STAT-S632

Assignment 5

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```r
import::from(magrittr, `%>%`, `%<>%`)
library(ggplot2)
import::from(nnet, multinom)

theme_set(theme_bw())
```

Problem 1

Part a

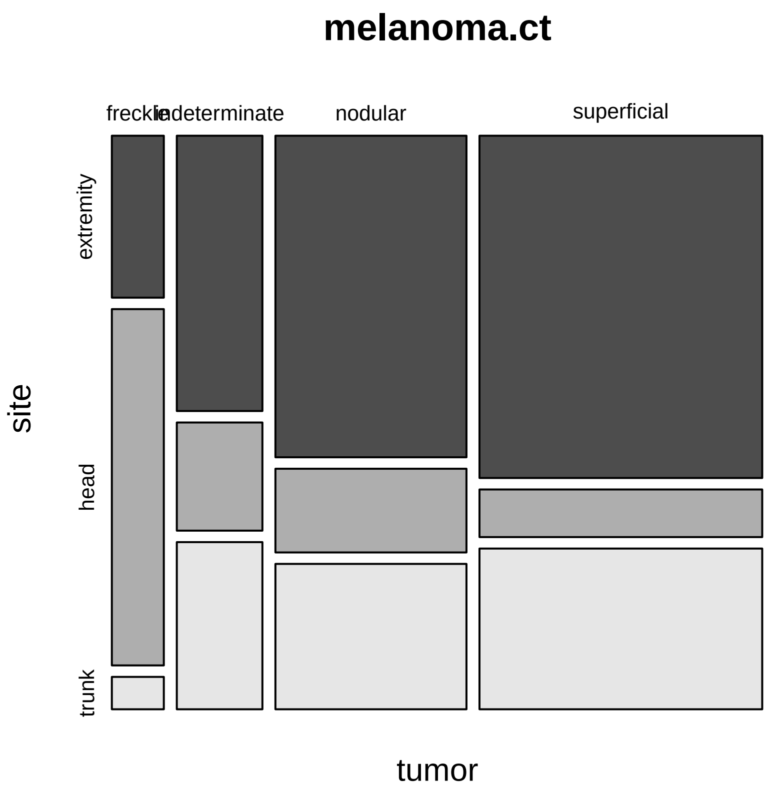
```r
# get the data
melanoma.df <- faraway::melanoma
summary(melanoma.df)
```

```
     count                  tumor          site  
 Min.   :  2.00   freckle      :3   extremity:4  
 1st Qu.: 14.75   indeterminate:3   head     :4  
 Median : 20.50   nodular      :3   trunk    :4  
 Mean   : 33.33   superficial  :3                
 3rd Qu.: 38.25                                  
 Max.   :115.00                                  
```

```r
# contingency table stuff
melanoma.ct <- xtabs(count ~ tumor + site, data = melanoma.df)
melanoma.ct
```

```
               site
tumor           extremity head trunk
  freckle              10   22     2
  indeterminate        28   11    17
  nodular              73   19    33
  superficial         115   16    54
```

```r
mosaicplot(melanoma.ct, color = TRUE)
```




```r
# poisson model
pois.mod <- glm(count ~ tumor + site, data = melanoma.df, family = poisson)
summary(pois.mod)
```

```
Call:
glm(formula = count ~ tumor + site, family = poisson, data = melanoma.df)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.0453  -1.0741   0.1297   0.5857   5.1354

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)          2.9554     0.1770  16.696  < 2e-16 ***
tumorindeterminate   0.4990     0.2174   2.295   0.0217 *
tumornodular         1.3020     0.1934   6.731 1.68e-11 ***
tumorsuperficial     1.6940     0.1866   9.079  < 2e-16 ***
sitehead            -1.2010     0.1383  -8.683  < 2e-16 ***
sitetrunk           -0.7571     0.1177  -6.431 1.27e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 295.203  on 11  degrees of freedom
Residual deviance:  51.795  on  6  degrees of freedom
AIC: 122.91

Number of Fisher Scoring iterations: 5
```

```r
pchisq(pois.mod$deviance, pois.mod$df.residual, lower.tail = FALSE)
```

```
[1] 2.050453e-09
```

The Poisson model is not a good fit according to a χ^2 test on the deviance of the model, and this could be due to the fact that the regressors `tumor` and `site` are not independent. We can see some of this in the mosaic plot—frekles are much more common on heads compared to other types of tumors.

Part b

```r
melanoma.df %<>% dplyr::mutate(pois.resid = residuals(pois.mod))
resid.ct <- xtabs(pois.resid ~ tumor + site, data = melanoma.df)
resid.ct
```

```
               site
tumor             extremity        head       trunk
  freckle       -2.31583297  5.13537787 -2.82829426
  indeterminate -0.66016102  0.46798432  0.54787007
  nodular        0.28104581 -0.49711084 -0.02173229
  superficial    1.00813975 -3.04533605  0.69899703
```

We see large residuals for the tumor type "freckle".

Problem 2

Part a

```r
uncviet.df <- faraway::uncviet
summary(uncviet.df)
```

```
       y           policy     sex          year   
 Min.   :  3.00   A:10   Female:20   Fresh :8  
 1st Qu.: 18.50   B:10   Male  :20   Grad  :8  
 Median : 42.00   C:10               Junior:8  
 Mean   : 78.67   D:10               Senior:8  
 3rd Qu.:131.25                      Soph  :8  
 Max.   :345.00                                
```

```r
uncviet.ct <- xtabs(y ~ policy + sex + year, data = uncviet.df)
uncviet.ct
```

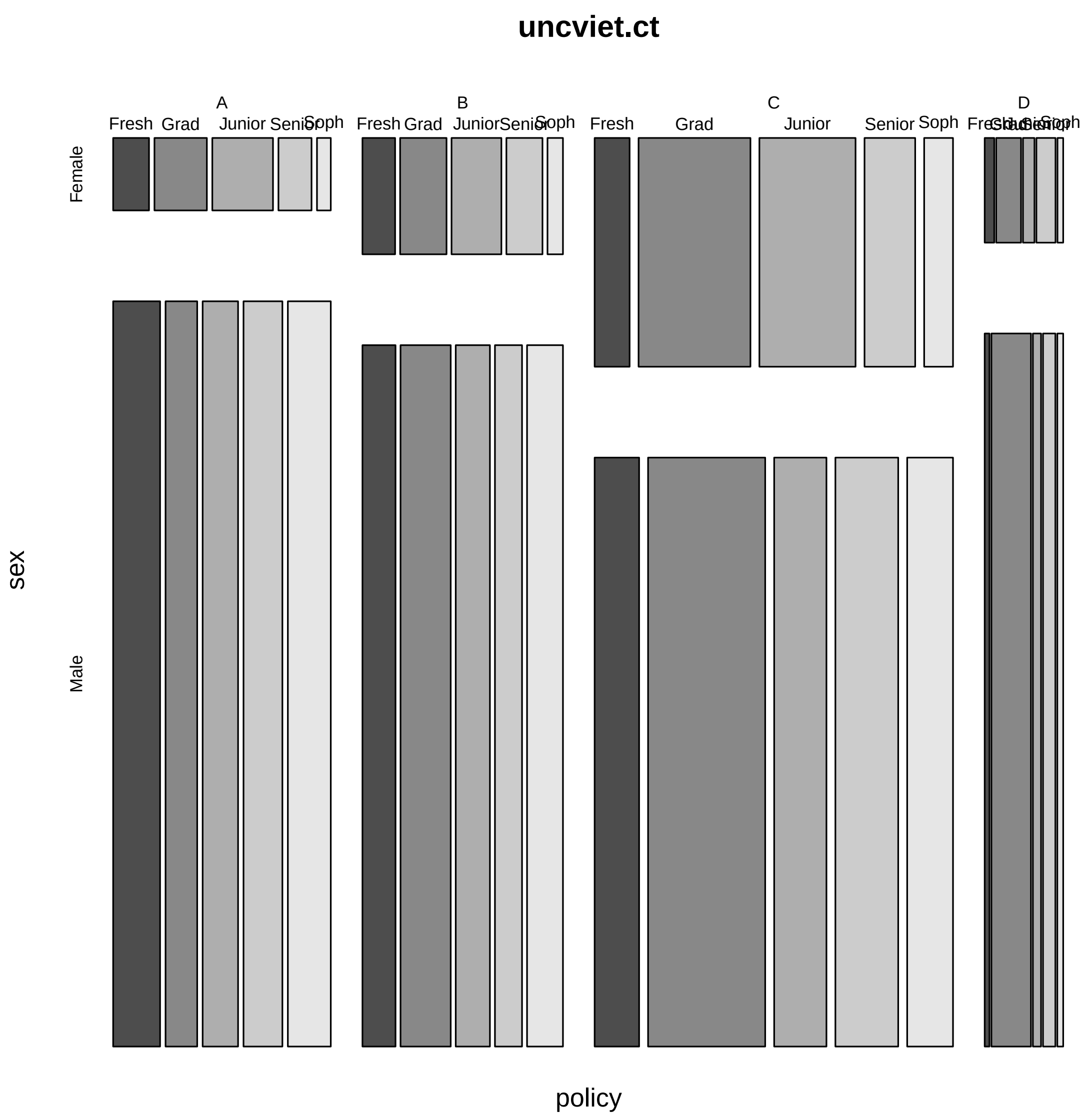
```
, , year = Fresh

      sex
policy Female Male
     A     13  175
```

```
     B     19  116
     C     40  131
     D      5   17

, , year = Grad

      sex
policy Female Male
     A     19  118
     B     27  176
     C    128  345
     D     13  141

, , year = Junior

      sex
policy Female Male
     A     22  132
     B     29  120
     C    110  154
     D      6   29

, , year = Senior

      sex
policy Female Male
     A     12  145
     B     21   95
     C     58  185
     D     10   44

, , year = Soph

      sex
policy Female Male
     A      5  160
     B      9  126
     C     33  135
     D      3   21
```

```r
summary(uncviet.ct)
```

```
Call: xtabs(formula = y ~ policy + sex + year, data = uncviet.df)
Number of cases in table: 3147
Number of factors: 3
Test for independence of all factors:
    Chisq = 449.2, df = 31, p-value = 1.118e-75
```

```r
mosaicplot(uncviet.ct, color = TRUE)
```




```
mantelhaen.test(uncviet.ct)
```

```

    Cochran-Mantel-Haenszel test

data:  uncviet.ct
Cochran-Mantel-Haenszel M^2 = 132.55, df = 3, p-value < 2.2e-16
```

```
uncviet.pois.mod <- glm(y ~ policy + sex + year, data = uncviet.df,
                        family = poisson)
summary(uncviet.pois.mod)
```

```

Call:
glm(formula = y ~ policy + sex + year, family = poisson, data = uncviet.df)
```

```
Deviance Residuals:
   Min       1Q   Median       3Q      Max
-6.323   -2.582   -0.810    0.673    7.873

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.19003    0.06534  48.823   <2e-16 ***
policyB     -0.08192    0.05102  -1.605   0.1084
policyC      0.49877    0.04479  11.134   <2e-16 ***
policyD     -1.01943    0.06862 -14.856   <2e-16 ***
sexMale      1.48324    0.04591  32.305   <2e-16 ***
yearGrad     0.62809    0.05452  11.521   <2e-16 ***
yearJunior   0.15415    0.05999   2.569   0.0102 *
yearSenior   0.09953    0.06076   1.638   0.1014
yearSoph    -0.04763    0.06301  -0.756   0.4497
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 2708.08  on 39  degrees of freedom
Residual deviance:  423.83  on 31  degrees of freedom
AIC: 666.22

Number of Fisher Scoring iterations: 5
```

```
pchisq(uncviet.pois.mod$deviance, uncviet.pois.mod$df.residual,
       lower.tail = FALSE)
```

```
[1] 1.591439e-70
```

We have evidence from the mosaic plot, contingency tables, Mantel-Haenszel test, and Poisson model that the three regressors are not independent. So we might be interested in seeing how they are dependent. Visually, we can see some relationship between sex and policy. We can also see some relationship between year and policy as well. Instead of considering the different possibilities, we can just use AIC:

```
uncviet.nominal.mod <- glm(y ~ (policy + sex + year) ** 2, data = uncviet.df,
                   family = poisson) %>%
  step(direction = 'both')
```

```
Start:  AIC=299.58
y ~ (policy + sex + year)^2

              Df Deviance    AIC
<none>               19.194 299.58
- sex:year     4   70.643 343.03
- policy:sex   3  153.935 428.32
- policy:year 12  216.312 472.70
```

```
summary(uncviet.nominal.mod)
```

```
Call:
glm(formula = y ~ (policy + sex + year)^2, family = poisson,
    data = uncviet.df)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.4849  -0.4420   0.0023   0.3962   1.8756

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)         2.69824    0.16895  15.970  < 2e-16 ***
policyB             0.13458    0.18626   0.723 0.469945
policyC             1.05527    0.16400   6.435 1.24e-10 ***
policyD            -1.78914    0.29955  -5.973 2.33e-09 ***
sexMale             2.45589    0.16548  14.841  < 2e-16 ***
yearGrad           -0.21730    0.18001  -1.207 0.227367
yearJunior          0.40703    0.17827   2.283 0.022415 *
yearSenior         -0.09396    0.18938  -0.496 0.619800
yearSoph           -0.57514    0.21360  -2.693 0.007090 **
policyB:sexMale    -0.51798    0.16448  -3.149 0.001637 **
policyC:sexMale    -1.35481    0.14116  -9.598  < 2e-16 ***
policyD:sexMale    -0.39366    0.21999  -1.789 0.073545 .
policyB:yearGrad    0.71910    0.15814   4.547 5.44e-06 ***
policyC:yearGrad    1.31478    0.14590   9.011  < 2e-16 ***
policyD:yearGrad    2.25855    0.25416   8.886  < 2e-16 ***
policyB:yearJunior  0.25659    0.16181   1.586 0.112799
policyC:yearJunior  0.49017    0.15030   3.261 0.001109 **
policyD:yearJunior  0.63363    0.29360   2.158 0.030915 *
policyB:yearSenior  0.02394    0.16669   0.144 0.885809
policyC:yearSenior  0.51505    0.15011   3.431 0.000601 ***
policyD:yearSenior  1.07484    0.27513   3.907 9.36e-05 ***
policyB:yearSoph    0.14893    0.16213   0.919 0.358320
policyC:yearSoph    0.18157    0.15499   1.171 0.241406
policyD:yearSoph    0.23077    0.31400   0.735 0.462372
sexMale:yearGrad   -0.10814    0.15328  -0.706 0.480479
sexMale:yearJunior -0.68075    0.15747  -4.323 1.54e-05 ***
sexMale:yearSenior -0.09400    0.16944  -0.555 0.579056
sexMale:yearSoph    0.47497    0.19722   2.408 0.016024 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 2708.080  on 39  degrees of freedom
Residual deviance:   19.194  on 12  degrees of freedom
AIC: 299.58

Number of Fisher Scoring iterations: 4
```

```r
pchisq(uncviet.nominal.mod$deviance,
       uncviet.nominal.mod$df.residual,
       lower.tail = FALSE)
```

```
[1] 0.08394884
```

It appears that the full model (with two-way interactions) provides the lowest AIC, and a χ^2 test suggests that this may be a decent fit. This implies that there is full dependence (including pairwise dependence between all three pairs of regressors).

Part b

```
uncviet.df %<>%
  dplyr::mutate(policy.ord = as.numeric(factor(policy, levels = LETTERS[1:4])),
                year.ord = as.numeric(factor(year, levels = c('Fresh',
                                                              'Soph',
                                                              'Junior',
                                                              'Senior',
                                                              'Grad'))))
uncviet.ord.mod <- glm(y ~ policy + sex + year + I(policy.ord * year.ord),
                       data = uncviet.df, family = poisson)
anova(uncviet.pois.mod, uncviet.ord.mod, test = 'Chi')
```

```
Analysis of Deviance Table

Model 1: y ~ policy + sex + year
Model 2: y ~ policy + sex + year + I(policy.ord * year.ord)
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1        31     423.83
2        30     246.13  1   177.69 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

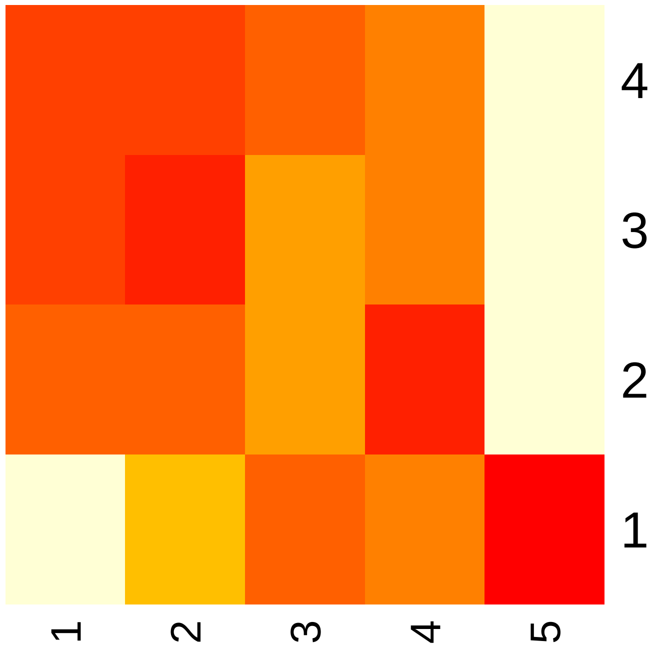
```
summary(uncviet.ord.mod)$coef['I(policy.ord * year.ord)', ]
```

```
    Estimate   Std. Error      z value     Pr(>|z|)
1.751092e-01 1.354426e-02 1.292867e+01 3.101548e-38
```

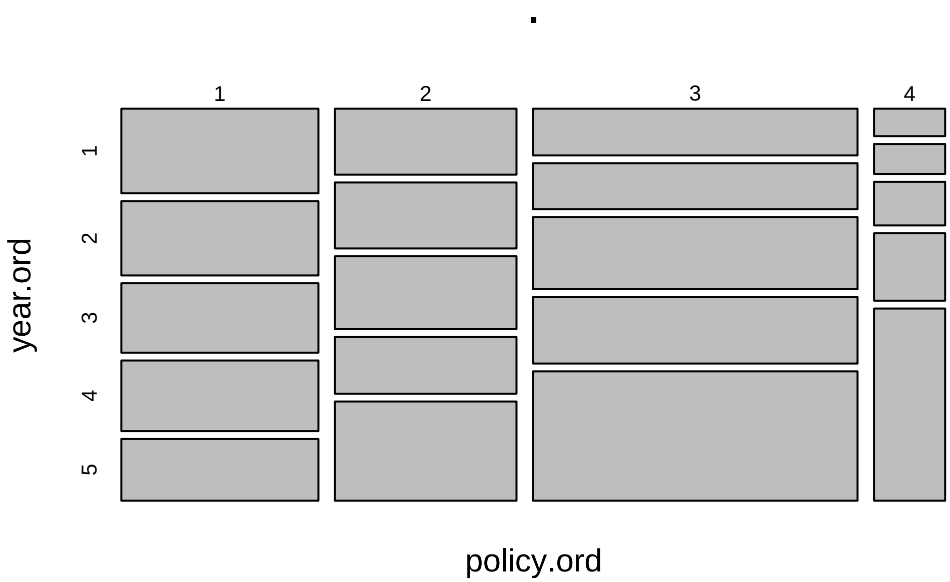
We have evidence of association from both the χ^2 test and the Wald test. The estimate $\hat{\gamma} > 0$, suggesting positive association. This suggests that as `year` increases, there is a higher probability that the responder favors less involvment in the war.

We can also try a different ordinal assignment. A heatmap of counts might give us some idea of how we might want to do this:

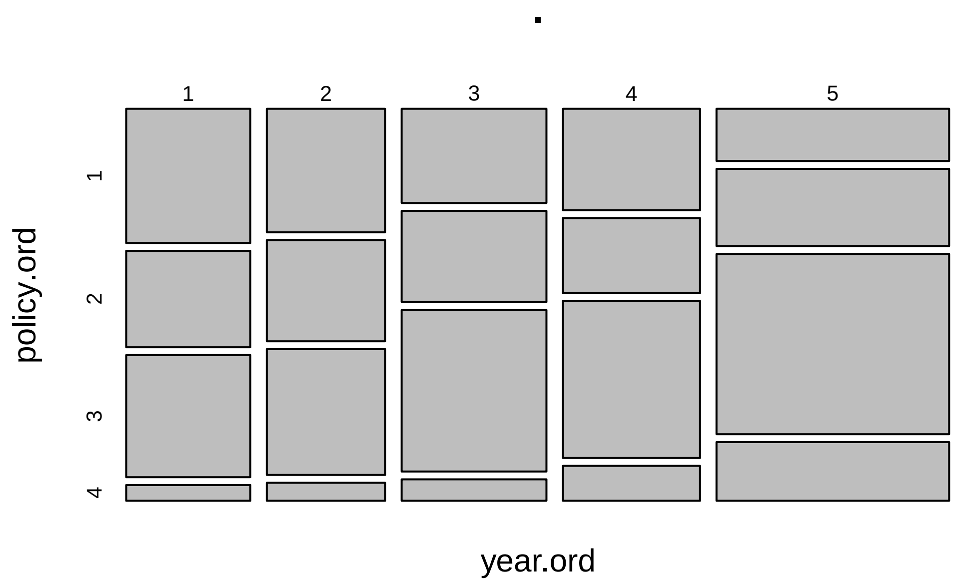
```
xtabs(y ~ policy.ord + year.ord, data = uncviet.df) %>%
  heatmap(Rowv = NA, Colv = NA)
```




```r
xtabs(y ~ policy.ord + year.ord, data = uncviet.df) %>%
  mosaicplot()
```




```r
xtabs(y ~ year.ord + policy.ord, data = uncviet.df) %>%
  mosaicplot()
```




```
policy.lookup <- list(1, 2, 2, 3)
year.lookup <- list(1, 1, 2, 2, 3)

uncviet.df %<>%
  dplyr::mutate(policy.ord.new = sapply(policy.ord,
                                         function(i) policy.lookup[[i]]),
                year.ord.new = sapply(year.ord,
                                       function(i) year.lookup[[i]]))

uncviet.ord.mod <- glm(y ~ policy + sex + year +
                         I(policy.ord.new * year.ord.new),
                       data = uncviet.df, family = poisson)
anova(uncviet.pois.mod, uncviet.ord.mod, test = 'Chi')
```

```
Analysis of Deviance Table

Model 1: y ~ policy + sex + year
Model 2: y ~ policy + sex + year + I(policy.ord.new * year.ord.new)
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1        31     423.83
2        30     260.30  1   163.53 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(uncviet.ord.mod)$coef['I(policy.ord.new * year.ord.new)', ]
```

```
    Estimate   Std. Error      z value     Pr(>|z|)
5.288723e-01 4.295635e-02 1.231185e+01 7.820686e-35
```

```r
policy.lookup <- list(1, 1, 1, 2)
year.lookup <- list(1, 1, 1, 1, 3)

uncviet.df %<>%
  dplyr::mutate(policy.ord.new = sapply(policy.ord,
                                        function(i) policy.lookup[[i]]),
                year.ord.new = sapply(year.ord,
                                      function(i) year.lookup[[i]]))

uncviet.ord.mod <- glm(y ~ policy + sex + year +
                         I(policy.ord.new * year.ord.new),
                       data = uncviet.df, family = poisson)
anova(uncviet.pois.mod, uncviet.ord.mod, test = 'Chi')
```

```
Analysis of Deviance Table

Model 1: y ~ policy + sex + year
Model 2: y ~ policy + sex + year + I(policy.ord.new * year.ord.new)
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1        31     423.83
2        30     353.56  1   70.265 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(uncviet.ord.mod)$coef['I(policy.ord.new * year.ord.new)', ]
```

```
    Estimate   Std. Error      z value     Pr(>|z|)
5.270499e-01 6.248985e-02 8.434168e+00 3.335661e-17
```

The ordinal assignments do not seem to be very sensitive to the actual values used.

Problem 3

We are given:

$$\eta_{ij} = \log \frac{p_{ij}}{p_{i1}}$$

Then we get:

$$e^{\eta_[ij}} = \frac{p_{ij}}{p_{i1}}$$
$$p_{i1} e^{\eta_{ij}} = p_{ij}$$
$$p_{i1} \sum_j e^{\eta_{ij}} = \sum_j p_{ij} = 1$$

We can also say that $\sum_j e^{\eta_{ij}} = \sum_{j=2} e^{\eta_{ij}} + e^{\eta_{i1}}$

We can also see that $\eta_{i1} = \log \frac{p_{i1}}{p_{i1}} = \log 1 = 0$, so $e^{\eta_{ij}} = 1$.

And finally, we can see that since $\eta_{ij} = \log \frac{p_{ij}}{p_{i1}}$, $p_{i1} = \frac{p_{ij}}{e^{\eta_{ij}}}$. Putting this all together:

$$p_{i1} \sum_j e^{\eta_{ij}} = 1$$

$$\frac{p_{ij}}{e^{\eta_{ij}}}(1 + \sum_{j=2}^{J} e^{\eta_{ij}}) = 1$$

$$p_{ij} = \frac{e^{\eta_{ij}}}{1 + \sum_{j=2}^{J} e^{\eta_{ij}}}$$

Problem 4

Part a

```
hsb.df <- faraway::hsb %>%
  dplyr::mutate(ses = factor(ses, levels = c('low', 'middle', 'high')))
summary(hsb.df)
```

```
       id             gender                race          ses
 Min.   :  1.00   female:109   african-amer: 20   low   :47
 1st Qu.: 50.75   male  : 91   asian       : 11   middle:95
 Median :100.50                hispanic    : 24   high  :58
 Mean   :100.50                white       :145
 3rd Qu.:150.25
 Max.   :200.00
     schtyp           prog          read           write
 private: 32   academic:105   Min.   :28.00   Min.   :31.00
 public :168   general : 45   1st Qu.:44.00   1st Qu.:45.75
               vocation: 50   Median :50.00   Median :54.00
                              Mean   :52.23   Mean   :52.77
                              3rd Qu.:60.00   3rd Qu.:60.00
                              Max.   :76.00   Max.   :67.00
      math          science          socst
 Min.   :33.00   Min.   :26.00   Min.   :26.00
 1st Qu.:45.00   1st Qu.:44.00   1st Qu.:46.00
 Median :52.00   Median :53.00   Median :52.00
 Mean   :52.65   Mean   :51.85   Mean   :52.41
 3rd Qu.:59.00   3rd Qu.:58.00   3rd Qu.:61.00
 Max.   :75.00   Max.   :74.00   Max.   :71.00
```

```
hsb.df %>%
  dplyr::group_by(prog, gender) %>%
  dplyr::summarise(y = n()) %>%
  dplyr::ungroup() %>%
  xtabs(y ~ gender + prog, data = .) %>%
  prop.table(1)
```

```
        prog
gender    academic   general  vocation
  female 0.5321101 0.2201835 0.2477064
  male   0.5164835 0.2307692 0.2527473
```

```
hsb.df %>%
  dplyr::group_by(prog, ses) %>%
  dplyr::summarise(y = n()) %>%
  dplyr::ungroup() %>%
```

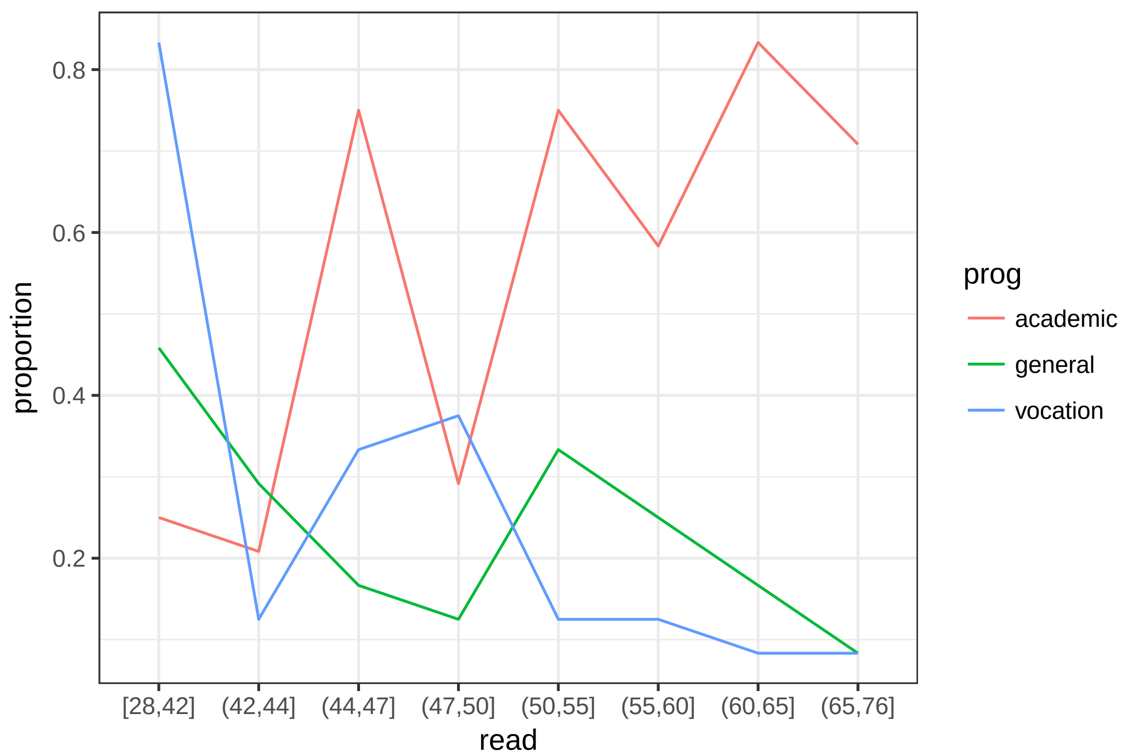
```r
  xtabs(y ~ ses + prog, data = .) %>%
  prop.table(1)
```

```
        prog
ses       academic   general  vocation
  low    0.4042553 0.3404255 0.2553191
  middle 0.4631579 0.2105263 0.3263158
  high   0.7241379 0.1551724 0.1206897
```

It appears that there is no strong association between `gender` and `prog`, but there is one between `ses` and `prog`.

Part b

```r
hsb.df %>%
  dplyr::mutate(read = cut_number(read, 8)) %>%
  dplyr::group_by(prog, read) %>%
  dplyr::summarise(y = n()) %>%
  dplyr::ungroup() %>%
  dplyr::mutate(proportion = y / n()) %>%
  ggplot() +
  geom_line(aes(x = read, y = proportion, group = prog, colour = prog))
```



It appears that as reading scores increase, the probability of being in an academic program increases, and as reading scores decrease, the probability of being in a vocational program increases.

Part c

```r
hsb.df %<>%
  dplyr::mutate(ses = as.numeric(ses))  # to ordinal
prog.mod <- multinom(prog ~ ., data = hsb.df) %>%
  step(direction = 'both', trace = 0)
```

```
# weights:  42 (26 variable)
initial  value 219.722458
iter  10 value 186.536640
iter  20 value 158.410762
iter  30 value 156.034011
final  value 156.033991
converged
trying - id
trying - gender
trying - race
trying - ses
trying - schtyp
trying - read
trying - write
trying - math
trying - science
trying - socst
# weights:  33 (20 variable)
initial  value 219.722458
iter  10 value 186.710606
iter  20 value 161.060816
final  value 159.177698
converged
trying - id
trying - gender
trying - ses
trying - schtyp
trying - read
trying - write
trying - math
trying - science
trying - socst
trying + race
# weights:  30 (18 variable)
initial  value 219.722458
iter  10 value 186.000556
iter  20 value 159.934297
final  value 159.409406
converged
trying - id
trying - ses
trying - schtyp
trying - read
trying - write
trying - math
trying - science
trying - socst
```

```
trying + gender
trying + race
# weights:  27 (16 variable)
initial  value 219.722458
iter  10 value 179.532582
iter  20 value 159.734855
final  value 159.730690
converged
trying - ses
trying - schtyp
trying - read
trying - write
trying - math
trying - science
trying - socst
trying + id
trying + gender
trying + race
# weights:  24 (14 variable)
initial  value 219.722458
iter  10 value 181.921322
iter  20 value 160.333721
final  value 160.333655
converged
trying - ses
trying - schtyp
trying - read
trying - math
trying - science
trying - socst
trying + id
trying + gender
trying + race
trying + write
# weights:  21 (12 variable)
initial  value 219.722458
iter  10 value 174.300997
iter  20 value 161.857206
iter  20 value 161.857205
iter  20 value 161.857205
final  value 161.857205
converged
trying - ses
trying - schtyp
trying - math
trying - science
trying - socst
trying + id
trying + gender
trying + race
trying + read
trying + write
# weights:  18 (10 variable)
initial  value 219.722458
```

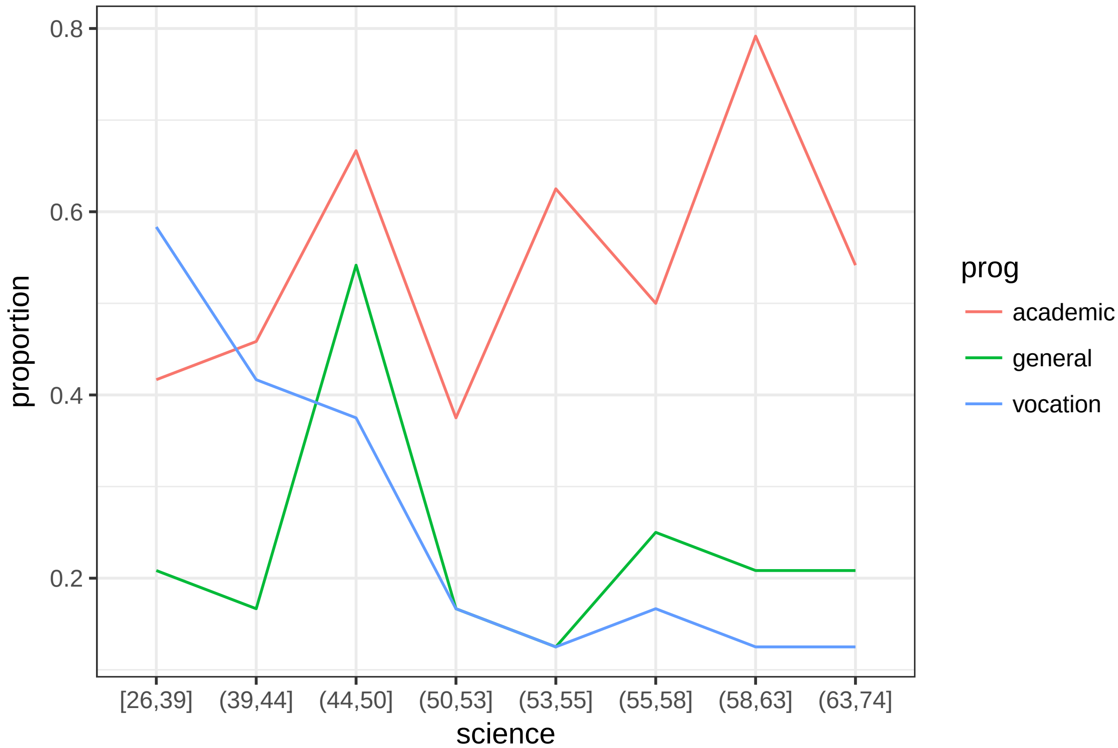
```
iter  10 value 166.035430
final  value 163.818866
converged
trying - schtyp
trying - math
trying - science
trying - socst
trying + id
trying + gender
trying + race
trying + ses
trying + read
trying + write
```

```r
summary(prog.mod)
```

```
Call:
multinom(formula = prog ~ schtyp + math + science + socst, data = hsb.df)

Coefficients:
         (Intercept) schtyppublic       math    science       socst
general     3.854099    0.6735847 -0.1205511 0.07441108 -0.05144098
vocation    7.022897    1.7880022 -0.1370433 0.04214340 -0.08672034

Std. Errors:
         (Intercept) schtyppublic       math    science      socst
general     1.512678    0.5336615 0.03182842 0.02727090 0.02314651
vocation    1.739585    0.8041796 0.03545611 0.02773962 0.02471897

Residual Deviance: 327.6377
AIC: 347.6377
```

We can see that while students who have higher math and social studies scores tend to go to academic programs, the opposite is the case for science scores. This is not consistent with what we see in the data:

```r
hsb.df %>%
  dplyr::mutate(science = cut_number(science, 8)) %>%
  dplyr::group_by(prog, science) %>%
  dplyr::summarise(y = n()) %>%
  dplyr::ungroup() %>%
  dplyr::mutate(proportion = y / n()) %>%
  ggplot() +
  geom_line(aes(x = science, y = proportion, group = prog, colour = prog))
```




```
summary(multinom(prog ~ science, data = hsb.df))
```

```
# weights:  9 (4 variable)
initial  value 219.722458
final  value 196.328070
converged
```

```
Call:
multinom(formula = prog ~ science, data = hsb.df)

Coefficients:
         (Intercept)     science
general  -0.04375373 -0.01512511
vocation  2.83772488 -0.07082091

Std. Errors:
         (Intercept)    science
general    1.0102263 0.01880946
vocation   0.9561635 0.01895089

Residual Deviance: 392.6561
AIC: 400.6561
```

However, there is some correlation between math and science scores, which is probably the culprit. $\hat{\rho}_{math,science} \approx 0.631$. This is also probably why reading scores and socioeconomic status were omitted.

Interpretations:

- The probability of being in a general program when being in a private school and when subject scores are 0 is $\frac{e^{3.854}}{1+e^{3.854}+e^{7.023}} \approx 0.0403$.
- The probability of being in a vocational program when being in a public school and when all subject

scores are 100 is $\frac{e^{7.023+1.788-13.70+4.214-8.672}}{1+e^{7.023+1.788-13.70+4.214-8.672}+e^{3.854+.6736-12.06+7.441-5.144}} \approx 8.6757 \times 10^{-5}$