DA420_Project 8_MattGraham

```
# install.packages("Rcpp")
# install.packages("aod")
```

Import libraries

```
library(aod)
library(ggplot2)
library(Rcpp)
```

Getting the data and data summaries

```
###Get the data
mydata <- read.csv (file="C:/mattgraham93.github.io/school/23_1_DA420/projects/binary.csv")
head(mydata)
```

	admit <int>	gre <int>	gpa <dbl>	rank <int>
1	0	380	3.61	3
2	1	660	3.67	3
3	1	800	4.00	1
4	1	640	3.19	4
5	0	520	2.93	4
6	1	760	3.00	2

6 rows

Get table summary

```
summary(mydata)
```

```
##      admit             gre             gpa             rank
##  Min.   :0.0000   Min.   :220.0   Min.   :2.260   Min.   :1.000
##  1st Qu.:0.0000   1st Qu.:520.0   1st Qu.:3.130   1st Qu.:2.000
##  Median :0.0000   Median :580.0   Median :3.395   Median :2.000
##  Mean   :0.3175   Mean   :587.7   Mean   :3.390   Mean   :2.485
##  3rd Qu.:1.0000   3rd Qu.:660.0   3rd Qu.:3.670   3rd Qu.:3.000
##  Max.   :1.0000   Max.   :800.0   Max.   :4.000   Max.   :4.000
```

We can see that the average admissions was ~32%, implying that as their admission rate. The mean GPA is near that of the median at 3.9.

The median and mean rank show that there may be a skew in ranking, and something worth investigating. The mean and median GRE is also nearly equal.

Viewing standard deviations

```
sapply(mydata, sd)
```

```
##       admit         gre         gpa        rank
##   0.4660867 115.5165364   0.3805668   0.9444602
```

We can note how much variation there is in GRE scores. GPA is relatively wide, as is admission, given it's binary, it makes sense.

Contingency table

```
## we want to make sure there are not 0 cells
xtabs(~ admit + rank, data = mydata)
```

```
##      rank
## admit  1  2  3  4
##     0 28 97 93 55
##     1 33 54 28 12
```

We can conclude all intersections of data exist

Logistic regression

Creating the model

```
mydata$rank <- factor(mydata$rank)
mylogit <- glm(admit ~ gre + gpa + rank, data = mydata, family = "binomial")
```

Model summary and testing

```
summary(mylogit)
```

```
##
## Call:
## glm(formula = admit ~ gre + gpa + rank, family = "binomial",
##     data = mydata)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6268  -0.8662  -0.6388   1.1490   2.0790
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.989979   1.139951  -3.500 0.000465 ***
## gre          0.002264   0.001094   2.070 0.038465 *
## gpa          0.804038   0.331819   2.423 0.015388 *
## rank2       -0.675443   0.316490  -2.134 0.032829 *
## rank3       -1.340204   0.345306  -3.881 0.000104 ***
## rank4       -1.551464   0.417832  -3.713 0.000205 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98  on 399  degrees of freedom
## Residual deviance: 458.52  on 394  degrees of freedom
## AIC: 470.52
##
## Number of Fisher Scoring iterations: 4
```

We can see the GRE has a positive impact on admission. GPA appears to be negative, and rank appears inconsequential

Coefficient 95% CI's

```
## CIs using profiled log-likelihood
confint(mylogit)
```

```
## Waiting for profiling to be done...
```

```
##                     2.5 %       97.5 %
## (Intercept) -6.2716202334 -1.792547080
## gre          0.0001375921  0.004435874
## gpa          0.1602959439  1.464142727
## rank2       -1.3008888002 -0.056745722
## rank3       -2.0276713127 -0.670372346
## rank4       -2.4000265384 -0.753542605
```

Coefficient 95% CI's (default)

```
## CIs using standard errors
confint.default(mylogit)
```

```
##                     2.5 %       97.5 %
## (Intercept) -6.2242418514 -1.755716295
## gre          0.0001202298  0.004408622
## gpa          0.1536836760  1.454391423
## rank2       -1.2957512650 -0.055134591
## rank3       -2.0169920597 -0.663415773
## rank4       -2.3703986294 -0.732528724
```

We can see our 95% confidence intervals and can conclude they're all valid in that they do not cross 0.

The default test appears to be more conservative.

Testing effect of all ranks

```
wald.test(b = coef(mylogit), Sigma = vcov(mylogit), Terms = 4:6)
```

```
## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 20.9, df = 3, P(> X2) = 0.00011
```

Based on our Wald test, we can conclude that Rank is a statistically significant when looking at all 3 ranks

Testing difference between rank 2 and rank 3

```
l <- cbind(0,0,0,1,-1,0)
wald.test(b = coef(mylogit), Sigma = vcov(mylogit), L = l)
```

```
## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 5.5, df = 1, P(> X2) = 0.019
```

Again, we can conclude there is a significant difference between rank 2 and rank 3.

Testing odds ratios

```
## odds ratios only
exp(coef(mylogit))
```

```
## (Intercept)         gre         gpa       rank2       rank3       rank4
##   0.0185001   1.0022670   2.2345448   0.5089310   0.2617923   0.2119375
```

We can see the odds ratio of 2.23 as compared to a gre rank of 1, we can see how/why GPA is a negative trait. The lower variability in GPA vs. higher variability in GRE help explain why GRE is a highly positive trait.

Odds ratios and 95% CIs

```
# odds ratios and 95% CI
exp(cbind(OR = coef(mylogit), confint(mylogit)))
```

```
## Waiting for profiling to be done...
```

```
##                    OR       2.5 %    97.5 %
## (Intercept) 0.0185001 0.001889165 0.1665354
## gre         1.0022670 1.000137602 1.0044457
## gpa         2.2345448 1.173858216 4.3238349
## rank2       0.5089310 0.272289674 0.9448343
## rank3       0.2617923 0.131641717 0.5115181
## rank4       0.2119375 0.090715546 0.4706961
```

We can see how much more likely GPA is to happen as compared to the relative consistency of GRE. Ranks 2 looks to highly variable having the highest delta between variables.

Calculating probabilities

```
# calculate predictive probability of admission for each rank
newdata1 <- with(mydata,
  data.frame(gre = mean(gre), gpa = mean(gpa), rank = factor(1:4)))
newdata1
```

gre	gpa	rank
<dbl>	<dbl>	<fct>
587.7	3.3899	1
587.7	3.3899	2
587.7	3.3899	3
587.7	3.3899	4

4 rows

```
newdata1$rankP <- predict(mylogit, newdata = newdata1, type = "response")
newdata1
```

gre	gpa	rank	rankP
<dbl>	<dbl>	<fct>	<dbl>
587.7	3.3899	1	0.5166016

gre <dbl>	gpa <dbl>	rank <fct>	rankP <dbl>
587.7	3.3899	2	0.3522846
587.7	3.3899	3	0.2186120
587.7	3.3899	4	0.1846684

4 rows

We can see that people who have the mean GRE and GPA, if you are ranked 1st, there's a 51.6% chance you are gaining admission. Rank 2 is also fair, 3 and 4 are a lot less likely.

Creating dataframe with range of GRE score and rank

```
newdata2 <- with(mydata,
  data.frame(gre = rep(seq(from = 200, to = 800, length.out = 100), 4),
  gpa = mean(gpa), rank = factor(rep(1:4, each = 100))))
head(newdata2)
```

	gre <dbl>	gpa <dbl>	rank <fct>
1	200.0000	3.3899	1
2	206.0606	3.3899	1
3	212.1212	3.3899	1
4	218.1818	3.3899	1
5	224.2424	3.3899	1
6	230.3030	3.3899	1

6 rows

Predicted probabilities with statistics for visualizations

```
newdata3 <- cbind(newdata2, predict(mylogit, newdata = newdata2, type="link",
se=TRUE))
newdata3 <- within(newdata3, {
  PredictedProb <- plogis(fit)
  LL <- plogis(fit - (1.96 * se.fit))
  UL <- plogis(fit + (1.96 * se.fit))
})

## view first few rows of final dataset
head(newdata3)
```

gre <dbl>	gpa <dbl>	ra… <fct>	fit <dbl>	se.fit <dbl>	residual.scale <dbl>	UL <dbl>	LL <dbl>

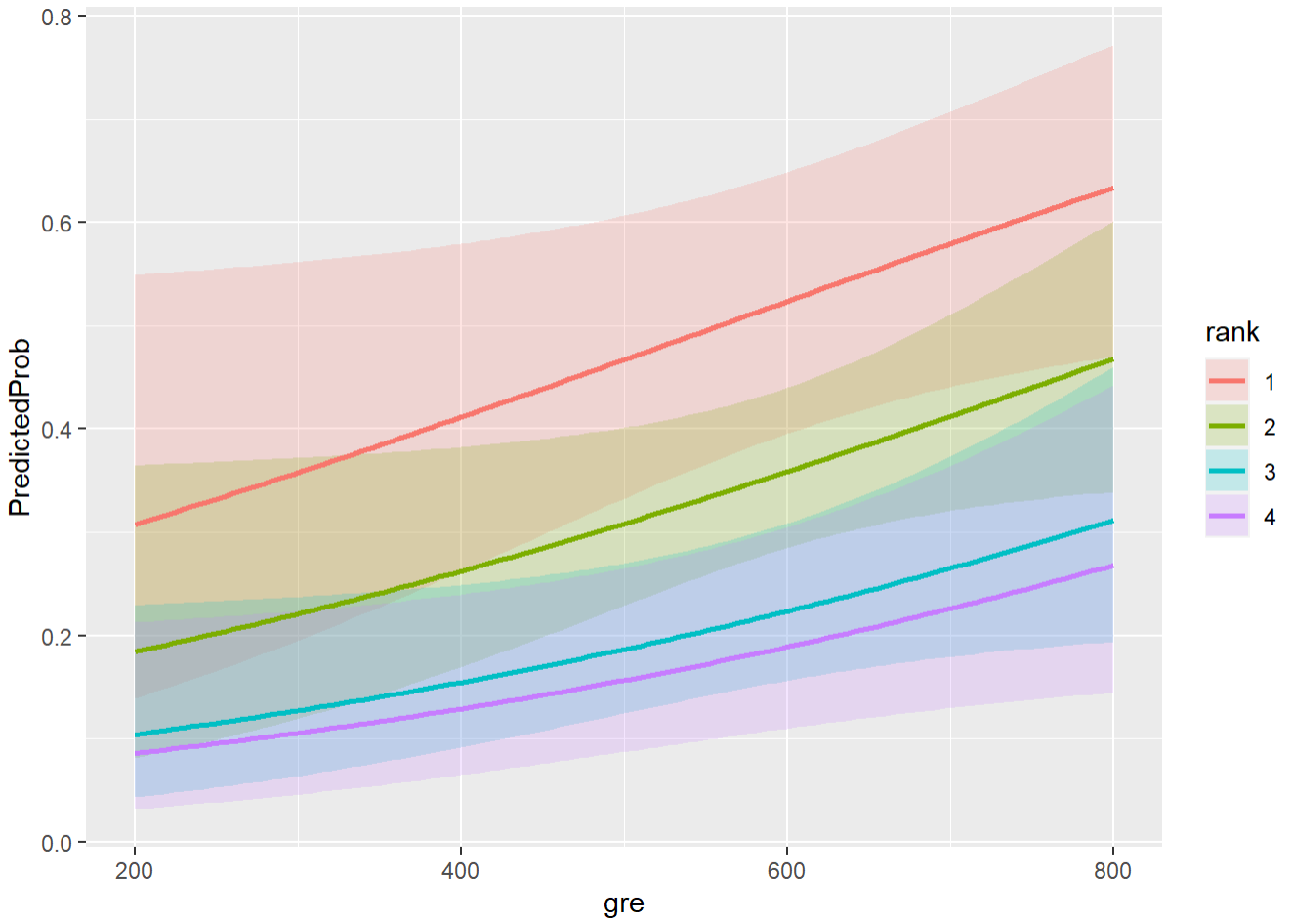
	gre <dbl>	gpa <dbl>	ra... <fct>	fit <dbl>	se.fit <dbl>	residual.scale <dbl>	UL <dbl>	LL <dbl>
1	200.0000	3.3899	1	-0.8114870	0.5147714	1	0.5492064	0.1393812
2	206.0606	3.3899	1	-0.7977632	0.5090986	1	0.5498513	0.1423880
3	212.1212	3.3899	1	-0.7840394	0.5034491	1	0.5505074	0.1454429
4	218.1818	3.3899	1	-0.7703156	0.4978239	1	0.5511750	0.1485460
5	224.2424	3.3899	1	-0.7565919	0.4922237	1	0.5518545	0.1516973
6	230.3030	3.3899	1	-0.7428681	0.4866494	1	0.5525464	0.1548966

6 rows | 1-9 of 10 columns

Visualizing our data

```
ggplot(newdata3, aes(x = gre, y = PredictedProb)) +
  geom_ribbon(aes(ymin = LL, ymax = UL, fill = rank), alpha = .2) +
  geom_line(aes(colour = rank), size=1)
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
```



We can see, overall - regardless of rank - all ranks are more likely to be admitted with higher GRE scores.

Final model analysis

Testing overall fit

```
with(mylogit, null.deviance - deviance)
```

```
## [1] 41.45903
```

Had we gone with a model with just an intercept, this model would out-perform it by a magnitude of 41.5

Degrees of freedom for difference between models

```
with(mylogit, df.null - df.residual)
```

```
## [1] 5
```

Final p-value of significance

```
with(mylogit, pchisq(null.deviance - deviance, df.null - df.residual, lower.tail = FALSE))
```

```
## [1] 7.578194e-08
```

We can conclude our model is significant

Final test for model fit and analysis

```
logLik(mylogit)
```

```
## 'log Lik.' -229.2587 (df=6)
```

While our model may be significant, our log-likelihood of -229.3 is not desirable. We may want to explore reducing total variables in our model, and explore interaction. This may open more insight into the intricacies of relationships.