1. **Exercise 1 – Agresti 7.36**

   Table 1 is based on a study involving British doctors.

	Person-Years		Coronary Deaths	
Age	Nonsmokers	Smokers	Nonsmokers	Smokers
35 – 44	18,793	52,407	2	32
45 – 54	10,673	43,248	12	104
55 – 64	5,710	28,612	28	206
65 – 74	2,585	12,663	28	186
75 – 84	1,462	5,317	31	102

Table 1: **Data on Coronary Death Rates**

   (a) Fit a main effects model for the log rates using age and smoking as factors. In discussing lack-of-fit, show that this model assumes a constant ratio of nonsmokers' to smokers' coronary death rates over age, and evaluate how the sample ratio depends on age.

```r
smokers<-data.frame(    c(  35 , 44 , 18793 , 52407 , 2 , 32 ),
  c( 45  , 54 , 10673 , 43248 , 12 , 104 ),  c( 55 , 64 , 5710 , 28612 , 28 , 206 ),
  c( 65  , 74 , 2585 , 12663 , 28 , 186 ),   c( 75 , 84 , 1462 , 5317 , 31 , 102 )  )

smokers<-t(as.matrix(smokers));smokers<-as.data.frame(smokers)
rownames(smokers)<-paste0( smokers$V1,"-", smokers$V2); smokers<-smokers[,-c(1:2)]
names(smokers)<-c(paste0("PY",c("nonsmokers", "smokers")),
    paste0("CD",c("nonsmokers", "smokers")))

smokers<-data.frame(rep(1:5,2),c(rep("NS",5),rep("S",5))    ,
    c(smokers$PYnonsmokers,smokers$PYsmokers),
    c(smokers$CDnonsmokers,smokers$CDsmokers))

names(smokers)<-c("age","smoker","PersonYears","Deaths")
smokers$age<-as.factor(smokers$age);smokers$ageQI<-as.numeric(smokers$age)
smokers$ratios<-smokers[,4]/smokers[,3];str(smokers)
```

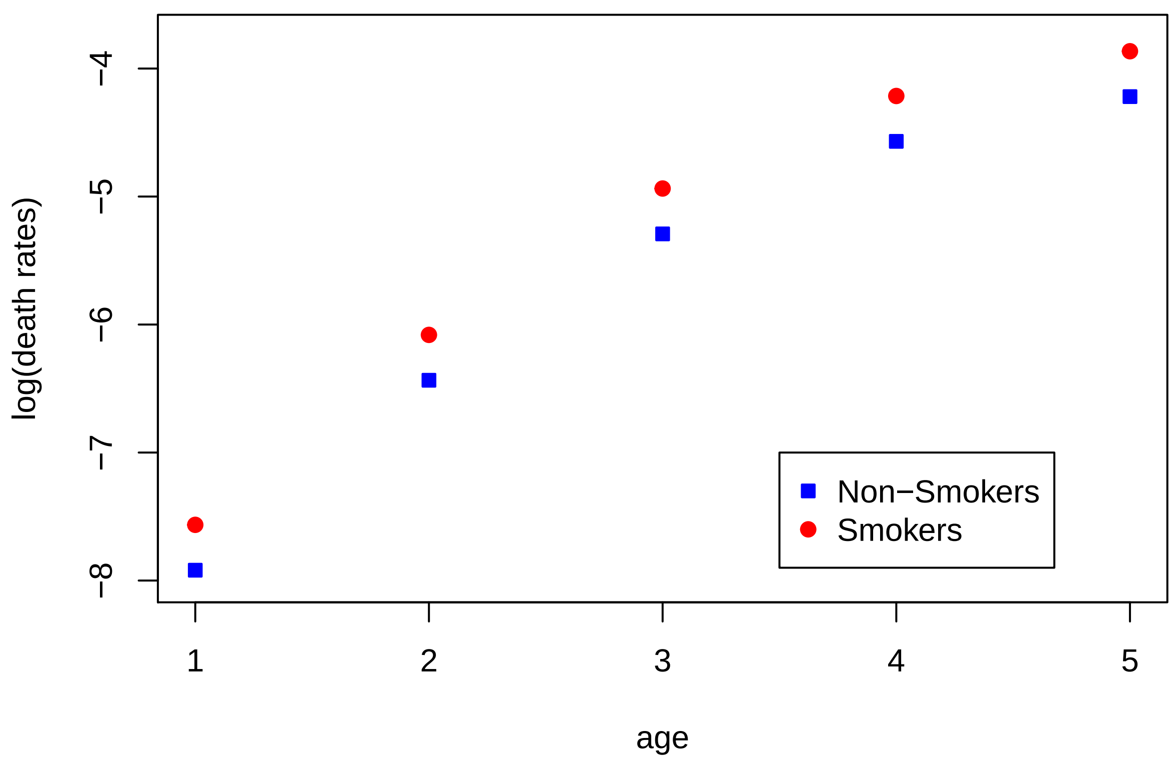
```
## 'data.frame':    10 obs. of  6 variables:
##  $ age        : Factor w/ 5 levels "1","2","3","4",..: 1 2 3 4 5 1 2 3 4 5
##  $ smoker     : Factor w/ 2 levels "NS","S": 1 1 1 1 1 2 2 2 2 2
##  $ PersonYears: num  18793 10673 5710 2585 1462 ...
##  $ Deaths     : num  2 12 28 28 31 32 104 206 186 102
##  $ ageQI      : num  1 2 3 4 5 1 2 3 4 5
##  $ ratios     : num  0.000106 0.001124 0.004904 0.010832 0.021204 ...
```

```r
smokers.fit<- glm(Deaths ~ age+smoker, offset = log(PersonYears), family=poisson, data=smokers)
summary(smokers.fit)
```

```
##
## Call:
## glm(formula = Deaths ~ age + smoker, family = poisson, data = smokers,
##     offset = log(PersonYears))
##
## Deviance Residuals:
##        1         2         3         4         5         6         7         8         9        10
## -2.18005  -1.30797  -0.13786   0.22886   1.91906   0.90176   0.51036   0.05133  -0.08734  -0.91239
##
```

```
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -7.9194     0.1918 -41.298  < 2e-16 ***
## age2          1.4840     0.1951   7.606 2.82e-14 ***
## age3          2.6275     0.1837  14.301  < 2e-16 ***
## age4          3.3505     0.1848  18.131  < 2e-16 ***
## age5          3.7001     0.1922  19.250  < 2e-16 ***
## smokerS       0.3545     0.1074   3.302  0.00096 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 935.091  on 9  degrees of freedom
## Residual deviance:  12.134  on 4  degrees of freedom
## AIC: 79.202
##
## Number of Fisher Scoring iterations: 4
```

```r
par(mar=c(5.1,4.1,2.1,2.1))
plot( ( smokers.fit$linear.predictors[1:5] )  - log(smokers$PersonYears)[1:5],
     ylim=c(-8,-3.75) , pch=22 ,col="blue", bg ="blue",
        ylab="log(death rates)",xlab="age")
points(smokers.fit$linear.predictors[6:10]  - log(smokers$PersonYears)[6:10],
    pch=21 , bg ="red",col="red")
legend(3.5,-7,c("Non-Smokers", "Smokers"), pch = c(22,21), col=c("blue","red") , pt.bg=c("blue","red"))
```



We note the rate of death is modeled by:

$$\log\left(\frac{\mu_i}{t_i}\right) = \boldsymbol{x}_i^T \boldsymbol{\beta}.$$

R is using a nequivalent offset for calculating the linear predictors,

$$\log(\mu_i) = \log(t_i) + \boldsymbol{x}_i^T \boldsymbol{\beta}.$$

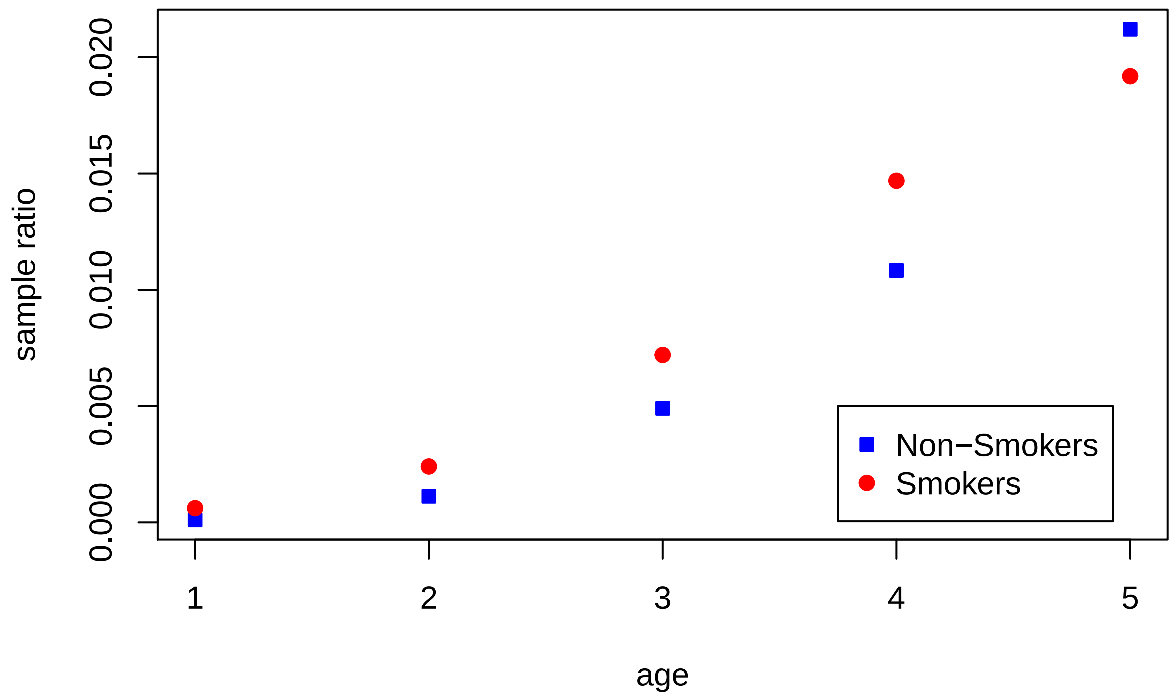
So we move the $\log(t_i)$ term back to the LHS to show the constant ratio of coronary deaths between nonsmokers to smokers. (Note: even if we kept the $\log(t_i)$ term on the RHS, the model would still have a constant ratio between nonsmokers to smokers coronary death counts).

We see the lack-of-fit with the model:

```
1-pchisq(12.134  , 4 )
```

```
## [1] 0.01638213
```

```
par(mar=c(5.1,4.1,1.1,2.1))
plot(1:5,smokers$ratios[1:5] , pch=22 ,col="blue", bg ="blue", ylab="sample ratio",xlab="age")
points(1:5,smokers$ratios[6:10],pch=21 , bg ="red",col="red")
legend(3.75,0.005,c("Non-Smokers", "Smokers"), pch = c(22,21), col=c("blue","red") , pt.bg=c("blue","red
```

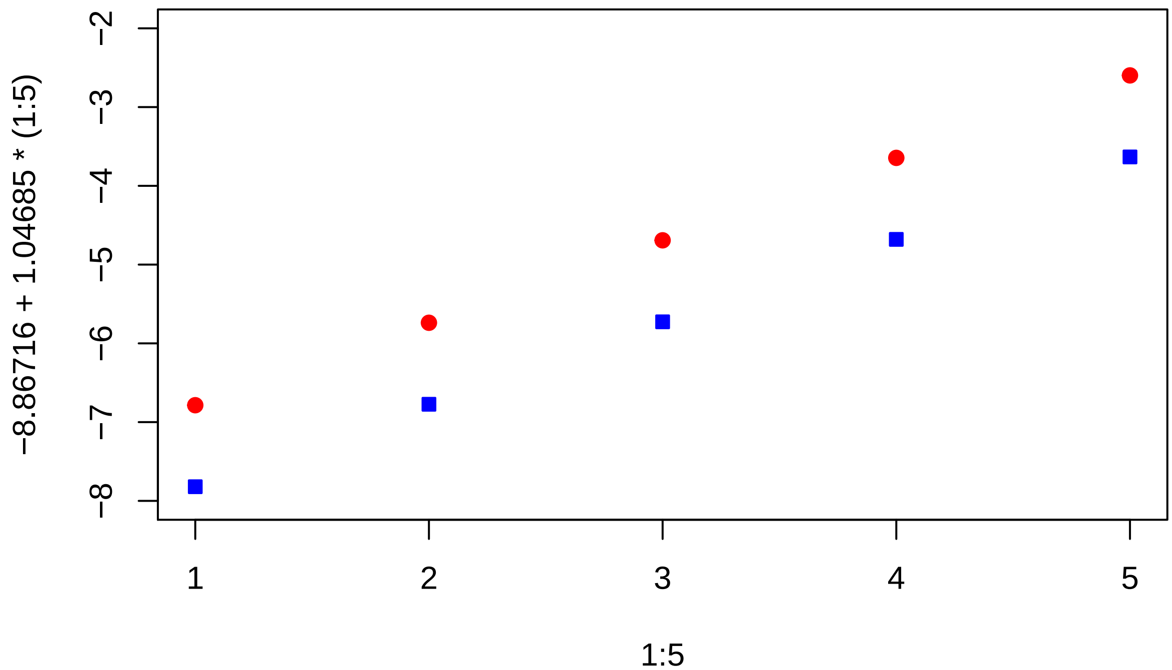


(b) Explain why it is sensible to add a quantitative interaction of age and smoking. For this model, show that the log ratio of coronary death rates changes linearly with age. Assign scores to age, fit the model, and interpret.

```
smokersQI.fit<-  glm(Deaths ~ ageQI*smoker, offset = log(PersonYears),family=poisson, data=smokers)
summary(smokersQI.fit)
```

```
##
## Call:
## glm(formula = Deaths ~ ageQI * smoker, family = poisson, data = smokers,
##     offset = log(PersonYears))
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.8784  -2.1219  -0.2482   1.7184   3.5269
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -8.86716    0.30567 -29.009  < 2e-16 ***
## ageQI          1.04685    0.07743  13.520  < 2e-16 ***
## smokerS        1.28369    0.32583   3.940 8.16e-05 ***
## ageQI:smokerS -0.24899    0.08359  -2.979  0.00289 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 935.091  on 9  degrees of freedom
## Residual deviance:  59.895  on 6  degrees of freedom
## AIC: 122.96
##
## Number of Fisher Scoring iterations: 4
```

```
plot(1:5,-8.86716 + 1.04685*(1:5) , ylim=c(-8,-2), pch=22 ,col="blue", bg ="blue")
points(1:5,-8.86716 + 1.04685*(1:5) +1.284  -0.249,pch=21 , bg ="red",col="red")
```


−8.86716 + 1.04685 * (1:5)
−2
−3
−4
−5
−6
−7
−8
1
2
3
4
5
1:5

2. **Exercise 2**

One question in the 1990 General Social Survey asked subjects how many times they had sexual intercourse in the preceding month. Table 2 shows responses classified by gender.

Response	Male	Female	Response	Male	Female	Response	Male	Female
0	65	128	9	2	2	20	7	6
1	11	17	10	24	13	22	0	1
2	13	23	12	6	10	23	0	1
3	14	16	13	3	3	24	1	0
4	26	19	14	0	1	25	1	3
5	13	17	15	3	10	27	0	1
6	15	17	16	3	1	30	3	1
7	7	3	17	0	1	50	1	0
8	21	15	18	0	1	60	1	0

Table 2: Data from the 1990 General Social Survey

(a) Fit a Poisson GLM with log link and a dummy variable for gender (1=males, 0=females) and explain if the model seems appropriate.

```
setwd("G:\\math\\661")
dat<-read.csv("sex.csv")
dat<-data.frame(
      (rep(dat$Response,2)),
    c(dat$Male,dat$Female),
    as.factor(c(rep(1,nrow(dat)),rep(0,nrow(dat)))) )
names(dat)<-c("response","counts","gender")
str(dat)
```

```
## 'data.frame':    54 obs. of  3 variables:
##  $ response: int  0 1 2 3 4 5 6 7 8 9 ...
##  $ counts  : int  65 11 13 14 26 13 15 7 21 2 ...
##  $ gender  : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
```

```
cbind(head(dat) ,tail(dat))
```

```
##   response counts gender response counts gender
## 1        0     65      1       24      0      0
## 2        1     11      1       25      3      0
## 3        2     13      1       27      1      0
## 4        3     14      1       30      1      0
## 5        4     26      1       50      0      0
## 6        5     13      1       60      0      0
```

```
dat.fit<-glm(response ~ gender, family=poisson, weights=counts, data=dat)
summary(dat.fit)
```

```
##
## Call:
## glm(formula = response ~ gender, family = poisson, data = dat,
##     weights = counts)
##
## Deviance Residuals:
```

```
##     Min       1Q   Median       3Q      Max
## -33.191    0.000    3.437    6.126   13.430
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.45936    0.02738  53.302  < 2e-16 ***
## gender1      0.30850    0.03822   8.071 6.95e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 4050.8  on 44  degrees of freedom
## Residual deviance: 3985.7  on 43  degrees of freedom
## AIC: 5271.3
##
## Number of Fisher Scoring iterations: 6
```

```
tab<-cbind(dat[which(dat$gender == 0),],dat[which(dat$gender == 1 ),-1])
tab<-tab[,c(1,2,4)];tab[19,2]<-sum(tab[19:nrow(tab),2]);
tab[19,3]<-sum(tab[19:nrow(tab),3]);tab<-tab[1:19,]
names(tab)[2:3]<-c("Female","Male")
head(tab)
```

```
##    response Female Male
## 28        0    128   65
## 29        1     17   11
## 30        2     23   13
## 31        3     16   14
## 32        4     19   26
## 33        5     17   13
```

```
c(sum(tab[,2]),sum(tab[,1]*tab[,2]));    sum(tab[,1]*tab[,2])/sum(tab[,2])
```

```
## [1]  310 1297
```

```
## [1] 4.183871
```

```
sum( tab[,2]*((tab[,1]- 4.183871 )^2) ) / ( sum(tab[,2]) -1)
```

```
## [1] 29.76867
```

```
c(sum(tab[,3]),sum(tab[,1]*tab[,3]));    sum(tab[,1]*tab[,3])/sum(tab[,3])
```

```
## [1]  240 1297
```

```
## [1] 5.404167
```

```
sum( tab[,3]*((tab[,1]- 4.183871 )^2) ) / ( sum(tab[,3]) -1)
```

```
## [1] 31.30203
```

```
1-pchisq(3985.7,43)
```

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

The sample mean for the 1297 women is 4.183871 with a variance of 29.76867. The sample mean for the 1297 men is 5.404167 with a variance of 31.30203. In both groups the sample variances are about

6-7 times the size of the sample means. This is suggesting overdispersion relative to the Poisson. We also see that the model does not give a good fit to the data (p-value ≈ 0).

(b) Interpret the regression coefficient of gender for the model in (a) and provide a 95% Wald confidence interval for the ratio of means for males versus females.

```
exp(0.30850 -1.96*0.03822);exp(0.30850 +1.96*0.03822)
```

```
## [1] 1.263125
```

```
## [1] 1.467281
```

When gender is male, the count of sexual intercourse is estimated to be 1.36 times that of females ($e^{0.30850}$). The Wald 95% confidence interval for the ratio of means for males versus females is:

$$\exp\left(0.30850 \pm 1.96 \cdot 0.03822\right) = (1.263125, 1.467281)$$

(c) Fit a negative binomial model. Is there evidence of overdispersion? What is the estimated difference in log means, its standard error, and the 95% Wald confidence interval for the ratio of means.

```
library(MASS)
nb.fit<-glm.nb(response ~ gender, weights=counts, data=dat)
summary(nb.fit)
```

```
##
## Call:
## glm.nb(formula = response ~ gender, data = dat, weights = counts,
##     init.theta = 0.5018752366, link = log)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -17.0366    0.0000    0.9873    1.5894    3.4336
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.45936    0.08472  17.226   <2e-16 ***
## gender1      0.30850    0.12724   2.425   0.0153 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.5019) family taken to be 1)
##
##     Null deviance: 606.53  on 44  degrees of freedom
## Residual deviance: 600.60  on 43  degrees of freedom
## AIC: 2883
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.5019
```

```
##           Std. Err.:  0.0387
##
##  2 x log-likelihood:  -2876.9770
```

```r
1-pchisq(600,43)
```

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

We note that $\widehat{Var}(Y) = \hat{\mu} + \hat{\gamma}\hat{\mu}^2$ is actually overestimating the sample variances. For females the sample variance is 29.76867, and the negative binomial model is estimating $4.303205 + \left(\frac{1}{0.5019}\right) * 4.303205^2 = 41.19815$. Likewise for males, the sample variance is 31.30203, and the negative binomial model is estimating $5.858303 + \left(\frac{1}{0.5019}\right) * 5.858303^2 = 74.23789$.

There is evidence that $\hat{\gamma} > 0$; $\hat{\gamma} = \left(\frac{1}{0.5019}\right) = 1.992429$ and a 95% confidence interval for γ is given by:

$$\frac{1}{0.5019 \pm 1.96 \cdot 0.0387} = (1.730846, 2.347153).$$

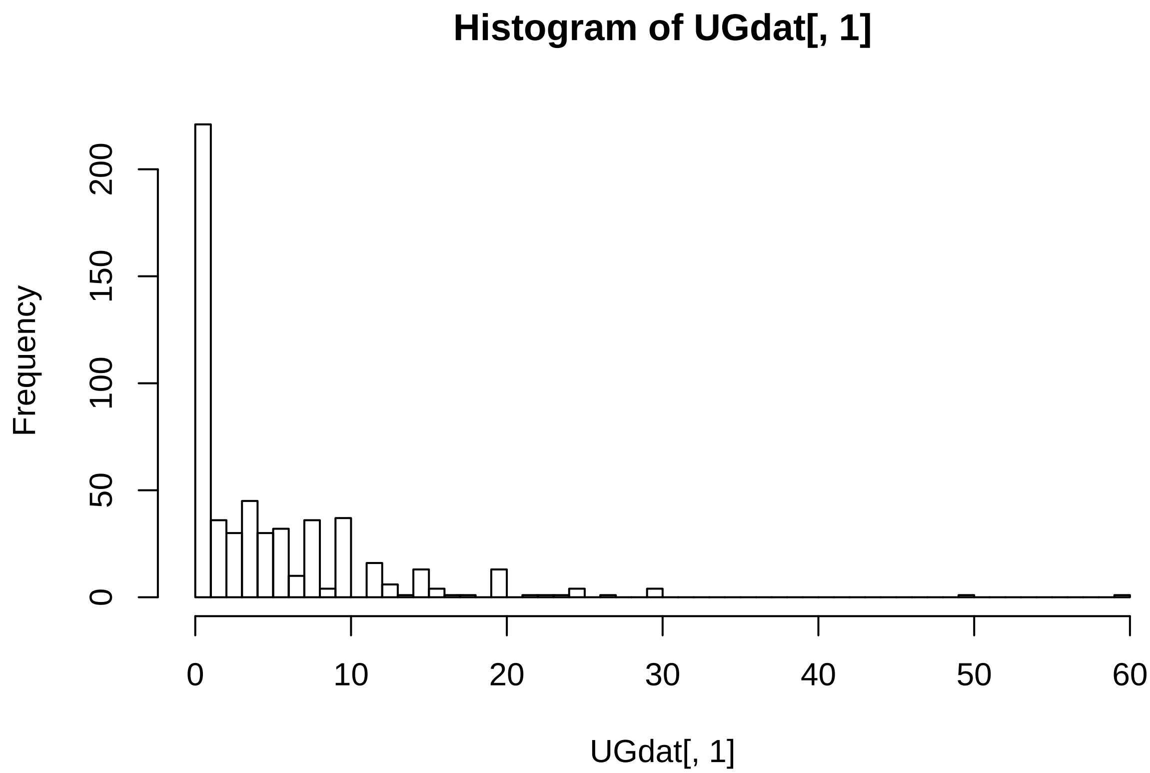
So the extra parameter is picking up some of the dispersion compared with the Poisson. But we recall that the negative binomial approaches the Poisson as $\gamma \to 0$, so there might be more overdispersion unaccounted for. We test the fit of the negative binomial model:

```r
1-pchisq(600.60,43)
```

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

and see the model does not fit well. We look at a histogram of the raw data and see an excessive amount of zeroes in the data, one reaspon for overdispersion.

```r
UGdat<-as.data.frame(lapply(dat, function(x,p) rep(x,p), dat[["counts"]]))
hist(UGdat[,1], breaks = seq(0,60,by=1))
```



(d) Consider a zero-inflated Poisson model with the zero-inflated component constant across subject (that is with intercept only for the model of ϕ_i). What are the mixing proportions for the degenerate distribution and the Poisson model? Interpret the regression coefficient of gender.

```
suppressWarnings(suppressMessages(library(pscl)))

fit.zip = zeroinfl(response ~ gender |  1 ,data=UGdat)
summary(fit.zip )
```

```
## Warning in deparse(x$call, width.cutoff = floor(getOption("width") * 0.85)): invalid 'cutoff' value f

##
## Call:
## zeroinfl(formula = response ~ gender | 1, data = UGdat)
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -1.1692 -1.1547 -0.4264  0.6238 12.2789
##
## Count model coefficients (poisson with log link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.99107    0.02747  72.493   <2e-16 ***
## gender1      0.09242    0.03830   2.413   0.0158 *
##
```

```
## Zero-inflation model coefficients (binomial with logit link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.61660    0.08944  -6.894 5.41e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 8
## Log-likelihood: -1835 on 3 Df
```

```
#mixing proportions
phi=as.numeric( exp(coef(fit.zip)[3])/(1+exp(coef(fit.zip)[3])) )
phi;1-phi
```

```
## [1] 0.3505542

## [1] 0.6494458
```

The mixing parameter $\phi = 0.3505542$, so the mixing proportion for the degenerate distribution is 0.6494458 and the mixing proportion for the Poisson distribution at $y_i = 0$ is 0.3505542.

Males have an expected log count that is 0.09242 higher than females.

(e) Consider a zero-inflated negative binomial model. What are the mixing proportions for the degenerate distribution and the negative binomial model? Interpret the regression coefficient of gender.

```
fit.zinb = zeroinfl(response ~ gender| 1 ,dist="negbin",data=UGdat)
summary(fit.zinb)
```

```
## Warning in deparse(x$call, width.cutoff = floor(getOption("width") * 0.85)): invalid 'cutoff' value :

##
## Call:
## zeroinfl(formula = response ~ gender | 1, data = UGdat, dist = "negbin")
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -0.8054 -0.7979 -0.2814  0.3961  8.2062
##
## Count model coefficients (negbin with log link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.89133    0.06990  27.059  < 2e-16 ***
## gender1      0.14584    0.09487   1.537 0.124254
## Log(theta)   0.43572    0.12576   3.465 0.000531 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.8439     0.1166  -7.238 4.54e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 1.5461
## Number of iterations in BFGS optimization: 9
```

```
## Log-likelihood: -1410 on 4 Df
```

```
#mixing proportions
phi=as.numeric( exp(coef(fit.zinb)[3])/(1+exp(coef(fit.zinb)[3])) )
phi;1-phi
```

```
## [1] 0.300723
## [1] 0.699277
```

The mixing parameter $\phi = 0.300723$, so the mixing proportion for the degenerate distribution is 0.6494458 and the mixing proportion for the Poisson distribution at $y_i = 0$ is 0.699277.

Males have an expected count that is 1.157011 $\left(e^{0.14584}\right)$ than females. The predictor `gender1` in the part of the negative binomial regression model predicting how many times they had sexual intercourse in the preceding month is not statistically significant.

(f) Provide a table with the observed counts and the fitted counts for each of the four models for $y_i = 0, \ldots, 20$ and $y_i > 20$.

```
tab<-cbind(dat[which(dat$gender == 0),],dat[which(dat$gender == 1 ),-1])
tab<-tab[,c(1,2,5)]
 names(tab)[2:3]<-c("Female","Male");head(tab)
```

```
##    response Female Male
## 28        0    128    1
## 29        1     17    1
## 30        2     23    1
## 31        3     16    1
## 32        4     19    1
## 33        5     17    1
```

```
sex.n = by(dat$counts, dat$gender, sum)
sex.nb = glm.nb(response ~ gender, weights=counts, data=dat)
sex.muhat = unique(sex.nb$fitted.values)



nfemale.poi = dpois(unique(dat[,1]), lambda=sex.muhat[1])*sex.n[1]
nmale.poi = dpois(unique(dat[,1]), lambda=sex.muhat[2])*sex.n[2]
nfemale.negb = round(dnbinom(unique(dat[,1]), size=sex.nb$theta,
mu=sex.muhat[1])*sex.n[1],3)
nmale.negb = round(dnbinom(unique(dat[,1]), size=sex.nb$theta,
    mu=sex.muhat[2])*sex.n[2],3)


tab$poiF<-round( nfemale.poi  ,3)
tab$poiM<-round( nmale.poi ,3)

tab$negbF<-  nfemale.negb
tab$negbM<-  nmale.negb
```

```r
tab$zipF<- round(c(  as.numeric(
    sex.n[1] * (     phi + (1-phi)  * dpois(0,exp(1.99107)) )    ),
    sex.n[1]*( (1-phi)* dpois(unique(dat[,1])[-1],exp(1.99107)) ) ) ,3)

tab$zipM<-round(c(  as.numeric(
    sex.n[2] * (     phi + (1-phi)  * dpois(0,exp(1.99107 + 0.09242)) )),
    sex.n[2]*((1-phi)*dpois(unique(dat[,1])[-1],exp(1.99107 + 0.09242)))),3)

tab$zinbF<-round(c( as.numeric(
    sex.n[1]*(  phi + (1-phi) * dnbinom(0,mu=exp(1.89133), exp(0.43572)))),
    sex.n[1]* ((1-phi) * dnbinom(unique(dat[,1])[-1], mu=exp(1.89133),
    exp(0.43572))   )   ),3)

tab$zinbM<-round(c( as.numeric(
    sex.n[2]*(  phi + (1-phi) * dnbinom(0,mu=exp(1.89133+0.14584),
        exp(0.43572))) ),
    sex.n[2]* ((1-phi) * dnbinom(unique(dat[,1])[-1], mu=exp(1.89133 +
        0.14584),exp(0.43572))   )),3)

print(tab,row.names = F)
```

```
##  response Female Male   poiF   poiM  negbF  negbM   zipF   zipM   zinbF  zinbM
##         0    128    1  0.885  3.246 86.667 77.236 93.367 72.228 109.739 82.797
##         1     17    1  5.187 13.968 40.064 34.714  1.048  0.438  20.703 13.668
##         2     23    1 15.193 30.054 27.712 23.345  3.836  1.758  21.371 14.481
##         3     16    1 29.668 43.110 21.287 17.436  9.365  4.708  20.483 14.245
##         4     19    1 43.452 46.378 17.165 13.670 17.145  9.453  18.877 13.473
##         5     17    1 50.911 39.915 14.236 11.023 25.112 15.187  16.978 12.437
##         6     17    1 49.709 28.627 12.024  9.052 30.651 20.331  15.020 11.293
##         7      3    1 41.601 17.598 10.287  7.530 32.067 23.330  13.129 10.131
##         8     15    1 30.464  9.466  8.885  6.323 29.355 23.425  11.372  9.007
##         9      2    1 19.830  4.526  7.731  5.349 23.886 20.906   9.781  7.951
##        10     13    1 11.617  1.948  6.766  4.552 17.493 16.793   8.364  6.978
##        12     10    1  3.020  0.273  5.253  3.341  7.107  8.208   6.035  5.304
##        13      3    1  1.361  0.090  4.653  2.877  4.004  5.072   5.099  4.599
##        14      1    1  0.570  0.028  4.134  2.485  2.094  2.910   4.296  3.977
##        15     10    1  0.222  0.008  3.681  2.152  1.023  1.558   3.610  3.430
##        16      1    1  0.081  0.002  3.285  1.867  0.468  0.782   3.027  2.952
##        17      1    1  0.028  0.001  2.937  1.623  0.202  0.370   2.534  2.536
##        18      1    1  0.009  0.000  2.630  1.413  0.082  0.165   2.117  2.174
##        20      6    1  0.001  0.000  2.119  1.076  0.012  0.028   1.471  1.591
##        22      1    1  0.000  0.000  1.715  0.824  0.001  0.004   1.017  1.159
##        23      1    1  0.000  0.000  1.546  0.722  0.000  0.001   0.844  0.987
##        24      0    1  0.000  0.000  1.394  0.633  0.000  0.000   0.700  0.840
##        25      3    1  0.000  0.000  1.259  0.555  0.000  0.000   0.580  0.715
##        27      1    1  0.000  0.000  1.028  0.429  0.000  0.000   0.397  0.516
##        30      1    1  0.000  0.000  0.763  0.292  0.000  0.000   0.224  0.314
##        50      0    1  0.000  0.000  0.114  0.025  0.000  0.000   0.004  0.010
##        60      0    1  0.000  0.000  0.046  0.008  0.000  0.000   0.001  0.002
```