Sections 5.1, 5.2, 5.3

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Stat 770: Categorical Data Analysis

The logistic regression model is

$$Y_i \sim \text{bin}(n_i, \pi_i), \quad \pi_i = \frac{\exp(\beta_0 + \beta_1 x_{i1} + \cdots + \beta_{p-1} x_{i,p-1})}{1 + \exp(\beta_0 + \beta_1 x_{i1} + \cdots + \beta_{p-1} x_{i,p-1})}.$$

- $\mathbf{x}_i = (1, x_{i1}, \ldots, x_{i,p-1})$ is a p-dimensional vector of explanatory variables including a place holder for the intercept.
- $\boldsymbol{\beta} = (\beta_0, \ldots, \beta_{p-1})$ is the p-dimensional vector of regression coefficients. These are the unknown population parameters.
- $\eta_i = \mathbf{x}_i' \boldsymbol{\beta}$ is called the linear predictor.
- Page 163: many, many uses including credit scoring, genetics, disease modeling, etc, etc...
- Many generalizations: ordinal data, complex random effects models, discrete choice models, etc.

5.1.1 Model interpretation

Lets start with simple logistic regression:

$$Y_i \sim \text{bin}\left(n_i, \frac{e^{\alpha+\beta x_i}}{1+e^{\alpha+\beta x_i}}\right).$$

An odds ratio: let's look at how the odds of success changes when we increase x by one unit:

$$\begin{aligned}
\frac{\pi(x+1)/[1-\pi(x+1)]}{\pi(x)/[1-\pi(x)]} &= \frac{\left[\frac{e^{\alpha+\beta x+\beta}}{1+e^{\alpha+\beta x+\beta}}\right] / \left[\frac{1}{1+e^{\alpha+\beta x+\beta}}\right]}{\left[\frac{e^{\alpha+\beta x}}{1+e^{\alpha+\beta x}}\right] / \left[\frac{1}{1+e^{\alpha+\beta x}}\right]} \\
&= \frac{e^{\alpha+\beta x+\beta}}{e^{\alpha+\beta x}} = e^{\beta}.
\end{aligned}$$

When we increase x by one unit, the odds of an event occurring increases by a factor of e^{β}, *regardless of the value of* x.

Another interpretation for β

So e^{β} is an odds ratio.

We also have

$$\frac{\partial \pi(x)}{\partial x} = \beta \pi(x)[1 - \pi(x)].$$

Note that $\pi(x)$ changes more when $\pi(x)$ is away from zero or one than when $\pi(x)$ is near 0.5.

This gives us *approximately* how $\pi(x)$ changes when x increases by a unit. This increase depends on x, unlike the odds ratio.

See Figure 5.1, p. 164.

5.1.3 Horseshoe crab data

Let's look at $Y_i = 1$ if a female crab has one or more satellites, and $Y_i = 0$ if not. So

$$\pi(x) = \frac{e^{\alpha+\beta x}}{1 + e^{\alpha+\beta x}},$$

is the probability of a female having more than her nest-mate around as a function of her width x.

```
data crabs;
input color spine width satell weight @@; weight=weight/1000; color=color-1;
y=0; if satell>0 then y=1;
datalines;

...DATA HERE...

;

proc logistic;
model y=width;
```

Crab data

3	3	28.3	8	3050	4	3	22.5	0	1550	2	1	26.0	9	2300	4	3	24.8	0	2100	4	3	26.0	4	2600
3	3	23.8	0	2100	2	1	26.5	0	2350	4	2	24.7	0	1900	3	1	23.7	0	1950	4	3	25.6	0	2150
4	3	24.3	0	2150	3	3	25.8	0	2650	3	3	28.2	11	3050	5	2	21.0	0	1850	3	1	26.0	14	2300
2	1	27.1	8	2950	3	3	25.2	1	2000	3	3	29.0	1	3000	5	3	24.7	0	2200	3	3	27.4	5	2700
3	2	23.2	4	1950	2	2	25.0	3	2300	3	1	22.5	1	1600	4	3	26.7	2	2600	5	3	25.8	3	2000
5	3	26.2	0	1300	3	3	28.7	3	3150	3	1	26.8	5	2700	5	3	27.5	0	2600	3	3	24.9	0	2100
2	1	29.3	4	3200	2	3	25.8	0	2600	3	2	25.7	0	2000	3	1	25.7	8	2000	3	1	26.7	5	2700
5	3	23.7	0	1850	3	3	26.8	0	2650	3	3	27.5	6	3150	5	3	23.4	0	1900	3	3	27.9	6	2800
4	3	27.5	3	3100	2	1	26.1	5	2800	2	1	27.7	6	2500	3	1	30.0	5	3300	4	1	28.5	9	3250
4	3	28.9	4	2800	3	3	28.2	6	2600	3	3	25.0	4	2100	3	3	28.5	3	3000	3	1	30.3	3	3600
5	3	24.7	5	2100	3	3	27.7	5	2900	2	1	27.4	6	2700	3	3	22.9	4	1600	3	1	25.7	5	2000
3	3	28.3	15	3000	3	3	27.2	3	2700	4	3	26.2	3	2300	3	1	27.8	0	2750	5	3	25.5	0	2250
4	3	27.1	0	2550	4	3	24.5	5	2050	4	1	27.0	3	2450	3	3	26.0	5	2150	3	3	28.0	1	2800
3	3	30.0	8	3050	3	3	29.0	10	3200	3	3	26.2	0	2400	3	1	26.5	0	1300	3	3	26.2	3	2400
4	3	25.6	7	2800	4	3	23.0	1	1650	4	3	23.0	0	1800	3	3	25.4	6	2250	4	3	24.2	0	1900
3	2	22.9	0	1600	4	2	26.0	3	2200	3	3	25.4	4	2250	4	3	25.7	0	1200	3	3	25.1	5	2100
4	2	24.5	0	2250	5	3	27.5	0	2900	4	3	23.1	0	1650	4	1	25.9	4	2550	3	3	25.8	0	2300
5	3	27.0	3	2250	3	3	28.5	0	3050	5	1	25.5	0	2750	5	3	23.5	0	1900	3	2	24.0	0	1700
3	1	29.7	5	3850	3	1	26.8	0	2550	5	3	26.7	0	2450	3	1	28.7	0	3200	4	3	23.1	0	1550
3	1	29.0	1	2800	4	3	25.5	0	2250	4	3	26.5	1	1967	4	3	24.5	1	2200	4	3	28.5	1	3000
3	3	28.2	1	2867	3	3	24.5	1	1600	3	3	27.5	1	2550	3	2	24.7	4	2550	3	1	25.2	1	2000
4	3	27.3	1	2900	3	3	26.3	1	2400	3	3	29.0	1	3100	3	3	25.3	2	1900	3	3	26.5	4	2300
3	3	27.8	3	3250	3	3	27.0	6	2500	4	3	25.7	0	2100	3	3	25.0	2	2100	3	3	31.9	2	3325
5	3	23.7	0	1800	5	3	29.3	12	3225	4	3	22.0	0	1400	3	3	25.0	5	2400	4	3	27.0	6	2500
4	3	23.8	6	1800	2	1	30.2	2	3275	4	3	26.2	0	2225	3	3	24.2	2	1650	3	3	27.4	3	2900
3	2	25.4	0	2300	4	3	28.4	3	3200	5	3	22.5	4	1475	3	3	26.2	2	2025	3	1	24.9	6	2300
2	2	24.5	6	1950	3	3	25.1	0	1800	3	1	28.0	4	2900	5	3	25.8	10	2250	3	3	27.9	7	3050
3	3	24.9	0	2200	3	1	28.4	5	3100	4	3	27.2	5	2400	3	2	25.0	6	2250	3	3	27.5	6	2625
3	1	33.5	7	5200	3	3	30.5	3	3325	4	3	29.0	3	2925	3	1	24.3	0	2000	3	3	25.8	0	2400
5	3	25.0	8	2100	3	1	31.7	4	3725	3	3	29.5	4	3025	4	3	24.0	10	1900	3	3	30.0	9	3000
3	3	27.6	4	2850	3	3	26.2	0	2300	3	1	23.1	0	2000	3	1	22.9	0	1600	5	3	24.5	0	1900
3	3	24.7	4	1950	3	3	28.3	0	3200	3	3	23.9	2	1850	4	3	23.8	0	1800	4	2	29.8	4	3500
3	3	26.5	4	2350	3	3	26.0	3	2275	3	3	28.2	8	3050	5	3	25.7	0	2150	3	3	26.5	7	2750
3	3	25.8	0	2200	4	3	24.1	0	1800	4	3	26.2	2	2175	4	3	26.1	3	2750	4	3	29.0	4	3275
2	1	28.0	0	2625	5	3	27.0	0	2625	3	2	24.5	0	2000										

Fit of $\text{logit}(\pi_i) = \alpha + \beta x_i$ where x_i is width

Parameter	DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept	1	-12.3508	2.6287	22.0749	<.0001
width	1	0.4972	0.1017	23.8872	<.0001

Odds Ratio Estimates

Effect	Point Estimate	95% Wald Confidence Limits	
width	1.644	1.347	2.007

We estimate the probability of a satellite as

$$\hat{\pi}(x) = \frac{e^{-12.35+0.50x}}{1 + e^{-12.35+0.50x}}.$$

The odds of having a satellite increases by a factor between 1.3 and 2.0 times for every *cm* increase in carapace width.

The coefficient table houses estimates $\hat{\beta}_j$, $\text{se}(\hat{\beta}_j)$, and the Wald statistic $z_j^2 = \{\hat{\beta}_j/\text{se}(\hat{\beta}_j)\}^2$ and p-value for testing $H_0 : \beta_j = 0$. What do we conclude here?

With a single predictor x, can plot $p_i = y_i/n_i$ versus x_i. This approach works well when $n_i \neq 1$. The plot should look like a "lazy s." Alternatively, the sample logits $\log p_i/(1-p_i) = \log y_i/(n_i - y_i)$ versus x_i should be approximately straight. If some categories have all successes or failures, an ad hoc adjustment is $\log\{(y_i + 0.5)/(n_i - y_i + 0.5)\}$.

When many n_i are small, you can group the data yourself into, say, 10-20 like categories and plot them. For the horseshoe crab data let's use the categories defined in Chapter 4. A new variable w is created that is the midpoint of the width categories:

```
data crab1; input color spine width satell weight;
  weight=weight/1000; color=color-1;
  y=0; n=1; if satell>0 then y=1; w=22.75;
  if width>23.25 then w=23.75;
  if width>24.25 then w=24.75;
  if width>25.25 then w=25.75;
  if width>26.25 then w=26.75;
  if width>27.25 then w=27.75;
  if width>28.25 then w=28.75;
  if width>29.25 then w=29.75;
```

Plot of sample logits vs. width windows

```
proc sort data=crab1; by w;
proc means data=crab1 noprint; by w; var y n; output out=crabs2 sum=sumy sumn;
data crabs3; set crabs2; p=sumy/sumn;
logit=log((sumy+0.5)/(sumn-sumy+0.5));
proc gplot;
 plot p*w; plot logit*w;
```

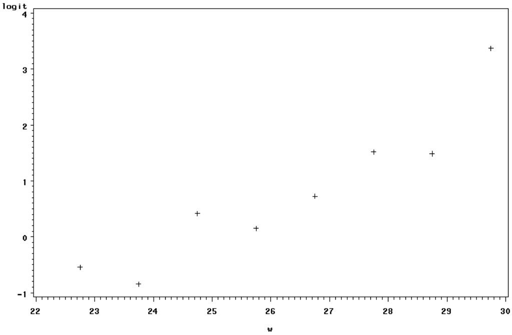


Figure: Sample logits versus width; is this “straight?”

Another option is to use loess

- loess (Cleveland, 1979) stands for *locally weighted scatterplot smoothing*.
- For data $\{(x_i, y_i)\}_{i=1}^n$, a weighted regression is fit at each x_0, where x-values further away from x_0 are given less weight.
- Essentially fits a nonparametric mean function $\mu(x) = E(y|x)$ to $\{(x_i, y_u)\}_{i=1}^n$.
- Useful for (a) exploratory visualization of data, e.g. "is the mean approximately a line?" and (b) residual plots for models where the response is binary or a count.
- However, loess does not restrict the mean to be between zero and one!

```
proc sgscatter;
 plot y*width / loess;
```

5.1.4 Retrospective sampling & logistic regression

In case-control studies the number of cases and the number of controls are set ahead of time. It is not possible to estimate the probability of being a case *from the general population* for these types of data, but just as with a 2×2 table, we *can still estimate an odds ratio e^{β}*.

Let Z indicate whether a subject is sampled (1=yes,0=no). Let $\rho_1 = P(Z = 1|y = 1)$ be the probability that a case is sampled and let $\rho_0 = P(Z = 1|y = 0)$ be the probability that a control is sampled.

In a simple random sample, $\rho_1 = P(Y = 1)$ and $\rho_0 = P(Y = 0) = 1 - \rho_1$.

Assume the logistic regression model

$$\pi(x) = P(Y_i = 1|x) = \frac{e^{\alpha+\beta x}}{1 + e^{\alpha+\beta x}}.$$

Case-control studies, cont.

Assume that the probability of choosing a case is independent of x, $P(Z=1|y=1,x)=P(Z=1|y=1)$ and the same for a control $P(Z=1|y=0,x)=P(Z=1|y=0)$. This is the case, for instance, when a fixed number of cases and controls are sampled retrospectively, regardless of their x values.

Bayes' rule gives us

$$\begin{aligned} P(Y=1|z=1,x) &= \frac{\rho_1\pi(x)}{\rho_1\pi(x)+\rho_0(1-\pi(x))} \\ &= \frac{e^{\alpha^*+\beta x}}{1+e^{\alpha^*+\beta x}}, \end{aligned}$$

where $\alpha^* = \alpha + \log(\rho_1/\rho_0)$.

The parameter β *has the same interpretation* in terms of odds ratios as with simple random sampling.

Comments

- This is very powerful & another reason why logistic regression is widely used.
- Other links (e.g. identity, probit) do not have this property.
- *Matched* case/controls studies require more thought; Chapter 11.
- 5.1.5 relates directly to ROC analysis where x is a diagnostic test score (e.g. ELISA) and Y indicates presence/absence of disease.

Consider the full model

$$\text{logit}\{\pi(\mathbf{x})\} = \beta_0 + \beta_1 x_1 + \cdots + \beta_{p-1} x_{p-1} = \mathbf{x}'\boldsymbol{\beta}.$$

Most types of inferences are functions of $\boldsymbol{\beta}$, say $g(\boldsymbol{\beta})$. Some examples:

- $g(\boldsymbol{\beta}) = \beta_j$, j^{th} regression coefficient.
- $g(\boldsymbol{\beta}) = e^{\beta_j}$, j^{th} odds ratio.
- $g(\boldsymbol{\beta}) = e^{\mathbf{x}'\boldsymbol{\beta}}/(1 + e^{\mathbf{x}'\boldsymbol{\beta}})$, probability $\pi(\mathbf{x})$.

If $\hat{\boldsymbol{\beta}}$ is the MLE of $\boldsymbol{\beta}$, then $g(\hat{\boldsymbol{\beta}})$ is the MLE of $g(\boldsymbol{\beta})$. This provides an estimate.

The *delta method* is an all-purpose method for obtaining a standard error for $g(\hat{\boldsymbol{\beta}})$.

Delta method

We know

$$\hat{\boldsymbol{\beta}} \overset{\bullet}{\sim} N_p(\boldsymbol{\beta}, \widehat{\text{cov}}(\hat{\boldsymbol{\beta}})).$$

Let $g(\boldsymbol{\beta})$ be a function from $\mathbb{R}^p$ to $\mathbb{R}$. Taylor's theorem implies, as long as the MLE $\hat{\boldsymbol{\beta}}$ is somewhat close to the true value $\boldsymbol{\beta}$, that

$$g(\boldsymbol{\beta}) \approx g(\hat{\boldsymbol{\beta}}) + [Dg(\hat{\boldsymbol{\beta}})](\boldsymbol{\beta} - \hat{\boldsymbol{\beta}}),$$

where $[Dg(\boldsymbol{\beta})]$ is the vector of first partial derivatives

$$Dg(\boldsymbol{\beta}) = \begin{bmatrix} \frac{\partial g(\boldsymbol{\beta})}{\partial \beta_1} \\ \frac{\partial g(\boldsymbol{\beta})}{\partial \beta_2} \\ \vdots \\ \frac{\partial g(\boldsymbol{\beta})}{\partial \beta_p} \end{bmatrix}.$$

Delta method

Then

$$(\hat{\boldsymbol\beta} - \boldsymbol\beta) \overset{\bullet}{\sim} N_p(\mathbf{0}, \widehat{\text{cov}}(\hat{\boldsymbol\beta})),$$

implies

$$[Dg(\boldsymbol\beta)]'(\hat{\boldsymbol\beta} - \boldsymbol\beta) \overset{\bullet}{\sim} N(0, [Dg(\boldsymbol\beta)]'\widehat{\text{cov}}(\hat{\boldsymbol\beta})[Dg(\boldsymbol\beta)]),$$

and finally

$$g(\hat{\boldsymbol\beta}) \overset{\bullet}{\sim} N(g(\boldsymbol\beta), [Dg(\hat{\boldsymbol\beta})]'\widehat{\text{cov}}(\hat{\boldsymbol\beta})[Dg(\hat{\boldsymbol\beta})]).$$

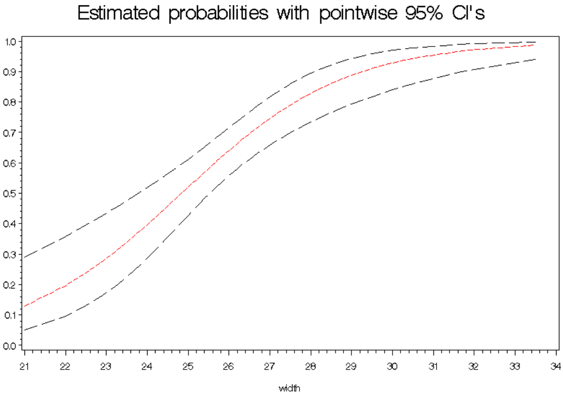
So

$$\text{se}\{g(\hat{\boldsymbol\beta})\} = \sqrt{[Dg(\hat{\boldsymbol\beta})]'\widehat{\text{cov}}(\hat{\boldsymbol\beta})[Dg(\hat{\boldsymbol\beta})]}.$$

This can be used to get confidence intervals for probabilities, etc.

Pointwise CIs for probability of success

```
proc logistic data=crabs1 descending;
 model y = width; output out=crabs2 pred=p lower=l upper=u;
proc sort data=crabs2; by width;
proc gplot data=crabs2;
 title "Estimated probabilities with pointwise 95% CI's";
 symbol1 i=join color=black; symbol2 i=join color=red line=3;
 symbol3 i=join color=black; axis1 label=('');
 plot (l p u)*width / overlay vaxis=axis1;
```



The deviance GOF statistic is defined to be

$$D = 2 \sum_{i=1}^{N} \left\{ y_i \log\left(\frac{y_i}{n_i \hat{\pi}_i}\right) + (n_i - y_i) \log\left(\frac{n_i - y_i}{n_i - n_i \hat{\pi}_i}\right) \right\},$$

where $\hat{\pi}_i = \frac{e^{\mathbf{x}_i' \hat{\beta}}}{1 + e^{\mathbf{x}_i' \hat{\beta}}}$ are fitted values.

Pearson's GOF statistic is

$$X^2 = \sum_{i=1}^{N} \frac{(y_i - n_i \hat{\pi}_i)^2}{n_i \hat{\pi}_i (1 - \hat{\pi}_i)}.$$

Both statistics are approximately χ^2_{N-p} in large samples assuming that the number of *trials* $n = \sum_{i=1}^{N} n_i$ increases in such a way that each n_i increases.

Group your data

Binomial data is often recorded as individual (Bernoulli) records:

i	y_i	n_i	x_i
1	0	1	9
2	0	1	14
3	1	1	14
4	0	1	17
5	1	1	17
6	1	1	17
7	1	1	20

Grouping the data yields an identical model:

i	y_i	n_i	x_i
1	0	1	9
2	1	2	14
3	2	3	17
4	1	1	20

- $\hat{\boldsymbol{\beta}}$, $\text{se}(\hat{\beta}_j)$, and $L(\hat{\boldsymbol{\beta}})$ don't care if data are grouped.
- The quality of residuals and GOF statistics *depend on how data are grouped*. D and Pearson's X^2 will change!

Comments

- In PROC LOGISTIC type AGGREGATE and SCALE=NONE after the MODEL statement to get D and X^2 based on grouped data. This option *does not* compute residuals based on the grouped data. You can aggregate over all variables or a subset, e.g. AGGREGATE=(width).
- The Hosmer and Lemeshow test statistic orders observations $(\mathbf{x}_i, Y_i)$ by fitted probabilities $\hat{\pi}(\mathbf{x}_i)$ from smallest to largest and divides them into (typically) $g = 10$ groups of roughly the same size. A Pearson test statistic is computed from these g groups.

Comments

- The statistic would have a χ^2_{g-p} distribution if each group had *exactly the same predictor* $\mathbf{x}$ for all observations. In general, the null distribution is *approximately* χ^2_{g-2} (see text). Termed a "near-replicate GOF test." The LACKFIT option in PROC LOGISTIC gives this statistic.
- Can also test $\text{logit}\{\pi(x)\} = \beta_0 + \beta_1 x$ versus more general model $\text{logit}\{\pi(x)\} = \beta_0 + \beta_1 x + \beta_2 x^2$ via $H_0 : \beta_2 = 0$.

Raw (Bernoulli) data with aggregate scale=none lackfit;

Deviance and Pearson Goodness-of-Fit Statistics

Criterion	Value	DF	Value/DF	Pr > ChiSq
Deviance	69.7260	64	1.0895	0.2911
Pearson	55.1779	64	0.8622	0.7761

Number of unique profiles: 66

Partition for the Hosmer and Lemeshow Test

		y = 1		y = 0	
Group	Total	Observed	Expected	Observed	Expected
1	19	5	5.39	14	13.61
2	18	8	7.62	10	10.38
3	17	11	8.62	6	8.38
4	17	8	9.92	9	7.08
5	16	11	10.10	5	5.90
6	18	11	12.30	7	5.70
7	16	12	12.06	4	3.94
8	16	12	12.90	4	3.10
9	16	13	13.69	3	2.31
10	20	20	18.41	0	1.59

Hosmer and Lemeshow Goodness-of-Fit Test

Chi-Square	DF	Pr > ChiSq
5.2465	8	0.7309

Comments

- There are 66 distinct widths $\{\mathbf{x}_i\}$ out of $N = 173$ crabs. For χ^2_{66-2} to hold, we must keep sampling crabs that only have one of the 66 *fixed number of widths*! Does that make sense here?
- The Hosmer and Lemeshow test gives a p-value of 0.73 based on $g = 10$ groups. Are assumptions going into this p-value met?
- None of the GOF tests have assumptions that are met in practice for continuous predictors. Are they still useful?
- The raw statistics do not tell you *where* lack of fit occurs. Deviance and Pearson residuals do tell you this (later). Also, the table provided by the H-L tells you which groups are ill-fit should you reject H_0 : logistic model holds.
- GOF tests are meant to detect *gross* deviations from model assumptions. No model ever truly fits data except hypothetically.

5.3 Categorical predictors

Let's say we wish to include variable X, a categorical variable that takes on values $x \in \{1, 2, \ldots, I\}$. We need to allow each level of $X = x$ to affect $\pi(x)$ differently. This is accomplished by the use of dummy variables. This is typically done one of two ways.

Define $z_1, z_2, \ldots, z_{I-1}$ as follows:

$$z_j = \begin{cases} 1 & X = j \\ -1 & X \neq j \end{cases}$$

This is the default in PROC LOGISTIC with a CLASS X statement. Say $I = 3$, then the model is

$$\text{logit } \pi(x) = \beta_0 + \beta_1 z_1 + \beta_2 z_2.$$

which gives

$$\begin{array}{lll} \text{logit } \pi(x) = \beta_0 + \beta_1 - \beta_2 & \text{when} & X = 1 \\ \text{logit } \pi(x) = \beta_0 - \beta_1 + \beta_2 & \text{when} & X = 2 \\ \text{logit } \pi(x) = \beta_0 - \beta_1 - \beta_2 & \text{when} & X = 3 \end{array}$$

Zero/One dummy variables

At alternative method uses "zero/one" dummies instead:

$$z_j = \begin{cases} 1 & X = j \\ 0 & X \neq j \end{cases}$$

This is the default if PROC GENMOD with a CLASS X statement. This can also be obtained in PROC LOGISTIC with the PARAM=REF option. This sets class $X = I$ as baseline. Say $I = 3$, then the model is

$$\text{logit } \pi(x) = \beta_0 + \beta_1 z_1 + \beta_2 z_2.$$

which gives

$$\begin{array}{lll} \text{logit } \pi(x) = \beta_0 + \beta_1 & \text{when} & X = 1 \\ \text{logit } \pi(x) = \beta_0 + \beta_2 & \text{when} & X = 2 \\ \text{logit } \pi(x) = \beta_0 & \text{when} & X = 3 \end{array}$$

SAS example

I prefer the latter method because it's easier to think about for me. You can choose a different baseline category with REF=FIRST next to the variable name in the CLASS statement. Table 3.8 (p. 89):

```
data mal;
 input cons present absent @@;
 total=present+absent;
 datalines;
 1 48 17066 2 38 14464 3 5 788 4 1 126 5 1 37
;
proc logistic;
 class cons / param=ref;
 model present/total = cons;
```

SAS output

Testing Global Null Hypothesis: BETA=0

Test	Chi-Square	DF	Pr > ChiSq
Likelihood Ratio	6.2020	4	0.1846
Score	12.0821	4	0.0168
Wald	9.2811	4	0.0544

Type 3 Analysis of Effects

Effect	DF	Wald Chi-Square	Pr > ChiSq
cons	4	9.2811	0.0544

Analysis of Maximum Likelihood Estimates

Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept		1	-3.6109	1.0134	12.6956	0.0004
cons	1	1	-2.2627	1.0237	4.8858	0.0271
cons	2	1	-2.3309	1.0264	5.1577	0.0231
cons	3	1	-1.4491	1.1083	1.7097	0.1910
cons	4	1	-1.2251	1.4264	0.7377	0.3904

Odds Ratio Estimates

Effect	Point Estimate	95% Wald Confidence Limits	
cons 1 vs 5	0.104	0.014	0.774
cons 2 vs 5	0.097	0.013	0.727
cons 3 vs 5	0.235	0.027	2.061
cons 4 vs 5	0.294	0.018	4.810

Interpretation

The model is

$$\text{logit}\, \pi(X) = \beta_0 + \beta_1 I\{X = 1\} + \beta_2 I\{X = 2\} + \beta_3 I\{X = 3\} + \beta_4 I\{X = 4\}$$

where X denotes alcohol consumption $X = 1, 2, 3, 4, 5$.

- Type 3 analyses test whether all dummy variables associated with a categorical predictor are simultaneously zero, here $H_0 : \beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$. If we accept this then the categorical predictor is not needed in the model.
- PROC LOGISTIC gives estimates and CIs for e^{β_j} for $j = 1, 2, 3, 4$. Here, these are interpreted as the odds of developing malformation when $X = 1, 2, 3$, or 4 versus the odds when $X = 5$.
- We are not as interested in the *individual* Wald tests $H_0 : \beta_j = 0$ for a categorical predictor. Why is that? Because they only compare a level $X = 1, 2, 3, 4$ to baseline $X = 5$, not to each other.

Comments

- The `Testing Global Null Hypothesis: BETA=0` are three tests that *no predictor* is needed; $H_0 : \text{logit}\{\pi(x)\} = \beta_0$ versus $H_1 : \text{logit}\{\pi(x)\} = \mathbf{x}'\boldsymbol{\beta}$. Anything wrong here? We'll talk about exact tests later.
- Note that the Wald test for $H_0 : \boldsymbol{\beta} = 0$ is the same as the Type III test that consumption is not important. Why is that?
- Let $Y = 1$ denote malformation for a randomly sampled individual. To get an odds ratio for malformation from increasing from, say, $X = 2$ to $X = 4$, note that

$$\frac{P(Y = 1|X = 2)/P(Y = 0|X = 2)}{P(Y = 1|X = 4)/P(Y = 0|X = 4)} = e^{\beta_2 - \beta_4}.$$

This is estimated with the CONTRAST command.