stat359_A6_wducharme

Wesley Ducharme

2024-11-26

Reading the file

```r
geriatric <- read.table(file="C:/Users/wesch/uvic/stat359 Data
→  Analysis/data1/geriatric.txt", header=TRUE)
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 4.3.3
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

Part a)

```r
# Fitting the model
modelp <- glm(Fall ~ Int + Sex + BI + SI, family = poisson, data = geriatric)

summary(modelp)
```

```
##
## Call:
## glm(formula = Fall ~ Int + Sex + BI + SI, family = poisson, data = geriatric)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.489467   0.336869   1.453  0.14623
## Int         -1.069403   0.133154  -8.031 9.64e-16 ***
## Sex         -0.046606   0.119970  -0.388  0.69766
## BI           0.009470   0.002953   3.207  0.00134 **
## SI           0.008566   0.004312   1.986  0.04698 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 199.19  on 99  degrees of freedom
## Residual deviance: 108.79  on 95  degrees of freedom
## AIC: 377.29
##
## Number of Fisher Scoring iterations: 5
```

```r
confint(modelp)
```

```
## Waiting for profiling to be done...
```

```
##                     2.5 %       97.5 %
## (Intercept) -0.1836076944  1.13605432
## Int         -1.3360219299 -0.81332114
## Sex         -0.2823288477  0.18838553
## BI           0.0036833502  0.01526299
## SI           0.0001457923  0.01704817
```

```r
# Table of coefs, std errors, and CIs
inference_table <- data.frame(
  Estimate = coef(modelp),
  StdError = summary(modelp)$coefficients[, "Std. Error"],
  LowerCI = confint(modelp)[, 1],
  UpperCI = confint(modelp)[, 2]
)
```

```
## Waiting for profiling to be done...
## Waiting for profiling to be done...
```

```r
inference_table
```

```
##                Estimate    StdError       LowerCI      UpperCI
## (Intercept)  0.489467165 0.336869309 -0.1836076944  1.13605432
## Int         -1.069402551 0.133153890 -1.3360219299 -0.81332114
## Sex         -0.046606063 0.119970256 -0.2823288477  0.18838553
## BI           0.009469987 0.002952922  0.0036833502  0.01526299
## SI           0.008565829 0.004312119  0.0001457923  0.01704817
```

Sex has 0 on its confidence interval so it will need to be looked at.

Part b)

Goodness of fit test. H0: Model Adequate H1: Model Not Adequate.

```r
# Model deviance
deviance(modelp)
```

```
## [1] 108.7899
```

```r
# goodness of fit test
p_val <- 1-pchisq(deviance(modelp), modelp$df.residual)
p_val
```

```
## [1] 0.157792
```

Model deviance is 108.7899

The p-value for the goodness of fit test is $0.1577 > 0.1$ so we have little or no evidence against H0. So we can conclude that the model is a good fit.

Part c)

```r
deviance_residuals <- residuals(modelp, type = "deviance")

plot(deviance_residuals,
     main = "Deviance Residuals vs Index",
     xlab = "Index",
     ylab = "Deviance Residuals",
     ylim= c(-3, 3),
     pch = 19,
     col = "blue")

# line at y = 0
abline(h = 0, col = "red", lty = 2)
```

Deviance Residuals vs Index
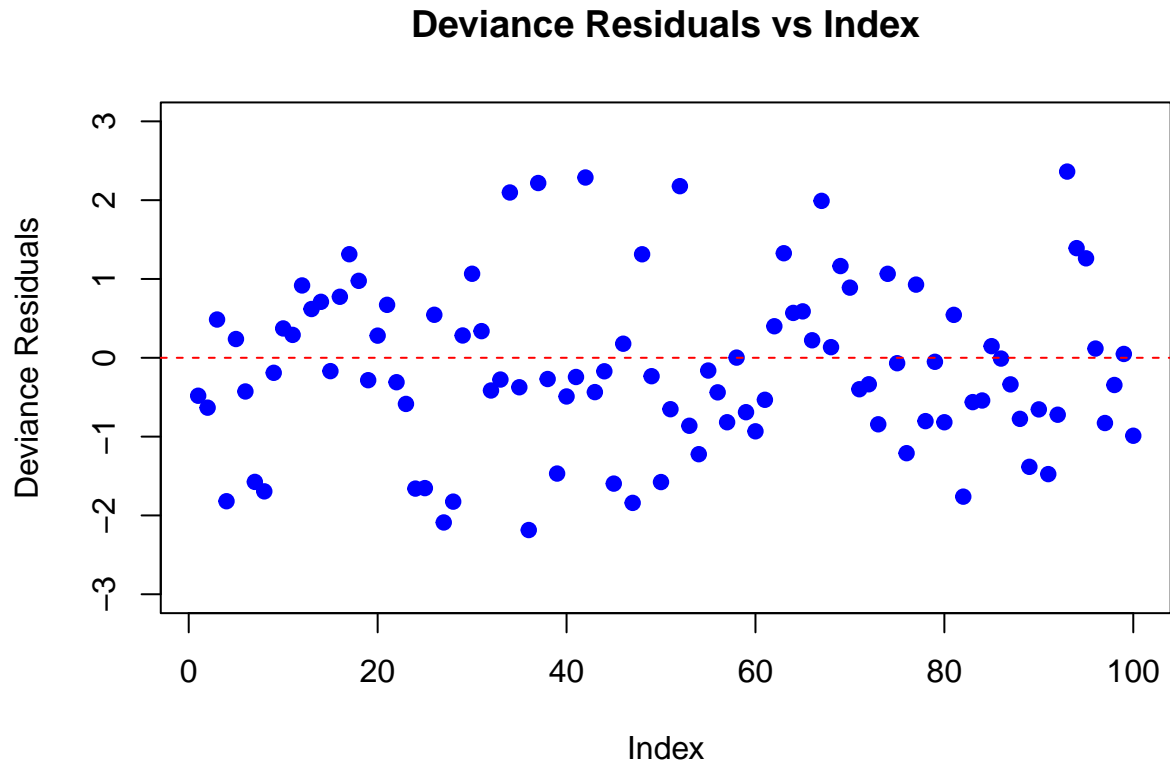
From viewing this residual plot there appears to be no extreme outliers in the data.

Part d)

Deviance test to determine if sex can be dropped from the model. H0: B3 = 0 H1: B3 not equal to 0

```
# remove sex and fit the smaller model
modelp2<-glm(Fall ~ Int + BI + SI, family = poisson, data = geriatric)
## assess the significance of sex using a deviance test
anova(modelp2,modelp,test="Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: Fall ~ Int + BI + SI
## Model 2: Fall ~ Int + Sex + BI + SI
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1        96     108.94
## 2        95     108.79  1    0.151   0.6976
```

p-value is 0.6976 so we have no evidence against H0. Therefore we can conclude that B3 = 0 and that sex can be removed from the model.

Part e)

Model without sex is already fitted above. Will make a 95% CI for the B1 the coeffiecent of Int.

4

```
confint(modelp2)
```

```
## Waiting for profiling to be done...
```

```
##                     2.5 %      97.5 %
## (Intercept) -0.1871313366  1.05602695
## Int         -1.3411096967 -0.82520388
## BI           0.0036752273  0.01527211
## SI           0.0007733914  0.01719607
```

95% Confidence interval for Int is -1.3411096967, -0.82520388.

The interval -1.341,-0.825 means we are 95% confident that the true value of B1 lies within this range of values.

Part f)

Since the entire confidence interval is below 0 it indicates that intervention is associated with a decrease in the rate of falls in this data set.