> data1<-read.csv("Table7.21.csv",header=TRUE,sep=",")

> loglinear1 <-glm(Count~EI+SN+JP+TF,family=poisson, data=data1)

> summary(loglinear1)

Call:

glm(formula = Count ~ EI + SN + JP + TF, family = poisson, data = data1)

Deviance Residuals:

Min 1Q Median 3Q Max

-4.3550 -2.1182 -1.0628 0.8506 5.7457

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 3.92723 0.07501 52.354 < 2e-16 \*\*\*

EIYes -0.26439 0.06226 -4.246 2.17e-05 \*\*\*

SNYes 0.87008 0.06765 12.861 < 2e-16 \*\*\*

JPYes 0.12971 0.06185 2.097 0.036 \*

TFYes -0.48551 0.06355 -7.640 2.17e-14 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 399.94 on 15 degrees of freedom

Residual deviance: 135.87 on 11 degrees of freedom

AIC: 238.7

Number of Fisher Scoring iterations: 4

> pearson <- sum(resid(loglinear1, type="pearson")^2)

> pearson

[1] 145.1028

> loglinear2<-glm(Count~EI\*SN+EI\*JP+EI\*TF+SN\*JP+SN\*TF+JP\*TF,family=poisson, data=data1)

> summary(loglinear2)

Call:

glm(formula = Count ~ EI \* SN + EI \* JP + EI \* TF + SN \* JP +

SN \* TF + JP \* TF, family = poisson, data = data1)

Deviance Residuals:

1 2 3 4 5 6 7 8 9 10 11 12 13

-0.72826 1.00215 0.05168 -0.01429 1.49947 -1.29325 -0.07596 0.00231 0.56850 -0.82975 -0.04948 0.01728 -1.57051

14 15 16

1.09960 0.08587 -0.00804

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 4.37035 0.09913 44.087 < 2e-16 \*\*\*

EIYes 0.01142 0.12516 0.091 0.92732

SNYes 0.29141 0.12138 2.401 0.01636 \*

JPYes -0.95183 0.14661 -6.492 8.45e-11 \*\*\*

TFYes -1.00681 0.14898 -6.758 1.40e-11 \*\*\*

EIYes:SNYes -0.30212 0.14233 -2.123 0.03378 \*

EIYes:JPYes 0.01766 0.13160 0.134 0.89326

EIYes:TFYes -0.19449 0.13121 -1.482 0.13826

SNYes:JPYes 1.22153 0.14547 8.397 < 2e-16 \*\*\*

SNYes:TFYes 0.40920 0.15243 2.684 0.00727 \*\*

JPYes:TFYes 0.55936 0.13512 4.140 3.48e-05 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 399.944 on 15 degrees of freedom

Residual deviance: 10.162 on 5 degrees of freedom

AIC: 125

Number of Fisher Scoring iterations: 4

> pearson <- sum(resid(loglinear2, type="pearson")^2)

> pearson

[1] 10.10336

> data2<-read.csv("table5.12.csv",header=TRUE,sep=",")

> data2.lm <-glm(cbind(yes,no)~city+smoking,family=binomial, data=data2)

> summary(data2.lm)

Call:

glm(formula = cbind(yes, no) ~ city + smoking, family = binomial,

data = data2)

Deviance Residuals:

Min 1Q Median 3Q Max

-34.539 -13.095 0.625 12.720 33.041

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -0.548682 0.118022 -4.649 3.34e-06 \*\*\*

cityHB 0.018187 0.129473 0.140 0.888

cityNC -0.054906 0.170996 -0.321 0.748

cityNJ 0.005764 0.140911 0.041 0.967

citySH 0.055618 0.119570 0.465 0.642

citySY -0.027739 0.120071 -0.231 0.817

cityTY -0.745683 0.185518 -4.019 5.83e-05 \*\*\*

cityZZ 0.028782 0.144755 0.199 0.842

smoking 0.777062 0.046775 16.613 < 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: 11663 on 31 degrees of freedom

Residual deviance: 11358 on 23 degrees of freedom

AIC: 11376

Number of Fisher Scoring iterations: 4

> pearson <- sum(resid(data2.lm, type="pearson")^2)

> pearson

[1] 8418.534