

# medical school

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medical school

references:

- Cannon, et al., Stat2, chapter 09, example 10.9
- Cannon, et al., Student R Manual, chapter 10

Import the data.

```
data <- read.csv("MedGPA.csv", header=TRUE)
head(data)
```

```
##   Accept Acceptance Sex BCPM  GPA VR PS WS BS MCAT Apps
## 1      D           0  F 3.59 3.62 11  9  9  9  38   5
## 2      A           1  M 3.75 3.84 12 13  8 12  45   3
## 3      A           1  F 3.24 3.23  9 10  5  9  33  19
## 4      A           1  F 3.74 3.69 12 11  7 10  40   5
## 5      A           1  F 3.53 3.38  9 11  4 11  35  11
## 6      A           1  M 3.59 3.72 10  9  7 10  36   5
```

```
dim(data)
```

```
## [1] 55 11
```

glm.

```
med.glm <- glm(Acceptance ~ Sex + GPA + I(GPA^2) + Sex:GPA + Sex:I(GPA^2), data=data, family=binomial)
options(show.signif.stars=FALSE)
summary(med.glm)
```

```
##
## Call:
## glm(formula = Acceptance ~ Sex + GPA + I(GPA^2) + Sex:GPA + Sex:I(GPA^2),
##      family = binomial, data = data)
##
## Deviance Residuals:
##   Min       1Q   Median       3Q      Max
## -1.8864  -0.8632   0.1388   0.6758   2.2370
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    63.2738   152.3272   0.415   0.678
## SexM           -9.7948   162.0299  -0.060   0.952
## GPA            -42.9622    87.5134  -0.491   0.623
## I(GPA^2)         7.1269   12.5577   0.568   0.570
## SexM:GPA         5.9204    93.4748   0.063   0.949
## SexM:I(GPA^2)  -0.9993    13.4642  -0.074   0.941
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 75.791 on 54 degrees of freedom
## Residual deviance: 52.066 on 49 degrees of freedom
## AIC: 64.066
##
## Number of Fisher Scoring iterations: 6
```

One predictor.

```
med.glm1 <- glm(Acceptance ~ GPA, data=data, family=binomial)
summary(med.glm1)
```

```
##
## Call:
## glm(formula = Acceptance ~ GPA, family = binomial, data = data)
##
## 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
## GPA 5.454 1.579 3.454 0.000553
##
## (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
```

Two predictors.

```
med.glm2 <- glm(Acceptance ~ GPA + MCAT, data=data, family=binomial)
summary(med.glm2)
```

```
##
## Call:
## glm(formula = Acceptance ~ GPA + MCAT, family = binomial, data = data)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -1.7132 -0.8132 0.3136 0.7663 1.9933
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -22.3727 6.4538 -3.467 0.000527
## GPA 4.6765 1.6416 2.849 0.004389
```

```
## MCAT          0.1645      0.1032      1.595 0.110786
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 75.791 on 54 degrees of freedom
## Residual deviance: 54.014 on 52 degrees of freedom
## AIC: 60.014
##
## Number of Fisher Scoring iterations: 5
```

Second order model.

```
med.glm3 <- glm(Acceptance ~ GPA + I(GPA^2), data=data, family=binomial)
summary(med.glm3)
```

```
##
## Call:
## glm(formula = Acceptance ~ GPA + I(GPA^2), family = binomial,
## data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8363  -0.8020   0.3207   0.7830   1.9553
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   33.332     45.275   0.736   0.462
## GPA           -24.752     26.366  -0.939   0.348
## I(GPA^2)        4.325       3.832   1.128   0.259
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 75.791 on 54 degrees of freedom
## Residual deviance: 55.800 on 52 degrees of freedom
## AIC: 61.8
##
## Number of Fisher Scoring iterations: 4
```

Three predictors.

```
med.glm4 <- glm(Acceptance ~ GPA + MCAT + Sex, data=data, family=binomial)
summary(med.glm4)
```

```
##
## Call:
## glm(formula = Acceptance ~ GPA + MCAT + Sex, family = binomial,
## data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.0326  -0.8438   0.2524   0.6130   2.1607
##
```

```
## Coefficients:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) -23.9851     6.9685  -3.442 0.000578
## GPA          5.1392     1.8508   2.777 0.005491
## MCAT         0.1809     0.1080   1.675 0.093946
## SexM        -1.2580     0.7303  -1.723 0.084965
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 75.791  on 54  degrees of freedom
## Residual deviance: 50.786  on 51  degrees of freedom
## AIC: 58.786
##
## Number of Fisher Scoring iterations: 5
```

Interaction.

```
med.glm5 <- glm(Acceptance ~ GPA + Sex * MCAT, data=data, family=binomial)
summary(med.glm5)
```

```
##
## Call:
## glm(formula = Acceptance ~ GPA + Sex * MCAT, family = binomial,
##      data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8644  -0.9001   0.2219   0.6508   2.1709
##
## Coefficients:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) -21.54913     7.32060  -2.944 0.00324
## GPA          5.81784     2.06611   2.816 0.00486
## SexM        -12.88778     8.94048  -1.442 0.14944
## MCAT         0.04467     0.13693   0.326 0.74425
## SexM:MCAT    0.32144     0.24474   1.313 0.18905
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 75.791  on 54  degrees of freedom
## Residual deviance: 48.849  on 50  degrees of freedom
## AIC: 58.849
##
## Number of Fisher Scoring iterations: 6
```