STAT3015/4030/7030: Generalised Linear Modelling GLMS - Analysis of Deviance

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- Null model no relationship between predictors and response. That is, fit a common mean μ for all y, and the data is represented entirely as random variation.
- ► Full/Saturated model data is explained exactly, estimate n parameters with exactly n data points. Drawbacks? the model tells us no more than the data itself, uninformative.

Likelihood ratio statistics for comparison between full (saturated) model and the model under consideration:

$$2\log LRT = 2\log \Lambda = 2(\log L(\hat{\theta}_{sat}, \phi|y) - \log L(\hat{\theta}, \phi|y)) \sim \chi_{\nu}^{2}$$

 ν : difference in number of parameters between two models

Provided observations are independent and for EF distributions this simplifies to

Scaled Deviance =
$$2\log \Lambda = 2\sum_{i}^{n} \frac{(y_{i}(\hat{\theta}_{sat} - \hat{\theta}) - b(\hat{\theta}_{sat}) + b(\hat{\theta}))}{\phi}$$

$$= \frac{D(Y, \hat{Y})}{\phi} \tag{2}$$

$$D(Y, \hat{Y})$$
 is called the *deviance*. $D^* = \frac{D(Y, \hat{Y})}{\phi}$ is called the *scaled deviance*.

Exercise: What is the deviance for the linear regression model with identity link and normal error structure, and fitted values \hat{Y}_i .

We showed previously that for the normal distribution, $\theta = \mu$, $\phi = \sigma^2$, $b(\theta) = \theta^2/2$.

$$D(Y, \hat{Y}) = \sum_{i} 2(y_{i}(\tilde{\theta}_{i} - \hat{\theta}_{i}) - b(\tilde{\theta}_{i}) + b(\hat{\theta}_{i}))$$

$$= \sum_{i} 2\left(y_{i}(y_{i} - \hat{y}_{i}) - \frac{y_{i}^{2}}{2} + \frac{\hat{y}_{i}^{2}}{2}\right)$$

$$= \sum_{i} 2y_{i}^{2} - 2y_{i}\hat{y}_{i} - y_{i}^{2} + \hat{y}_{i}^{2}$$

$$= \sum_{i} y_{i}^{2} - 2y_{i}\hat{y}_{i} + \hat{y}_{i}^{2}$$

$$= \sum_{i} (y_{i} - \hat{y}_{i})^{2} = SSE$$

Alternatively, working from first principles, and noting that the log-likelihood for $Y \sim N(\mu, \sigma^2)$ is

$$\log L(Y|\mu, \sigma^2) = -\frac{1}{2\sigma^2} \sum_{i=1}^n (y_i - \mu)^2 - \frac{n}{2} \log(2\pi\sigma^2)$$

$$D(Y, \hat{Y}) = 2\log\Lambda \times \sigma^2 = 2\sigma^2 \left\{ -\frac{1}{2\sigma^2} \sum_i (y_i - y_i)^2 - n\phi \log(2\pi\sigma^2) \right\}$$
$$+ 2\sigma^2 \left\{ -\frac{1}{2\sigma^2} \sum_i (y_i - \hat{y}_i)^2 + n\phi \log(2\pi\sigma^2) \right\}$$
$$= \sum_i (y_i - \hat{y}_i)^2 = SSE$$

A larger value of $D(Y, \hat{Y})$ suggests a poorer fit. How can we use the deviance statistic to assess model fit? If ϕ is known,

$$\frac{D(Y, \hat{Y})}{\phi} \sim \chi_{n-p}^2 \text{ under } H_0$$

So if $\phi = 1$, then

$$D(Y, \hat{Y}) \sim \chi^2_{n-p}$$
 under H_0

In R, $D(Y, \hat{Y})$ is reported as the <u>residual deviance</u>. Because ϕ must be known, we can only apply the goodness of fit test to Poisson and Binomial GLMS where $\phi=1$. For GLMS such as the Gaussian and Gamma, we usually do not know the value of the dispersion parameter ϕ , and so this test cannot be used. Though, as we will see later, we can often estimate the dispersion and use a suitably scaled deviance test.

 $\label{eq:local_equation} \begin{array}{l} \underline{IMPORTANT} \text{: the goodness-of-fit test is not appropriate for binary} \\ \text{data (that is, observations are reported as Y=0,1)}. Why? Because \\ \text{the chi-squared approximation requires expected frequencies of} \\ \text{success for each observation to exceed one, this is not possible} \\ \text{with the definition of binary data.} \end{array}$

Like the sums of squared errors under the least-squares approach to parameter estimation, the deviance measures the deviation of the fitted values from the observed data.

Similarly, we will use a <u>difference in deviances</u> measure to test if a larger model provides a significantly better fit to the data.

The difference in deviance is a measure of how important the subset of predictors which have been left out of the smaller model are to explain relationships in the observed data.

To compare a large model "L" to a small model "S", we calculate the difference in deviances

Suppose the extra parameters in the larger model are denoted by

Suppose the extra parameters in the larger model are denoted by $\beta_{\overline{\bf 5}}.$

$$H_0: \beta_{\bar{S}} = 0 \text{ vs } H_A: \beta_{\bar{S}} \neq 0$$

1. Dispersion ϕ known (Poisson and Binomial GLM) For α significance level, reject H_0 if

$$D(Y, \hat{Y}_S) - D(Y, \hat{Y}_L) \ge \chi^2_{(df_S - df_L)}(1 - \alpha)$$

That is, the difference in deviances $D(Y, \hat{Y}_S) - D(Y, \hat{Y}_L)$ is asymptotically χ^2 with degrees of freedom equal to the difference in the number of identifiable parameters in the two models.

2. Dispersion ϕ unknown (Normal and Gamma GLM) The χ^2 test for nested models cannot be used if ϕ must be estimated. Where ϕ is usually not known, we can insert an estimate for ϕ and compute an F-statistic of the form

$$F = \frac{(D(Y, \hat{Y}_S) - D(Y, \hat{Y}_L))/(df_S - df_L)}{\hat{\phi}_L}$$

Compare the F-stat to the quantiles of a $F_{df_S-df_L,df_L}$ distribution.

For the normal linear model (Gaussian GLM) the F-statistic has an exact F-distribution. For other GLMs with a free dispersion parameter that must be estimated, the statistic is only approximately F distributed.

Exercise: Specify the drop in deviance test statistic for the overall significance of a normal linear multiple regression with (p-1 predictors). That is, testing the null hypothesis $(H_0: \beta_1 = ... = \beta_{p-1} = 0)$

In this case the smaller model is the null model with just an intercept term $Y_i = \beta_0 + \epsilon_i$. The fitted values are $\hat{Y}_i = \bar{Y}$ for all data points. So $D(Y, \hat{Y}_S) = \sum_i (Y_i - \bar{Y})^2 = SST$.

The larger model has fitted values $\hat{Y}_i = X_i^T \hat{\beta}$. So $D(Y, \hat{Y}_L) = \sum_i (Y_i - \hat{Y}_i)^2 = SSE$.

Hence, we have

$$\frac{(SST - SSE)/(p-1)}{\hat{\phi}_L} = \frac{SSR/(p-1)}{\hat{\sigma}_L^2} = \frac{MSR}{MSE} = F$$

So the deviance statistic is equivalent to the standard F-statistic in multiple linear regression to test for significance of subsets of predictors.

(R code example - Weighted regression on pages 46 to 48 of the brick)

(R code example - Car insurance data on pages 48 to 54 of the brick)

(Additional R code example - Bliss insect data)