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 \( \log\{-\log[1-\pi(x)]\} = X_p^T \beta_{p1} \). 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 \( \pi(x) = 1 - \exp[-\exp(X_p^T \beta_{p1})] \).

Both logit and probit links have the same property, which is link[\(\pi(x)\)] = 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 ($\ln[\pi(x)]=\ln[1-\pi(x)]$). 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 $\log[-\log(1-\pi(x_1))] - \log[-\log(1-\pi(x_2))]=\beta(x_2-x_1)$, so that

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

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 \leq t). For fixed dosage x, the probability a randomly selected subject dies is 
\pi(x)=P(Y=1| X=x)=P(T \leq x)=F(x)

That is the appropriate binary model is the one having the shape of the cdf F of the tolerance distribution. Let \Phi denote the standard cdf for the family to which F belongs. A common standardization uses the mean and standard deviation of T, so that 
\pi(x)=F(x)=\Phi[(x - \mu)/\sigma]
Then, the model has form \pi(x)=\Phi(\alpha+\beta x).

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**

The LOGISTIC Procedure

Model Fit Statistics

<table>
<thead>
<tr>
<th></th>
<th>Intercept Only</th>
<th>Covariates</th>
</tr>
</thead>
<tbody>
<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>Standard Parameter</th>
<th>Wald DF</th>
<th>Wald Estimate</th>
<th>Wald Error</th>
<th>Wald Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></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>

The LOGISTIC Procedure

#### Analysis of Maximum Likelihood Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>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>175.9925</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>Estimate</th>
<th>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>
For logistic proc:

```
logdose 1 19.7408 1.4880 175.9925 <.0001
```

For logistic proc:
```
For logistic proc:

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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 -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.
```

For logistic proc:
```
For logistic proc:

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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 3.5992 0.5599
Scaled Pearson X2 6 3.5992 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 175.15 <.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.
```

For logistic proc:
```
For logistic proc:

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The GENMOD Procedure
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 
$$\hat{\pi}(x) = \exp[-\exp(-39.5224 + 22.0148 \times 1.7)] = 0.884445$$
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 ≈ (0.884445)^{9.03838} (0.3296027 = (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 to mention that the complementary log-log model is not only used for binary response 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:

$$\text{logit}[\pi(x)] = \log[\pi(x)/(1-\pi(x))]$$

$$= -\log[(1-\pi(x))/\pi(x)]$$

$$= -\logit[1-\pi(x)]$$

$$\Phi^{-1}[\pi(x)] = \alpha + \beta x$$

$$\Phi^{-1}[1 - \pi(x)] = -\Phi^{-1}[\pi(x)]$$

$$\Phi^{-1}[\pi(x)] = -\Phi^{-1}[1 - \pi(x)]$$

$$\log\{-\log[\pi(x)]\} = \log\{-\log[1-\exp(\alpha + \beta x)]\}$$

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

F(x) = \exp\{-\exp[-(x-a)/b]\}
\[
\log[-\log(1-\pi(x_i))] - \log[-\log(1-\pi(x_j))] = \beta(x_j - x_i)
\]

\[
\log[1-\pi(x_i)] = \exp[\beta(x_j - x_i)]
\]

\[
1 - \pi(x_i) = [1 - \pi(x_j)]^{\exp[\beta(x_j - x_i)]}
\]

\[
\text{link}[\pi(x)] = -\text{link}[1-\pi(x)]
\]

\[
\pi(x) = \exp[-\exp(\alpha+\beta x)]
\]

\[
\log[-\log(1-\pi(x))] = \alpha+\beta x
\]

\[
F(x) = \exp\{-\exp[-(x-a)/b]\}
\]

\[
x_j - x_i = 1
\]

\[
\pi(x) = \exp[-\exp(\alpha+\beta x)]
\]

\[
F(t) = P(T \leq t)
\]

\[
\pi(x) = P(Y=1|X=x) = P(T \leq x) = F(x)
\]

\[
\Phi
\]

\[
\pi(x) = F(x) = \Phi[(x - \mu)/\sigma]
\]

\[
\pi(x) = 1 - \exp[-\exp(\alpha+\beta x)]
\]

\[
\pi(x) = [1 - \exp(-\exp(\alpha+\beta x))]
\]

\[
\text{link}[\pi(x)] = -\text{link}[1-\pi(x)]
\]

\[
\logit[\pi(x)] = \log[\pi(x)/(1-\pi(x))]
\]

\[
= -\log[(1-\pi(x))/\pi(x)]
\]

\[
= -\log[-\log(1-\exp[-\exp(\alpha+\beta x)])]
\]

\[
\log[-\log(\pi(x))] = \beta^T x
\]

\[
p \in [0.1 \ 0.9]
\]

\[
\pi(x) = 1 - \exp[-\exp(X_{psn}^T \beta_{psn})]
\]

\[
(-\infty, +\infty)
\]

\[
1 - \pi(x) = \exp[-\exp(-39.5224+22.0148 \times 1.7)]
\]

\[
\exp(\beta)
\]

\[
\Phi^{-1}[\pi(x)] = \alpha+\beta x
\]

\[
\Phi^{-1}[1 - \pi(x)] = -(\alpha+\beta x)
\]

\[
\Phi^{-1}[\pi(x)] = -\Phi^{-1}[1 - \pi(x)]
\]

\[
\log \{-\log(1-\exp[-\exp(\alpha+\beta x)])\} = \alpha_j + \beta^T x
\]

\[
\log[-\log(1-\pi(x))] = -39.5224+22.0148 \times \log\text{dose}
\]

\[
\text{Exp}(22.0148 \times 0.1) = 9.03838
\]

\[
0.3296029 \approx (0.884445)^{0.03838}
\]

\[
0.3296027 = (0.884445)^{0.03838}
\]

\[
\text{Deviance-G}^2 = 3.5143
\]

\[
\log \{-\log(P(Y \leq j \mid x))\} = \alpha_j + \beta^T x
\]
\log[-\log(1 - \pi(x_2))] - \log[-\log(1 - \pi(x_1))] = \beta(x_2 - x_1)

\log[1 - \pi(x_2)] = \exp[\beta(x_2 - x_1)]

\log[1 - \pi(x_2)] = \frac{1}{\log[1 - \pi(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[(x - \mu) / \sigma]

\pi(x) = 1 - \exp[-\exp(\alpha + \beta x)]

\text{link}[\pi(x)] = -\text{link}[1 - \pi(x)]

\text{logit}[\pi(x)] = \log[\pi(x)/(1 - \pi(x))]

\quad = -\log[(1 - \pi(x))/\pi(x)]

\quad = -\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^T \beta_{p+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
  */
  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=NULL 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';
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
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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
Intercept Only Covariates
AIC 647.441 376.354
SC 651.617 384.706
-2 Log L 645.441 372.354

Testing Global Null Hypothesis: BETA=0
Test Chi-Square DF Pr > ChiSq
Likelihood Ratio 273.0869 1 <.0001
Score 227.5973 1 <.0001
Wald 138.5112 1 <.0001

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The LOGISTIC Procedure
Analysis of Maximum Likelihood Estimates

Parameter Standard Wald
DF Estimate Error Chi-Square Pr > ChiSq
Intercept 1 -60.7339 5.1814 137.3964 <.0001
logdose 1 34.2824 2.9129 138.5112 <.0001

Odds Ratio Estimates

Point 95% Wald
Effect Estimate Confidence Limits
logdose >999.999 >999.999 >999.999
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 complementary log log model for beetles data                    33
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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 cloglog
Optimization Technique Fisher’s scoring

Response Profile

<table>
<thead>
<tr>
<th>Ordered Value</th>
<th>Binary</th>
<th>Total Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Event</td>
<td>291</td>
</tr>
<tr>
<td>2</td>
<td>Nonevent</td>
<td>190</td>
</tr>
</tbody>
</table>

Model Convergence Status

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

Model Fit Statistics

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

the complementary log log model for beetles data                    34
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The LOGISTIC Procedure

Analysis of Maximum Likelihood Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Standard DF</th>
<th>Wald</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate</td>
<td>Error</td>
<td>Chi-Square</td>
</tr>
<tr>
<td>Intercept</td>
<td>-39.5224</td>
<td>3.2356</td>
<td>149.1990</td>
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<tr>
<td>logdose</td>
<td>22.0148</td>
<td>1.7970</td>
<td>150.0854</td>
</tr>
</tbody>
</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 probit model for beetles data                            35
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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 probit
Optimization Technique Fisher's scoring

Response Profile

<table>
<thead>
<tr>
<th>Ordered</th>
<th>Binary</th>
<th>Total Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Event</td>
<td>291</td>
</tr>
<tr>
<td>2</td>
<td>Nonevent</td>
<td>190</td>
</tr>
</tbody>
</table>

Model Convergence Status

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

Model Fit Statistics

<table>
<thead>
<tr>
<th>Intercept Only</th>
<th>Covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIC</td>
<td>647.441</td>
</tr>
<tr>
<td>SC</td>
<td>651.617</td>
</tr>
<tr>
<td>-2 Log L</td>
<td>645.441</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>175.9925</td>
<td>1</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

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>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>-34.9557</td>
<td>2.6490</td>
<td>174.1309</td>
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<tr>
<td>logdose</td>
<td>1</td>
<td>19.7408</td>
<td>1.4880</td>
<td>175.9925</td>
<td>&lt;.0001</td>
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</table>

Association of Predicted Probabilities and Observed Responses

<table>
<thead>
<tr>
<th>Percent Concordant</th>
<th>87.0</th>
<th>Somers' D</th>
<th>0.802</th>
</tr>
</thead>
<tbody>
<tr>
<td>Percent Discordant</td>
<td>8.8</td>
<td>Gamma</td>
<td>0.856</td>
</tr>
<tr>
<td>Percent Tied</td>
<td>6.3</td>
<td>Tau-a</td>
<td>0.384</td>
</tr>
<tr>
<td>Pairs</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;
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 */
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>
<td>6</td>
<td>3.5143</td>
<td>0.5857</td>
</tr>
<tr>
<td>Scaled Deviance</td>
<td>6</td>
<td>3.5143</td>
<td>0.5857</td>
</tr>
<tr>
<td>Pearson Chi-Square</td>
<td>6</td>
<td>3.3592</td>
<td>0.5599</td>
</tr>
<tr>
<td>Scaled Pearson X2</td>
<td>6</td>
<td>3.3592</td>
<td>0.5599</td>
</tr>
<tr>
<td>Log Likelihood</td>
<td></td>
<td>-182.3765</td>
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</tr>
</tbody>
</table>

Algorithm converged.

Analysis Of Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Standard Estimate</th>
<th>Wald 95% Confidence Limits</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
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<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
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<td>3.2229</td>
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<td>Scale</td>
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<td>1.0000</td>
<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
</tbody>
</table>

NOTE: The scale parameter was held fixed.

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

SAS ONLINE TUTOR SOFTWARE