

Homework 5

Shun-Lung Chang, Dilip Hiremath

```
# import packages
library(vcd)
library(RcmdrMisc) # stepwise()
library(tidyr) # spread()
```

1. (2 points) Construct the two-way table for gender and whether admitted. Find the odds ratio for admission of males vs. females and interpret. For which gender is the probability of admission higher?

The table below shows the numbers of admitted students with respect to genders, and the odds ratio for admission of males vs. females is 1.84108. Given that this ratio is greater than 1, male students are more likely to get admission than the females ones.

```
UCBAdmissions_m <- margin.table(UCBAdmissions, c(2, 1))
UCBAdmissions_m
```

| Gender | Admit | |
|--------|----------|----------|
| | Admitted | Rejected |
| Male | 1198 | 1493 |
| Female | 557 | 1278 |

```
oddsratio(UCBAdmissions_m, log = FALSE)
```

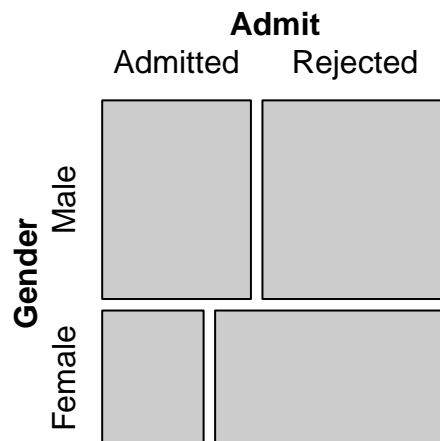
odds ratios for Gender and Admit

```
[1] 1.84108
```

2. Draw a mosaic plot for the data aggregated over departments.

The mosaic plot for the aggregated data is shown below.

```
mosaic(UCBAdmissions_m)
```



3. (3 points) Fit a saturated log-linear model to the frequencies using A and G as predictors. Calculate the odds ratio for admission of males vs. females. Display the predicted frequencies in a table and compare them to the observed frequencies displayed in Question 1.

The log-linear model with frequency as the response and A and G as predictors is shown below. The odds ratio for admission of males vs. females can be obtained by taking exponential of the coefficient of *AdmitRejected:GenderFemale*, and the odd ratio is 1.84108, which is same as the ratio in task 1.

```
berkeley <- data.frame(UCBAdmissions)
mod_1 <- glm(Freq ~ Admit * Gender,
             family = 'poisson', data = berkeley)
summary(mod_1)
```

Call:

```
glm(formula = Freq ~ Admit * Gender, family = "poisson", data = berkeley)
```

Deviance Residuals:

| Min | 1Q | Median | 3Q | Max |
|----------|---------|---------|--------|---------|
| -18.9074 | -7.8908 | -0.1399 | 5.6871 | 18.4285 |

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|----------------------------|----------|------------|---------|--------------|
| (Intercept) | 5.29665 | 0.02889 | 183.329 | < 2e-16 |
| AdmitRejected | 0.22013 | 0.03879 | 5.675 | 0.0000000138 |
| GenderFemale | -0.76584 | 0.05128 | -14.933 | < 2e-16 |
| AdmitRejected:GenderFemale | 0.61035 | 0.06389 | 9.553 | < 2e-16 |

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 2650.1 on 23 degrees of freedom
 Residual deviance: 2163.7 on 20 degrees of freedom
 AIC: 2330.8

Number of Fisher Scoring iterations: 5

```
exp(unname(mod_1$coefficients[4]))
```

```
[1] 1.84108
```

The predicted frequency table is same as the observed frequency table in task 1.

```
mod_table <- xtabs(mod_1$fitted.values ~ berkeley$Admit + berkeley$Gender)
mod_table
```

| | berkeley\$Gender | |
|-----------------|------------------|--------|
| berkeley\$Admit | Male | Female |
| Admitted | 1198 | 557 |
| Rejected | 1493 | 1278 |

4. (2 points) Fit an independence log-linear model to the frequencies using A, D and G as predictors. Display the predicted frequencies in a table and compare them to the observed frequencies. Calculate the estimated odds ratios for admission of males vs. females for each department.

The requested model is shown as follows. In the predicted frequency table, the ratio of the accepted to the rejected, regardless of gender, is always the same (0.6333454) in each department. The reason is that this ratio can be simplified to total number of accepted students dividing by the total number of rejected students. Given the identical ratios, the estimated odds ratios are all equal to 1.

```
mod_2 <- glm(Freq ~ Admit + Gender + Dept,
             family = 'poisson',
             data = berkeley)
summary(mod_2)
```

Call:

```
glm(formula = Freq ~ Admit + Gender + Dept, family = "poisson",
    data = berkeley)
```

Deviance Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|--------|--------|-------|--------|
| -18.170 | -7.719 | -1.008 | 4.734 | 17.153 |

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|---------------|----------|------------|---------|--------------|
| (Intercept) | 5.37111 | 0.03964 | 135.498 | < 2e-16 |
| AdmitRejected | 0.45674 | 0.03051 | 14.972 | < 2e-16 |
| GenderFemale | -0.38287 | 0.03027 | -12.647 | < 2e-16 |
| DeptB | -0.46679 | 0.05274 | -8.852 | < 2e-16 |
| DeptC | -0.01621 | 0.04649 | -0.349 | 0.727355 |
| DeptD | -0.16384 | 0.04832 | -3.391 | 0.000696 |
| DeptE | -0.46850 | 0.05276 | -8.879 | < 2e-16 |
| DeptF | -0.26752 | 0.04972 | -5.380 | 0.0000000744 |

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 2650.1 on 23 degrees of freedom
 Residual deviance: 2097.7 on 16 degrees of freedom
 AIC: 2272.7

Number of Fisher Scoring iterations: 5

```
# predicted values (mod_2)
mod_2_table <- xtabs(mod_2$fitted.values ~ berkeley$Gender +
                    berkeley$Admit + berkeley$Dept)

# observed values
obs_table <- xtabs(berkeley$Freq ~ berkeley$Gender +
                  berkeley$Admit + berkeley$Dept)

structable(obs_table)
```

```

                    berkeley$Admit Admitted Rejected
berkeley$Gender berkeley$Dept
```

| | | | |
|--------|---|-----|-----|
| Male | A | 512 | 313 |
| | B | 353 | 207 |
| | C | 120 | 205 |
| | D | 138 | 279 |
| | E | 53 | 138 |
| | F | 22 | 351 |
| Female | A | 89 | 19 |
| | B | 17 | 8 |
| | C | 202 | 391 |
| | D | 131 | 244 |
| | E | 94 | 299 |
| | F | 24 | 317 |

```
structable(mod_2_table)
```

```

              berkeley$Admit  Admitted  Rejected
berkeley$Gender berkeley$Dept
Male            A            215.10146 339.62744
                B            134.87069 212.94968
                C            211.64324 334.16719
                D            182.59417 288.30110
                E            134.64014 212.58566
                F            164.61141 259.90781
Female          A            146.67825 231.59285
                B             91.96868 145.21095
                C            144.32008 227.86949
                D            124.51144 196.59328
                E             91.81147 144.96272
                F            112.24895 177.23182

```

```
# odds ratio for observed values
```

```
(obs_table[1, 1, ]/obs_table[1, 2, ])/(obs_table[2, 1, ]/obs_table[2, 2, ])
```

```

      A      B      C      D      E      F
0.3492120 0.8025007 1.1330596 0.9212838 1.2216312 0.8278727

```

```
# odds ratio for predicted values
```

```
(mod_2_table[1, 1, ]/mod_2_table[1, 2, ])/(mod_2_table[2, 1, ]/mod_2_table[2, 2, ])
```

```

A B C D E F
1 1 1 1 1 1

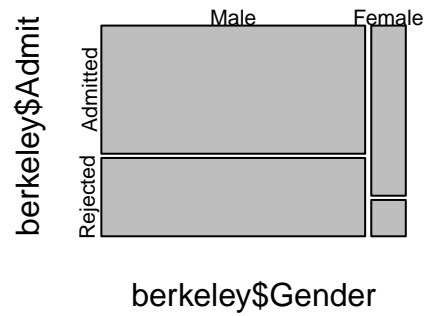
```

5. Draw mosaic plots of admission versus gender for each department separately.

The following plots demonstrate admission versus gender for each department separately.

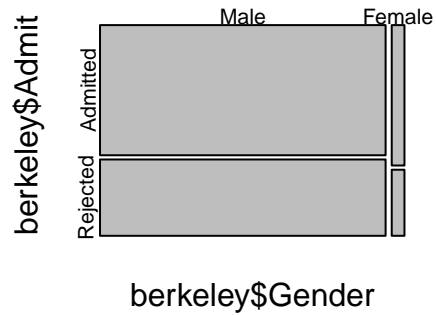
```
mosaicplot(obs_table[1:2,1:2,1], main = "Dept. A")
```

Dept. A



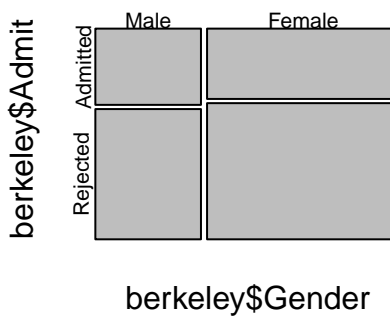
```
mosaicplot(obs_table[1:2,1:2,2], main = "Dept. B")
```

Dept. B



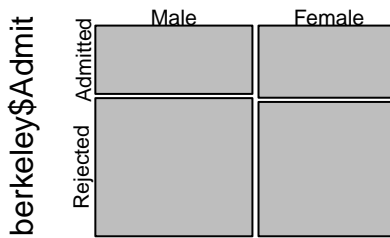
```
mosaicplot(obs_table[1:2,1:2,3], main = "Dept. C")
```

Dept. C



```
mosaicplot(obs_table[1:2,1:2,4], main = "Dept. D")
```

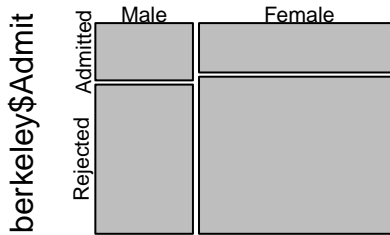
Dept. D



berkeley\$Gender

```
mosaicplot(obs_table[1:2,1:2,5], main = "Dept. E")
```

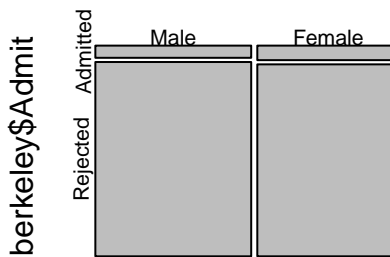
Dept. E



berkeley\$Gender

```
mosaicplot(obs_table[1:2,1:2,6], main = "Dept. F")
```

Dept. F



berkeley\$Gender

6. (3 points) Fit a log-linear model to the frequencies using A, D and G as predictors that includes all two-way interactions but not the three-way interaction. Display the predicted frequencies in a table and compare them to the predicted frequencies displayed in Question 4 as well as the observed frequencies. Calculate the estimated odds ratio for admission of males vs. females in this model.

The requested model and the predicted frequencies are shown below. We can see the ratios of the accepted to the rejected differ accross departments and genders, since the interactions were included in this model. Besides, the predicted frequencies are more closer to the observed frequencies than that of the model in task

4. The estimated odds ratio for admission of males vs. females was also computed, and the value is 1.84108, which is the same as the odds ratio in task 1.

```
mod_3 <- glm(Freq ~ Admit + Gender + Dept +
              Admit * Dept + Gender * Dept + Admit * Gender,
              family = 'poisson',
              data = berkeley)
summary(mod_3)
```

Call:

```
glm(formula = Freq ~ Admit + Gender + Dept + Admit * Dept + Gender *
     Dept + Admit * Gender, family = "poisson", data = berkeley)
```

Deviance Residuals:

| | | | | | | |
|----------|---------|----------|----------|----------|---------|----------|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| -0.75481 | 0.99471 | 1.96454 | -3.15768 | -0.03402 | 0.04449 | 0.15709 |
| 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| -0.22034 | 1.01273 | -0.73839 | -0.74367 | 0.54896 | 0.06760 | -0.04741 |
| 15 | 16 | 17 | 18 | 19 | 20 | 21 |
| -0.06911 | 0.05080 | 1.05578 | -0.61236 | -0.73617 | 0.42678 | -0.20117 |
| 22 | 23 | 24 | | | | |
| 0.05113 | 0.19803 | -0.05370 | | | | |

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|----------------------------|----------|------------|---------|---------------|
| (Intercept) | 6.27150 | 0.04271 | 146.855 | < 2e-16 |
| AdmitRejected | -0.58205 | 0.06899 | -8.436 | < 2e-16 |
| GenderFemale | -1.99859 | 0.10593 | -18.866 | < 2e-16 |
| DeptB | -0.40322 | 0.06784 | -5.944 | 0.00000000278 |
| DeptC | -1.57790 | 0.08949 | -17.632 | < 2e-16 |
| DeptD | -1.35000 | 0.08526 | -15.834 | < 2e-16 |
| DeptE | -2.44982 | 0.11755 | -20.840 | < 2e-16 |
| DeptF | -3.13787 | 0.16174 | -19.401 | < 2e-16 |
| AdmitRejected:DeptB | 0.04340 | 0.10984 | 0.395 | 0.693 |
| AdmitRejected:DeptC | 1.26260 | 0.10663 | 11.841 | < 2e-16 |
| AdmitRejected:DeptD | 1.29461 | 0.10582 | 12.234 | < 2e-16 |
| AdmitRejected:DeptE | 1.73931 | 0.12611 | 13.792 | < 2e-16 |
| AdmitRejected:DeptF | 3.30648 | 0.16998 | 19.452 | < 2e-16 |
| GenderFemale:DeptB | -1.07482 | 0.22861 | -4.701 | 0.00000258269 |
| GenderFemale:DeptC | 2.66513 | 0.12609 | 21.137 | < 2e-16 |
| GenderFemale:DeptD | 1.95832 | 0.12734 | 15.379 | < 2e-16 |
| GenderFemale:DeptE | 2.79519 | 0.13925 | 20.073 | < 2e-16 |
| GenderFemale:DeptF | 2.00232 | 0.13571 | 14.754 | < 2e-16 |
| AdmitRejected:GenderFemale | -0.09987 | 0.08085 | -1.235 | 0.217 |

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 2650.095 on 23 degrees of freedom
 Residual deviance: 20.204 on 5 degrees of freedom
 AIC: 217.26

Number of Fisher Scoring iterations: 4

```
# predicted values (mod_3)
```

```
mod_3_table <- xtabs(mod_3$fitted.values ~ berkeley$Gender +
                    berkeley$Admit + berkeley$Dept)
structable(mod_3_table)
```

| | | berkeley\$Admit | Admitted | Rejected |
|------------------|----------------|-----------------|------------|------------|
| berkeley\$Gender | berkeley\$Dept | | | |
| Male | A | | 529.269919 | 295.730081 |
| | B | | 353.639509 | 206.360491 |
| | C | | 109.245276 | 215.754724 |
| | D | | 137.207390 | 279.792610 |
| | E | | 45.680810 | 145.319190 |
| | F | | 22.957096 | 350.042904 |
| Female | A | | 71.730081 | 36.269919 |
| | B | | 16.360491 | 8.639509 |
| | C | | 212.754724 | 380.245276 |
| | D | | 131.792610 | 243.207390 |
| | E | | 101.319190 | 291.680810 |
| | F | | 23.042904 | 317.957096 |

```
(sum(mod_3_table[1, 1, ])/sum(mod_3_table[1, 2, ]))/(sum(mod_3_table[2, 1, ])/sum(mod_3_table[2, 2, ]))
```

```
[1] 1.84108
```

7. (2 points) Starting with the model in Question 6, use the stepwise method with the backward/forward option and BIC as criterion. Does this result in a simpler model? Interpret this model in plain English.

The model obtained by stepwise method is shown below, and it omitted the interaction term between *Admit* and *Gender*. In a three-main-effect model, if we have already known that the interaction between A and B is independent of that between B and C (denoted as (AB, BC)) and the interaction between B and C is independent of that between A and C, which is (BC, AC), we can safely conclude that the interaction between A and B is independent of that between A and C ((AB, AC)). Therefore, the redundant interaction term was omitted.

```
mod_4 <- stepwise(mod_3, direction = 'backward/forward', criterion = 'BIC')
```

```
summary(mod_4)
```

Call:

```
glm(formula = Freq ~ Admit + Gender + Dept + Admit:Dept + Gender:Dept,
    family = "poisson", data = berkeley)
```

Deviance Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|---------|--------|--------|--------|
| -3.4776 | -0.4144 | 0.0098 | 0.3089 | 2.2321 |

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|---------------|----------|------------|---------|---------------|
| (Intercept) | 6.27557 | 0.04248 | 147.744 | < 2e-16 |
| AdmitRejected | -0.59346 | 0.06838 | -8.679 | < 2e-16 |
| GenderFemale | -2.03325 | 0.10233 | -19.870 | < 2e-16 |
| DeptB | -0.40575 | 0.06770 | -5.993 | 0.00000000206 |

| | | | | |
|---------------------|----------|---------|---------|---------------|
| DeptC | -1.53939 | 0.08305 | -18.536 | < 2e-16 |
| DeptD | -1.32234 | 0.08159 | -16.207 | < 2e-16 |
| DeptE | -2.40277 | 0.11014 | -21.816 | < 2e-16 |
| DeptF | -3.09624 | 0.15756 | -19.652 | < 2e-16 |
| AdmitRejected:DeptB | 0.05059 | 0.10968 | 0.461 | 0.645 |
| AdmitRejected:DeptC | 1.20915 | 0.09726 | 12.432 | < 2e-16 |
| AdmitRejected:DeptD | 1.25833 | 0.10152 | 12.395 | < 2e-16 |
| AdmitRejected:DeptE | 1.68296 | 0.11733 | 14.343 | < 2e-16 |
| AdmitRejected:DeptF | 3.26911 | 0.16707 | 19.567 | < 2e-16 |
| GenderFemale:DeptB | -1.07581 | 0.22860 | -4.706 | 0.00000252480 |
| GenderFemale:DeptC | 2.63462 | 0.12343 | 21.345 | < 2e-16 |
| GenderFemale:DeptD | 1.92709 | 0.12464 | 15.461 | < 2e-16 |
| GenderFemale:DeptE | 2.75479 | 0.13510 | 20.391 | < 2e-16 |
| GenderFemale:DeptF | 1.94356 | 0.12683 | 15.325 | < 2e-16 |

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 2650.095 on 23 degrees of freedom
 Residual deviance: 21.736 on 6 degrees of freedom
 AIC: 216.8

Number of Fisher Scoring iterations: 4

8. (2 points) Calculate the saturated model using all three predictors and compare this model to the one obtained in Question 7 using AIC, BIC and the deviance criterion. Give a verbal summary of your findings.

The saturated model is shown below. A decrease can be seen in AIC and BIC scores and deviance criterion if we compare the model to the one in task 7. Furthermore, the predicted frequency table is the same as the observed table, since all the interaction terms were all taken into account in this model.

```
mod_5 <- glm(Freq ~ Admit * Gender * Dept,
             family = 'poisson',
             data = berkeley)
summary(mod_5)
```

Call:

```
glm(formula = Freq ~ Admit * Gender * Dept, family = "poisson",
    data = berkeley)
```

Deviance Residuals:

```
[1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[24] 0
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|---------------|----------|------------|---------|----------|
| (Intercept) | 6.23832 | 0.04419 | 141.157 | < 2e-16 |
| AdmitRejected | -0.49212 | 0.07175 | -6.859 | 6.94e-12 |
| GenderFemale | -1.74969 | 0.11484 | -15.235 | < 2e-16 |
| DeptB | -0.37186 | 0.06918 | -5.375 | 7.65e-08 |
| DeptC | -1.45083 | 0.10142 | -14.305 | < 2e-16 |
| DeptD | -1.31107 | 0.09591 | -13.669 | < 2e-16 |

| | | | | |
|----------------------------------|----------|---------|---------|----------|
| DeptE | -2.26803 | 0.14430 | -15.718 | < 2e-16 |
| DeptF | -3.14728 | 0.21773 | -14.455 | < 2e-16 |
| AdmitRejected:GenderFemale | -1.05208 | 0.26271 | -4.005 | 6.21e-05 |
| AdmitRejected:DeptB | -0.04163 | 0.11319 | -0.368 | 0.71304 |
| AdmitRejected:DeptC | 1.02764 | 0.13550 | 7.584 | 3.34e-14 |
| AdmitRejected:DeptD | 1.19608 | 0.12641 | 9.462 | < 2e-16 |
| AdmitRejected:DeptE | 1.44908 | 0.17681 | 8.196 | 2.49e-16 |
| AdmitRejected:DeptF | 3.26187 | 0.23120 | 14.109 | < 2e-16 |
| GenderFemale:DeptB | -1.28357 | 0.27358 | -4.692 | 2.71e-06 |
| GenderFemale:DeptC | 2.27046 | 0.16270 | 13.954 | < 2e-16 |
| GenderFemale:DeptD | 1.69763 | 0.16754 | 10.133 | < 2e-16 |
| GenderFemale:DeptE | 2.32269 | 0.20663 | 11.241 | < 2e-16 |
| GenderFemale:DeptF | 1.83670 | 0.31672 | 5.799 | 6.66e-09 |
| AdmitRejected:GenderFemale:DeptB | 0.83205 | 0.51039 | 1.630 | 0.10306 |
| AdmitRejected:GenderFemale:DeptC | 1.17700 | 0.29956 | 3.929 | 8.53e-05 |
| AdmitRejected:GenderFemale:DeptD | 0.97009 | 0.30262 | 3.206 | 0.00135 |
| AdmitRejected:GenderFemale:DeptE | 1.25226 | 0.33032 | 3.791 | 0.00015 |
| AdmitRejected:GenderFemale:DeptF | 0.86318 | 0.40267 | 2.144 | 0.03206 |

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 2.6501e+03 on 23 degrees of freedom
 Residual deviance: 1.1191e-13 on 0 degrees of freedom
 AIC: 207.06

Number of Fisher Scoring iterations: 3

```
# compare AIC scores
AIC(mod_4)
```

```
[1] 216.7952
```

```
AIC(mod_5)
```

```
[1] 207.0597
```

```
# compare BIC scores
BIC(mod_4)
```

```
[1] 238.0002
```

```
BIC(mod_5)
```

```
[1] 235.333
```

```
# Compute DIC = -2 * log(likelihood)
-2 * logLik(mod_4)
```

```
'log Lik.' 180.7952 (df=18)
```

```
-2 * logLik(mod_5)
```

```
'log Lik.' 159.0597 (df=24)
```

```
# predicted values (mod_5)
mod_5_table <- xtabs(mod_5$fitted.values ~ berkeley$Gender +
  berkeley$Admit + berkeley$Dept)
structable(mod_5_table)
```

| | | berkeley\$Admit | Admitted | Rejected |
|------------------|----------------|-----------------|----------|----------|
| berkeley\$Gender | berkeley\$Dept | | | |
| Male | A | | 512 | 313 |
| | B | | 353 | 207 |
| | C | | 120 | 205 |
| | D | | 138 | 279 |
| | E | | 53 | 138 |
| | F | | 22 | 351 |
| Female | A | | 89 | 19 |
| | B | | 17 | 8 |
| | C | | 202 | 391 |
| | D | | 131 | 244 |
| | E | | 94 | 299 |
| | F | | 24 | 317 |

9. To run a logistic regression model with aggregated data it is best to create a data frame that comprises two frequency variables: one for the numbers of admitted students, and one for the numbers of rejected students.

```
UCBAdmissions <- as.data.frame(UCBAdmissions)
attach(UCBAdmissions)
UCBAdmit <- cbind(UCBAdmissions[Admit=="Rejected",-1],
  A=UCBAdmissions[Admit=="Admitted", "Freq"])
names(UCBAdmit)[3] <- "R"
detach()
```

Treating cbind(A,R) as response and D and G as qualitative predictors, fit the logit model having main effects only.

```
berkeley_t <- spread(berkeley, Admit, Freq)

mod_6 <- glm(cbind(Rejected, Admitted) ~ Gender * Dept,
  family = binomial(link = "logit"),
  data = berkeley_t)
summary(mod_6)
```

Call:

```
glm(formula = cbind(Rejected, Admitted) ~ Gender * Dept, family = binomial(link = "logit"),
  data = berkeley_t)
```

Deviance Residuals:

```
[1] 0 0 0 0 0 0 0 0 0 0 0 0 0
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|--------------|----------|------------|---------|----------|
| (Intercept) | -0.49212 | 0.07175 | -6.859 | 6.94e-12 |
| GenderFemale | -1.05208 | 0.26271 | -4.005 | 6.21e-05 |
| DeptB | -0.04163 | 0.11319 | -0.368 | 0.71304 |
| DeptC | 1.02764 | 0.13550 | 7.584 | 3.34e-14 |
| DeptD | 1.19608 | 0.12641 | 9.462 | < 2e-16 |

| | | | | |
|--------------------|---------|---------|--------|----------|
| DeptE | 1.44908 | 0.17681 | 8.196 | 2.49e-16 |
| DeptF | 3.26187 | 0.23120 | 14.109 | < 2e-16 |
| GenderFemale:DeptB | 0.83205 | 0.51039 | 1.630 | 0.10306 |
| GenderFemale:DeptC | 1.17700 | 0.29956 | 3.929 | 8.53e-05 |
| GenderFemale:DeptD | 0.97009 | 0.30262 | 3.206 | 0.00135 |
| GenderFemale:DeptE | 1.25226 | 0.33032 | 3.791 | 0.00015 |
| GenderFemale:DeptF | 0.86318 | 0.40267 | 2.144 | 0.03206 |

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 877.0564132197750951 on 11 degrees of freedom
 Residual deviance: 0.0000000000001088 on 0 degrees of freedom
 AIC: 92.94

Number of Fisher Scoring iterations: 3

(a) (1.5 points) Report the prediction equation. Interpret the coefficients of D, G and the interaction in this equation.

The prediction equation and the coefficients of each term are shown above. If we add the coefficient of *GenderFemale* and the coefficients of interaction terms between *Dept*, and *Gender*, the results are exactly the logarithmic odds ratios for admission of males vs. females in each department. And the exponential of the results are the observed odd ratios in task 4.

```
exp(c(mod_6$coefficients[2], mod_6$coefficients[2] + mod_6$coefficients[8:12]))
```

| | | |
|--------------------|--------------------|--------------------|
| GenderFemale | GenderFemale:DeptB | GenderFemale:DeptC |
| 0.3492120 | 0.8025007 | 1.1330596 |
| GenderFemale:DeptD | GenderFemale:DeptE | GenderFemale:DeptF |
| 0.9212838 | 1.2216312 | 0.8278727 |

(b) (half a point) To which log-linear model is this model equivalent?

The model is equivalent to the saturated model using all three predictors in task 8.