Part II: Generalized Linear Models

Chapter II.2

Theory of Generalized Linear Models

Model Fit Evaluation - Model Selection

Evaluating Model Fit for GLMs

№ II.2.32 Definition

Consider a random sample $\mathbf{Y}=(Y_1,\ldots,Y_n)'$ of n independent responses with $Y_i\sim \mathsf{EDF}(\vartheta_i,\varphi)$, modeled by a GLM $\eta=g(\mathsf{E}(\mathbf{Y})=\mathbf{X}\boldsymbol{\beta},$ denoted as $\mathfrak{M},$ with (known) design matrix $X\in\mathbb{R}^{n\times p}$ and (unknown) parameter vector $\boldsymbol{\beta}\in\Theta\subseteq\mathbb{R}^p$.

Then

- $\hat{\mu}$ denotes the MLE of $\mu = E(Y)$ under \mathcal{M} and the vector $\hat{Y} = \hat{\mu} = g^{-1} \left(\mathbf{X} \hat{\beta} \right)$ is called the vector of predicted values,
- $e = \hat{\epsilon} = Y \hat{Y} = Y \hat{\mu}$ is the vector of raw residuals, and
- $\ell(\hat{\beta}) = \ell(\hat{\mu}; y)$ is the maximum log-likelihood corresponding to model \mathcal{M} evaluated at the MLE $\hat{\mu}$ (i.e. $\hat{\beta}$).

II.2.33 Definition (saturated model)

A GLM that describes $Y=(Y_1,\ldots,Y_n)'$ perfectly is called **saturated model** and is denoted by \mathfrak{M}_{sat} . If β_{sat} is the parameter vector of \mathfrak{M}_{sat} and $\hat{\mu}_{sat}$ the corresponding vector of predicted values, then it holds $\beta_{sat} \in \Theta \subseteq \mathbb{R}^n$ (i.e. p=n), $\hat{\mu}_{sat} = Y$ and consequently e=0.

II.2.34 Remark

- The quality of the fit of a model \mathcal{M} is assessed by comparing the maximum log-likelihood $\ell(\hat{\mu}; y)$ for \mathcal{M} to $\ell_{sat} = \ell(y; y)$, which is the *saturated* maximum log-likelihood (corresponding to model \mathcal{M}_{sat}).
- It is obvious that $\ell(\hat{\mu}; y) < \ell_{sat}$ always, with the fit of model \mathcal{M} being as better as its log-likelihood approaches the saturated log-likelihood.

$$l_sat = l(y^n, y)$$

№ II.2.35 Definition (Deviance)

The goodness of fit of a GLM $\mathfrak M$ is expressed, in terms of the log-likelihood difference, by the statistic $-2\,[\ell(\hat\mu;y)-\ell_{s\,at}]$. For the exponential dispersion family (s. slide 38) it equals

$$-2\left[\ell(\hat{\mu};y)-\ell_{sat}\right]=2\left(\sum_{i=1}^{n}\frac{y_{i}\tilde{\theta}_{i}-b(\tilde{\theta}_{i})}{a(\varphi;i)}-\sum_{i=1}^{n}\frac{y_{i}\hat{\theta}_{i}-b(\hat{\theta}_{i})}{a(\varphi;i)}\right),$$

with $\hat{\theta}_i$ and $\tilde{\theta}_i$ the MLE of θ_i under models \mathcal{M} and \mathcal{M}_{sat} , respectively.

Furthermore, for $a(\phi; i) = \phi/w_i$ (s. Remark II.2.8), the statistic becomes

$$D_s(\mathbf{y}; \hat{\mathbf{\mu}}) = \frac{D(\mathbf{y}; \hat{\mathbf{\mu}})}{\Phi} = \frac{2}{\Phi} \sum_{i=1}^n w_i \left(y_i(\tilde{\theta}_i - \hat{\theta}_i) - [b(\tilde{\theta}_i) - b(\hat{\theta}_i)] \right)$$

and is called the scaled deviance. The statistic $D(\boldsymbol{y};\hat{\boldsymbol{\mu}})$ is known as deviance.

II.2.36

Since $\ell(\hat{\mu}; y) < \ell_{sat}$, it always holds $D(y; \hat{\mu}) \geqslant 0$, with the fit of model M becoming poorer as the deviance becomes greater.

II.2.37 Remark (deviance of GLMs with canonical link)

1 For normal GLMs, the deviance equals the residual sum of squares (SSE):

$$D(y; \hat{\mu}) = \sum_{i=1}^{n} (y_i - \hat{\mu}_i)^2.$$

② For Poisson GLMs, the deviance equals the **likelihood ratio statistic (LRS)** G^2 for testing model \mathcal{M} (H₀) against the saturated model \mathcal{M}_{sat} (H₁):

$$D(\mathbf{y}; \hat{\mathbf{\mu}}) = G^2(\mathcal{M}) = 2\sum_{i=1}^n y_i \log(\frac{y_i}{\hat{\mu}_i}).$$

3 For GLMs with response distributions satisfying $Var(Y_i) = \nu(\mu_i)$, i = 1, ..., n (s. Remark II.2.18), and $\phi = 1$, the corresponding score statistic ^a is of the form

$$W_{S}(\mathcal{M}) = \sum_{i=1}^{n} \frac{(y_i - \hat{\mu}_i)^2}{\nu(\hat{\mu}_i)}.$$

For Poisson distributed Y_i s $(\nu(\mu_i) = \mu_i)$, it becomes the *Pearson's* X^2 statistic.

 $^{^{}a}$ For the LRS, the score statistic and the corresponding asymptotic statistical tests see Theorems S1.59, S1.61 and S1.63 of the course 'Mathematics of Data Science'.

II.2.38 Remark

For normal GLMs and under the assumption that $\mathfrak M$ is true, the deviance and the score statistics are both exact \succ^2 distributed.

For the other response distributions, these statistics can be used for testing model's $\mathfrak M$ goodness of fit, if their asymptotic distribution can be specified, which is not always the case. This is possible for example, for Poisson GLMs with large means $\mu_i s$ or for binomial GLMs with $Y_i \sim \mathfrak B(\mathfrak m_i, \mu_i)/\mathfrak m_i$) having sufficiently large $\mathfrak m_i s$.

In this case, $D(y;\hat{\mu})$ and $G^2(\mathcal{M})$, for example, are both approximately \succeq_{df}^2 distributed, with $\mathrm{df}=n-p$ (e.g. sample size – number of parameters in the model).

Model Complexity

These goodness-of-fit tests do not account for **model complexity** while they are increasing in sample size n, giving thus significant values for good models if the sample size is large.

Alternatively, the fit of a GLM can be evaluated by the criteria introduced below.

№ II.2.39 Definition (AIC and BIC)

Tthe fit of a model ${\mathfrak M}$ can be evaluated by

- **Akaike's Information Criterion** (Akaike, 1974): $AIC = -2\ell(\hat{\mu}; y) + 2p$. It is based on the maximum likelihood under $\mathfrak M$ but penalizes its value for model complexity, where p is the number of parameters in the model. The better is a model, the smaller is the corresponding AIC.
- **Bayesian Information Criteron** (Schwarz, 1978): BIC = $-2\ell(\hat{\mu}; y) + (\log n)p$, which is another maximum likelihood based measure, incorporating Bayesian thinking, that beyond complexity takes into account also the sample size.

Model Selection in GLMs

Deviance plays a predominant role in comparing GLMs. Model selection is based on comparing *nested models*.

► II.2.40 Definition (nested models)

Let \mathcal{M}_1 be a GLM having p_1 parameters. Let also \mathcal{M}_0 be a simpler GLM, produced from \mathcal{M}_1 by eliminating r of its p_1 parameters. Then, \mathcal{M}_0 is said to be *nested* in \mathcal{M}_1 and denoted by $\mathcal{M}_0 \subset \mathcal{M}_1$. Model \mathcal{M}_0 is more parsimonious than \mathcal{M}_1 having $p_0 = p_1 - r$ parameters.

II.2.41 Remark

If the response distributions are in the EDF with $\varphi=1$ (like Poisson and binomial responses), then the deviance of a model is equal to the corresponding LRS for testing its fit.

If $\hat{\mu}_0$ and $\hat{\mu}_1$ are the MLEs of μ under \mathcal{M}_0 and \mathcal{M}_1 , respectively, then, for $\varphi=1$, the deviances of models \mathcal{M}_0 and \mathcal{M}_1 are

$$D(y; \hat{\mu}_j) = -2 [\ell(\hat{\mu_j}; y) - \ell(y; y)], \quad j = 0, 1.$$

If $(\mathcal{M}_0 \subset \mathcal{M}_1)$, since reducing the number of model's parameters implies increase of model's distance from the perfect fit of the saturated model, it will always be $D(y; \hat{\mu}_0) > D(y; \hat{\mu}_1)$.

► II.2.42 Comparison of two nested models

Consider models \mathfrak{M}_0 and \mathfrak{M}_1 with $\mathfrak{M}_0\subset \mathfrak{M}_1$, for response distributions in EDF with $\varphi=1$, both applied on the same observations y. Then the difference in their deviances is

$$D(y; \hat{\mu}_0) - D(y; \hat{\mu}_1) = -2 [\ell(\hat{\mu_0}; y) - \ell(\hat{\mu_1}; y)] = G^2(\mathcal{M}_0, \mathcal{M}_1)$$
,

where $G^2(\mathcal{M}_0,\mathcal{M}_1)$ is the LRS for testing the null hypothesis that \mathcal{M}_0 holds against the alternative that \mathcal{M}_1 holds.

II.2.43 Remark

In particular, if the appropriate assumptions hold (see Remark II.2.38), then the difference in deviances

$$D(\hat{\mu}_0; \hat{\mu}_1) = D(y; \hat{\mu}_0) - D(y; \hat{\mu}_1),$$

is under \mathcal{M}_0 approximately \succ_r^2 distributed, where $r=p_1-p_0$ is the difference between the number of parameters of the two compared models. This result is the key for asymptotic comparison of models.

For Poisson log-linear models, $D(\hat{\mu}_0; \hat{\mu}_1)$ simplifies to

$$G^2(\mathcal{M}_0|\mathcal{M}_1) = 2\sum_{i=1}^n y_i \log \left(\frac{\hat{\mu}_{i1}}{\hat{\mu}_{i0}}\right) = G^2(\mathcal{M}_0) - G^2(\mathcal{M}_1) \ .$$

'Best Model' Selection

II.2.44 Remark

Upon considering a sequence of nested models from a very simple \mathcal{M}_0 up to the saturated \mathcal{M}_{sat} ,

$$\mathfrak{M}_0\subset \mathfrak{M}_1\subset \mathfrak{M}_2\subset \ldots \subset \mathfrak{M}_{\mathsf{sat}}$$
 ,

the importance of the parameters added gradually can be evaluated by successive comparisons of neighbor models, in a **stepwise** manner, moving "forwards" or "backwards".

Hence, comparisons of nested models serve for developing procedures of 'best model' selection. Furthermore, once the 'best model' is selected, models comparison can serve as a tool for evaluating the individual importance of each parameter or group of parameters.

Model selection can also be based on AIC or BIC.

These issues will be discussed and illustrated in the context of log-linear models for multi-way tables.