

STAT347: Generalized Linear Models

Lecture 6

Today's topics: Chapters 5.3 - 5.5, 5.7

- Binary GLM inference
- Fitting logistic regression and the infinite estimates
- Binary GLM example

1 Binary GLM model inference

We have already learnt the inference of a general GLM model, we now look what the specific forms are for a binary GLM.

1.1 Score equation in logistic regression

For logistic regression, as the logit link is the canonical link, the score equation is:

$$\frac{\partial L}{\partial \beta_j} = \sum_i (y_i - n_i p_i) x_{ij} = \sum_i \left(y_i - \frac{n_i e^{X_i^T \beta}}{1 + e^{X_i^T \beta}} \right) x_{ij} = 0$$

We have derived that as $n \rightarrow \infty$

$$\text{Var}(\hat{\beta}) \rightarrow (X^T W X)^{-1}$$

where $W = D^2 V^{-1}$ is a diagonal matrix. For logistic regression where the logit link is the canonical link, we have $W = V$ so

$$W_{ii} = n_i p_i (1 - p_i), \quad \widehat{W}_{ii} = n_i \frac{e^{X_i^T \hat{\beta}}}{(1 + e^{X_i^T \hat{\beta}})^2}$$

1.2 Hypothesis testing

Consider the simple null model for binomial data we discussed earlier. Under the null model, the group data is $\sum_i y_i \sim \text{Binomial}(N, p)$ which has only one sample. We want to test for $H_0 : \beta = \text{logit}(p_0)$ (or equivalently: $H_0 : p \equiv p_0$) where β is the constant coefficient. Define $y = \sum_i y_i / N$, under the null model, we can quickly find the MLE, which is $\hat{p} = y$ and $\hat{\beta} = \text{logit}(y)$.

The test statistics are

Wald test:

$$\left(\frac{\hat{\beta} - \text{logit}(p_0)}{\widehat{\text{SE}}(\hat{\beta})} \right)^2 = [\text{logit}(y) - \text{logit}(p_0)]^2 N y (1 - y),$$

Or

$$\left(\frac{\hat{p} - p_0}{\widehat{\text{SE}}(\hat{p})} \right)^2 = \frac{(y - p_0)^2}{[y(1 - y)/N]}$$

Likelihood ratio test:

$$-2(L_0 - L_1) = -2 \log \left[\frac{p_0^{Ny} (1 - p_0)^{N - Ny}}{y^{Ny} (1 - y)^{N - Ny}} \right]$$

Score test:

$$T = \frac{\dot{L}(\beta_0)^T \dot{L}(\beta_0)}{-\ddot{L}(\beta_0)} = \frac{(y - p_0)^2}{[p_0(1 - p_0)/N]}$$

- Wald test depends on the scale
- Wald test is less stable when y is close to 0 or 1. Read Chapter 5.3.3

1.3 Deviance

The total (residual) deviance for a binary GLM (the deviance between the saturated model and the fitted model) is

$$\begin{aligned} D_+(y, \hat{\mu}) &= \sum_i D(y_i, n_i \hat{p}_i) \\ &= -2 \sum_i \log \left[f(y_i, \hat{\theta}_i) / f(y_i, \theta_{y_i}) \right] \\ &= -2 \sum_i \log \left[\frac{\hat{p}_i^{y_i} (1 - \hat{p}_i)^{n_i - y_i}}{(y_i/n_i)^{y_i} (1 - y_i/n_i)^{n_i - y_i}} \right] \\ &= 2 \sum_i y_i \log \frac{y_i}{n_i \hat{p}_i} + 2 \sum_i (n_i - y_i) \log \frac{n_i - y_i}{n_i - n_i \hat{p}_i} \end{aligned}$$

- The total deviance is different for grouped data and ungrouped data as the saturated model is different.
 - Ungrouped data: the saturated model is $\hat{p}_i = y_i$ for each individual sample
 - grouped data: the saturated model is $\hat{p}_k = \tilde{y}_k$ for each group k . Thus all samples in the same group should have the same \hat{p}_i even in the saturated model.

1.4 Goodness-of-fit test

The group level data can be presented by a $K \times 2$ count table, where each row is a group, and the two columns store the number of success \tilde{y}_k and the number of failure $n_k - \tilde{y}_k$ respectively in each cell.

- Residual deviance for the grouped data:

$$G^2 = D_+(y, \hat{\mu}) = 2 \sum_{2K \text{ cells}} \text{observed} \times \log \left(\frac{\text{observed}}{\text{expected}} \right)$$

- When the number of groups K is fixed while the total samples size $N = \sum_k n_k$ is large, then the residual deviance is the likelihood ratio satisfying

$$G^2 = D_+(y, \hat{\mu}) \xrightarrow{p} \chi_{K-p}^2$$

which can be used for goodness-of-fit test of the fitted model.

- Pearson's statistics for goodness of fit:

$$\begin{aligned} X^2 &= \sum_{2K \text{ cells}} \frac{(\text{observed} - \text{fitted})^2}{\text{fitted}} \\ &= \sum_k \frac{(n_k \tilde{y}_k - n_k \hat{p}_k)^2}{n_k \hat{p}_k} + \sum_k \frac{[(n_k - \tilde{y}_k) - (n_k - n_k \hat{p}_k)]^2}{n_k - n_k \hat{p}_k} \\ &= \sum_k \frac{(\tilde{y}_k - n_k \hat{p}_k)^2}{n_k \hat{p}_k (1 - \hat{p}_k)} \xrightarrow{p} \chi_{K-p}^2 \end{aligned}$$

- Comparison between G^2 and X^2
 - $X^2 = \sum_k e_k^2$: sum square of Pearson residuals of group data. X^2 converges to χ_{K-p}^2 more quickly, so it works better than G^2 for N not to large.
 - $G^2 = \sum_k d_k^2$: sum square of deviance residuals of group data. G^2 gives more reliable p-values than X^2 when some cells have small expected counts (≤ 5).

2 Binary GLM computation

For logistic regression, Newton's method = Fisher scoring = IRLS.

For IRLS, the t th iteration is

$$X^T W^{(t)} (z^{(t)} - X\beta) = 0$$

where

$$\begin{aligned} z_i^{(t)} &= X_i^T \beta^{(t)} + \left(D_{ii}^{(t)}\right)^{-1} (y_i - \mu_i^{(t)}) \\ &= \log\left(\frac{p_i^{(t)}}{1 - p_i^{(t)}}\right) + \frac{y_i - n_i p_i^{(t)}}{n_i p_i^{(t)} (1 - p_i^{(t)})} \end{aligned}$$

and

$$W_{ii}^{(t)} = V_{ii}^{(t)} = n_i p_i^{(t)} (1 - p_i^{(t)})$$

2.1 Infinite parameter estimates

One may sometimes see this warning message using R to solve the logistic regression:

Warning message: glm.fit: fitted probabilities numerically 0 or 1 occurred

You may see very large estimates of β . What happened?

- Perfect separation:

There exists β_s such that if $X_i^T \beta_s > 0$ then $y_i = 1$ otherwise $y_i = 0$.

We prove that the MLE for β does not exist. Let $\eta_i = kX_i^T\beta_s$.

When $k \rightarrow \infty$, then

$$p_i = \frac{e^{kX_i^T\beta_s}}{1 + e^{kX_i^T\beta_s}} \rightarrow \begin{cases} 1 & \text{if } X_i^T\beta_s > 0, \text{ or equivalently } y_i = 1 \\ 0 & \text{else} \end{cases}$$

Thus, $\frac{\partial L}{\partial \beta} \rightarrow 0$ if $k \rightarrow \infty$ so the solution of the score equation is infinite. In other words, the MLE does not exist.

- Quasi-complete separation:

There exists β_s such that if $X_i^T\beta_s > 0$ then $y_i = 1$, if $X_i^T\beta_s < 0$ then $y_i = 0$, and if $X_i^T\beta_s = 0$ then $y_i = 0$ or 1 (allow data points on the separation hyperplane with both outcomes).

We can also show that the MLE for β does not exist (Albert and Anderson, *Biometrika* 1984). Any value β can be decomposed as $\beta = \beta_s + \gamma$. Denote $\beta_k = k\beta_s + \gamma$. Let $\eta_i = kX_i^T\beta_s + X_i^T\gamma$. When $k \rightarrow \infty$, then

$$p_i = \frac{e^{kX_i^T\beta_s + X_i^T\gamma}}{1 + e^{kX_i^T\beta_s + X_i^T\gamma}} \rightarrow \begin{cases} 1 & \text{if } X_i^T\beta_s > 0 \\ 0 & \text{if } X_i^T\beta_s < 0 \\ \frac{e^{X_i^T\gamma}}{1 + e^{X_i^T\gamma}} & \text{if } X_i^T\beta_s = 0 \end{cases}$$

This tells us that for any β , we can find β_k with large enough k so that the log-likelihood $L(\beta_k) > L(\beta)$, so the log-likelihood function $L(\cdot)$ does not have a finite maximum point. In other words, the MLE does not exist.

- How to deal with perfect/quasi-complete separation? (Read Chapter 5.4.2)

We can add a penalization or add a prior of the parameter to obtain finite estimates of β .

3 Two data examples

Chapter 5.7. Please check the R notebook 3.

Next time: Chapter 6.1, multivariate GLM: nominal response