Computer Lab 3: Binary Data

Example 1:

Use models to analyze and interpret the data in the following table on smoking habits of students in some high schools.

	Student Smokes	Student Not Smoke
Both parents smoke	400	1380
One parent smoke	416	1823
Neither parent smoke	188	1168

[code:]

```
options (contrasts=c("contr.treatment","contr.poly"))
students.smoke=c(400,416,188)
students.no.smoke=c(1380,1823,1168)
students=cbind(students.smoke,students.no.smoke)
parents=factor(c("both.smoke","one.smoke","neither.smoke"))
smoke.glm=glm(students~parents, family =binomial(link=logit))
out=summary(smoke.glm)
out
anova(smoke.glm,test="Chisq")

pearsonResiduals=residuals(smoke.glm,type="pearson")     ### Pearson
                                                         ### residuals
devianceResiduals=residuals(smoke.glm,type="deviance")    # ## Deviance
                                                         ### residuals
plot(pearsonResiduals)
plot(devianceResiduals)
```

Example 2:

The following table refers to 661 children with birth weights 650 g and 1749 g all of whom survived for at least one year. The variables of interest are:

Cardiac: mild heart problems of the mother during pregnancy

Comps: gynaecological problems during pregnancy

Smoking: mother smoked at least one cigarette per day during the first months of pregnancy.

BW: was the birth weight less than 1250

Cardiac	Yes				No			
Comps	Yes		No		Yes		No	
Smoking	Yes	No	Yes	No	Yes	No	Yes	No
BW Yes	10	25	12	15	18	12	42	45
No	7	5	22	19	10	12	202	205

Analyze the data and interpret the relationship of the children weights and mother's habits and health conditions.

[code:]
```
options(contrasts=c("contr.treatment","contr.poly"))
BW.yes=c(10,25,12,15,18,12,42,45)
BW.no=c(7,5,22,19,10,12,202,205)
BW=cbind(BW.yes,BW.no)
cardiac=factor(rep(c("0","1"),each=4))
comps=factor(rep(rep(c("0","1"),each=2),2))
smoking=factor(rep(c("0","1"),4))
survived.glm=glm(BW~cardiac+comps+smoking,family=binomial(link=logit))
summary(survived.glm)
anova(survived.glm,test="Chisq")
survived.glm2=glm(BW~cardiac+comps,family=binomial(link=logit))
summary(survived.glm2)
anova(survived.glm2,test="Chisq")

pearsonResiduals=residuals(survived.glm2,type="pearson")     ### Pearson
                                                              ### residuals
devianceResiduals=residuals(survived.glm2,type="deviance")   # ## Deviance
                                                              ### residuals
plot(pearsonResiduals)
plot(devianceResiduals)
```