Goodness of Fit in Logistic Regression

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Collection of Binomial Random Variables

Suppose that we have k samples of n 0/1 variables, as with a binomial Bin(n,p), and suppose that $\hat{p}_1, \hat{p}_2, \ldots, \hat{p}_k$ are the sample proportions. We know that

$$\begin{aligned} E(\hat{p}) &= p \\ V(\hat{p}) &= p(1-p)/n \end{aligned}$$

- If $\bar{p} = \mathrm{Ave}(\hat{\mathrm{p}}_\mathrm{i})$ then if the distribution really is binomial, we should have that the sample variance s^2 of the $\hat{p}_i$ should be close to $\bar{p}(1-\bar{p})/n$. If it is not, then there is something wrong.
- The sample variance can be as small as 0 if all the $\hat{p}_i$ are the same, and is largest if some of the $\hat{p}_i$ are 0 and the remainder are 1.

- For example, suppose that $k = 20$ and $n = 50$, If $p = 0.1$, then $\bar{p} \sim 0.1$ and $s^2 \sim p(1-p)/n = (0.1)(0.9)/50 = 0.0018$.
- If 5 of the sample proportions are 1 and 45 are 0, then $\bar{p} = 0.1$ but $s^2 = \left[(5)(0.90)^2 + (45)((0.1)^2\right] /39 = 0.0918$, which is a factor of 50 too big.
- If the variance is too big, then either the distribution is not binomial, or we need more predictors (we have only one in this example).

The deviance is

$$D = 2\sum [y_i \ln(y_i/\hat{\mu}_i) + (n - y_i)\ln((n - y_i)/(n - \hat{\mu}_i))]$$

If we have k groups from a single binomial distribution, then $\hat{\mu}_i = kp$. The expression

$$y_i \ln(y_i/kp) + (n - y_i)\ln((n - y_i)/(n - kp)$$

is like

$$(\hat{p}_i - p)^2 = (y_i - kp)^2/k^2$$

in that both get larger as the difference between the observed and expected get larger.

Residual Deviance

- Suppose we have k groups and n observations. The (residual) deviance of a model is the difference between the minus twice the log likelihood of that model and that of the saturated model that fits each group with its own proportion.
- So we could consider the deviance of the given model as a likelihood ratio test of whether the given model is satisfactory.

- If our model has p predictors (counting categorical variables as one less than the number of levels and an intercept, then the difference from the saturated model is $k - p - 1$, and we could compare the deviance to a χ^2_{k-p-1} which has mean $k - p - 1$.
- If the deviance is too big, then something is wrong: Omitted predictors? Not binomial?

```
> summary(hyp.glm)
glm(formula = hyp.tbl ~ smoking + obesity + snoring, family = binomial)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.37766    0.38018  -6.254    4e-10 ***
smokingYes  -0.06777    0.27812  -0.244   0.8075
obesityYes   0.69531    0.28509   2.439   0.0147 *
snoringYes   0.87194    0.39757   2.193   0.0283 *
---
Signif. codes:  0 ?***? 0.001 ?**? 0.01 ?*? 0.05 ?.? 0.1 ? ? 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 14.1259  on 7  degrees of freedom
Residual deviance:  1.6184  on 4  degrees of freedom
```

- Residual deviance: 1.6184 on 4 degrees of freedom
- The residual deviance is not too large, so we don't appear to have a problem.
- $\Pr(\chi^2_4 < 1.6184) = 0.20$ so it is not too small either.

Deviance for Grouped Data

- When data are entered as groups with disease/notdisease, then R uses the definition of deviance comparing it to a model saturated by groups.
- In the hypertension data, there are 8 groups and deviance is relative to an 8df model like Smoking*Obesity*Snoring.

Deviance for Ungrouped Data

- If the data are given in observation form with 0/1 response, then R uses a definition of deviance relative to an observation-saturated model where each response is perfectly predicted.
- This means that the deviance is just minus twice the log likelihood.
- We can still use the deviance test when the analysis is grouped.

```
> main.model <- glm(CHD~CAT+SMK+HPT,family=binomial,evans)
> full.model <- glm(CHD~CAT*SMK*HPT,family=binomial,evans)
> anova(main.model,full.model,test="Chisq")
Analysis of Deviance Table

Model 1: CHD ~ CAT + SMK + HPT
Model 2: CHD ~ CAT * SMK * HPT
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1       605     414.05
2       601     404.92  4   9.1367  0.05777 .

> summary(main.model)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.0324     0.3056  -9.924  < 2e-16 ***
CAT           0.8055     0.2963   2.719  0.00655 **
SMK           0.7098     0.2969   2.391  0.01681 *
HPT           0.5956     0.2844   2.094  0.03623 *

    Null deviance: 438.56  on 608  degrees of freedom
Residual deviance: 414.05  on 605  degrees of freedom
```

Goodness of Fit for Uncategorized Data

- The procedure above works well only if the number of groups in which the predictors are the same is small compared to n.
- A commonly used procedure if there are continuous predictors is the Hosmer-Lemeshow goodness of fit test.
- This works poorly if there are too many ties, but is useful when almost all the observations have distinct predictors.

- Order the data by the predicted values and cut into classes of equal size, say 10.
- Calculate observed and expected cases in each group.
- Use χ^2 test as usual from $(O - E)^2/E$.
- This can be done using `hoslem.test()` from the `ResourceSelection` package in R.
- This is very commonly used, but has low power, and interpretation in case of rejection can be difficult.

```
> library(ResourceSelection)
ResourceSelection 0.2-6   2016-02-15
Warning message:
package ResourceSelection was built under R version 3.2.5
> mod2.glm <- glm(CHD~CAT+CHL+SMK+HPT,family=binomial,evans)
> hoslem.test(mod2.glm$y,fitted(mod2.glm))

Hosmer and Lemeshow goodness of fit (GOF) test

data:  mod2.glm$y, fitted(mod2.glm)
X-squared = 1.4748, df = 8, p-value = 0.9931
```

Note that the model omits interactions we know are important, but still passes the HL test.

Model Checking and Diagnostics

Linear Regression

- In linear regression, the major assumptions in order of importance:
- **Linearity:** The mean of y is a linear (in the coefficients) function of the predictors.
- **Independence:** Different observations are statistically independent.
- **Constant Variance:** The residual variance is the same for each observation.
- **Normality:** The error distribution is normal.

Diagnostics

Linear Regression

- Plot residuals vs. fitted values
- Plot residuals vs. predictors
- Look for influential observations with dffits and dfbeta. These are observations that have a large effect on the coefficients.
- We can use many of these techniques in logistic regression.

Model Checking and Diagnostics

Logistic Regression

- In logistic regression, the major assumptions in order of importance:
- **Linearity:** The logit of the mean of y is a linear (in the coefficients) function of the predictors.
- **Independence:**Different observations are statistically independent.
- **Variance Function:** The variance of an observation with mean p is $p(1-p)/n$.
- **Binomial:** The error distribution is binomial.

Diagnostics for Grouped Logistic Regression

- Deviance test for goodness of fit.
- Plot deviance residuals vs. fitted values. In this case, there are as many residuals and fitted values as there are distinct categories.
- Plot dfffits vs. fitted values. This is the scaled change in the predicted value of point i when point i itself is removed from the fit. This has to be the whole category in this case.
- All this works well automatically only when the data are given to R in aggregated form.

```
> summary(main.model)

Call:
glm(formula = CHD ~ CAT + SMK + HPT, family = binomial, data = evans)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.8185  -0.5721  -0.4325  -0.3068   2.4817

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.0324     0.3056  -9.924  < 2e-16 ***
CAT           0.8055     0.2963   2.719  0.00655 **
SMK           0.7098     0.2969   2.391  0.01681 *
HPT           0.5956     0.2844   2.094  0.03623 *
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 438.56  on 608  degrees of freedom
Residual deviance: 414.05  on 605  degrees of freedom
AIC: 422.05

Number of Fisher Scoring iterations: 5
```

```
> evans.cat1 <- aggregate(cbind(CHD,1-CHD,1)~CAT+SMK+HPT,FUN=sum,data=evans)

> print(evans.cat1)
  CAT SMK HPT CHD  V2  V3
1   0   0   0   5 117 122
2   1   0   0   1   5   6
3   0   1   0  15 193 208
4   1   1   0   7  11  18
5   0   0   1   4  51  55
6   1   0   1   7  32  39
7   0   1   1  20  82 102
8   1   1   1  12  47  59

> res <- as.matrix(evans.cat1)[,4:5]
> evans.cat1.glm <- glm(res~CAT+SMK+HPT,family=binomial,data=evans.cat1)
```

```
> summary(evans.cat1.glm)

Call:
glm(formula = res ~ CAT + SMK + HPT, family = binomial, data = evans.cat1)

Deviance Residuals:
      1       2       3       4       5       6       7       8
-0.2685  0.5256 -0.8950  2.0789 -0.2128  0.2638  1.2263 -1.4307

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.0324     0.3056  -9.924  < 2e-16 ***
CAT           0.8055     0.2963   2.719  0.00655 **
SMK           0.7098     0.2969   2.391  0.01681 *
HPT           0.5956     0.2844   2.094  0.03623 *
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 33.6416  on 7  degrees of freedom
Residual deviance:  9.1367  on 4  degrees of freedom
AIC: 45.737

Number of Fisher Scoring iterations: 4
```

```
> summary(main.model)

Call:
glm(formula = CHD ~ CAT + SMK + HPT, family = binomial, data = evans)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.8185  -0.5721  -0.4325  -0.3068   2.4817

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.0324     0.3056  -9.924  < 2e-16 ***
CAT           0.8055     0.2963   2.719  0.00655 **
SMK           0.7098     0.2969   2.391  0.01681 *
HPT           0.5956     0.2844   2.094  0.03623 *
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 438.56  on 608  degrees of freedom
Residual deviance: 414.05  on 605  degrees of freedom
AIC: 422.05

Number of Fisher Scoring iterations: 5
```

The goodness of fit test is to compare 9.1367, the residual deviance, with a χ^2_4.

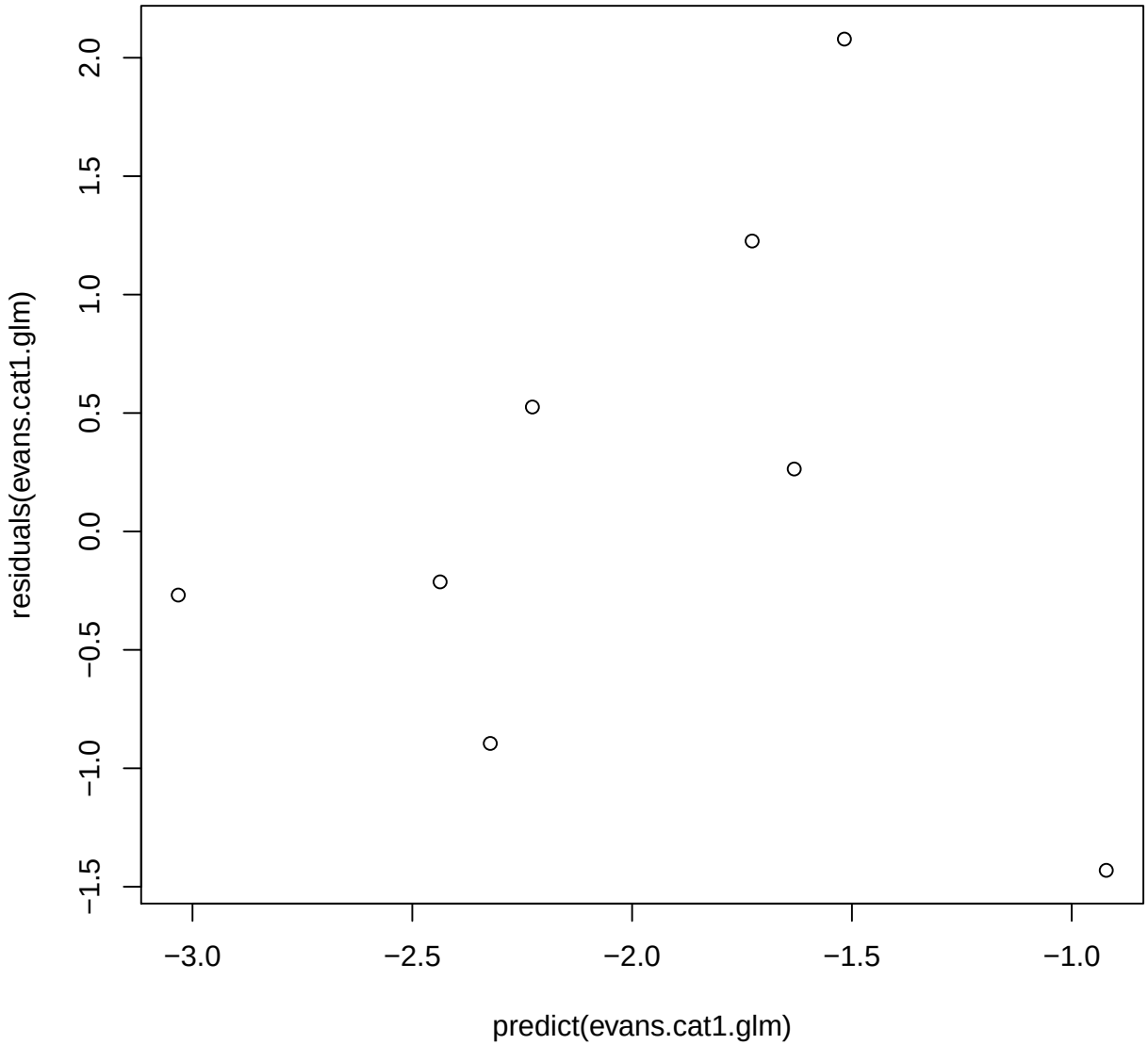
```
> pchisq(deviance(evans.cat1.glm),4,lower=F)
[1] 0.05777162
```

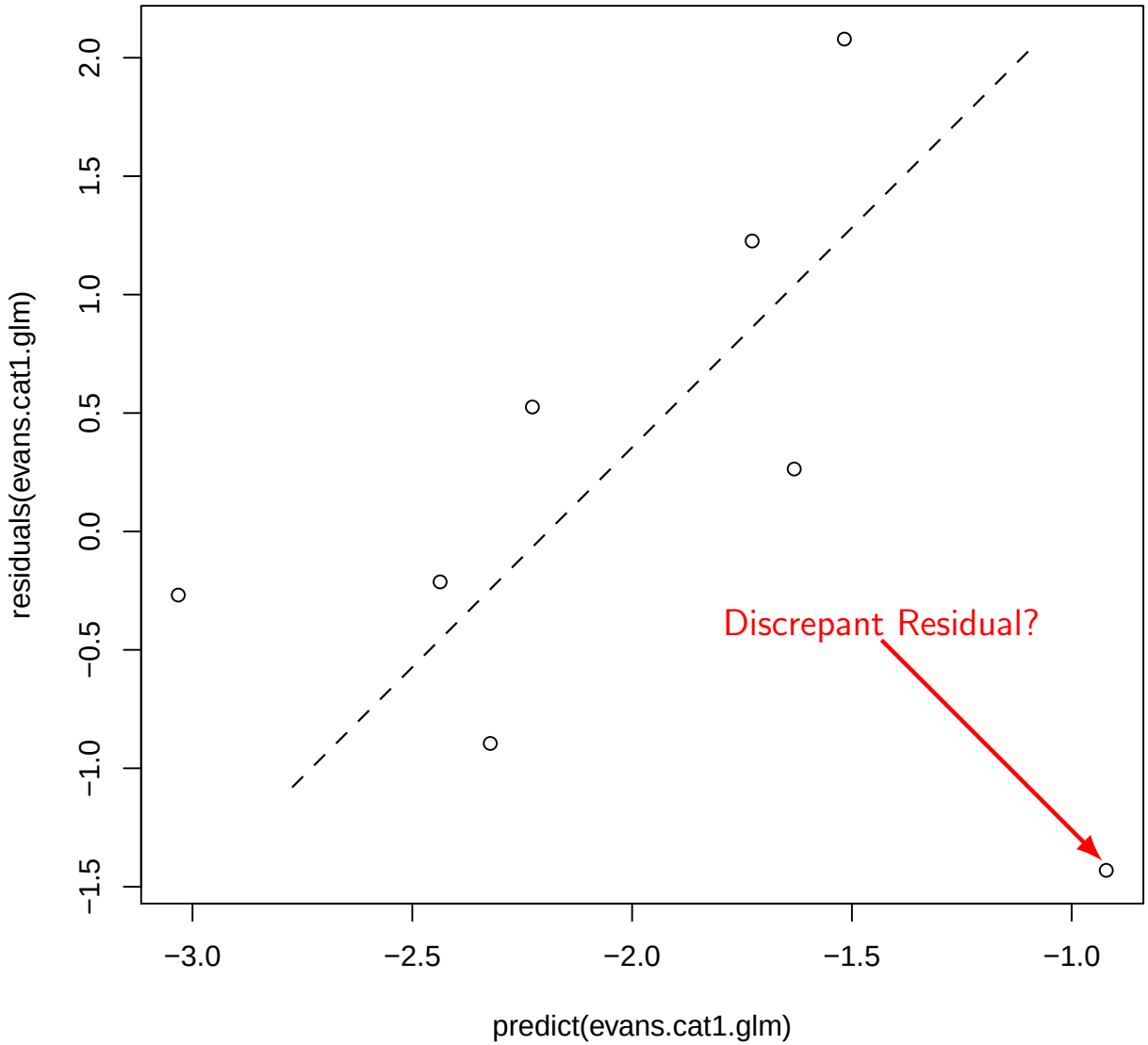
We know that the `CAT:HPT` interaction is significant, which is somewhat indicated by the relatively high value of the residual deviance.

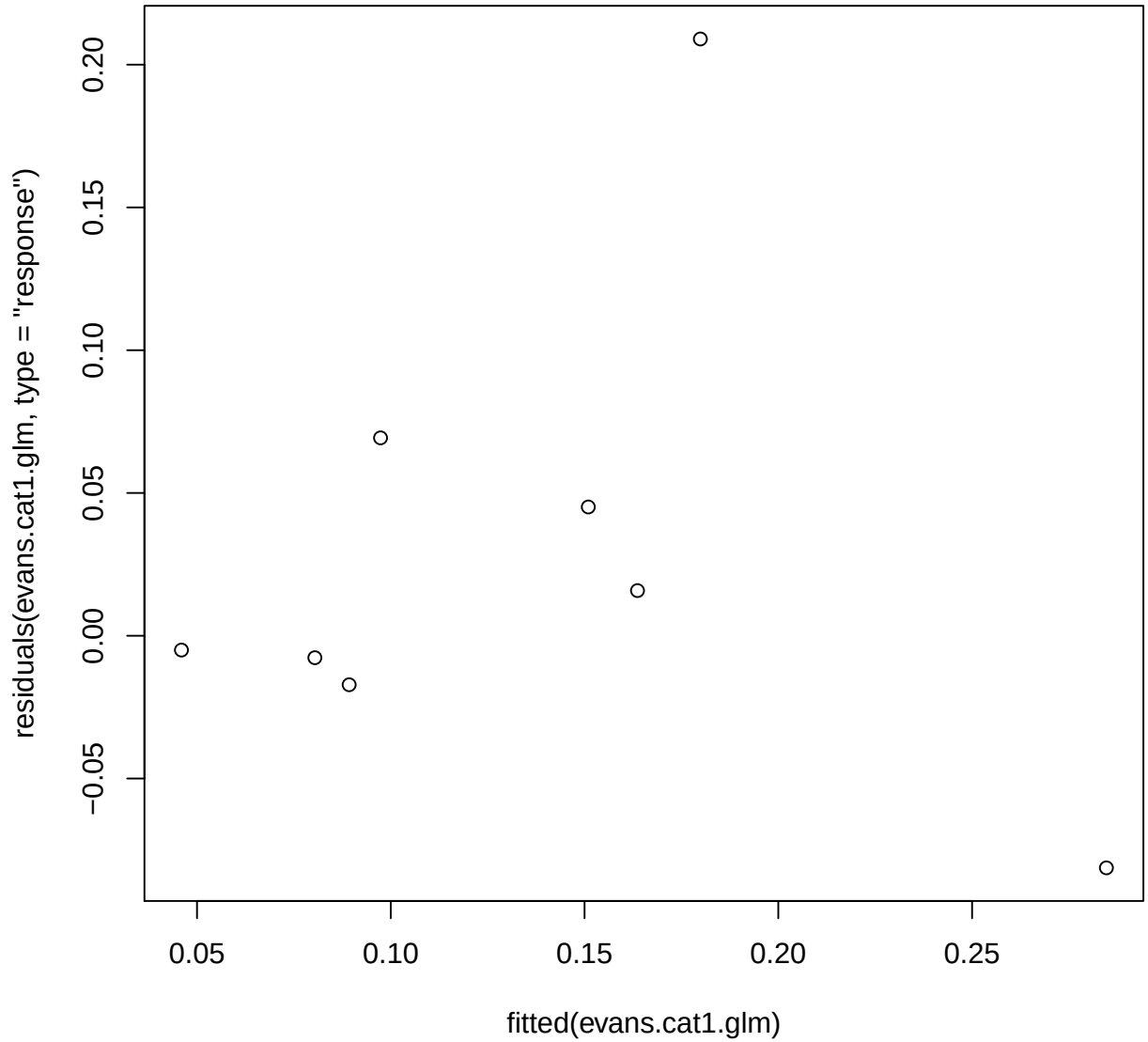
```
> summary(glm(res~CAT+SMK+HPT+CAT:HPT,family=binomial,data=evans.cat1))

Call:
glm(formula = res ~ CAT + SMK + HPT + CAT:HPT, family = binomial,
    data = evans.cat1)

Deviance Residuals:
       1         2         3         4         5         6         7         8
 0.10972  -0.38331  -0.06311   0.18549  -0.74483   0.78093   0.40560  -0.54343

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.2032     0.3227  -9.925  < 2e-16 ***
CAT           1.9958     0.4941   4.039 5.37e-05 ***
SMK           0.6655     0.2981   2.232  0.02560 *
HPT           1.0246     0.3213   3.189  0.00143 **
CAT:HPT      -1.6750     0.6007  -2.789  0.00529 **
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 33.6416  on 7  degrees of freedom
Residual deviance:  1.8218  on 3  degrees of freedom
AIC: 40.422
```

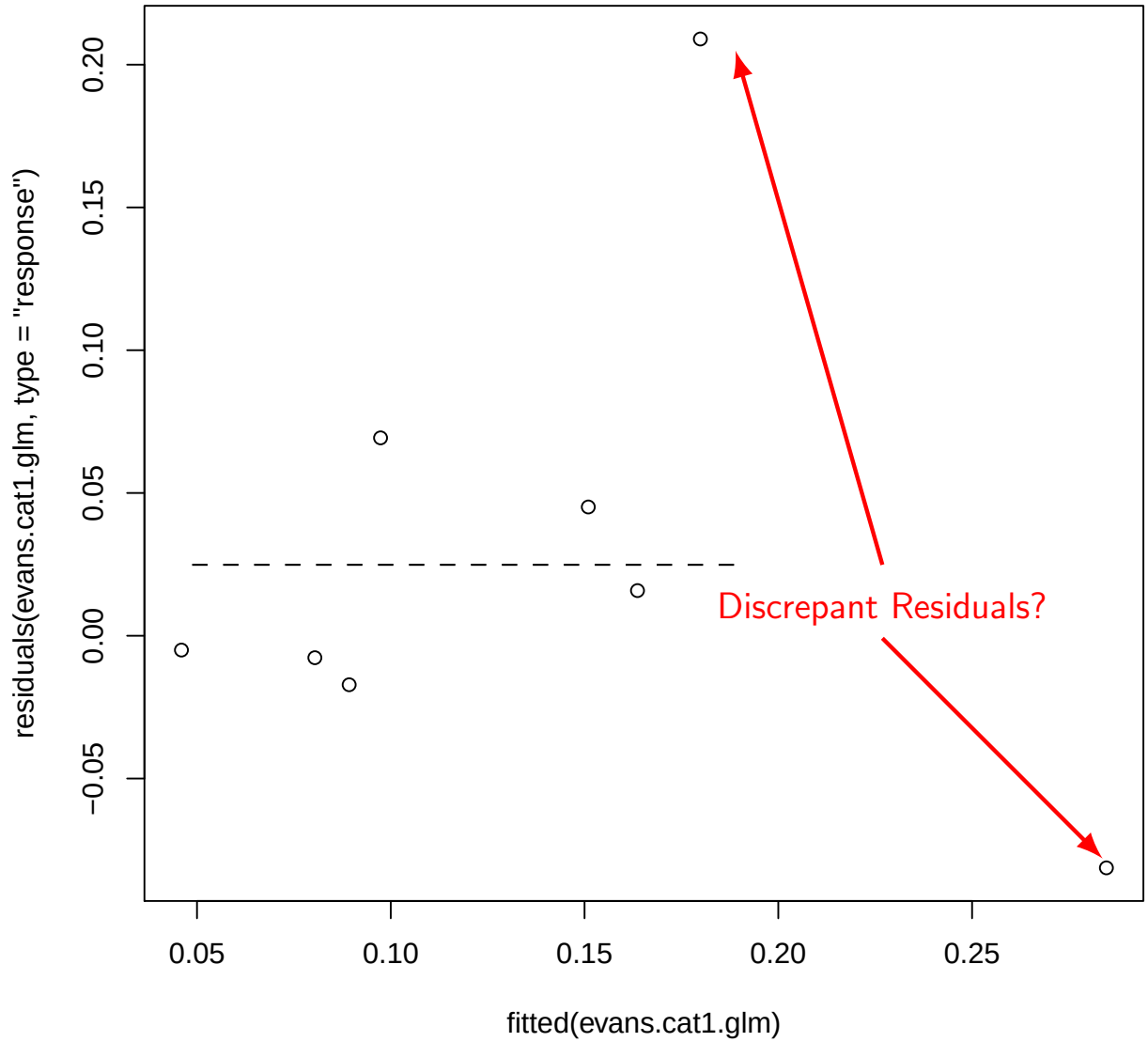
```
> pdf("evanscat1res1.pdf")
> plot(predict(evans.cat1.glm),residuals(evans.cat1.glm))
> dev.off()
windows
      2
> pdf("evanscat1res2.pdf")
> plot(fitted(evans.cat1.glm),residuals(evans.cat1.glm,type="response"))
> dev.off()
```

The first is on the scale of the linear predictor, the second on the [0, 1] scale. Note that the last point $(1, 1, 1)$ has a discordant residual.

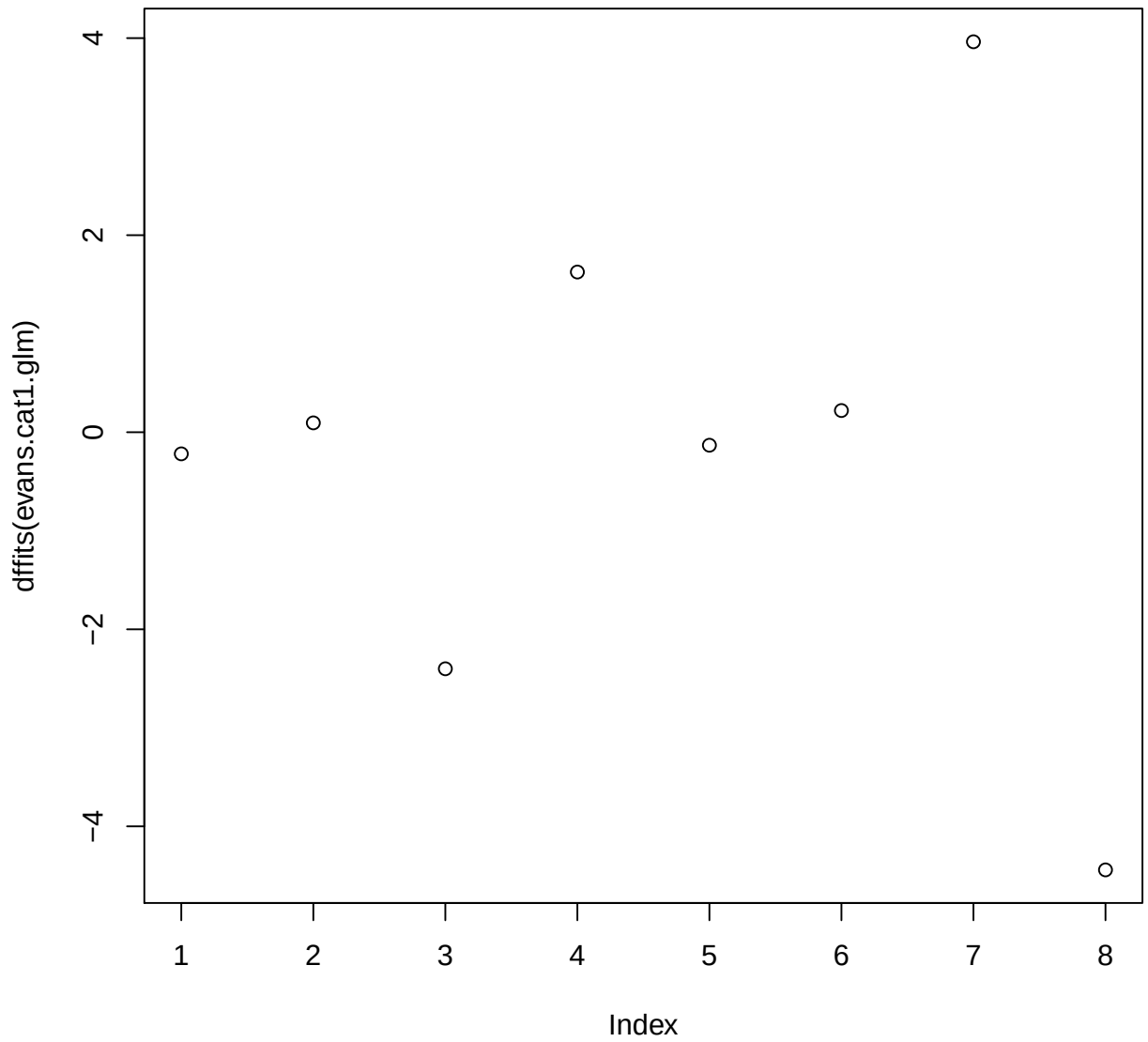

residuals(evans.cat1.glm)
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3.0
−2.5
−2.0
−1.5
−1.0
predict(evans.cat1.glm)

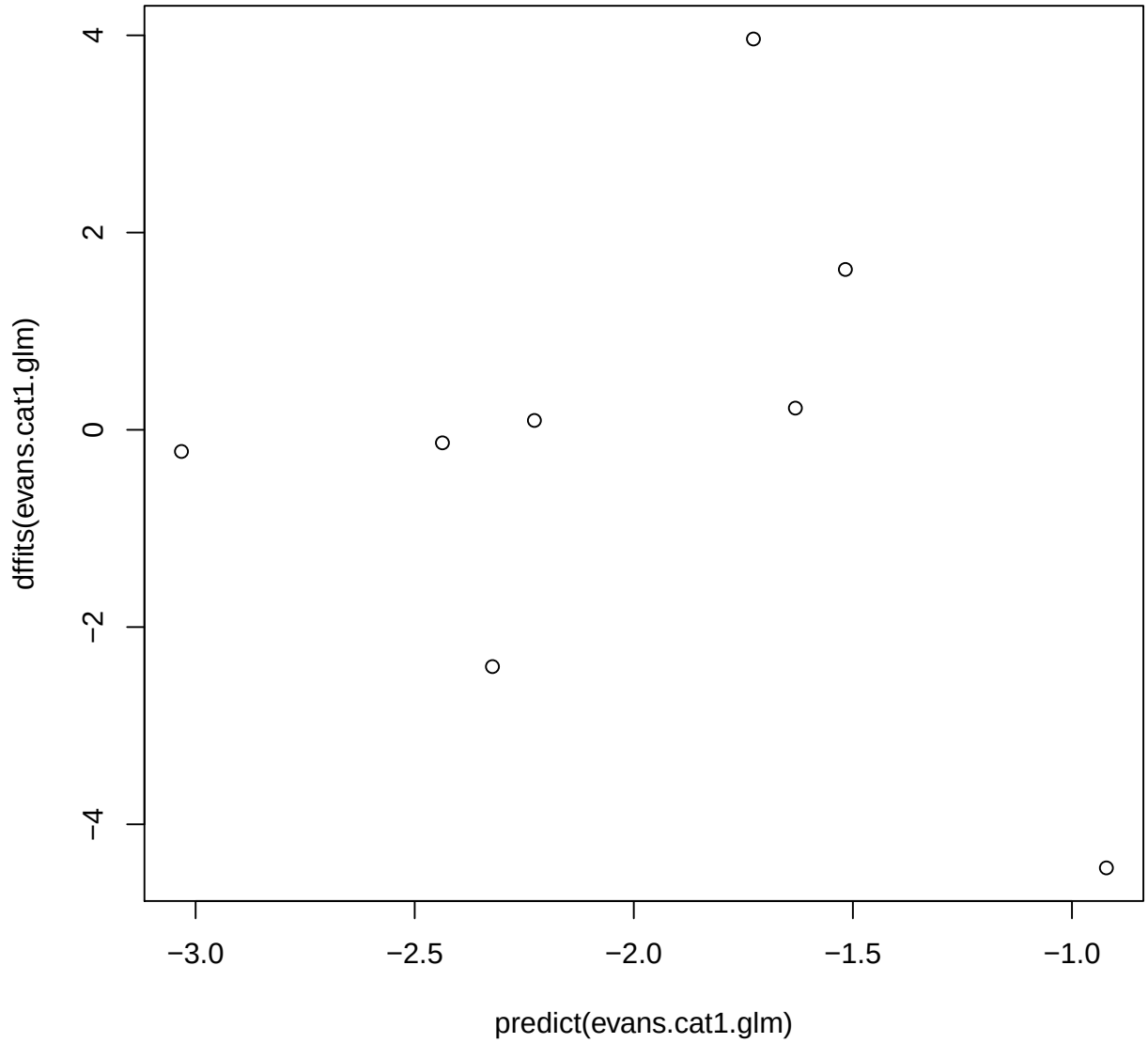

residuals(evans.cat1.glm)
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3.0
−2.5
−2.0
−1.5
−1.0
predict(evans.cat1.glm)
Discrepant Residual?


residuals(evans.cat1.glm, type = "response")
0.20
0.15
0.10
0.05
0.00
−0.05
0.05
0.10
0.15
0.20
0.25
fitted(evans.cat1.glm)


residuals(evans.cat1.glm, type = "response")
0.20
0.15
0.10
0.05
0.00
−0.05
0.05
0.10
0.15
0.20
0.25
fitted(evans.cat1.glm)
Discrepant Residuals?

```
> pdf("evanscat1dff1.pdf")
> plot(dffits(evans.cat1.glm))
> dev.off()

> pdf("evanscat1dff2.pdf")
> plot(predict(evans.cat1.glm),dffits(evans.cat1.glm))
> dev.off()
```


dffits(evans.cat1.glm)
4
2
0
−2
−4
1
2
3
4
5
6
7
8
Index


dffits(evans.cat1.glm)
4
2
0
−2
−4
−3.0
−2.5
−2.0
−1.5
−1.0
predict(evans.cat1.glm)

Types of Residuals in Logistic Regression

- In linear regression, the residual is always $y - \hat{y}$.
- In logistic regression we have multiple types, partly because we have multiple scales.
- The deviance is the sum of $y_i \ln(y_i/\hat{\mu}_i) + (n - y_i) \ln((n - y_i)/(n - \hat{\mu}_i))$, which is always positive and lives on the χ^2 scale.
- The deviance residual is the signed square root of the deviance contribution, positive if $y > \hat{y}$ and negative otherwise.
- When $y = 1$, all the residuals are positive and when $y = 0$ they are all negative.

Types of Residuals in Logistic Regression

- Pearson and response residuals are on the response scale

$$r = \frac{p - \hat{p}}{\sqrt{\hat{p}(1-\hat{p})/n}}$$

- This is approximately standard normal if n is large.
- If the data are not grouped, then

$$r_{response} = y - \hat{y} \qquad r_{Pearson} = \frac{y - \hat{y}}{\sqrt{\hat{y}(1-\hat{y})}}$$

Types of Residuals in Logistic Regression

- The **partial residual** is useful for assessing the linearity of the relationship between a quantitative variable and the response.
- The partial residual for observation i and predictor j is

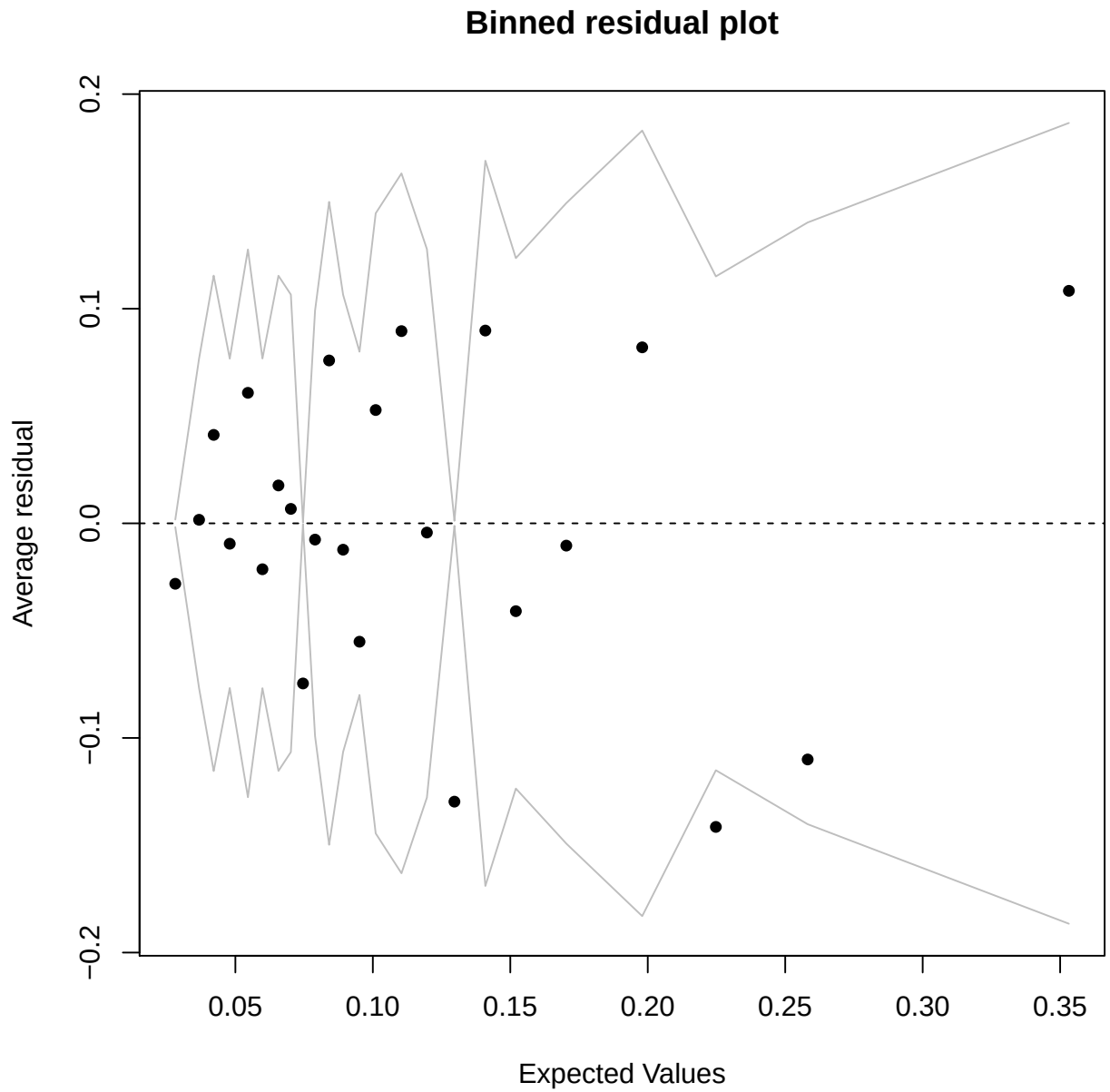
$$r_{ij} = \hat{\beta}_j x_{ij} + \frac{y_i - \hat{y}_i}{\hat{y}_i(1 - \hat{y}_i)}$$

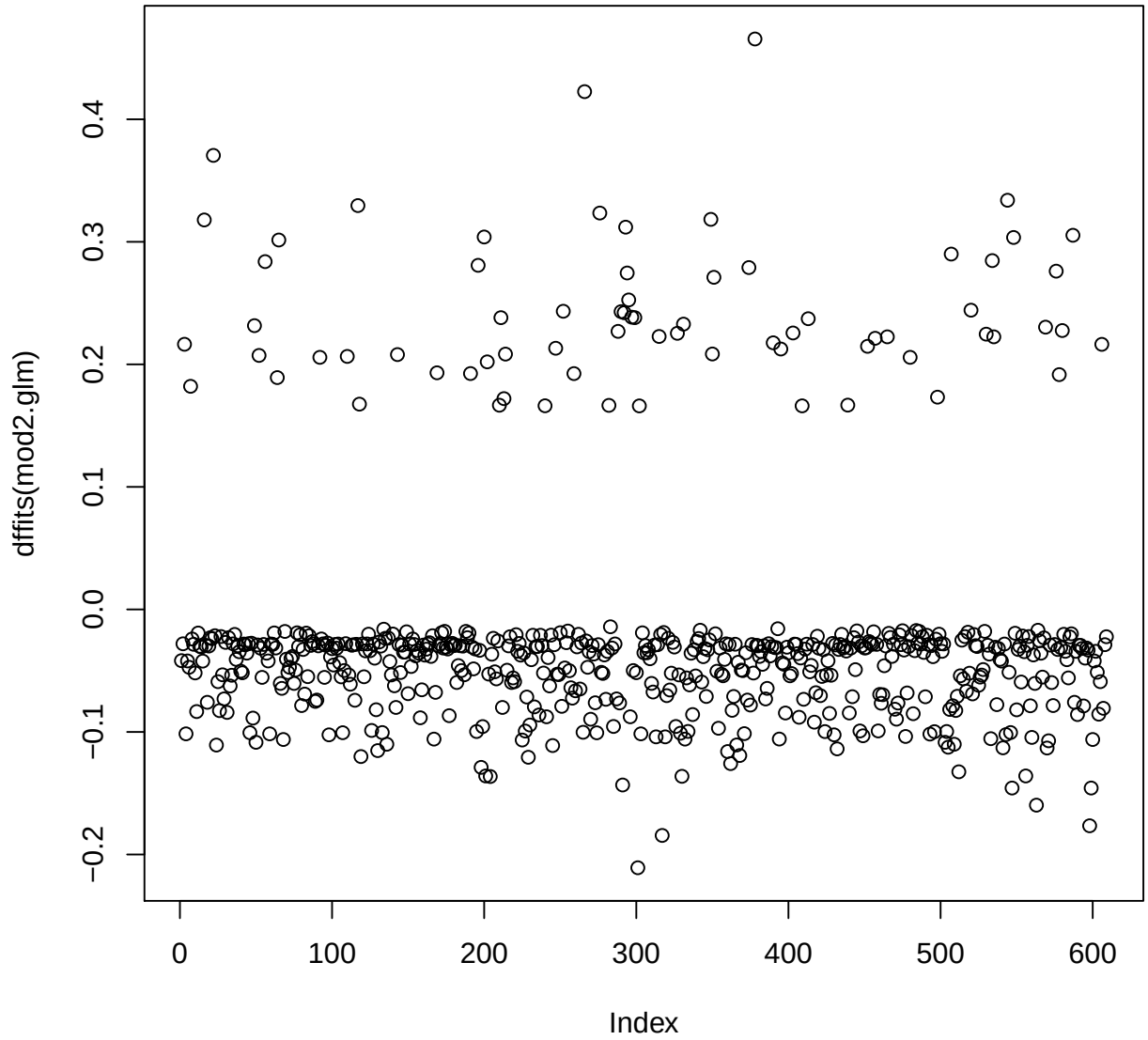
- The second term on the RHS is called the **working residual** and is related to the algorithm that minimizes the deviance.

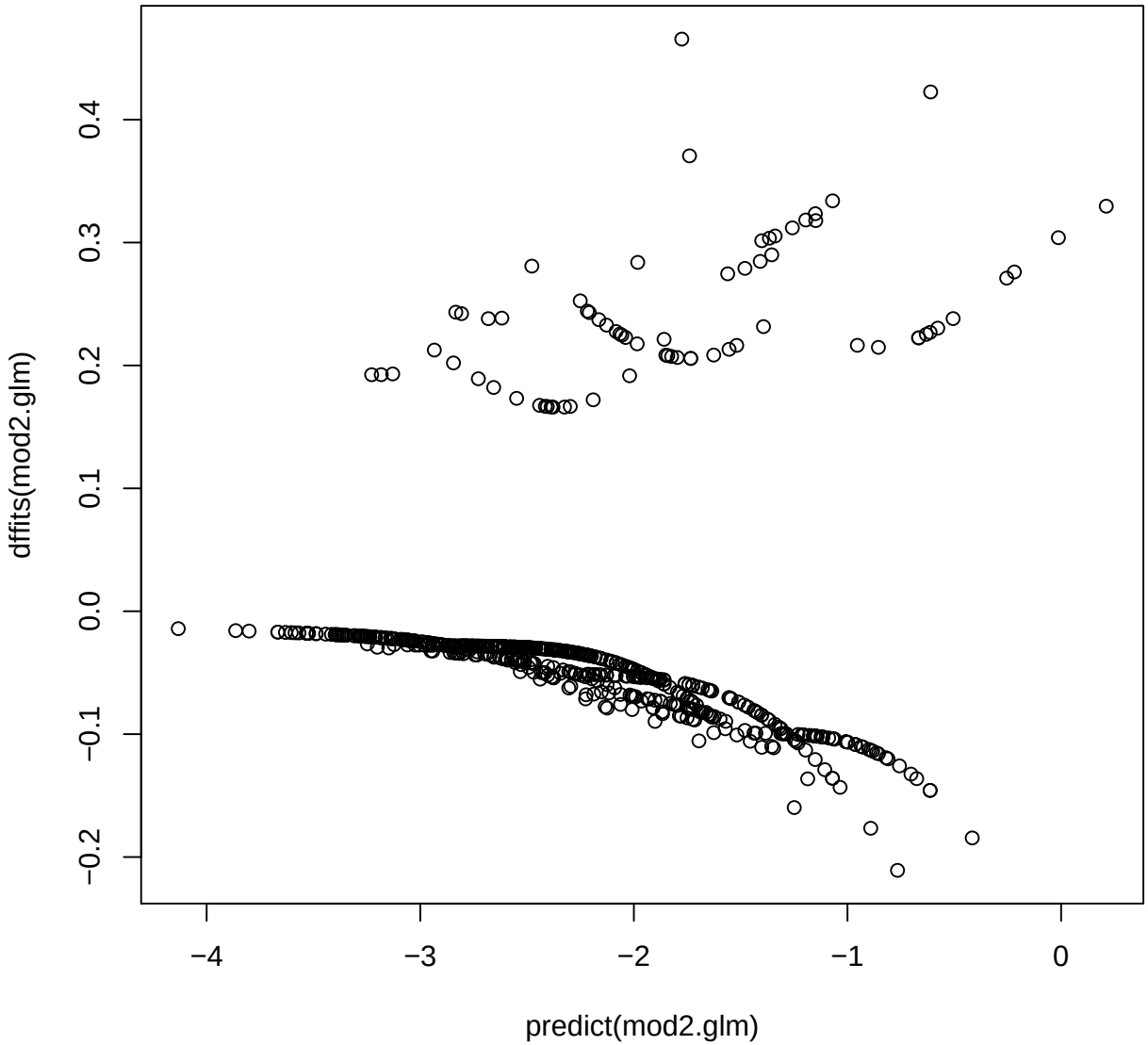
Diagnostics for Ungrouped Logistic Regression

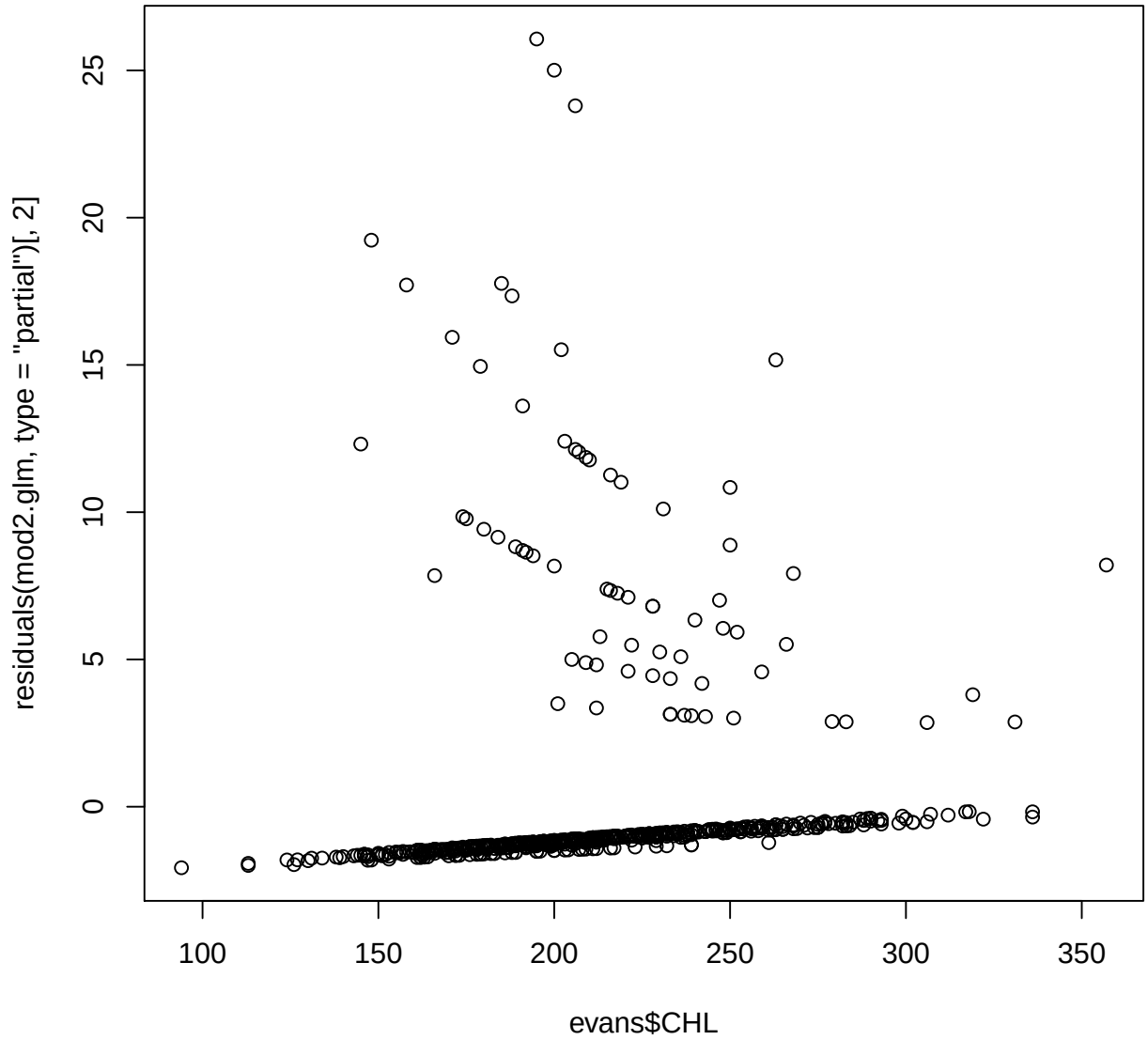
- Possible HL test for goodness of fit
- Plot deviance residuals vs. fitted values. We can either group the fitted values as in the HL test using the, `binnedplot` function in the `arm` package or smooth the plot with `lowess`.
- Plot partial residuals for each quantitative variable vs. the value of the variable.
- Plot dfffits vs. fitted values.
- Plot dfbetas vs. index and/or fitted value for each quantitative variable. This is the change in the coefficient of variable j when point i is removed.

```
> mod2.glm <- glm(CHD~CAT+CHL+SMK+HPT,family=binomial,evans)
> binnedplot(fitted(mod2.glm),residuals(mod2.glm,type="response"))
> plot(dffits(mod2.glm))
> plot(predict(mod2.glm),dffits(mod2.glm))
> which(dffits(mod2.glm) > .3)
 16  22  65 117 200 266 276 293 349 378 544 548 587
 16  22  65 117 200 266 276 293 349 378 544 548 587
> plot(evans$CHL,residuals(mod2.glm,type="partial")[,2])
> plot(dfbeta(mod2.glm)[,1])
> plot(dfbeta(mod2.glm)[,2])
> plot(dfbeta(mod2.glm)[,3])
> plot(dfbeta(mod2.glm)[,4])
> plot(dfbeta(mod2.glm)[,5])
```

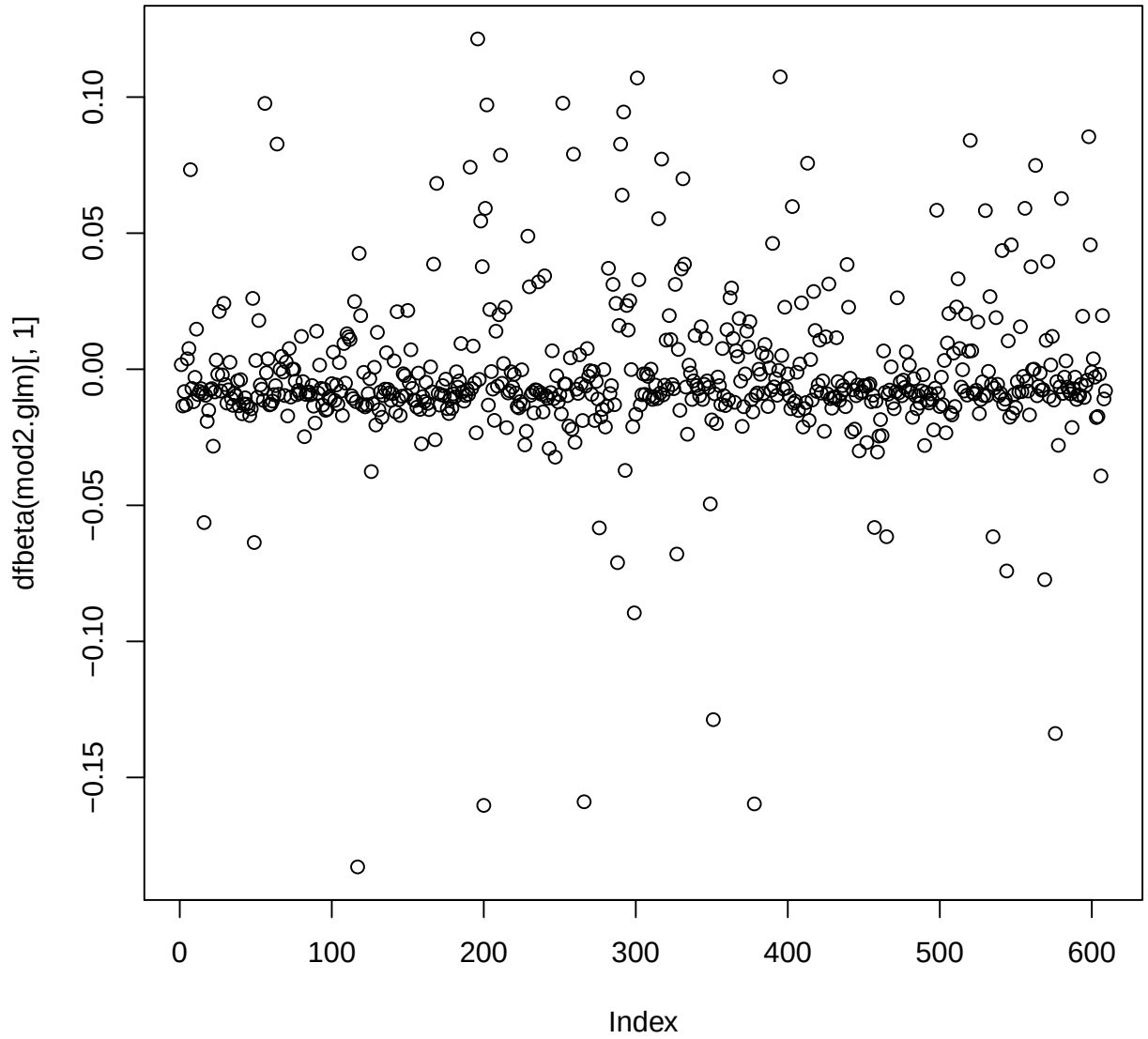

Binned residual plot
Average residual
0.2
0.1
0.0
−0.1
−0.2
0.05
0.10
0.15
0.20
0.25
0.30
0.35
Expected Values


dffits(mod2.glm)
0.4
0.3
0.2
0.1
0.0
−0.1
−0.2
0
100
200
300
400
500
600
Index


dffits(mod2.glm)
0.4
0.3
0.2
0.1
0.0
−0.1
−0.2
−4
−3
−2
−1
0
predict(mod2.glm)

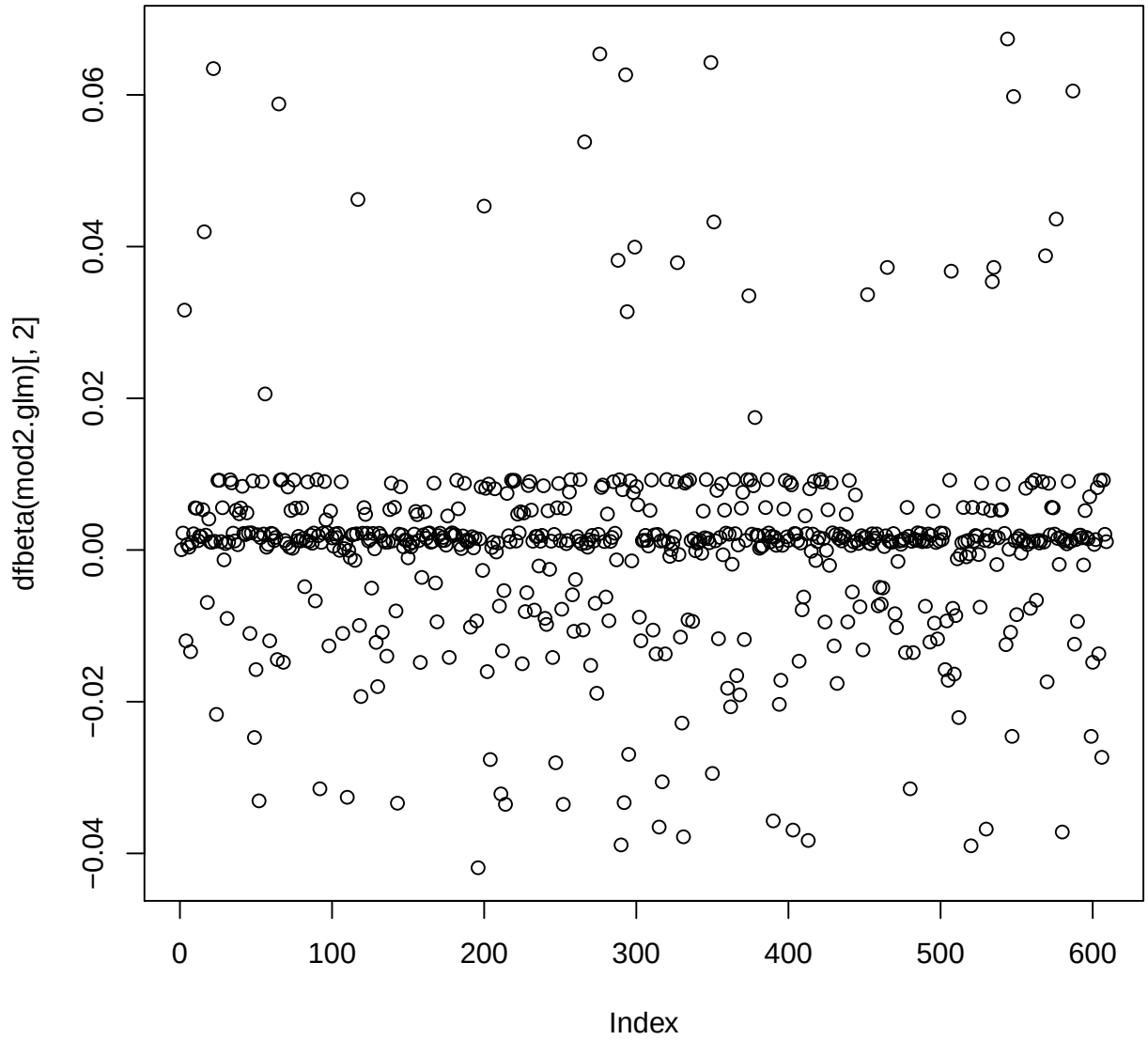

residuals(mod2.glm, type = "partial")[, 2]
0
5
10
15
20
25
100
150
200
250
300
350
evans$CHL

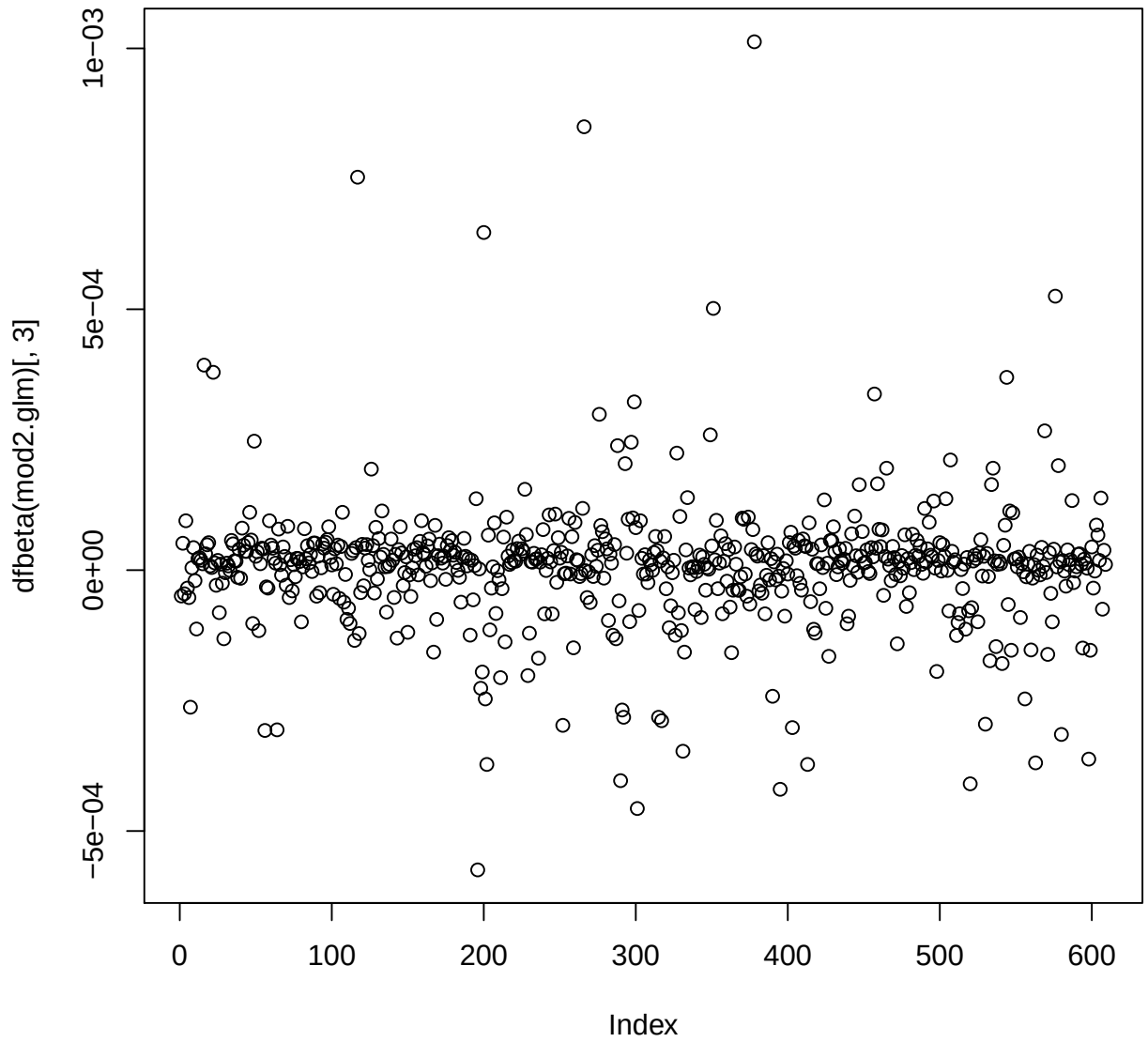
- Curvature in the partial residual plot for CHL may indicate non-linearity.
- This is supported by the curvature in the dffits plot vs. predicted values.


dfbeta(mod2.glm)[, 1]
0.10
0.05
0.00
−0.05
−0.10
−0.15
0
100
200
300
400
500
600
Index

- There are 6 points with high influence for the intercept.
- Omission will increase the intercept.
- Most have high CAT, most are hypertensive, all have CHD.
- It would seem that omission of a CHD case would tend to decrease the intercept, but it increases instead.

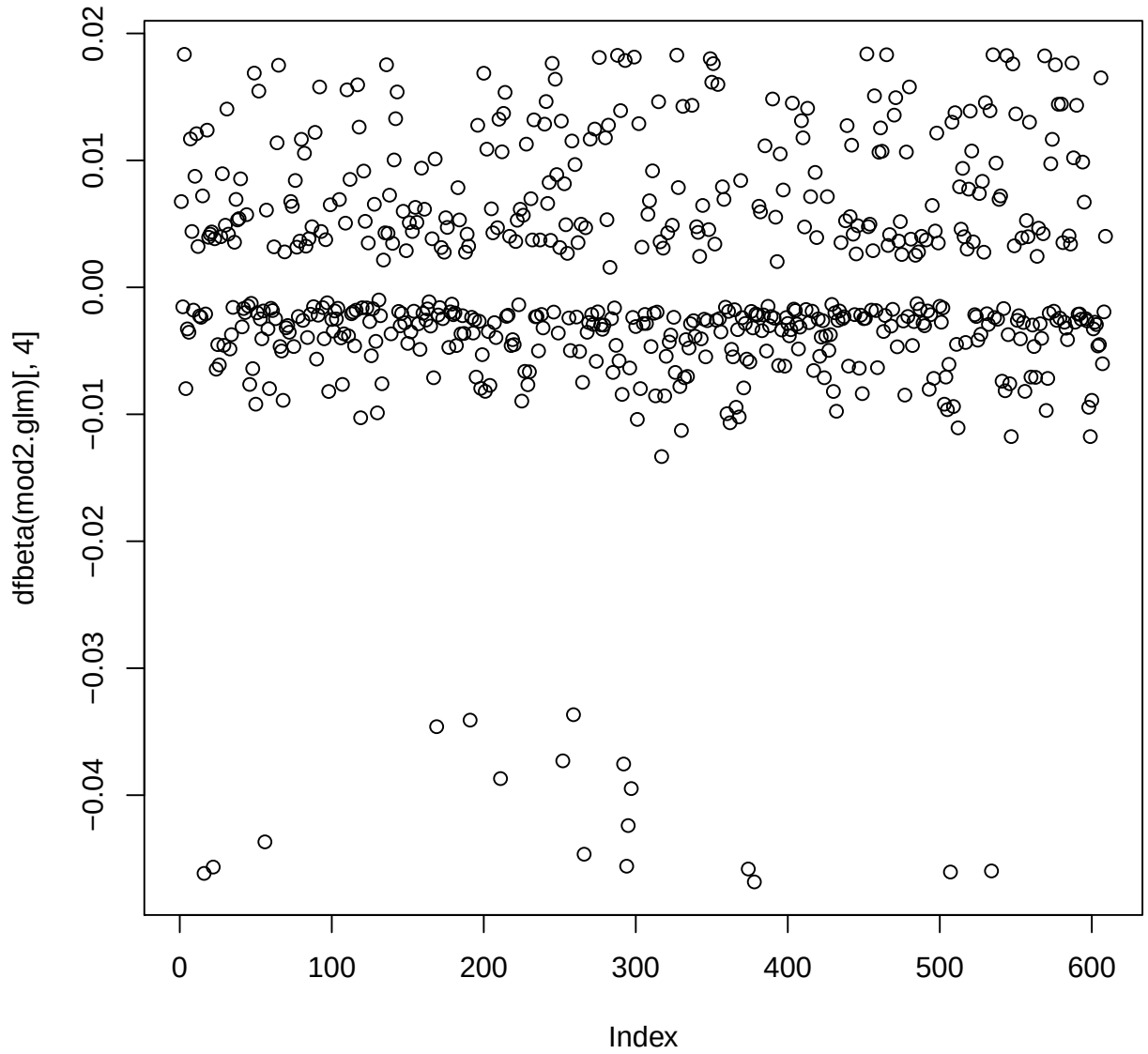
```
> evans[order(dfbeta(mod2.glm)[,1])[1:6],]
       ID CHD CAT AGE CHL SMK ECG DBP SBP HPT CH  CC
117  2891   1   1  56 331   1   0 110 190   1  1 331
200  5131   1   1  52 306   1   0 108 178   1  1 306
378 12051   1   0  67 357   0   0  90 129   0  0   0
266  7051   1   1  67 319   0   0 104 182   1  1 319
576 18131   1   1  56 283   1   0 100 188   1  1 283
351 11361   1   1  76 279   1   0  96 136   1  1 279
```


dfbeta(mod2.glm)[, 2]
0.06
0.04
0.02
0.00
−0.02
−0.04
0
100
200
300
400
500
600
Index


dfbeta(mod2.glm)[, 3]
1e−03
5e−04
0e+00
−5e−04
0
100
200
300
400
500
600
Index

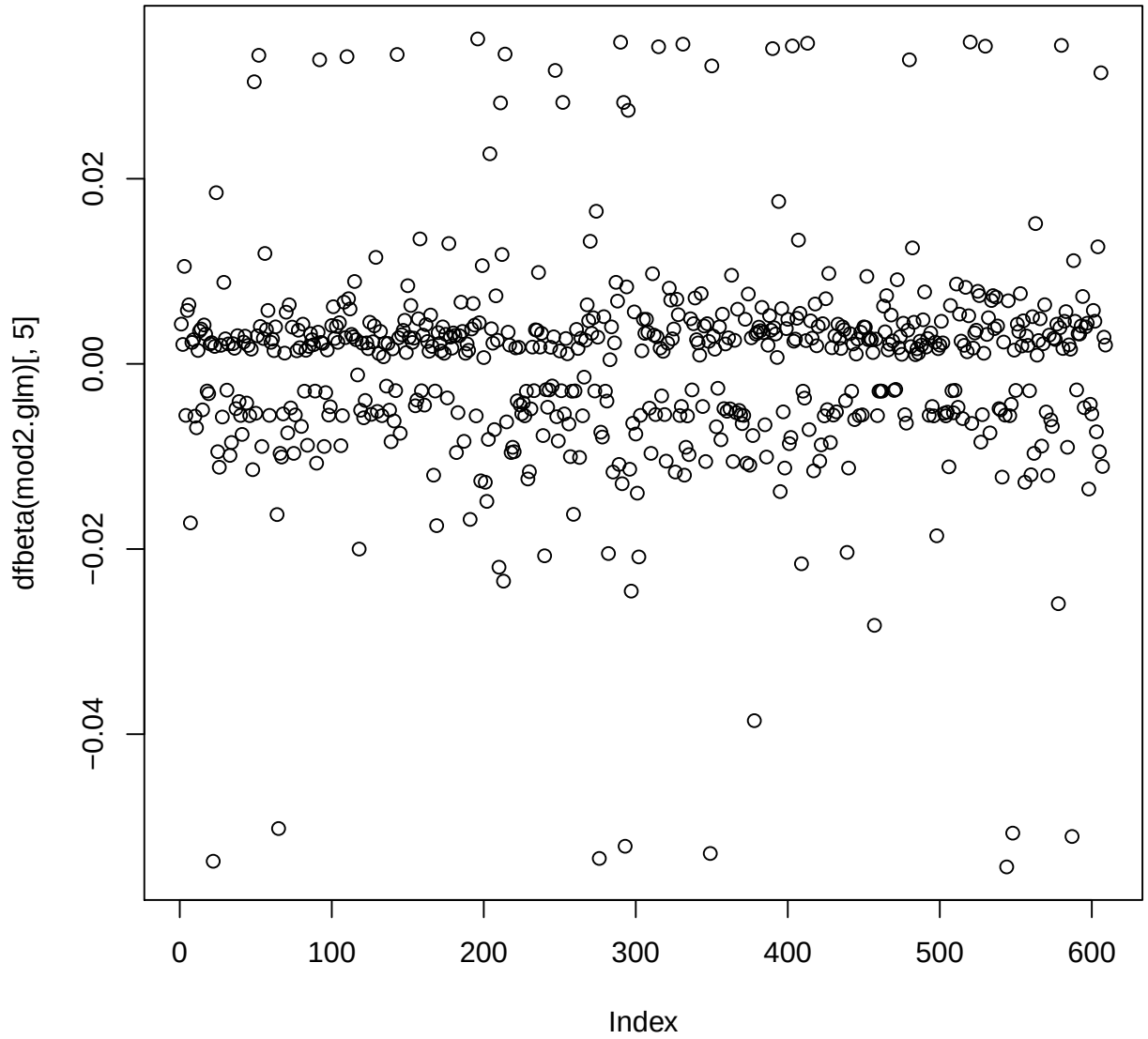
- There are 4 points with high influence for CHL.
- Omission will decrease the coefficient.
- All have CHD and very high CHL.

```
> head(sort(evans$CHL,decreasing=T))
[1] 357 336 336 331 322 319

> evans[order(dfbeta(mod2.glm)[,3],decreasing=T)[1:4],]
       ID CHD CAT AGE CHL SMK ECG DBP SBP HPT CH  CC
378 12051   1   0  67 357   0   0  90 129   0  0   0
266  7051   1   1  67 319   0   0 104 182   1  1 319
117  2891   1   1  56 331   1   0 110 190   1  1 331
200  5131   1   1  52 306   1   0 108 178   1  1 306
```


dfbeta(mod2.glm)[, 4]
0.02
0.01
0.00
−0.01
−0.02
−0.03
−0.04
0
100
200
300
400
500
600
Index

- There are 17 points with high influence for SMK.
- Omission will increase the coefficient.
- All have CHD and don't smoke. In fact, these points consist of all the subjects with CHD who don't smoke. Omission of even 1 has a high effect on the coefficient.

```
> evans[order(dfbeta(mod2.glm)[,4])[1:17],]
       ID CHD CAT AGE CHL SMK ECG DBP SBP HPT CH  CC
378 12051   1   0  67 357   0   0  90 129   0  0   0
16    283   1   1  51 259   0   1 102 135   1  1 259
507 15511   1   1  67 236   0   1 106 200   1  1 236
534 16481   1   1  69 230   0   1 100 170   1  1 230
374 11941   1   1  65 222   0   1  88 162   1  1 222
22    381   1   1  64 247   0   1  75 130   0  0 247
294  9201   1   1  63 213   0   1 156 256   1  1 213
266  7051   1   1  67 319   0   0 104 182   1  1 319
56   1061   1   1  46 166   0   1  76 162   1  1 166
295  9261   1   0  67 250   0   0 100 158   1  0   0
297  9601   1   0  45 263   0   0  86 132   0  0   0
211  5451   1   0  63 202   0   0 110 160   1  0   0
292  9101   1   0  67 188   0   1 102 168   1  0   0
252  6821   1   0  65 185   0   0 105 156   1  0   0
169  4551   1   0  54 206   0   1  76 142   0  0   0
191  4961   1   0  72 200   0   1  86 138   0  0   0
259  6931   1   0  56 195   0   1  94 150   0  0   0
```


dfbeta(mod2.glm)[, 5]
0.02
0.00
−0.02
−0.04
0
100
200
300
400
500
600
Index

- There are 8 points with high influence for the coefficient of hypertension.
- Omission will increase the coefficient.
- Only 71 cases of CHD out of 609, and only 28 are not hypertensive.

	Not Hypertensive	Hypertensive
No CHD	326	212
CHD	28	43

```
evans[order(dfbeta(mod2.glm)[,5])[1:8],]
        ID CHD CAT AGE CHL SMK ECG DBP SBP HPT CH  CC
544 16711   1   1  68 242   1   0  84 128   0  0 242
22    381   1   1  64 247   0   1  75 130   0  0 247
276  8721   1   1  64 233   1   0  94 140   0  0 233
349 11341   1   1  56 228   1   0  92 152   0  0 228
293  9191   1   1  56 221   1   1  78 154   0  0 221
587 18491   1   1  74 212   1   1  70 144   0  0 212
548 16871   1   1  58 209   1   1  94 140   0  0 209
65   1201   1   1  66 205   1   0  80 150   0  0 205
```

- All have CHD, all have high CAT, none are hypertensive, almost all smoke.
- Blood pressure is high "normal".
- One would expect that omission of a CHD case without hypertension would decrease the coefficient, but this is affected by correlation of the predictors.

The Role of Diagnostics

- Diagnostics can be useful for identifying problems in a model or in the data.
- The Evans County data are already cleaned, but if there were erroneous observations, residual and leverage plots could identify them.

Overdispersion

- A common problem with logistic regression is overdispersion.
- This is when $V(\hat{p}) >> p(1-p)/n$
- This can happen if the true parameter p varies even when the covariates do not.
- We can/should then use the quasibinomial, in which $V(\hat{p}) = \theta p(1-p)/n$

```
> summary(glm(CHD~CAT+CHL+SMK+HPT,family=quasibinomial,evans))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.0066  -0.5276  -0.4102  -0.3108   2.5560

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -4.975282   0.797487  -6.239  8.3e-10 ***
CAT          1.021916   0.313496   3.260  0.00118 **
CHL          0.008963   0.003289   2.725  0.00662 **
SMK          0.714577   0.301457   2.370  0.01808 *
HPT          0.483481   0.290735   1.663  0.09684 .
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

(Dispersion parameter for quasibinomial family taken to be 1.021549)

    Null deviance: 438.56  on 608  degrees of freedom
Residual deviance: 406.52  on 604  degrees of freedom
AIC: NA
```

- In this case, there is no sign of overdispersion.
- Note that this can depend on the model as well as the data.
- Fitting the quasibinomial model is the best test of this.
- You should always check for overdispersion in a binomial (or Poisson) model.
- If there is overdispersion and you use a standard logistic regression, the inferences are wrong.

Homework: Due 5/4/17

Try some of these diagnostic techniques on your model for the Evans County Data.