Practice 7 Solutions

1. The data below come from a survey of opinion on the Vietnam war conducted among 1st – 3rd year undergraduate students at the University of North Carolina in 1967.

   The policies listed were:

   A – defeat power of Vietnam by widespread bombing and land invasion

   B – follow the present policy

   C – withdraw troops to strong points and open negotiations on elections involving the Vietcong

   D – immediate withdrawal of all U.S. troops.

Gender	Year	Opinion (op)			
		A	B	C	D
Male	1	175	116	131	17
	2	160	126	135	21
	3	132	120	154	29
Female	1	13	19	40	5
	2	5	9	33	3
	3	22	29	110	6

	Model	scaled deviance	residual df
1	gender+year+op	181.42	17
2	gender*year+op	120.05	15
3	gender*op+year	78.88	14
4	gender+year*op	157.33	11
5	gender*year+gender*op	17.51	12
6	gender*year+year*op	95.96	9
7	gender*op+year*op	54.79	8
8	gender*year+gender*op+year*op	5.70	6

   (a) Which of the three factors, `Opinion`, `Gender` and `Year`, can serve as the response variable? Why? Based on your answer, which of the eight models is (or are) not worth to consider? Why not?

   - `Opinion` should be used as the response variable because the distribution of `Opinion` across `Gender` and `Year` is the focus of study.
   - Model 7 `gender*op+year*op`, i.e. [GO][YO] is not worth to consider, because this model studies the association between `Gender` and `Year` given `Opinion` which is not related to the focus of the `Opinion` study.

   (b) Which of the following conclusions are reasonable for the data? Why or why not?

   i. Opinion is independent of year level and gender.

   ii. Given the year level, opinion is independent of gender.

   iii. Given gender, opinion is independent of year level.

    iv. The ratio of the odds between any two opinions (B and C say) for males and females is the same for each year level.

Which, if any, of these conclusions do you consider to be the most appropriate based on the model deviance output provided? Justify your answer.

-    i. It refers to the model $[GY][O]$, i.e. `gender*year+op`: $D = 120.05$ on 15 df, p-value ≈ 0. Not a good fit, consequently not a reasonable conclusion.
  - ii. $[GY][YO]$, i.e. `gender*year +year*op`: $D = 95.96$ on 9 df, p-value ≈ 0. Not a good fit, consequently not a reasonable conclusion.
  - iii. $[GY][GO]$, i.e. `gender*year +gender*op`: $D = 17.51$ on 12 df, p-value $= 0.13$. A good fit, consequently a reasonable conclusion. (AIC=17.51+24=41.51, equivalent to 171.5871 given by `R` which is computed using AIC=$-2\times$ maxLoglik $+2p$).
  - iv. $[GY][GO][YO]$, i.e. `gender*year +gender*op+year*op`: $D = 5.70$ on 6 df, p-value $= 0.46$. A good fit, consequently a reasonable conclusion. (AIC=5.70+36=41.70. AIC=171.7841 by `R`, equivalent).

- Most appropriate model is $[GY][GO]$ according to AIC. The "bigger" model $[GY][GO][YO]$ is not significantly better ($\Delta D = 17.51 - 5.70 = 11.81$ on $12 - 6 = 6$ df, $< 12.59 = \chi^2_{0.95}(6)$.)

(c) It has been suggested that the most appropriate model found above might be improved by including year as a variable (as yr) rather than as a factor in some way. Write down the form of such a model which is likely to provide an adequate fit to the data, and give an interpretation of the model.

- An improved model is $[GY][GO][yrO]$, i.e. `gender*year +gender*op+yr*op`. Interpretation: `Opinion` depends on both `gender` and `year`, with simple log-linear trends in `Opinion` with `yr`. Further, the deviance of $[GY][GO][yrO]$ is 5.9787 with df=9 and p-value=0.742, indicating an adequate fit. The trend terms `yr*op` is significant with $\Delta D = 17.51 - 5.9787 = 11.528$, Δdf $= 3$ and p-value=0.009. AIC of $[GY][GO][yrO]$=166.06.

```
> summary(mod5a)

Call: glm(formula = freq ~ gender * year + gender * op + yr * op, family = poisson)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.93002  -0.36383  -0.03652   0.42052   0.97094

Coefficients: (1 not defined because of singularities)
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  5.16762    0.07040  73.405  < 2e-16 ***
gender2     -2.58984    0.19348 -13.385  < 2e-16 ***
year2       -0.11430    0.07851  -1.456 0.145468
year3       -0.26262    0.10976  -2.393 0.016726 *
op2         -0.50365    0.17296  -2.912 0.003593 **
op3         -0.58228    0.16545  -3.519 0.000433 ***
op4         -2.55012    0.33448  -7.624 2.46e-14 ***
yr                NA         NA      NA       NA
```

```
        gender2:year2 -0.49913     0.19482  -2.562 0.010406 *
        gender2:year3  0.66556     0.15863   4.196 2.72e-05 ***
        gender2:op2    0.57600     0.21891   2.631 0.008508 **
        gender2:op3    1.56371     0.18826   8.306  < 2e-16 ***
        gender2:op4    0.81147     0.33964   2.389 0.016885 *
        op2:yr         0.12733     0.08069   1.578 0.114551
        op3:yr         0.23903     0.07577   3.155 0.001606 **
        op4:yr         0.30226     0.14753   2.049 0.040474 *
        ---
        Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

        (Dispersion parameter for poisson family taken to be 1)

            Null deviance: 1390.5648  on 23  degrees of freedom
        Residual deviance:    5.9787  on  9  degrees of freedom
        AIC: 166.06

        Number of Fisher Scoring iterations: 4
```

(d) Write down the deviance and the degrees of freedom that would be obtained by fitting the model `year+op` to the 2–way table obtained by collapsing over `gender`. State, with reasons, whether collapsing over `gender` would be a reasonable thing to do.

- The deviance wanted here is actually the reduction of deviance achieved by adding the interaction term `year:op` to the model `year + op` . Therefore, the wanted deviance is the same as the reduction of deviance between models 1 an 4, or models 2 and 6, or models 3 and 7. Namely, scale deviance = $181.42 - 157.33 = 120.05 - 95.96 = 78.88 - 54.79 = 24.09$ (on 6 df) which is highly significant ($> \chi^2_{0.95}(6) = 12.59$).

- Collapsing over `gender` is not reasonable as both `gender:year` and `gender:opinion` are significant in those 3-factor models (models 1 to 8).

2. The following data were obtained from a study of coronary heart disease, where `N` is the total number of subjects in each group and `Y` is the number diagnosed with coronary heart disease. The factor `CHOL` refers to serum cholesterol in mg/100cc where:

$$1 = < 200, \ 2 = 200 - 219, \ 3 = 220 - 259, \ 4 = 260+$$

while the factor `BP` refers to blood pressure in mm of mercury where:

$$1 = < 127, \ 2 = 127 - 146, \ 3 = 147 - 166, \ 4 = 167+$$

		BP			
CHOL		1	2	3	4
1	Y	2	3	3	4
	N	119	124	50	26
2	Y	3	2	0	3
	N	88	100	43	23
3	Y	8	11	6	6
	N	127	220	74	49
4	Y	7	12	11	11
	N	74	111	57	44

Four models have been fitted to these data, R output for which is given below.

```
> Y <- c(2, 3, 3, 4, 3, 2, 0, 3, 8, 11, 6, 6, 7, 12, 11, 11)
> N <- c(119, 124, 50, 26, 88, 100, 43, 23, 127, 220, 74, 49, 74,
+     111, 57, 44)
> BP <- factor(rep(1:4, 4))
> CHOL <- factor(rep(1:4, rep(4, 4)))
> fit.1 <- glm(Y/N ~ 1, weights = N, family = "binomial")
> summary(fit.1)

Call:
glm(formula = Y/N ~ 1, family = "binomial", weights = N)

Deviance Residuals:
    Min       1Q    Median       3Q       Max
-2.67546  -1.63956   0.06465   1.37102   3.74137

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.5987     0.1081  -24.05   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 58.726  on 15  degrees of freedom
Residual deviance: 58.726  on 15  degrees of freedom
AIC: 111.83

Number of Fisher Scoring iterations: 5
```

```
> fit.2 <- glm(Y/N ~ CHOL, weights = N, family = "binomial")
> summary(fit.2)

Call:
glm(formula = Y/N ~ CHOL, family = "binomial", weights = N)

Deviance Residuals:
       Min          1Q      Median          3Q         Max
-1.6589861  -1.0203129   0.0009951   1.1270950   2.3674007

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.2419     0.2943 -11.017  < 2e-16 ***
CHOL2        -0.1839     0.4644  -0.396   0.6920
CHOL3         0.5914     0.3480   1.699   0.0893 .
CHOL4         1.4543     0.3392   4.287 1.81e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 58.726  on 15  degrees of freedom
Residual deviance: 26.805  on 12  degrees of freedom
AIC: 85.909

Number of Fisher Scoring iterations: 5

> fit.3 <- glm(Y/N ~ BP, weights = N, family = "binomial")
> summary(fit.3)

Call:
glm(formula = Y/N ~ BP, family = "binomial", weights = N)

Deviance Residuals:
    Min      1Q   Median      3Q      Max
-2.8361  -1.0499  -0.3808   0.8645   2.4265

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.96527    0.22930 -12.932  < 2e-16 ***
BP2          0.03028    0.30032   0.101   0.9197
BP3          0.64289    0.32784   1.961   0.0499 *
BP4          1.37264    0.32050   4.283 1.85e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

```
    Null deviance: 58.726  on 15  degrees of freedom
Residual deviance: 35.163  on 12  degrees of freedom
AIC: 94.267

Number of Fisher Scoring iterations: 5


> fit.4 <- glm(Y/N ~ CHOL + BP, weights = N, family = "binomial")
> summary(fit.4)

Call:
glm(formula = Y/N ~ CHOL + BP, family = "binomial", weights = N)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.89259  -0.34946  -0.02072   0.52307   0.99198

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.48194    0.34865  -9.987  < 2e-16 ***
CHOL2       -0.20798    0.46641  -0.446 0.655663
CHOL3        0.56223    0.35080   1.603 0.108998
CHOL4        1.34412    0.34297   3.919 8.89e-05 ***
BP2         -0.04146    0.30365  -0.137 0.891393
BP3          0.53236    0.33240   1.602 0.109251
BP4          1.20042    0.32689   3.672 0.000240 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 58.7262  on 15  degrees of freedom
Residual deviance:  8.0762  on  9  degrees of freedom
AIC: 73.18

Number of Fisher Scoring iterations: 4
```

The data have been analysed using logistic regression models as shown above. An alternative would have been to use log-linear models in a 3-way contingency table with factors CHOL1, BP1 and CHD, where CHD is a factor with 2 levels indicating whether or not subjects have coronary heart disease. For each of the four (logistic regression) models given in the R output, specify the equivalent log-linear model (eg CHOL1 + BP1 + CHD). Also analyze these log-linear models using R, and compare the results with that of the logistic models.

- Log-linear model Freq~ CHOL1*BP1+CHD (given in fitP.1) is equivalent to logistic model fit.1 in that the intercept value -2.5987 of fit.1 and its standard error are the same as those of the coefficient of CHD2 in Freq~ CHOL1*BP1+CHD, except

a minus sign. Note if we set CHD2 as the base level of CHD, these values will be exactly the same of each other. Also both `fit.1` and `Freq~ CHOL1*BP1+CHD` give the same residual deviance 58.726 on 15 degrees of freedom.

- Note that log-linear model `Freq~ CHOL1+BP1+CHD` (given in `fitP.5`) has a value 2.59866 for its CHD2 coefficient which is the same as the intercept value -2.5987 of `fit.1` except a minus sign. But `fitP.5` and `fit.1` are not equivalent in that they don't have the same residual deviance.

- The equivalent model to `fit.2` is `Freq~ BP1+CHD*CHOL1`. The coefficients of CHD2 and CHD2:CHOL1 are the same as those in `fit.2` except the sign is opposite. Deviance reduction 31.92 due to CHOL in `fit.2` is the same as the deviance reduction due to CHD:CHOL1 in the log-linear model.

- The equivalent model to `fit.3` is `Freq~ CHOL1+CHD*BP1`. The coefficients of CHD2 and CHD2:BP1 are the same as those in `fit.3` except the sign is opposite. Deviance reduction 23.56 due to BP in `fit.3` is the same as the deviance reduction due to CHD:BP1 in the log-linear model.

- The equivalent model to `fit.4` is `Freq~ CHOL1*BP1+CHD*CHOL1+CHD*BP1`. The coefficients of CHD2, CHD2:CHOL1 and CHD2:BP1 are the same as those in `fit.4` except the sign is opposite. Deviance reduction 31.92 due to CHOL and reduction 18.73 due to BP in `fit.4` are the same as the deviance reductions due to CHD:CHOL1 and CHD:BP1 respectively in the log-linear model.

```
Freq<- c(Y, N-Y)
CHD <- factor(rep(1:2, each=16))
BP1<- factor(rep(1:4,8))
CHOL1 <- factor(rep(rep(1:4,each=4),2))

fitP.1 <- glm(Freq ~ CHOL1*BP1+CHD, family=poisson)
summary(fitP.1)

Call: glm(formula = Freq ~ CHOL1 * BP1 + CHD, family = poisson)

Deviance Residuals:
    Min      1Q   Median      3Q      Max
-2.6102  -0.5885  -0.0192  0.5336   3.5131

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.10873    0.13609  15.495  < 2e-16 ***
CHOL12      -0.30179    0.14060  -2.146 0.031834 *
CHOL13       0.06506    0.12758   0.510 0.610071
CHOL14      -0.47506    0.14804  -3.209 0.001332 **
BP12         0.04116    0.12833   0.321 0.748417
BP13        -0.86710    0.16853  -5.145 2.68e-07 ***
BP14        -1.52103    0.21648  -7.026 2.12e-12 ***
CHD2         2.59866    0.10806  24.047  < 2e-16 ***
CHOL12:BP12  0.08668    0.19450   0.446 0.655869
CHOL13:BP12  0.50828    0.16996   2.991 0.002785 **
CHOL14:BP12  0.36431    0.19746   1.845 0.065042 .
```

```
CHOL12:BP13  0.15096    0.25104    0.601 0.547610
CHOL13:BP13  0.32698    0.22314    1.465 0.142823
CHOL14:BP13  0.60609    0.24385    2.486 0.012936 *
CHOL12:BP14  0.17918    0.31892    0.562 0.574214
CHOL13:BP14  0.56866    0.27413    2.074 0.038040 *
CHOL14:BP14  1.00115    0.28828    3.473 0.000515 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1653.680  on 31  degrees of freedom
Residual deviance:   58.726  on 15  degrees of freedom
AIC: 241.3

anova(fitP.1, test="Chi")

Analysis of Deviance Table

Model: poisson, link: log

Response: Freq

Terms added sequentially (first to last)


          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                         31    1653.68
CHOL1      3    77.90        28    1575.78 < 2.2e-16 ***
BP1        3   319.07        25    1256.70 < 2.2e-16 ***
CHD        1  1173.55        24      83.15 < 2.2e-16 ***
CHOL1:BP1  9    24.42        15      58.73  0.003678 **

fitP.2 <- glm(Freq ~ BP1+CHD*CHOL1, family=poisson)
summary(fitP.2)

Call: glm(formula = Freq ~ BP1 + CHD * CHOL1, family = poisson)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.0071  -0.9625  -0.4881   1.1220   2.6488

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.30399    0.29160   4.472 7.76e-06 ***
BP12         0.30770    0.06521   4.718 2.38e-06 ***
BP13        -0.59962    0.08316  -7.211 5.57e-13 ***
BP14        -1.05544    0.09743 -10.832  < 2e-16 ***
CHD2         3.24194    0.29426  11.017  < 2e-16 ***
CHOL12      -0.40547    0.45644  -0.888 0.374363
CHOL13       0.94908    0.33999   2.792 0.005246 **
CHOL14       1.22867    0.32821   3.744 0.000181 ***
CHD2:CHOL12  0.18395    0.46439   0.396 0.692023
CHD2:CHOL13 -0.59143    0.34803  -1.699 0.089253 .
```

```
CHD2:CHOL14 -1.45425    0.33921  -4.287 1.81e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1653.68  on 31  degrees of freedom
Residual deviance:   51.23  on 21  degrees of freedom
AIC: 221.81

anova(fitP.2)


Analysis of Deviance Table
Model: poisson, link: log
Response: Freq
Terms added sequentially (first to last)

          Df Deviance Resid. Df Resid. Dev
NULL                         31    1653.68
BP1        3   319.07        28    1334.61
CHD        1  1173.55        27     161.06
CHOL1      3    77.90        24      83.15
CHD:CHOL1  3    31.92        21      51.23

anova(fit.2)


Analysis of Deviance Table
Model: binomial, link: logit
Response: Y/N
Terms added sequentially (first to last)

     Df Deviance Resid. Df Resid. Dev
NULL                    15      58.726
CHOL  3   31.921        12      26.805

fitP.3 <- glm(Freq ~ CHOL1+ CHD*BP1, family=poisson)
summary(fitP.3)


Call: glm(formula = Freq ~ CHOL1 + CHD * BP1, family = poisson)


Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.7649  -0.9855  -0.4258   0.7715   2.6929

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.569e+00  2.289e-01   6.854 7.17e-12 ***
CHOL12      -2.279e-01  8.409e-02  -2.710  0.00674 **
CHOL13       3.875e-01  7.254e-02   5.342 9.18e-08 ***
CHOL14      -1.092e-01  8.143e-02  -1.341  0.17993
CHD2         2.965e+00  2.293e-01  12.932  < 2e-16 ***
BP12         3.365e-01  2.928e-01   1.149  0.25044
BP13         1.142e-12  3.162e-01   0.000  1.00000
BP14         1.823e-01  3.028e-01   0.602  0.54705
```

```
CHD2:BP12   -3.028e-02  3.003e-01  -0.101  0.91970
CHD2:BP13   -6.429e-01  3.278e-01  -1.961  0.04988 *
CHD2:BP14   -1.373e+00  3.205e-01  -4.283 1.85e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for poisson family taken to be 1)


    Null deviance: 1653.680  on 31  degrees of freedom
Residual deviance:   59.588  on 21  degrees of freedom
AIC: 230.17


anova(fitP.3)


Analysis of Deviance Table
Model: poisson, link: log
Response: Freq
Terms added sequentially (first to last)


        Df Deviance Resid. Df Resid. Dev
NULL                       31     1653.68
CHOL1    3    77.90         28     1575.78
CHD      1  1173.55         27      402.22
BP1      3   319.07         24       83.15
CHD:BP1  3    23.56         21       59.59


anova(fit.3)


Analysis of Deviance Table
Model: binomial, link: logit
Response: Y/N
Terms added sequentially (first to last)


     Df Deviance Resid. Df Resid. Dev
NULL                    15      58.726
BP    3   23.563        12      35.163


fitP.4 <- glm(Freq ~ CHOL1*BP1+CHD*CHOL1+CHD*BP1, family=poisson)
summary(fitP.4)


Call: glm(formula = Freq ~ CHOL1 * BP1 + CHD * CHOL1 + CHD * BP1, family = poisson)


Deviance Residuals:
    Min       1Q    Median       3Q       Max
-1.87305  -0.23880   0.00775   0.22834   0.93502


Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.2668998  0.3504512   3.615  0.00030 ***
CHOL12      -0.5041469  0.4753197  -1.061  0.28885
CHOL13       0.6050325  0.3612351   1.675  0.09395 .
CHOL14       0.7878843  0.3576814   2.203  0.02761 *
BP12         0.0009095  0.3214834   0.003  0.99774
BP13        -0.3554966  0.3606777  -0.986  0.32431
```

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```
BP14           -0.3875643  0.3751954  -1.033  0.30162
CHD2            3.4819392  0.3486498   9.987  < 2e-16 ***
CHOL12:BP12     0.0864531  0.1945107   0.444  0.65671
CHOL13:BP12     0.5091512  0.1700846   2.994  0.00276 **
CHOL14:BP12     0.3673877  0.1987569   1.848  0.06454 .
CHOL12:BP13     0.1547335  0.2511958   0.616  0.53790
CHOL13:BP13     0.3123810  0.2234962   1.398  0.16220
CHOL14:BP13     0.5553161  0.2462449   2.255  0.02412 *
CHOL12:BP14     0.1911206  0.3200390   0.597  0.55039
CHOL13:BP14     0.5233331  0.2757203   1.898  0.05769 .
CHOL14:BP14     0.8490860  0.2935642   2.892  0.00382 **
CHOL12:CHD2     0.2079774  0.4664196   0.446  0.65567
CHOL13:CHD2    -0.5622288  0.3507980  -1.603  0.10900
CHOL14:CHD2    -1.3441207  0.3429663  -3.919 8.89e-05 ***
BP12:CHD2       0.0414608  0.3036517   0.137  0.89139
BP13:CHD2      -0.5323561  0.3323976  -1.602  0.10925
BP14:CHD2      -1.2004221  0.3268887  -3.672  0.00024 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1653.6802  on 31  degrees of freedom
Residual deviance:    8.0762  on  9  degrees of freedom
AIC: 202.65


anova(fitP.4)


Analysis of Deviance Table
Model: poisson, link: log
Response: Freq
Terms added sequentially (first to last)


          Df Deviance Resid. Df Resid. Dev
NULL                         31     1653.68
CHOL1      3    77.90        28     1575.78
BP1        3   319.07        25     1256.70
CHD        1  1173.55        24       83.15
CHOL1:BP1  9    24.42        15       58.73
CHOL1:CHD  3    31.92        12       26.80
BP1:CHD    3    18.73         9        8.08


anova(fit.4)


Analysis of Deviance Table
Model: binomial, link: logit
Response: Y/N
Terms added sequentially (first to last)

     Df Deviance Resid. Df Resid. Dev
NULL                    15       58.726
CHOL  3   31.921        12       26.805
BP    3   18.729         9        8.076
```

```
fitP.5 <- glm(Freq ~ BP1+CHOL1+CHD, family=poisson)
summary(fitP.5)


Call:
glm(formula = Freq ~ BP1 + CHOL1 + CHD, family = poisson)


Deviance Residuals:
    Min      1Q   Median      3Q      Max
-2.4346  -1.1397  -0.3287   0.8674   4.3013


Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.91388    0.12227  15.653  < 2e-16 ***
BP12         0.30770    0.06521   4.718 2.38e-06 ***
BP13        -0.59962    0.08316  -7.211 5.57e-13 ***
BP14        -1.05544    0.09743 -10.832  < 2e-16 ***
CHOL12      -0.22786    0.08409  -2.710  0.00674 **
CHOL13       0.38754    0.07254   5.342 9.18e-08 ***
CHOL14      -0.10920    0.08143  -1.341  0.17993
CHD2         2.59866    0.10806  24.047  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for poisson family taken to be 1)


    Null deviance: 1653.680  on 31  degrees of freedom
Residual deviance:   83.151  on 24  degrees of freedom
AIC: 247.73
```