Tutorial 9

STAT3015/4030/7030 Generalised Linear Modelling

The Australian National University

Week 9, 2017

Overview

Summary

Difference between "ANOVA()" commands

anova(model, test="Chisq") scales by the assumed dispersion ($\hat{\phi}_{assumed}$). Produces chi-squared test p-values.

anova(model, test="F") scales by the assumed dispersion $(\hat{\phi}_{assumed})$. Produces F test p-values.

Note: Here we treat the assumed dispersion as an estimated variance. This assumption is only appropriate for normally distributed models.

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We use **chi-square tests** for all drop-in-deviance tests on **non normal** GLMs in this course.

Pearson residual

If we define $e_i = Y_i - \hat{Y}_i$ as residual, e_i for a GLM does not behave quite nicely as in SLR models. In particular, we know that the variance of the Y_i 's is not constant, but is instead proportional to the variance function $V(\mu_i)$. Thus, even if the chosen model is correct, the residuals will not display a homoscedastic spread.

Pearson residual as

$$r_i = \frac{e_i}{\sqrt{V(\hat{Y}_i)}}$$

residuals(model, "pearson")

(see "R Example: Residual Plots" on Wattle)

Deviance residual

Deviance residual d_i is defined based on $D(\hat{Y}, Y)$, so that

$$\sum_{i=1}^n d_i^2 = D(\hat{Y}, Y).$$

residuals(model, "deviance")

(see "R Example: Residual Plots" on Wattle)

Partial residual

To check the appropriate scale for the j^{th} predictor variable, X_j , we plot the partial residual values versus the values of the predictor variable under investigation (i.e. values of X_j). The partial residuals can be written as

$$u_i = g(Y_i) - x_i^T \hat{\beta} + x_i \hat{\beta}_j$$

In other words, we "adjust" the $g(Y_i)$ values for the other covariates in the model (i.e., we subtract off the predicted value calculated without using the predictor in question).

We need to manually code this. (see "R Example: Model Building" on Wattle)

Commonly used residual plots in this course

Main residual vs fitted values plot:

```
plot(model$linear.predictors,residuals(model,"deviance"))
```

Normal quantile plot:

```
qqnorm(residuals(model, "pearson"))
qqline(residuals(model, "pearson"))
```

Partial residual plot:

```
plot(x, u1)
```