COMPLEMENTARY LOG-LOG MODEL

Under the assumption of binary response, there are two alternatives to logit model: probit model and complementary-log-log model. They all follow the same form

\[ \pi(x) = \Phi(\alpha + \beta x) \]  

for a continuous cdf \( \Phi \).

Complementary log-log model says \( \log\{-\log[1 - \pi(x)]\} = X^T \beta_{\text{probit}} \). The expression on the left-hand side is called Complementary Log-Log transformation. Like the logit and the probit transformation, the complementary log-log transformation takes a response restricted to the (0,1) interval and converts it into something in \((-\infty, +\infty)\) interval. Here, we need mentioned that the log of \(1-\pi(x)\) is always a negative number. This is changed to a positive number before taking the log a second time. We can also write the model down like form (1), as \( \pi(x) = 1 - \exp[-\exp(X^T \beta_{\text{probit}})] \).

Both logit and probit links have the same property, which is \( \text{link}[\pi(x)] = -\text{link}[1-\pi(x)] \). This means that the response curve for \( \pi(x) \) has a symmetric appearance about the point \( \pi(x) = 0.5 \) and so \( \pi(x) \) has the same rate for approaching 0 as well as for approaching 1. When the data given is not symmetric in the \([0,1]\) interval and increase slowly at small to moderate value but increases sharply near 1. The logit and probit models are inappropriate. However, in this situation, the complementary log-log model might give a satisfied answer.

Unlike logit and probit the complementary log-log model is asymmetrical, it is frequently used when the probability of an event is very small or very large. Under the assumption
that the general features are not lost, let us only consider a simple complementary log-log model with one predictor \( \pi(x) = 1 - \exp[-\exp(\alpha + \beta x)] \) in the report left. The response has an S-shaped curve, it approach 0 fairly slowly but approaching 1 quite sharply, when \( \beta > 0 \).

Since the log-log applies to the complement of \( \pi(x) \), the link for this GLM is called the complementary log-log link.

From the three-model comparison plot above, we also can get more information. All link function are increasing, continuous, and differentiable over \( 0 < p < 1 \), the logit and probit are almost linearly related over the interval \( p \in [0.1, 0.9] \). For small \( p \), the complementary log-log close to logit. The complementary log-log approaches 0 infinitely slower than any other link function.

Because logit and probit models are symmetrical, reversing the coding of the dependent variable (from 0,1 to 1,0) only change the sign of the coefficients \( \log[\pi(x)] = -\log[1 - \pi(x)] \). For the complementary log-log model, on the other hand, reversing the coding can give us completely different results. It is crucial to setup the model to predict the probability of an event, not the absence of the event.

Now let us talk more details about complementary log-log model \( \pi(x) = 1 - \exp[-\exp(\alpha + \beta x)] \). To interpret it, we note that at \( x_1 \) and \( x_2 \) two predictors’ points, we have \( \log[-\log(1 - \pi(x_1))] - \log[-\log(1 - \pi(x_2))] = \beta (x_1 - x_2) \), so that

\[
\frac{\log[1 - \pi(x_i)]}{\log[1 - \pi(x_i) - \beta (x_2 - x_1)]} = \exp[\beta (x_2 - x_1)]
\]

and

\[
1 - \pi(x_i) = [1 - \pi(x_i)]^{\exp[\beta (x_2 - x_1)]}
\]
For $x_2 - x_1 = 1$, the complement probability at $x_2$ equals the complement probability at $x_1$ raised to the power $\exp(\beta)$.

Here, we will give out another related model $\pi(x) = \exp[-\exp(\alpha + \beta x)]$, it is called log-log model. For it, $\pi(x)$ approaches 0 sharply but approaches 1 slowly. As $x$ increases, the curve is monotone decreasing when $\beta > 0$, and monotone increasing when $\beta < 0$. in GLM form it uses the log-log link $\log[-\log(\pi(x))] = \alpha + \beta x$. When the complementary log-log model holds for the probability of a success, the log-log model holds for the probability of a failure.

Most data can be modeled well by either logit or probit model. Why should we ever want an asymmetrical model? Because the complementary log-log model is closely related to continuous-time models for the occurrence of events., so it has an important application in the area of survival analysis. Here, we just talk about a specific case with binary response.

Survival analysis with binary response model

In toxicology, binary response models describe the effect of dosage of a toxin on whether a subject dies. The tolerance distribution provides justification for model $\pi(x) = \Phi(\alpha + \beta x)$. Let $x$ denote the dosage level. For a randomly selected subject, let $Y=1$ if the subject dies. Suppose that the subject has tolerance $T$ for the dosage, with $(Y=1)$ equivalent to $(T \leq x)$. For instance, an insect survive if the dosage $x$ is less than $T$ and Dies if the dosage is at least $T$. Tolerances vary among subjects, and let
F(t) = P(T ≤ t). For fixed dosage x, the probability a randomly selected subject dies is
\[ π(x) = P(Y = 1| X=x) = P(T ≤ x) = F(x) \]
That is the appropriate binary model is the one having the shape of the cdf F of the
tolerance distribution. Let \( Φ \) denote the standard cdf for the family to which F belongs.
A common standardization uses the mean and standard deviation of T, so that
\[ π(x) = F(x) = \Phi\left(\frac{x - μ}{σ}\right) \]
Then, the model has form \( π(x) = Φ(α + βx) \).
Let us use the beetle data as an example.

Beetles Killed after Exposure to Carbon Disulfide

<table>
<thead>
<tr>
<th>Log Dose</th>
<th>Number of Beetles</th>
<th>Number Killed</th>
<th>Fitted Values</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Comp. Log-Log</td>
</tr>
<tr>
<td>1.691</td>
<td>59</td>
<td>6</td>
<td>5.7</td>
</tr>
<tr>
<td>1.724</td>
<td>60</td>
<td>13</td>
<td>11.3</td>
</tr>
<tr>
<td>1.755</td>
<td>62</td>
<td>18</td>
<td>20.9</td>
</tr>
<tr>
<td>1.784</td>
<td>56</td>
<td>28</td>
<td>30.3</td>
</tr>
<tr>
<td>1.811</td>
<td>63</td>
<td>52</td>
<td>47.7</td>
</tr>
<tr>
<td>1.837</td>
<td>59</td>
<td>53</td>
<td>54.2</td>
</tr>
<tr>
<td>1.861</td>
<td>62</td>
<td>61</td>
<td>61.1</td>
</tr>
<tr>
<td>1.884</td>
<td>60</td>
<td>60</td>
<td>59.9</td>
</tr>
</tbody>
</table>

In the table, we find that the underlying cdf of number killed increases moderately before
x=1.811, then there is a big jump on the number of beetles killed.

SAS result:
For logistic proc:

```
the logit model for beetles data
21:41 Sunday, March 14, 2004

The LOGISTIC Procedure

Model Fit Statistics

<table>
<thead>
<tr>
<th>Intercept</th>
<th>Only</th>
<th>Covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AIC</td>
<td>647.441</td>
<td>376.354</td>
</tr>
<tr>
<td>SC</td>
<td>651.817</td>
<td>384.706</td>
</tr>
<tr>
<td>-2 Log L</td>
<td>645.441</td>
<td>372.354</td>
</tr>
</tbody>
</table>

Testing Global Null Hypothesis: BETA=0

<table>
<thead>
<tr>
<th>Test</th>
<th>Chi-Square</th>
<th>DF</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Likelihood Ratio</td>
<td>273.0869</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Score</td>
<td>227.5973</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Wald</td>
<td>138.5112</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

The LOGISTIC Procedure

Analysis of Maximum Likelihood Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Standard Wald</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estimate</td>
<td>Error</td>
<td>Chi-Square</td>
</tr>
</tbody>
</table>
```
the complementary log log model for beetles data

The LOGISTIC Procedure

Model Fit Statistics

<table>
<thead>
<tr>
<th>Criterion</th>
<th>Intercept Only</th>
<th>Intercept and Covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIC</td>
<td>647.441</td>
<td>368.753</td>
</tr>
<tr>
<td>SC</td>
<td>651.617</td>
<td>377.105</td>
</tr>
<tr>
<td>-2 Log L</td>
<td>645.441</td>
<td>364.753</td>
</tr>
</tbody>
</table>

Testing Global Null Hypothesis: BETA=0

<table>
<thead>
<tr>
<th>Test</th>
<th>Chi-Square</th>
<th>DF</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Likelihood Ratio</td>
<td>280.6881</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Score</td>
<td>227.5973</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Wald</td>
<td>150.0854</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Analysis of Maximum Likelihood Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Standard Estimate</th>
<th>Wald Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>-39.5224</td>
<td>3.2356</td>
<td>149.1990</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>logdose</td>
<td>1</td>
<td>22.0148</td>
<td>1.7970</td>
<td>150.0854</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

the probit model for beetles data

The LOGISTIC Procedure

Model Fit Statistics

<table>
<thead>
<tr>
<th>Criterion</th>
<th>Intercept Only</th>
<th>Intercept and Covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIC</td>
<td>647.441</td>
<td>375.226</td>
</tr>
<tr>
<td>SC</td>
<td>651.617</td>
<td>383.577</td>
</tr>
<tr>
<td>-2 Log L</td>
<td>645.441</td>
<td>371.226</td>
</tr>
</tbody>
</table>

Testing Global Null Hypothesis: BETA=0

<table>
<thead>
<tr>
<th>Test</th>
<th>Chi-Square</th>
<th>DF</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Likelihood Ratio</td>
<td>274.2155</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Score</td>
<td>227.5973</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Wald</td>
<td>157.9925</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Analysis of Maximum Likelihood Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Standard Estimate</th>
<th>Wald Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>-34.9557</td>
<td>2.6490</td>
<td>174.1309</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>
logdose       1     19.7408      1.4880      175.9925        <.0001

For logistic proc:

The SAS System        23:18 Monday, March 15, 2004   4

The GENMOD Procedure

Model Information

Data Set                      WORK.BEETLES1
Distribution                       Binomial
Link Function                        Probit
Response Variable (Events)          nkilled
Response Variable (Trials)         nbeetles
Observations Used                         8
Number Of Events                          291
Number Of Trials                         481

Criteria For Assessing Goodness Of Fit

Criterion                 DF           Value        Value/DF
Deviance                   6          9.9870          1.6645
Scaled Deviance            6          9.9870          1.6645
Pearson Chi-Square         6          9.3690          1.5615
Scaled Pearson X2          6          9.3690          1.5615
Log Likelihood                     -185.6128
Algorithm converged.

Analysis Of Parameter Estimates

Standard     Wald 95% Confidence       Chi-
Parameter    DF    Estimate       Error           Limits            Square    Pr > ChiSq
Intercept     1    -34.9561      2.6413    -40.1330    -29.7793     175.15        <.0001
logdose       1     19.7410      1.4853     16.8300     22.6521     176.66        <.0001
Scale         0      1.0000      0.0000      1.0000      1.0000

NOTE: The scale parameter was held fixed.

--------------------------------------------------------------------------------------------------------------------

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The GENMOD Procedure

Model Information

Data Set                      WORK.BEETLES1
Distribution                       Binomial
Link Function                           CLL
Response Variable (Events)          nkilled
Response Variable (Trials)         nbeetles
Observations Used                         8
Number Of Events                          291
Number Of Trials                         481

Criteria For Assessing Goodness Of Fit

Criterion                 DF           Value        Value/DF
Deviance                   6          3.5143          0.5857
Scaled Deviance            6          3.5143          0.5857
Pearson Chi-Square         6          3.3592          0.5599
Scaled Pearson X2          6          3.3592          0.5599
Log Likelihood                     -182.3765
Algorithm converged.

Analysis Of Parameter Estimates

Standard     Wald 95% Confidence       Chi-
Parameter    DF    Estimate       Error           Limits            Square    Pr > ChiSq
Intercept     1    -39.5223      3.2229    -45.8391    -33.2055     150.38        <.0001
logdose       1     22.0148      1.7899     18.5067     25.5228     176.66        <.0001
Scale         0      1.0000      0.0000      1.0000      1.0000

NOTE: The scale parameter was held fixed.

--------------------------------------------------------------------------------------------------------------------

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The GENMOD Procedure
Model Information
Data Set                      WORK.BEETLES1
Distribution                       Binomial
Link Function                         Logit
Response Variable (Events)          nkilled
Response Variable (Trials)         nbeetles
Observations Used                         8
Number Of Events                        291
Number Of Trials                        481

Criteria For Assessing Goodness Of Fit
Criterion                 DF           Value        Value/DF
Deviance                   6         11.1156          1.8526
Scaled Deviance            6         11.1156          1.8526
Pearson Chi-Square         6          9.9067          1.6511
Scaled Pearson X2          6          9.9067          1.6511
Log Likelihood                     -186.1771
Algorithm converged.

Analysis Of Parameter Estimates
Standard     Wald 95% Confidence       Chi-
Parameter    DF    Estimate       Error           Limits            Square    Pr > ChiSq
Intercept     1    -60.7401      5.1819    -70.8964    -50.5838     137.40        <.0001
logdose       1     34.2859      2.9132     28.5761     39.9957     138.51        <.0001
Scale         0      1.0000      0.0000      1.0000      1.0000

NOTE: The scale parameter was held fixed.

SAS plot:

For the beetles mortality data, the complementary log-log model has ML estimate model
\[ \log[-\log(1-\pi(x))] = -39.5224 + 22.0148 \times \text{logdose} \]. At dosage=1.7 the fitted probability
of survival is $1 - \pi(x) = \exp[-\exp(-39.5224 + 22.0148 \times 1.7)] = 0.884445$ where at dosage = 1.8 it is 0.3296029, and at dosage = 1.9, it is 4.39966e-05, the probability of survival at dosage + 0.1 equals the probability at dosage raised to the power $\exp(22.0148 \times 0.1) = 9.03838$. For instance, 0.3296029 $\approx (0.884445)^{9.03838}$ (0.3296027 $\approx (0.884445)^{9.03838}$)

Underlying the LOGISTIC proc:

<table>
<thead>
<tr>
<th>Model</th>
<th>intercept</th>
<th>logdose</th>
<th>Standard Error</th>
<th>AIC with Intercept and Covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td>logit</td>
<td>-60.7339</td>
<td>34.2824</td>
<td>5.1814/2.9129</td>
<td>376.354</td>
</tr>
<tr>
<td>probit</td>
<td>-34.9557</td>
<td>19.7408</td>
<td>2.6490/1.4880</td>
<td>375.226</td>
</tr>
<tr>
<td>Complementary log-log</td>
<td>-39.5224</td>
<td>22.0148</td>
<td>3.2356/1.7970</td>
<td>368.753</td>
</tr>
</tbody>
</table>

Underlying the GENMOD proc:

<table>
<thead>
<tr>
<th>Model</th>
<th>intercept</th>
<th>logdose</th>
<th>Standard Error</th>
<th>Deviance-G^2</th>
<th>DF</th>
</tr>
</thead>
<tbody>
<tr>
<td>logit</td>
<td>-60.7401</td>
<td>34.2859</td>
<td>5.1819/2.9132</td>
<td>11.1156</td>
<td>6</td>
</tr>
<tr>
<td>probit</td>
<td>-34.9561</td>
<td>19.7410</td>
<td>2.6413/1.4853</td>
<td>9.9870</td>
<td>6</td>
</tr>
</tbody>
</table>

From the table we can find that under logistic proc, complementary log-log has the smallest AIC = 368.753, under Genmod proc, it is still complementary log-log that has the smallest $G^2 = 3.5143$.

The last few things I need mentioned are there are
The reason is that GENMOD uses the Newton-Raphson algorithm to get the ML estimates, and LOGISTIC uses iteratively reweighed least squares(also called Fisher scoring), these two algorithms are equivalent for logit models but diverge for any other model.(That is because logit is the unique “canonical” link function).
(With the coefficients, we can see with the one unit change on x, the logit will
Finally, we need mentioned that complementary log-log model is not only used for binary respond but also can be used for ordinal responses with cumulative link, the form is 
\[
\log\{-\log[1 - P(Y \leq j | x)]\} = \alpha_j + \beta^T x
\]
and the ordinal model using this link is sometimes called a Proportional hazards model for survival data to handle grouped survival times.

proof for symmetric property of logit distribution and probit model:
\[
\text{logit}\left(\pi(x)\right) = \log\left(\frac{\pi(x)}{1 - \pi(x)}\right)
\]
\[
= -\log\left(\frac{1 - \pi(x)}{\pi(x)}\right)
\]
\[
= -\text{logit}\left[1 - \pi(x)\right]
\]
\[
\Phi^{-1}[\pi(x)] = \alpha + \beta x
\]
\[
\Phi^{-1}[1 - \pi(x)] = -(\alpha + \beta x)
\]
\[
\Phi^{-1}[\pi(x)] = -\Phi^{-1}[1 - \pi(x)]
\]
\[
\log\{-\log[\pi(x)]\} = \log\{-\log(1 - \exp[-\exp(\alpha + \beta x)])\}
\]

The model says that
for large p, log-log close to logit

/*************storage plant****************************/
\[
F(x) = \exp\{-\exp[-(x-a)/b]\}
\]
\[
\begin{align*}
\log[-\log(1-\pi(x_i))] - \log[-\log(1-\pi(x_j))] &= \beta(x_j - x_i) \\
\log[1-\pi(x_i)] &= \exp[\beta(x_j - x_i)] \\
1 - \pi(x_i) &= [1-\pi(x_i)]^{\exp[\beta(x_j - x_i)]} \\
\text{link}[^\pi](x) &= -\text{link}[1-\pi(x)] \\
\pi(x) &= \exp[-\exp(\alpha+\beta x)] \\
\log[-\log(1-\pi(x)) &= \alpha + \beta x \\
F(x) &= \exp\{-\exp[-(x-a)/b]\} \\
x_j - x_i &= 1 \\
\pi(x) &= \exp[-\exp(\alpha + \beta x)] \\
F(t) &= P(T \leq t) \\
\pi(x) &= P(Y=1|X=x) = P(T \leq x) = F(x) \\
\Phi \\
\pi(x) &= F(x) = \Phi[(x - \mu)/\sigma] \\
\pi(x) &= 1 - \exp[-\exp(\alpha + \beta x)] \\
\pi(x) &= 1 - \exp[-\exp(\alpha + \beta x)] \\
\text{link}[^\pi](x) &= -\text{link}[1-\pi(x)] \\
\logit[^\pi](x) &= \log[\pi(x)/(1-\pi(x))] \\
&= -\log[(1-\pi(x))/\pi(x)] \\
&= -\text{logit}[1-\pi(x)] \\
\log[-\log(\pi(x))] &= \beta^T x \\
p &\in [0.1, 0.9] \\
\pi(x) &= 1 - \exp[-\exp(X_{p}\times\beta_{p,x})] \\
&(-\infty, +\infty) \\
1 - \pi(x) &= \exp[-\exp(-39.5224+22.0148+1.7)] \\
\exp(\beta) \\
\Phi^{-1}[\pi(x)] &= \alpha + \beta x \\
\Phi^{-1}[1-\pi(x)] &= -(\alpha + \beta x) \\
\Phi^{-1}[\pi(x)] &= -\Phi^{-1}[1-\pi(x)] \\
\log \{-\log(\pi(x))\} &= \log \{-\log(1-\exp[-\exp(\alpha+\beta x)])\} \\
\log[-\log(1-\pi(x))] &= -39.5224 + 22.0148 \times \log\text{dose} \\
\text{Exp}(22.0148 \times 0.1) &= 9.03838 \\
0.3296029 &\approx (0.884445)^{9.03838} \\
0.3296027 &=(0.884445)^{9.03838} \\
\text{Deviance-G}^2 &= 3.5143 \\
\log \{-\log[1-P(Y \leq j \mid x)]\} = \alpha_j + \beta^T x
\end{align*}
\]
\[
\log[-\log(1 - \pi(x_2))] - \log[-\log(1 - \pi(x_1))] = \beta(x_2 - x_1)
\]
\[
\frac{\log[1 - \pi(x_2)]}{\log[1 - \pi(x_1)]} = \exp[\beta(x_2 - x_1)]
\]
\[
1 - \pi(x_2) = [1 - \pi(x_1)]^{\exp[\beta(x_2 - x_1)]}
\]
\[
\text{link}[\pi(x)] = -\text{link}[1 - \pi(x)]
\]
\[
\pi(x) = \exp[-\exp(\alpha + \beta x)]
\]
\[
\log[-\log(\pi(x))] = \alpha + \beta x
\]
\[
F(x) = \exp[-\exp(-(x-a)/b)]
\]
\[
x_2 - x_1 = 1
\]
\[
\pi(x) = \exp[-\exp(\alpha + \beta x)]
\]
\[
F(t) = P(T \leq t)
\]
\[
\pi(x) = P(Y=1 | X=x) = P(T \leq x) = F(x)
\]
\[
\Phi
\]
\[
\pi(x) = F(x) = \Phi\left[(x - \mu) / \sigma\right]
\]
\[
\pi(x) = 1 - \exp[-\exp(\alpha + \beta x)]
\]
\[
\text{link}[\pi(x)] = -\text{link}[1 - \pi(x)]
\]
\[
\logit[\pi(x)] = \log[\pi(x)/(1 - \pi(x))]
\]
\[
= -\log[(1 - \pi(x))/\pi(x)]
\]
\[
= -\log[1 - \pi(x)]
\]
\[
\log[-\log(\pi(x))] = \beta^T x
\]
\[
p \in [0.1, 0.9]
\]
\[
\pi(x) = 1 - \exp[-\exp(X^T_{p \times n} \beta_{p \times 1})]
\]
\[(-\infty, +\infty)\]

/*****************************/
APPENDIX I

- For logistic proc

/*the begin of sas code
the code is used for two goal, so there is some result
that got from it and use it back to the code again fro plotting
*/

```sas
data beetles1;
input logdose nbeetles nkilled;
nsurvive=nbeetles-nkilled;/*for sample proportion*/
rprob1=nkilled/nbeetles;/*for logit model*/
ylogit=exp(-60.7339+34.2824*logdose)/(1+exp(-60.7339+34.2824*logdose));/*for complementary log log*/
ycll=1-exp(-exp(-39.5224+22.0148*logdose));
datalines;
1.691 59 6
1.724 60 13
1.755 62 18
1.784 56 28
1.811 63 52
1.837 59 53
1.861 62 61
1.884 60 60;
/****using logistic proc for test comparing the three kinds of model */
proc logistic data= beetles1; /*for logit*/
model nkilled/nbeetles = logdose;
title 'the logit model for beetles data';

proc logistic data= beetles1; /*for cloglog*/
model nkilled/nbeetles = logdose / link=cloglog OUTROC=cllplotd;
title 'the complementary log log model for beetles data';

proc logistic data= beetles1; /*for probit*/
model nkilled/nbeetles = logdose / link=probit;
title 'the probit model for beetles data';
/*plot a curve*/
symbol1 color=red value=star interpol=NONE height=1 width=1;
symbol2 color=green value=plus interpol=spline height=1 width=1;
symbol3 color=blue value=DIAMOND interpol=spline height=1 width=1;
proc gplot data=beetles1;
plot rprob1*logdose ylogit*logdose ycll*logdose/haxis=1.65 to 1.90 by .05 overlay legend=legend2;
title 'sample proportion, cll and logit model comparison';
```

/*the end of sas code
run;
/***the end of using logistic for test comparing the three kind of model  */
/*/the end of sas code*/

/*result begin*/
/*/for logistic proc*/

the logit model for beetles data                            31
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The LOGISTIC Procedure

Model Information

Data Set WORK.BEETLES1
Response Variable (Events) nkilled
Response Variable (Trials) nbeetles
Number of Observations 8
Model binary logit
Optimization Technique Fisher's scoring

Response Profile

Ordered Binary Total
Value Outcome Frequency
1 Event 291
2 Nonevent 190

Model Convergence Status

Convergence criterion (GCONV=1E-8) satisfied.

Model Fit Statistics

<table>
<thead>
<tr>
<th>Criterion</th>
<th>Intercept Only</th>
<th>Intercept and Covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIC</td>
<td>647.441</td>
<td>376.354</td>
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<tr>
<td>SC</td>
<td>651.617</td>
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Testing Global Null Hypothesis: BETA=0

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<th>Test</th>
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<td>Score</td>
<td>227.5973</td>
<td>1</td>
<td>&lt;.0001</td>
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<tr>
<td>Wald</td>
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<td>&lt;.0001</td>
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the logit model for beetles data                            32
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The LOGISTIC Procedure

Analysis of Maximum Likelihood Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Standard Coef</th>
<th>Wald Chisq</th>
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Odds Ratio Estimates

<table>
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<th>Effect</th>
<th>Point Estimate</th>
<th>95% Wald Confidence Limits</th>
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the logit model for beetles data                            33
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The LOGISTIC Procedure

Analysis of Maximum Likelihood Estimates

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<tr>
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<td>logdose</td>
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Odds Ratio Estimates

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<th>Effect</th>
<th>Point Estimate</th>
<th>95% Wald Confidence Limits</th>
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<tr>
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the logit model for beetles data                            34
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The LOGISTIC Procedure

Analysis of Maximum Likelihood Estimates

<table>
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<th>Pr &gt; Chisq</th>
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<td>138.5112</td>
<td>&lt;.0001</td>
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Odds Ratio Estimates

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<th>Point Estimate</th>
<th>95% Wald Confidence Limits</th>
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</table>
Association of Predicted Probabilities and Observed Responses

Percent Concordant  87.0  Somers' D  0.802
Percent Discordant  6.8  Gamma  0.856
Percent Tied  6.3  Tau-a  0.384
Pairs  55290  c  0.901

The LOGISTIC Procedure

Model Information

Data Set WORK.BEETLES1
Response Variable (Events) nkilled
Response Variable (Trials) nbeetles
Number of Observations 8
Model binary cloglog
Optimization Technique Fisher's scoring

Response Profile

Ordered     Binary           Total
Value     Outcome      Frequency
1     Event              291
2     Nonevent           190

Model Convergence Status

Convergence criterion (GCONV=1E-8) satisfied.

Model Fit Statistics

<table>
<thead>
<tr>
<th></th>
<th>Intercept</th>
<th>Only</th>
<th>Covariates</th>
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Testing Global Null Hypothesis: BETA=0

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<td>Wald</td>
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Analysis of Maximum Likelihood Estimates

<table>
<thead>
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<th>Standard DF Estimate</th>
<th>Wald Chi-Square</th>
<th>Pr &gt; ChiSq</th>
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Association of Predicted Probabilities and Observed Responses

Percent Concordant  87.0  Somers' D  0.802
Percent Discordant  6.8  Gamma  0.856
Percent Tied  6.3  Tau-a  0.384
Pairs  55290  c  0.901

The LOGISTIC Procedure
The LOGISTIC Procedure

Model Information
Data Set WORK.BEETLES1
Response Variable (Events) nkilled
Response Variable (Trials) nbeetles
Number of Observations 8
Model binary probit
Optimization Technique Fisher's scoring

Response Profile

<table>
<thead>
<tr>
<th>Ordered</th>
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<td>Value</td>
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<tr>
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<td>291</td>
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<tr>
<td>2</td>
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<td>190</td>
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</table>

Model Convergence Status
Convergence criterion (GCONV=1E-8) satisfied.

Model Fit Statistics

<table>
<thead>
<tr>
<th>Criterion</th>
<th>Intercept Only</th>
<th>Intercept and Covariates</th>
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<tr>
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Testing Global Null Hypothesis: BETA=0

<table>
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<th>DF</th>
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<tr>
<td>Wald</td>
<td>175.9925</td>
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the probit model for beetles data

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The LOGISTIC Procedure
Analysis of Maximum Likelihood Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Wald Chi-Square</th>
<th>Pr &gt; ChiSq</th>
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Association of Predicted Probabilities and Observed Responses

<table>
<thead>
<tr>
<th>Percent Concordant</th>
<th>Somers' D</th>
<th>Percent Discordant</th>
<th>Gamma</th>
<th>Percent Tied</th>
<th>Tau-a</th>
<th>Pairs</th>
<th>c</th>
<th>0.901</th>
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<tbody>
<tr>
<td>87.0</td>
<td>0.802</td>
<td>6.8</td>
<td>0.856</td>
<td>6.3</td>
<td>0.384</td>
<td>55290</td>
<td>c</td>
<td>0.901</td>
</tr>
</tbody>
</table>

• For Genmod Proc
/*the begin of sas code*/
data beetles1;
input logdose nbeetles nkilled;
datalines;
1.691 59 6
1.724 60 13
1.755 62 18
1.784 56 28
1.811 63 52
1.837 59 53
1.861 62 61
1.884 60 60
;
/*the end of sas code*/

proc genmod data= beetles1;
  model nkilled/nbeetles= logdose /dist=bin link=probit;

proc genmod data= beetles1;
  model nkilled/nbeetles= logdose /dist=bin link=cloglog;

proc genmod data= beetles1;
  model nkilled/nbeetles= logdose /dist=bin link=logit;
quit;
run;
/***the end of using genmode for test comparing the three kind of model */

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The GENMOD Procedure
Model Information
  Data Set                      WORK.BEETLES1
  Distribution                       Binomial
  Link Function                        Probit
  Response Variable (Events)          nkilled
  Response Variable (Trials)         nbeetles
  Observations Used                         8
  Number Of Events                        291
  Number Of Trials                        481

Criteria For Assessing Goodness Of Fit
  Criterion                 DF           Value        Value/DF
    Deviance                   6          9.9870          1.6645
    Scaled Deviance            6          9.9870          1.6645
    Pearson Chi-Square         6          9.3690          1.5615
    Scaled Pearson X2          6          9.3690          1.5615
    Log Likelihood             6  -185.6128

Algorithm converged.
Analysis Of Parameter Estimates
  Standard     Wald 95% Confidence       Chi-
  Parameter    DF    Estimate       Error           Limits            Square    Pr > ChiSq
    Intercept     1    -34.9561      2.6413    -40.1330    -29.7793     175.15        <.0001
    logdose       1     19.7410      1.4853     16.8300     22.6521     176.66        <.0001
    Scale         0      1.0000      0.0000      1.0000      1.0000

NOTE: The scale parameter was held fixed.

The SAS System 23:18 Monday, March 15, 2004 5
The GENMOD Procedure
Model Information
  Data Set                      WORK.BEETLES1
  Distribution                       Binomial
  Link Function                        CLL
  Response Variable (Events)          nkilled
Response Variable (Trials)         nbeetles
Observations Used                         8
Number Of Events                        291
Number Of Trials                        481

Criteria For Assessing Goodness Of Fit

<table>
<thead>
<tr>
<th>Criterion</th>
<th>DF</th>
<th>Value</th>
<th>Value/DF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Deviance</td>
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<td>Pearson Chi-Square</td>
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<td>Log Likelihood</td>
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Algorithm converged.

Analysis Of Parameter Estimates

<table>
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<tr>
<th>Parameter</th>
<th>DF</th>
<th>Standard Estimate</th>
<th>Wald 95% Confidence Limits</th>
<th>Chi-Square</th>
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NOTE: The scale parameter was held fixed.

The SAS System         23:18 Monday, March 15, 2004   6
The GENMOD Procedure
Model Information
Data Set                      WORK.BEETLES1
Distribution                       Binomial
Link Function                         Logit
Response Variable (Events)          nkilled
Response Variable (Trials)         nbeetles
Observations Used                         8
Number Of Events                        291
Number Of Trials                        481

Criteria For Assessing Goodness Of Fit

<table>
<thead>
<tr>
<th>Criterion</th>
<th>DF</th>
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Algorithm converged.

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NOTE: The scale parameter was held fixed.

Reference:
LOGISTIC REGRESSION USING THE SAS SYSTEM
Theory and Application
--Paul D. Allison

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