MONASH
BUSINESS
SCHOOL

ETC3580: Advanced Statistical Modelling

Week 3: Binary responses

Outline

Logistic regression

Suppose response variable Y_i takes values 0 or 1 with probability $P(Y_i = 1) = p_i$. (i.e., a Bernoulli distribution)

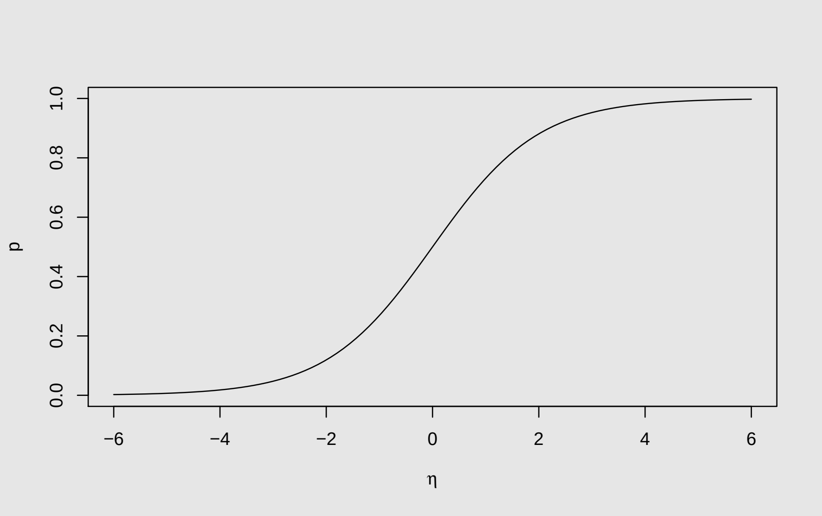
We relate p_i to the predictors:

$$p_i = e^{\eta_i}/(1 + e^{\eta_i}) = P(Y_i = 1)$$

$$\eta_i = \beta_0 + \beta_1 x_{i,1} + \cdots + \beta_q x_{i,q}$$

- $g(p) = \log(p/(1 - p))$ is the "logit" function. It maps $(0, 1) \to \mathbb{R}$.
- The inverse logit is $g^{-1}(\eta) = e^{\eta}/(1 + e^{\eta})$ which maps $\mathbb{R} \to (0, 1)$.
- g is called the "link" function.

Inverse logit function



- If $p_i \approx 0.5$, logistic and linear regression similar.

Log-likelihood

Likelihood

$$L = \prod_{i=1}^{n} p_i^{y_i}(1 - p_i)^{1-y_i}$$

$$\begin{aligned}
\log L(\beta) &= \sum_{i=1}^{n} y_i \log(p_i) + (1 - y_i)\log(1 - p_i) \\
&= \sum_{i=1}^{n} y_i[\eta_i - \log(1 + e^{\eta_i})] - (1 - y_i)\log(1 + e^{\eta_i}) \\
&= \sum_{i=1}^{n} [y_i\eta_i - \log(1 + e^{\eta_i})]
\end{aligned}$$

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\end{aligned}$$

- MLE: maximize $\log L$ to obtain $\hat{\beta}$
- Equivalent to iterative weighted least squares
- No closed form expressions

Logistic regression in R

```r
fit <- glm(y ~ x1 + x2, family=binomial,
                data=df)
```

- Bernoulli is equivalent to Binomial with only two levels.
- First (alphabetical) level is set to 0, other to 1. Use `relevel` if you want to change it.
- `glm` uses MLE with a logit link function (when `family=binomial`).

Interpreting a logistic regression

Odds = $p/(1-p)$.

- Example: 3-1 odds means $p = 3/4$.
- Example: 5-2 odds means $p = 5/7$.
- A horse at "15-1 against" means $p = 1/16$.
- Odds are unbounded.
- $\log(\text{odds}) = \log(p/(1-p)) = \beta_0 + \beta_1 x_1 + \beta_2 x_2$
- A unit increase in x_1 with x_2 held fixed increases log-odds of success by β_1.
- A unit increase in x_1 with x_2 held fixed increases odds of success by a factor of e^{β_1}.

Outline

Fitted values

Link: on $(-\infty, \infty)$

$$\hat{\eta}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i,1} + \cdots + \hat{\beta}_q x_{i,q}$$

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$$e^{\hat{\eta}_i} / (1 + e^{\hat{\eta}_i})$$

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$$e^{\hat{\eta}_i}/(1 + e^{\hat{\eta}_i})$$

```
fit <- glm(y ~ x1 + x2, family='binomial',
           data=df)
library(broom)
augment(fit, type.predict='link') # default
augment(fit, type.predict='response')
```

OLS Residuals

Response residuals: Observation – estimate

$$e_i = y_i - \hat{y}_i$$

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Deviance residuals: Signed root contribution to $-2 \log L$.

$$-2 \log L = c + \frac{1}{\hat{\sigma}^2} \sum e_i^2 = c + \sum d_i^2$$

$$d_i = e_i / \hat{\sigma}$$

Logistic regression residuals

Response residuals: Observation – estimate

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$$r_i = \frac{y_i - \hat{p}_i}{\sqrt{\hat{p}_i(1 - \hat{p}_i)}}$$

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- Mean 0, variance 1.

Deviance residuals: Signed root contribution to

$$-2 \log L = -2 \sum [y_i \eta_i - \log(1 + e^{\eta_i})] = \sum d_i^2$$

$$d_i = \text{sign}(y_i - \hat{p}_i) \sqrt{2 \left[-y_i \log(\hat{p}_i) - (1 - y_i) \log(1 - \hat{p}_i) \right]}$$

Logistic regression residuals

```
fit <- glm(y ~ x1 + x2, family='binomial',
           data=df)
library(broom)
augment(fit, type.resid='response')
augment(fit, type.resid='pearson')
augment(fit, type.resid='deviance') # default
```

- Residual plots can be hard to interpret
- Don’t expect residuals to be normally distributed

Partial residuals

- Let $e_i = y_i - \hat{p}_i$ be a response residual. Then

$$e_i^* = \frac{e_i}{\hat{p}_i(1-\hat{p}_i)}$$

  is the "logit residual" (compare Pearson residuals).

- The "logit partial residual" for the jth variable is

$$e_i^* + \hat{\beta}_j x_{i,j}$$

- We can plot these against $x_{i,j}$ to identify potential nonlinearity.
- `visreg` plots $d_i + \hat{\beta}_j x_{i,j}$ instead.

Outline

Deviance

Generalization of sum of squared residuals based on likelihood ratio:

$$D = \sum d_i^2 = -2 \log L + c$$

where L is the likelihood of the model and c is constant that depends on data but not model.

- Difference between deviances equivalent to a likelihood ratio test.
- $D_1 - D_2 \sim \chi^2_{q_2 - q_1}$ where q_i is df for model i assuming
  1. smaller model is correct
  2. models are nested
  3. distributional assumptions true
- Null deviance is for model with only an intercept.

Deviance test

In R:

```
fit <- glm(y ~ x1 + x2, family='binomial',
           data=df)
anova(fit, test="Chisq")
drop1(fit, test="Chisq")
anova(fit1, fit2, test="Chisq")
```

- NOT equivalent to t-tests on coefficients
- Deviance tests preferred

Confidence intervals for coefficients

- Standard intervals based on normal distribution are poor approximations.
- Better to use “profile likelihood” confidence intervals
- Let $L_p(\theta)$ be the profile likelihood (the likelihood without the nuisance parameters). LR test for $H_0 : \theta = \theta_0$ is

  $$LR = 2\left[\log L_p(\hat{\theta}) - \log L_p(\theta_0)\right]$$

  Confidence interval consists of those values θ_0 for which test is not significant. (A contour region of the likelihood.)
- Implemented in R using `confint`

Model selection

Akaike's Information Criterion

$$\text{AIC} = -2\log L + 2q = c + D + 2q$$

- Select model with smallest AIC
- Beware of hypothesis tests after variable selection
- `step()` works for `glm` objects in the same way as for `lm` objects, and minimizes the AIC.

Outline

Latent variable interpretation

- Suppose z is a latent (unobserved) random variable:

$$y = \begin{cases} 1 & z = \beta_0 + \beta_1 x_1 + \cdots + \beta_q x_q + \varepsilon > 0 \\ 0 & \text{otherwise} \end{cases}$$

  where ε has cdf F.
- If F is "standard logistic", then $F(w) = 1/[1 + e^{-w}]$.
- So $\text{logit}(p) = \beta_0 + \beta_1 x_1 + \cdots + \beta_q x_q$.

That is, we can think of logistic regression as an ordinary regression with logistic noise, and we observe only if it is above or below 0.

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That is, probit regression is an ordinary regression with normal noise, and we observe only if it is above or below 0.

Latent variable interetation

General binary model

$$p_i = g(\eta_i) = P(Y_i = 1)$$

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where g maps $\mathbb{R} \to (0, 1)$.

- $g(\eta) = e^\eta/(1 + e^\eta)$: logit link, logistic regression
- $g(\eta) = \Phi(\eta)$: normal cdf link, probit regression
- $g(\eta) = 1 - \exp(-\exp(\eta))$: log-log link

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```
fit <- glm(y ~ x1 + x2,
  family=binomial(link=probit), data=df)
```

Why prefer logit over probit?

- odds ratio interpretation of coefficients
- non-biased with disproportionate stratified sampling. Only link function with this property.
- non-biased with clustered observations. Only link function with this property.
- logit link is “canonical”: ensures $\sum x_{ij} y_i$ ($j = 1, \ldots, q$) are sufficient for estimation. So p-values are exact.