

Homework 3: The Application of Logistic Regression to Examine the Predictors of Car Crashes Caused by Alcohol

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```
mydata <- read.csv("Logistic Regression Data.csv")  
  
DRINKING_D.tab <- table(mydata$DRINKING_D)  
prop.table(DRINKING_D.tab) #94% of crashes did not involve drunk driver while 5.75 did
```

```
0           1  
0.9426944 0.0573056
```

```
CrossTable(mydata$DRINKING_D, mydata$FATAL_OR_M, prop.r=FALSE, prop.chisq=FALSE, chisq=FALSE,
```

Cell Contents	
	N
N / Col Total	

Total Observations in Table: 43364

	mydata\$FATAL_OR_M		Row Total
mydata\$DRINKING_D	0	1	

0	39698	1181	40879	
	0.945	0.863		
-----	-----	-----	-----	-----
1	2297	188	2485	
	0.055	0.137		
-----	-----	-----	-----	-----
Column Total	41995	1369	43364	
	0.968	0.032		
-----	-----	-----	-----	-----

```
CrossTable(mydata$DRINKING_D, mydata$OVERTURNED, prop.r=FALSE,prop.chisq=FALSE, chisq=FALSE,
```

Cell Contents	
-----	-----
	N
	N / Col Total
-----	-----

Total Observations in Table: 43364

mydata\$DRINKING_D	mydata\$OVERTURNED		Row Total
	0	1	
0	40267	612	40879
	0.944	0.848	
-----	-----	-----	-----
1	2375	110	2485
	0.056	0.152	
-----	-----	-----	-----
Column Total	42642	722	43364
	0.983	0.017	
-----	-----	-----	-----

```
CrossTable(mydata$DRINKING_D, mydata$CELL_PHONE ,prop.r=FALSE,prop.chisq=FALSE, chisq=FALSE, pr
```

Cell Contents

	N	
	N / Col Total	

Total Observations in Table: 43364

		mydata\$CELL_PHONE		Row Total
mydata\$DRINKING_D	0	1		
0	40453	426	40879	
	0.943	0.938		
1	2457	28	2485	
	0.057	0.062		
Column Total	42910	454	43364	
	0.990	0.010		

```
CrossTable(mydata$DRINKING_D, mydata$SPEEDING ,prop.r=FALSE,prop.chisq=FALSE, chisq=FALSE, pr
```

Cell Contents

	N	
	N / Col Total	

Total Observations in Table: 43364

		mydata\$SPEEDING		Row Total
		0	1	
mydata\$DRINKING_D	0	39618	1261	40879
		0.947	0.829	
mydata\$DRINKING_D	1	2225	260	2485
		0.053	0.171	
Column Total		41843	1521	43364
		0.965	0.035	

```
CrossTable(mydata$DRINKING_D, mydata$AGGRESSIVE ,prop.r=FALSE,prop.chisq=FALSE, chisq=FALSE,)
```

Cell Contents	
	N
	N / Col Total

Total Observations in Table: 43364

		mydata\$AGGRESSIVE		Row Total
		0	1	
mydata\$DRINKING_D	0	22357	18522	40879
		0.934	0.953	
mydata\$DRINKING_D	1	1569	916	2485
		0.066	0.047	
Column Total		23926	19438	43364
		0.552	0.448	

```
-----|-----|-----|-----|
```

```
CrossTable(mydata$DRINKING_D, mydata$DRIVER1617 ,prop.r=FALSE,prop.chisq=FALSE, chisq=FALSE, p
```

Cell Contents

```
|-----|  
| N |  
| N / Col Total |  
|-----|
```

Total Observations in Table: 43364

		mydata\$DRIVER1617		Row Total
mydata\$DRINKING_D	0	1		
0	40205	674	40879	
	0.942	0.983		
1	2473	12	2485	
	0.058	0.017		
Column Total	42678	686	43364	
	0.984	0.016		

```
CrossTable(mydata$DRINKING_D, mydata$DRIVER65PLUS ,prop.r=FALSE,prop.chisq=FALSE, chisq=FALSE, p
```

Cell Contents

```
|-----|  
| N |  
| N / Col Total |  
|-----|
```

```
|-----|
```

Total Observations in Table: 43364

		mydata\$DRIVER65PLUS		Row Total
mydata\$DRINKING_D		0	1	
0	36642	4237	40879	
	0.939	0.973		
1	2366	119	2485	
	0.061	0.027		
Column Total	39008	4356	43364	
	0.900	0.100		

```
CrossTable(mydata$DRINKING_D, mydata$FATAL_OR_M, prop.r=FALSE,prop.chisq=FALSE, chisq=TRUE, p
```

```
Cell Contents  
|-----|  
| N |  
| N / Col Total |  
|-----|
```

Total Observations in Table: 43364

		mydata\$FATAL_OR_M		Row Total
mydata\$DRINKING_D		0	1	
0	39698	1181	40879	
	0.945	0.863		
1	2297	188	2485	

	0.055	0.137	
Column Total	41995	1369	43364
	0.968	0.032	

Statistics for All Table Factors

Pearson's Chi-squared test

Pearson's Chi-squared test with Yates' continuity correction

```
CrossTable(mydata$DRINKING_D, mydata$OVERTURNED, prop.r=FALSE, prop.chisq=TRUE, chisq=FALSE, p=FALSE)
```

Cell Contents

		N
Chi-square contribution	N / Col Total	

Total Observations in Table: 43364

	mydata\$OVERTURNED		
mydata\$DRINKING_D	0	1	Row Total
0	40267	612	40879
	0.117	6.919	
	0.944	0.848	

1	2375	110	2485	
	1.927	113.824		
	0.056	0.152		
-----	-----	-----	-----	-----
Column Total	42642	722	43364	
	0.983	0.017		
-----	-----	-----	-----	-----

```
CrossTable(mydata$DRINKING_D, mydata$CELL_PHONE ,prop.r=FALSE,prop.chisq=FALSE, chisq=TRUE,p
```

Cell Contents	

	N
	N / Col Total

Total Observations in Table: 43364

		mydata\$CELL_PHONE		Row Total
mydata\$DRINKING_D	0	1		
0	40453	426	40879	
	0.943	0.938		
-----	-----	-----	-----	-----
1	2457	28	2485	
	0.057	0.062		
-----	-----	-----	-----	-----
Column Total	42910	454	43364	
	0.990	0.010		
-----	-----	-----	-----	-----

Statistics for All Table Factors

Pearson's Chi-squared test

```

-----  

Chi^2 = 0.162071      d.f. = 1      p = 0.6872569  

Pearson's Chi-squared test with Yates' continuity correction  

-----  

Chi^2 = 0.09065262      d.f. = 1      p = 0.7633491

```

```
CrossTable(mydata$DRINKING_D, mydata$SPEEDING, prop.r=FALSE, prop.chisq=FALSE, chisq=TRUE, prop
```

Cell Contents	
	N
	N / Col Total

Total Observations in Table: 43364

		mydata\$SPEEDING		Row Total
mydata\$DRINKING_D		0	1	
0	0	39618	1261	40879
	1	0.947	0.829	
1	1	2225	260	2485
	1	0.053	0.171	
Column Total		41843	1521	43364
		0.965	0.035	

Statistics for All Table Factors

```
Pearson's Chi-squared test
```

```
CrossTable(mydata$DRINKING_D, mydata$AGGRESSIVE ,prop.r=FALSE, prop.chisq=FALSE, chisq=TRUE, pp=TRUE)
```

Cell Contents

		N
	N / Col Total	

Total Observations in Table: 43364

	mydata\$AGGRESSIVE		
mydata\$DRINKING_D	0	1	Row Total
0	22357	18522	40879
	0.934	0.953	
1	1569	916	2485
	0.066	0.047	
Column Total	23926	19438	43364
	0.552	0.448	

Statistics for All Table Factors

Pearson's Chi-squared test

Chi^2 = 67.60186 d.f. = 1 p = 0.000000000000000200079

```
Pearson's Chi-squared test with Yates' continuity correction
-----
Chi^2 = 67.2607      d.f. = 1      p = 0.0000000000000002378758
```

```
CrossTable(mydata$DRINKING_D, mydata$DRIVER1617 ,prop.r=FALSE,prop.chisq=FALSE, chisq=TRUE,p
```

Cell Contents	
	N
N / Col Total	

Total Observations in Table: 43364

		mydata\$DRIVER1617		Row Total
mydata\$DRINKING_D	0	1		
0	40205	674	40879	
	0.942	0.983		
1	2473	12	2485	
	0.058	0.017		
Column Total	42678	686	43364	
	0.984	0.016		

Statistics for All Table Factors

```
Pearson's Chi-squared test
-----
Chi^2 = 20.45167      d.f. = 1      p = 0.000006115619
```

Pearson's Chi-squared test with Yates' continuity correction

Chi^2 = 19.7097 d.f. = 1 p = 0.000009014275

```
CrossTable(mydata$DRINKING_D, mydata$DRIVER65PLUS ,prop.r=FALSE,prop.chisq=FALSE, chisq=TRUE)
```

Cell Contents

	N	
	N / Col Total	

Total Observations in Table: 43364

		mydata\$DRIVER65PLUS		Row Total
mydata\$DRINKING_D	0	1		
0	36642	4237	40879	
	0.939	0.973		
1	2366	119	2485	
	0.061	0.027		
Column Total	39008	4356	43364	
	0.900	0.100		

Statistics for All Table Factors

Pearson's Chi-squared test

Chi^2 = 80.6047 d.f. = 1 p = 0.0000000000000000275703

Pearson's Chi-squared test with Yates' continuity correction

```
-----  
Chi^2 = 79.9888      d.f. = 1      p = 0.00000000000000003765375
```

```
tapply(mydata$PCTBACHMOR,  
mydata$DRINKING_D, mean)
```

```
0          1  
16.56986 16.61173
```

```
tapply(mydata$PCTBACHMOR, mydata$DRINKING_D, sd)
```

```
0          1  
18.21426 18.72091
```

```
tapply(mydata$MEDHHINC,  
mydata$DRINKING_D, mean)
```

```
0          1  
31483.05 31998.75
```

```
tapply(mydata$MEDHHINC, mydata$DRINKING_D, sd)
```

```
0          1  
16930.1 17810.5
```

```
t.test(mydata$PCTBACHMOR~mydata$DRINKING_D)
```

Welch Two Sample t-test

```
data: mydata$PCTBACHMOR by mydata$DRINKING_D  
t = -0.10842, df = 2777.5, p-value = 0.9137  
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to  
95 percent confidence interval:  
-0.7991398  0.7153982  
sample estimates:  
mean in group 0 mean in group 1  
16.56986       16.61173
```

```
t.test(mydata$MEDHHINC~mydata$DRINKING_D)
```

Welch Two Sample t-test

```
data: mydata$MEDHHINC by mydata$DRINKING_D
t = -1.4053, df = 2763.9, p-value = 0.16
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to
95 percent confidence interval:
-1235.2508 203.8544
sample estimates:
mean in group 0 mean in group 1
31483.05 31998.75
```

```
cor(mydata$PCTBACHMOR, mydata$DRINKING_D, method="pearson")
```

[1] 0.0005334492

```
cor(mydata$MEDHHINC, mydata$DRINKING_D, method="pearson")
```

[1] 0.007058232

```
cor(mydata$FATAL_OR_M, mydata$DRINKING_D, method="pearson")
```

[1] 0.06216164

```
cor(mydata$OVERTURNED, mydata$DRINKING_D, method="pearson")
```

[1] 0.05321245

```
cor(mydata$CELL_PHONE, mydata$DRINKING_D, method="pearson")
```

[1] 0.00193325

```
cor(mydata$SPEEDING, mydata$DRINKING_D, method="pearson")
```

[1] 0.09321369

```
cor(mydata$AGGRESSIVE, mydata$DRINKING_D, method="pearson")
```

```
[1] -0.03948341
```

```
cor(mydata$DRIVER1617, mydata$DRINKING_D, method="pearson")
```

```
[1] -0.02171699
```

```
cor(mydata$DRIVER65PLUS, mydata$DRINKING_D, method="pearson")
```

```
[1] -0.04311372
```

```
#no severe multicollinearity :)
```

```
full_logit <- glm(DRINKING_D ~ FATAL_OR_M +
OVERTURNED + CELL_PHONE + SPEEDING + AGGRESSIVE + DRIVER1617 +
DRIVER65PLUS + PCTBACHMOR + MEDHHINC, data = mydata, family = "binomial")
```

```
full_logit_output <- summary(full_logit)
full_logit_output
```

Call:

```
glm(formula = DRINKING_D ~ FATAL_OR_M + OVERTURNED + CELL_PHONE +
SPEEDING + AGGRESSIVE + DRIVER1617 + DRIVER65PLUS + PCTBACHMOR +
MEDHHINC, family = "binomial", data = mydata)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.732506616	0.045875659	-59.563	< 0.0000000000000002 ***
FATAL_OR_M	0.814013802	0.083806924	9.713	< 0.0000000000000002 ***
OVERTURNED	0.928921376	0.109166324	8.509	< 0.0000000000000002 ***
CELL_PHONE	0.029550085	0.197777821	0.149	0.8812
SPEEDING	1.538975665	0.080545894	19.107	< 0.0000000000000002 ***
AGGRESSIVE	-0.596915946	0.047779238	-12.493	< 0.0000000000000002 ***
DRIVER1617	-1.280295964	0.293147168	-4.367	0.000012572447127933 ***
DRIVER65PLUS	-0.774664640	0.095858315	-8.081	0.00000000000000641 ***
PCTBACHMOR	-0.000370634	0.001296387	-0.286	0.7750

MEDHHINC 0.000002804 0.000001341 2.091 0.0365 *

—

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 19036 on 43363 degrees of freedom
Residual deviance: 18340 on 43354 degrees of freedom
AIC: 18360

Number of Fisher Scoring iterations: 6

```
or_ci <- exp(cbind(OR = coef(full_logit), confint(full_logit)))
```

Waiting for profiling to be done...

```
full_logit_coef <- full_logit_output$coefficients
```

```
final_full_output <- cbind(full_logit_coef, or_ci)  
final_full_output
```

	Estimate	Std. Error	z value
(Intercept)	-2.732506616128	0.045875659265	-59.5633209
FATAL_OR_M	0.814013801855	0.083806923855	9.7129660
OVERTURNED	0.928921376176	0.109166323622	8.5092302
CELL_PHONE	0.029550084767	0.197777821226	0.1494105
SPEEDING	1.538975665492	0.080545894089	19.1068171
AGGRESSIVE	-0.596915945677	0.047779237535	-12.4932079
DRIVER1617	-1.280295964022	0.293147167807	-4.3674171
DRIVER65PLUS	-0.774664640320	0.095858315238	-8.0813505
PCTBACHMOR	-0.000370633604	0.001296386538	-0.2858974
MEDHHINC	0.000002804492	0.000001340972	2.0913870

```
fit <- full_logit$fitted  
  
fit.binary = (fit>=0.02)  
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

Cell Contents

|

|

| N |

| N / Col Total |

Total Observations in Table: 43364

		mydata\$DRINKING_D		Row Total
fit.binary	0	1		
FALSE	2374	41	2415	
	0.058	0.016		
TRUE	38505	2444	40949	
	0.942	0.984		
Column Total	40879	2485	43364	
	0.943	0.057		

```
|-----|-----|-----|-----|
```

```
fit.binary = (fit>=0.03)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

Cell Contents

```
|-----|
|           N |
|       N / Col Total |
|-----|
```

Total Observations in Table: 43364

		mydata\$DRINKING_D		Row Total
fit.binary	0	1		
FALSE	2613	48	2661	
	0.064	0.019		
TRUE	38266	2437	40703	
	0.936	0.981		
Column Total	40879	2485	43364	
	0.943	0.057		

```
fit.binary = (fit>=0.05)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

Cell Contents

```
|-----|
```

	N
	N / Col Total
<hr/>	

Total Observations in Table: 43364

	mydata\$DRINKING_D		Row Total
fit.binary	0	1	
FALSE	19176	659	19835
	0.469	0.265	
TRUE	21703	1826	23529
	0.531	0.735	
Column Total	40879	2485	43364
	0.943	0.057	

```
fit.binary = (fit>=0.07)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

	Cell Contents
<hr/>	
	N
	N / Col Total
<hr/>	

Total Observations in Table: 43364

	mydata\$DRINKING_D		Row Total
fit.binary	0	1	
FALSE	37356	1935	39291

	0.914	0.779		
TRUE	3523	550	4073	
	0.086	0.221		
Column Total	40879	2485	43364	
	0.943	0.057		

```
fit.binary = (fit>=0.08)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

Cell Contents	
	N
	N / Col Total

Total Observations in Table: 43364

	mydata\$DRINKING_D		Row Total
fit.binary	0	1	
FALSE	38370	2026	40396
	0.939	0.815	
TRUE	2509	459	2968
	0.061	0.185	
Column Total	40879	2485	43364
	0.943	0.057	

```

fit.binary = (fit>=0.09)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)

```

Cell Contents

	N	
	N / Col Total	

Total Observations in Table: 43364

	mydata\$DRINKING_D		Row Total
fit.binary	0	1	
FALSE	38670	2067	40737
	0.946	0.832	
TRUE	2209	418	2627
	0.054	0.168	
Column Total	40879	2485	43364
	0.943	0.057	

```

fit.binary = (fit>=0.1)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)

```

Cell Contents

	N	
	N / Col Total	

Total Observations in Table: 43364

	mydata\$DRINKING_D		
fit.binary	0	1	Row Total
FALSE	38762	2077	40839
	0.948	0.836	
TRUE	2117	408	2525
	0.052	0.164	
Column Total	40879	2485	43364
	0.943	0.057	

```
fit.binary = (fit>=0.15)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

Cell Contents

N
N / Col Total

Total Observations in Table: 43364

	mydata\$DRINKING_D		
fit.binary	0	1	Row Total
FALSE	39743	2226	41969
	0.972	0.896	
TRUE	1136	259	1395
	0.028	0.104	

Column Total	40879	2485	43364	
	0.943	0.057		

```
fit.binary = (fit>=0.2)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

Cell Contents	
	N
	N / Col Total

Total Observations in Table: 43364

	mydata\$DRINKING_D		Row Total
fit.binary	0	1	
FALSE	40690	2428	43118
	0.995	0.977	
TRUE	189	57	246
	0.005	0.023	
Column Total	40879	2485	43364
	0.943	0.057	

```
fit.binary = (fit>=0.5)
CrossTable(fit.binary, mydata$DRINKING_D, prop.r=FALSE, prop.t=FALSE, prop.chisq=FALSE)
```

```

Cell Contents
|-----|
|           N |
|       N / Col Total |
|-----|

```

Total Observations in Table: 43364

	mydata\$DRINKING_D			
fit.binary	0	1	Row Total	
FALSE	40875	2481	43356	
	1.000	0.998		
TRUE	4	4	8	
	0.000	0.002		
Column Total	40879	2485	43364	
	0.943	0.057		

```

a <- cbind(mydata$DRINKING_D, fit)

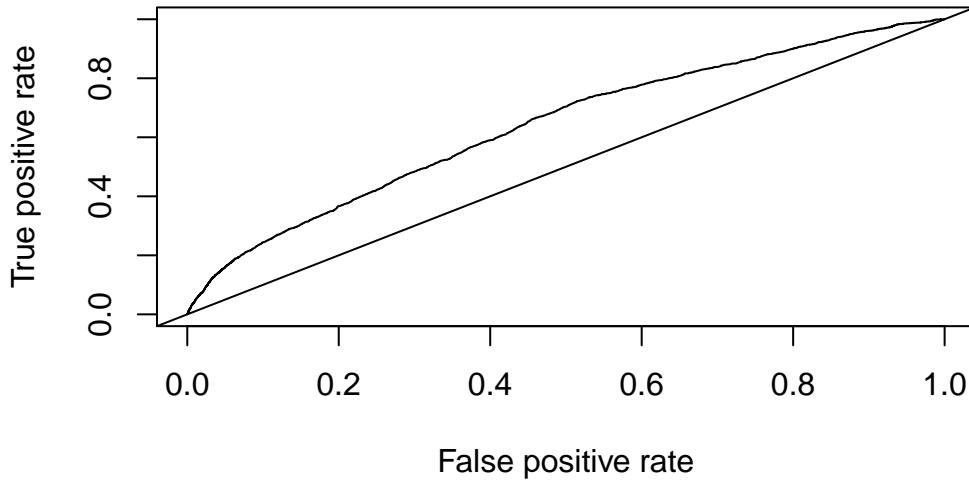
colnames(a) <- c("labels", "predictions")

roc <- as.data.frame(a)

pred <- prediction(roc$predictions, roc$labels)

roc.perf = performance(pred, measure = "tpr", x.measure="fpr")
plot(roc.perf)
abline(a=0,b=1)

```



```

opt.cut = function(perf, pred){
  cut.ind = mapply(FUN=function(x, y, p){
    d = (x - 0)^2 + (y-1)^2
    ind = which(d == min(d))
    c(sensitivity = y[[ind]], specificity = 1-x[[ind]],
      cutoff = p[[ind]])
  }, perf@x.values, perf@y.values, pred@cutoffs)
}

print(opt.cut(roc.perf, pred))

```

```

[,1]
sensitivity 0.66076459
specificity 0.54524328
cutoff      0.06365151

```

```

auc.perf = performance(pred, measure ="auc")
auc.perf@y.values #statisticians says that area >.7 is acceptable

```

```

[[1]]
[1] 0.6398695

```

```

binary_logit <- glm(DRINKING_D ~ FATAL_OR_M +
OVERTURNED + CELL_PHONE + SPEEDING + AGGRESSIVE + DRIVER1617 +
DRIVER65PLUS, data = mydata, family = "binomial")

binary_logit_output <- summary(binary_logit)
binary_logit_output

```

Call:

```

glm(formula = DRINKING_D ~ FATAL_OR_M + OVERTURNED + CELL_PHONE +
    SPEEDING + AGGRESSIVE + DRIVER1617 + DRIVER65PLUS, family = "binomial",
    data = mydata)

```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.65190	0.02753	-96.324	< 0.0000000000000002 ***
FATAL_OR_M	0.80932	0.08376	9.662	< 0.0000000000000002 ***
OVERTURNED	0.93978	0.10903	8.619	< 0.0000000000000002 ***
CELL_PHONE	0.03107	0.19777	0.157	0.875
SPEEDING	1.54032	0.08053	19.128	< 0.0000000000000002 ***
AGGRESSIVE	-0.59365	0.04775	-12.433	< 0.0000000000000002 ***
DRIVER1617	-1.27158	0.29311	-4.338	0.00001436374143265 ***
DRIVER65PLUS	-0.76646	0.09576	-8.004	0.000000000000000121 ***

Signif. codes:	0 '***'	0.001 '**'	0.01 '*'	0.05 '.'
	0.1	' '	1	

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 19036 on 43363 degrees of freedom
Residual deviance: 18344 on 43356 degrees of freedom
AIC: 18360

```

Number of Fisher Scoring iterations: 6

```

or_ci <- exp(cbind(OR = coef(binary_logit), confint(binary_logit)))

```

Waiting for profiling to be done...

```

binary_logit_coef <- binary_logit_output$coefficients

final_binary_output <- cbind(binary_logit_coef, or_ci)
final_binary_output

```

	Estimate	Std. Error	z value
(Intercept)	-2.65189961	0.02753107	-96.3238683
FATAL_OR_M	0.80931557	0.08376150	9.6621431
OVERTURNED	0.93978420	0.10903433	8.6191585
CELL_PHONE	0.03107367	0.19777088	0.1571195
SPEEDING	1.54032033	0.08052787	19.1277908
AGGRESSIVE	-0.59364687	0.04774781	-12.4329656
DRIVER1617	-1.27157607	0.29310969	-4.3382260
DRIVER65PLUS	-0.76645727	0.09576440	-8.0035718

	OR	2.5 %	97.5 %
(Intercept)	0.07051713	0.06678642	0.0743978
FATAL_OR_M	2.24636998	1.90112455	2.6404533
OVERTURNED	2.55942903	2.05736015	3.1556897
CELL_PHONE	1.03156149	0.68459779	1.4907150
SPEEDING	4.66608472	3.97961862	5.4573472
AGGRESSIVE	0.55230941	0.50268818	0.6061758
DRIVER1617	0.28038936	0.14904734	0.4751771
DRIVER65PLUS	0.46465631	0.38318289	0.5579332

```

AIC(full_logit, binary_logit)

```

	df	AIC
full_logit	10	18359.63
binary_logit	8	18360.47

1 Introduction

2 Methods

2.1 a) + b) - Sujan

2.2 c) + d) - Angel

In logistic regression, each predictor x_i is tested for the null hypothesis, H_0 , that the beta coefficient, β_i , is 0 against the alternative hypothesis H_a that β_i is not 0:

$$H_0 : \beta_i = 0$$

$$H_a : \beta_i \neq 0$$

The z-value, also known as the Wald statistic in logistic regression, is the test statistic that we calculate under the null hypothesis. We calculate this statistic by dividing the estimated beta coefficient, $\hat{\beta}_i$, by its standard error or $\sigma_{\hat{\beta}_i}$:

$$z = \frac{\hat{\beta}_i}{\sigma_{\hat{\beta}_i}}$$

Under the null hypothesis, the Wald statistic follows an approximately standard normal distribution, $N(0,1)$. This property allows us to compute the two-tailed p-value as the probability of observing a statistic as extreme, or more extreme, than the calculated statistic if the null hypothesis were true. If the p-value is < 0.05 , we can reject the null hypothesis in favor of the alternative hypothesis that β_i is not 0. Rather than interpreting the raw beta coefficients, statisticians prefer use the odds ratio, OR_i , which can be calculated by exponentiating $\hat{\beta}_i$:

$$OR_i = e^{\hat{\beta}_i}$$

The odds ratio expresses the effect of a predictor on the dependent variable in multiplicative terms. Specifically, it represents how the odds of the event change for a one-unit increase in the predictor, holding other variables constant. The null and alternative hypothesis can be adapted for the odds ratio, where the null hypothesis is the predictor has no effect on the odds ($OR = 1$) and the alternative hypothesis is that the predictor increases or decrease the odds of the event ($OR \neq 1$):

$$H_0 : OR = 1$$

$$H_a : OR \neq 1$$

Conceptually, the odds ratio is the ratio of the odds with the predictor present to the odds with the predictor absent. Thus, if the odds ratio equals 1, it indicates that the odds are

the same: the predictor did not change the odds of the outcome. Alternatively, if the odds ratio is significantly above or below 1, the predictor increased or decreased the odds. The confidence intervals for the odds ratios can be calculated by exponentiating the coefficient confidence intervals. These intervals provide a range of plausible values for the true odds ratio, reflecting the uncertainty of the estimate. In the context of logistic regression, the presence of a 1 in the confidence interval indicates the predictor's effect is not statistically significant while a confidence interval entirely above or below 1, indicates that the predictor increased or decreased the odds.

All coefficient estimates, z-values, and p-values were extracted in R from the fitted logistic regression model's summary. Odds ratios and their confidence intervals were calculated by exponentiating the original coefficient estimates and confidence intervals, then merged with the extracted coefficients for interpretation.

In our analysis, goodness of the model's fit was evaluated in various ways. In Ordinary Least Squares (OLS) regression, R^2 is used to evaluate model fit as it is a statistic that returns the proportion of total variance in the dependent variable explained by the independent variable. Unlike in OLS regression, logistic regression doesn't model a continuous outcome. In logistic regression the dependent variable, Y is binary, taking a value of 1 to indicate the occurrence of an event or 0 to indicate its absence. Therefore, since there is no longer a meaningful attribution of unexplained and explained variance in the dependent variable, R^2 can no longer be interpreted as the percent of variance explained by the model. Similarly to linear regression, residuals, ε_i , are calculated as the difference between the observed values of the dependent variable, y_i , and the predicted values of the dependent variable, \hat{y}_i :

$$\varepsilon_i = y_i - \hat{y}_i$$

In logistic regression, however, the predicted values, \hat{y}_i , represent the probability that $Y = 1$, while y_i represent the binary outcome ($Y = 1$ or $Y = 0$). Thus, residuals represent the difference between the observed binary outcome and the model's predicted probabilities. Theoretically a model of good fit predicts high probabilities of $Y = 1$ if y_i actually equals 1 and a low probability of $Y = 1$ if y_i is actually 0. In order to determine what is considered high probability and low probability, a cut-off value is imposed on the \hat{y}_i values. Cut-off values are then evaluated based on their specificity, sensitivity, and misclassification rates. Sensitivity, also called the true positive rate, is the proportion of actual positives that are correctly identified:

$$\text{Sensitivity} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}$$

In this analysis, the sensitivity rate is the proportion of observed $y_i = 1$ values correctly predicted as 1. Specificity, also called the true negative rate, is the proportion of actual negatives that are correctly identified as negatives:

$$\text{Specificity} = \frac{\text{True Negatives}}{\text{True Negatives} + \text{False Positives}}$$

The specificity rate in this analysis is the proportion of observed $y_i = 0$ values correctly predicted as 0. The misclassification rate is the proportion of incorrectly identified positive and negative y_i values based on the total number of predictions:

$$\text{Misclassification} = \frac{\text{False Negatives} + \text{False Positives}}{\text{True Negatives} + \text{True Positives} + \text{False Positives} + \text{False Negatives}}$$

In R, we called upon `fit.binary` and set the fit parameter to various different values to simulate how various cut off values would impact the sensitivity, specification, and misclassification rate. In other words, we use multiple cut-off values to compare the trade-offs of each cut-off threshold. Ideally, the chosen threshold will achieve higher sensitivity and specificity while minimizing the misclassification rate.

Receiver Operating Characteristics (ROC) curves are another tool for evaluating cut-off values. The ROC curve plots sensitivity against the false positive rate ($1 - \text{specificity}$) across all possible cut-off values of \hat{y}_i . The baseline for evaluating ROC curves called the “worthless” ROC is a 45 degree line where sensitivity and the false positive rate are equal across all cut-off values, meaning the predictions are no better than a random guess. Effective models produce ROC curves that lie above this diagonal baseline. ROC curves can be used to determine the cut-off value that balances the sensitivity and specificity rate, characteristics that indicate a good model. One common way to determine the optimal cut-off value is to use the Youden Index, which identifies the cut-off that maximizes the sum of sensitivity and specificity is maximized:

$$J = \text{Sensitivity} + \text{Specificity} - 1$$

This corresponds to the point on the ROC curve farthest above the diagonal line, or equivalently, the point closest to the top-left corner of the graph where sensitivity and specificity both equal 1. To identify the optimal cut-off value, we implemented a function in R that is conceptually similar to the Youden Index as it attempts to find the point that minimizes the distance to this ideal point.

In addition to identifying an optimal cut-off, we can also calculate Area Under Curve (AUC) for our ROC curve as a measure of the model’s overall predictive accuracy. The AUC quantifies the model’s ability to discriminate between positive and negative outcomes across all possible cut-offs. An AUC of 1 (area of the entire graph) indicates perfect classification or discrimination while a value of 0.5 (area under the 45 degree line) indicates no better than random guessing. Higher AUC values indicate that the model achieves strong predictive accuracy regardless of any single cut-off value, which in turn means that there exists at least one cut-off value where both sensitivity and specificity are relatively high. In this analysis, the AUC was computed in R using the `performance` function from the ROCR package. The threshold for evaluating accuracy based on AUC was that an area > 0.7 indicates at least moderate predictive accuracy. A guide for classifying accuracy based on other values of AUC is as follows:

A rough guide for classifying accuracy:

- 0.90–1.00 = Excellent
- 0.80–0.90 = Good
- 0.70–0.80 = Fair
- 0.60–0.70 = Poor
- 0.50–0.60 = Fail

Another measure used to evaluate logistic regression model fit is the Akaike Information Criterion (AIC). Although the absolute value of the AIC is not interpretable on its own, it provides a basis for comparing two or more models. Specifically, AIC combines the log-likelihood of the predicted probabilities with a penalty for the number of estimated parameters. Lower AIC values indicate a more favorable balance between model complexity and goodness of fit.

2.3 e) + f) - Ming

3 Results

3.1 a) - Sujan

3.2 b) - Angel

3.3 c) - Ming

4 Discussion