
MedGPA_binned<-MedGPA_binned%>%mutate(log_odds=log(acceptance_rate/(1 - acceptance_rate)))

#Plot the log of the odds of acceptance for the binned GPA
data_point<-ggplot(data = MedGPA_binned, aes(x = mean_GPA, y = log_odds)) +geom_point() + geom_line()

# compute log odds for observations
MedGPA_plus<-MedGPA_plus%>%mutate(log_odds_hat = log(.fitted/(1 - .fitted)))

#Plot the logistic model on the log odds scale
data_point+geom_line(data = MedGPA_plus, aes(x = GPA, y = log_odds_hat), color = "red")
```

