

BACKTRAN: A Computer Program for Converting Probit-Transformed
Data Back to the Original Units and Calculating Residuals

James E. Throne
USDA, ARS
U. S. Grain Marketing Research Laboratory
1515 College Ave.
Manhattan, KS 66502

David K. Weaver
USDA, ARS, IABBRL
1700 SW 23rd Drive
Gainesville, FL 32608

James E. Baker
USDA, ARS
U. S. Grain Marketing Research Laboratory
1515 College Ave.
Manhattan, KS 66502

PROBIT ANALYSIS is used to analyze data from bioassay experiments, such as the proportions of insects killed by several concentrations of an insecticide or at several time intervals at one or more concentrations of an insecticide (Finney 1964). Typically, results of probit analyses are reported as a concentration or time required to kill a certain proportion of the test insects (e.g., LC50) and the slope and intercept of the regression line of the probit-transformed data (e.g., Cilek & Greene 1994). Goodness of fit of the regression line is indicated by the chi-square statistic, which is calculated using residuals (observed minus predicted numbers of insects killed).

Results of probit analyses are rarely reported in the original units, that is, proportion of insects killed. The researcher should examine and report the results in the original units because the purpose of a bioassay is to make inferences about the proportions of insects killed by the insecticide, not to make inferences about probits (Finney 1964). A plot of observed and predicted proportions of insects killed aids in assessing goodness of fit of the regression line. Goodness of fit also should be assessed by examination of residuals and standardized residuals in the original units, particularly to try to determine the possible causes of lack of fit when the chi-square statistic is significant (Robertson & Preisler 1992).

In addition to the probit transformation, the complementary log-log and logit transformations also are used to linearize bioassay data (Robertson & Preisler 1992). Complementary log-log- and logit-transformed data are converted easily back to the original units. Converting probit-transformed data back to the original units is not straightforward, and is most easily accomplished using tables (Beyer 1987) or mathematical computer programs (e.g., Mathematica, Wolfram Research, Champaign, IL). We present a computer program (BACKTRAN) that uses the slope and intercept from probit analysis programs (e.g., Russell et al. 1977, Throne et al.

1995) to calculate the predicted proportion of insects killed by various concentrations of an insecticide or at various times by one concentration of an insecticide, including transforming the data from probits (or logits or the complementary log-log transformation) back to proportion killed. The user may also choose to have the program calculate residuals and standardized residuals.

Methods

Numerical Methods. The predicted proportion of insects killed (\hat{p}), in transformed units, is calculated as:

$$\hat{p} = a + bx , \quad (1)$$

where a = slope and b = intercept from the regression of transformed data and x is the concentration or time. If a logarithmic transformation of x was used in the original analysis, x should be replaced by $\log(x)$ in equation 1.

The formulas for calculating the predicted proportion of insects killed (\hat{q}), transformed back to the original units, are: 1)

$$\hat{q} = 1 - e^{-e^{\hat{p}}} \quad (2)$$

for the complementary log-log transformation; 2)

$$\hat{q} = \frac{e^{\hat{p}}}{1 + e^{\hat{p}}} \quad (3)$$

for the logit transformation; and 3)

$$\hat{q} = \int_{-\infty}^{\hat{p}} \frac{e^{-\frac{u^2}{2}}}{\sqrt{2\pi}} du \quad (4)$$

for the probit transformation (Beyer 1987).

If the user chooses to have residuals calculated, the program automatically modifies the input data set. Observations at the beginning of a time-mortality test or at low dosages when no insects were dead are deleted, except for the last observation where no mortality occurred. Observations where all insects are dead also are deleted. The proportion of insects killed during each time interval in the treatments is corrected for control mortality (Abbott 1925). The correction suggested by McCullagh and Nelder (1989) is applied if corrected proportion mortality ≤ 0 or $=1$. Standardized residuals are calculated by dividing the residuals of proportion kill at each x by their standard errors (Snedecor & Cochran 1976):

$$SE = \sqrt{\frac{p(1 - p)}{n}} , \quad (5)$$

where p = observed proportion killed and n = number tested at each x .

The Computer Program. The transformation was programmed in the Mathematica® language. The program, which is listed in Appendix I, can be modified using any text editor. A name for the output file and a page header may be specified (lines 22 and 26-31, respectively). Inputs to the program (lines 59-66) are the starting (intstart) and ending (intend) x values; the size of the intervals between x values (ints; e.g., 1-h time steps or 1 ppm dose steps; the size of the step does not have to be the same as that used in the original analysis, but the units must be the same); a variable indicating whether a logarithmic transformation (base 10) of x was used in the original analysis (tranx); a variable indicating which transformation of proportion kill (complementary log-log, logit, or probit) was used in the analysis

(trany); the slope (a) and intercept (b) from the original analysis; and a variable indicating whether residuals should be calculated. If residuals will be calculated, the results of the bioassay will need to be entered. Additional inputs required (lines 84-89) are the number of time intervals or doses in the data set (notimes); vectors containing the number of organisms dead in the control and treatment at each time interval or dose (contdead and expdead); a vector containing the actual times or doses at which observations were made (times); and the number of organisms in the control and experimental treatments (ncont and nexp). Note that these additional data need not be entered if calculation of residuals is not desired. The program is then saved, imported into a Mathematica® session, and executed.

The program can write three output data sets to a file (Appendix II). The first two data sets are written only when residual output is requested. The first data set (lines 31-36) contains column listings of x , the corrected observed proportions of insects killed by the treatment, the proportions of insects killed corresponding to probits (or logits or complementary log-log transforms) predicted by the regression equation, the residuals (observed minus predicted proportion killed), and the standardized residuals. The second data set (lines 44-49) contains column listings of x , the probits corresponding to the corrected observed proportion insects killed, the probits predicted using the regression equation, and the residuals (observed minus predicted probits). The third data set (lines 53-71) contains a column listing of x at intervals specified by the user, the probits predicted by the regression equation, and the proportion of insects killed corresponding to probits predicted by the regression equation. Input data are written to the output file for verification of data entry (lines 5-20). Five graphs are output to the screen: observed vs. predicted proportion kill, residual proportion kill, standardized residual proportion kill,

observed and predicted probits, and residual probits.

Versions of Mathematica® are available for Macintosh and IBM-compatible computers. The program shown in Appendix I took 7 sec to run on a 120 Mhz Pentium computer using the OS/2 version of Mathematica®.

References Cited

- Abbott, W. S.** 1925. A method of computing the effectiveness of an insecticide. *J. Econ. Entomol.* 18: 265-267.
- Baker, J. E., D. K. Weaver, J. E. Throne & J.L. Zettler.** 1994. Resistance to protectant insecticides in two field strains of the parasitoid *Bracon hebetor* (Hymenoptera: Braconidae). *J. Econ. Entomol.* 88: 512-519.
- Beyer, W. H.** 1987. CRC standard mathematical tables, 28th edition. CRC Press, Inc., Boca Raton, FL.
- Cilek, J. E. & G. L. Greene.** 1994. Stable fly (Diptera: Muscidae) insecticide resistance in Kansas cattle feedlots. *J. Econ. Entomol.* 87: 275-279.
- Finney, D. J.** 1964. Probit analysis: a statistical treatment of the sigmoid response curve, 2nd ed. Cambridge Univ. Press, London, England.
- McCullagh, P. & J. A. Nelder.** 1989. Generalized linear models, second edition. Chapman & Hall, New York, NY.
- Naylor, A. F.** 1964. Comparisons of regression constants fitted by maximum likelihood to four common transformations of binomial data. *Ann. Hum. Genet.* 27: 241-246.
- Preisler, H. K.** 1988. Assessing insecticide bioassay data with extra-binomial variation. *J. Econ. Entomol.* 81: 759-765.
- Robertson, J. L. & H. K. Preisler.** 1992. Pesticide bioassays with arthropods. CRC Press, Boca Raton, FL.
- Russell, R. M., J. L. Robertson & N. E. Savin.** 1977. POLO: A new computer program for probit analysis. *Bull. Entomol. Soc. Am.* 23: 209-213.
- Snedecor, G. W. & W. G. Cochran.** 1976. Statistical methods, sixth edition. Iowa State Univ. Press, Ames, IA.
- Throne, J. E., D. K. Weaver, V. Chew & J. E. Baker.** 1995. Probit analysis for correlated data: multiple observations over time at one concentration. *J. Econ. Entomol.* 88: 1510-1512.

APPENDIX I - PROGRAM LISTING

```
1      (* BACKTRAN - This program is used to calculate back transformations
2      (transform back to proportion organisms responding to stimulus) after
3      probit, logit, or complementary log-log transformation of bioassay
4      data. Time or dose may be transformed as log10(time or dose). The
5      user may also choose to calculate residuals of both untransformed
6      and transformed data. Follow the instructions below for modifying
7      the program to include your data. I would suggest that you save the
8      original version of the program and make changes to a copy of the
9      program. *)

10     (* This program was developed by:

11         Jim Throne
12         USDA, ARS, USGMRL
13         1515 College Avenue
14         Manhattan, KS 66502
15         (913)776-2796
16         throne@crunch.usgmrl.ksu.edu

17         Please notify me of problems or suggestions.  5 Oct 95 *)

18     Off[]

19     (* You may change the name of the output file where the
20     backtransformed data are written by changing the name in
21     quotation marks on the next line. *)

22     out=OpenWrite["outbt",FormatType->OutputForm,PageWidth->78]

23     (* You may type in a heading for the output file between the
24     quotation marks on the next program lines. Total line length
25     should not exceed 72 characters. *)

26     WriteString[out,"probit - backtransformed data"]
27     WriteString[out," \n"]
28     WriteString[out,"S. granarius on wheat"]
29     WriteString[out," \n"]
30     WriteString[out,"malathion - 7 mg/kg - Table 1"]
31     WriteString[out," \n\n"]

32     (* The lines following these descriptions are where you enter your
33     data. *)

34     (*   intstart   Initial time interval or dose at which observations
35                were made. For example, hour 1 or dose 1. Note: a
36                control dose or time of 0 should not be included.
37                Control data are not used to calculate the regression
38                line, but are used only to adjust for control mortality.
39                *)

40     (*   intend     Last time interval or dose at which observations were
41                made. For example, hour 120 or dose 5. *)

42     (*   ints       Size of intervals desired for output data set. For
43                example, if time goes from hours 1 to 120 you may want
44                output in hourly intervals so set ints equal to 1. If
45                dose goes from 0 to 1 mg you may want output in 0.1 mg
46                intervals so set ints equal to 0.1. *)

47     (*   tranx      Set to yes if log10 of time or dose was used in
48                analysis. Otherwise, set to no. Enclose in quotation
49                marks. *)
```

```

50      (*   tranx      Indicate whether probit, logit, or gompertz
51                    transformation of y was used in analysis. Note that
52                    gompertz is being used to represent the complementary
53                    log-log transformation. Enclose in quotation marks. *)

54      (*   a          Intercept from analysis.  *)

55      (*   b          Slope from analysis.  *)

56      (*   resids     Indicate whether residuals should be calculated and
57                    printed to the output file (yes or no in quotation
58                    marks).  *)

59      intstart=3
60      intend=21
61      ints=1
62      tranx="no"
63      tranx="probit"
64      a=-1.807
65      b=0.112272
66      resids="yes"

67      (* The following data need to be entered only if you wish to have
68         residuals calculated. If you don't want residuals calculated,
69         don't bother entering the following data. *)

70      (*   notimes     Number of time intervals for which data will be
71                    entered.  *)

72      (*   contdead    The observed cumulative number of insects dead in the
73                    control at each time interval, enclosed in brackets. *)

74      (*   expdead     The observed cumulative number of insects dead in the
75                    treatment at each time interval, enclosed in brackets.
76                    *)

77      (*   times       The times at which observations were made, enclosed in
78                    brackets.  *)

79      (*   ncont       The initial number of insects in the control.  *)

80      (*   nexpt       The initial number of insects in the treatment.  *)

81      (* The following data need to be changed only if you wish to have
82         residuals calculated - that is, resids=yes. If resids=no , don't
83         bother changing the following data. *)

84      notimes=6
85      contdead={0,0,0,0,0,0}
86      expdead={6,12.5,14.25,19,44,72}
87      times={3,6,7,10,14,21}
88      ncont=100
89      nexpt=100

90      (* The user should not make any further changes to the program. *)

91      WriteString[out,"Input data: \n\n"]
92      WriteString[out,"Starting time or dose = "]
93      Write[out,intstart]
94      WriteString[out,"Ending time or dose = "]
95      Write[out,intend]
96      WriteString[out,"Size of intervals = "]
97      Write[out,ints]
98      WriteString[out,"Logarithmic transformation of time or dose = "]
99      Write[out,tranx]

```

```

100 WriteString[out,"Transformation = "]
101 Write[out,trans]
102 WriteString[out,"Intercept = "]
103 Write[out,a]
104 WriteString[out,"Slope = "]
105 Write[out,b]
106 WriteString[out,"Residuals desired = "]
107 Write[out,resids]
108 WriteString[out," \n\n"]
109 Needs["Statistics`ContinuousDistributions`"]
110 ndist=NormalDistribution[0,1]

111 Do[If[resids=="no",Goto[no]]];

112 (* This section of the program calculates residuals. *)

113 WriteString[out,"Input data for calculating residuals: \n\n"];
114 WriteString[out,"Number of time intervals = "];
115 Write[out,notimes];
116 WriteString[out,"Number dead in controls = "];
117 Write[out,contdead];
118 WriteString[out,"Number dead in treatments = "];
119 Write[out,expdead];
120 WriteString[out,"Time intervals = "];
121 Write[out,times];
122 WriteString[out,"Number of controls = "];
123 Write[out,ncont];
124 WriteString[out,"Number treated = "];
125 Write[out,nexp];
126 WriteString[out," \n\n"];

127 (* Delete data for time periods when no mortality occurred or in
128 which all insects were dead. Apply log10 transformation to time. *)

129 If[tranx=="yes",times=Log[10,times] //N];
130 input=Table[0,{i,notimes},{j,3}];
131 input[[1,1]]=times[[1]];
132 input[[1,2]]=contdead[[1]];
133 input[[1,3]]=expdead[[1]];
134 inc=1;
135 Do[If[expdead[[i]]==0,Goto[elim],Goto[add]];
136 Label[add];
137 inc=inc+1;
138 input[[inc,1]]=times[[i]];
139 input[[inc,2]]=contdead[[i]];
140 input[[inc,3]]=expdead[[i]];
141 Goto[end1];
142 Label[elim];
143 If[expdead[[i]]==0,input[[1,1]]=times[[i]]];
144 If[expdead[[i]]==0,input[[1,3]]=contdead[[i]]];
145 Label[end1];
146 ,{i,2,notimes}];

147 (* Set up vectors containing the time intervals (t), the number dead
148 at each time interval in the control (dcont), the number dead at
149 each time interval in the treatment (dexp), and the number of time
150 intervals that had valid data (m) *)

151 t=Table[input[[i,1]],{i,inc}];
152 dcont=Table[input[[i,2]],{i,inc}];
153 dexp=Table[input[[i,3]],{i,inc}];
154 m=inc;

155 (* Calculate the number of insects that die during each time
156 interval (kexp or kcont), and the proportion that die during each

```

```

157         time interval (pexp or pcont). *)

158         kexp=Table[If[i==1,dexp[[1]],dexp[[i]]-dexp[[i-1]]],{i,m}];
159         pexpinit=kexp/nexp //N;
160         kcont=Table[If[i==1,dcont[[1]],dcont[[i]]-dcont[[i-1]]],{i,m}];
161         pcont=Table[kcont[[i]]/ncont,{i,m}];

162         (* Apply Abbott's formula to correct for control mortality, and
163            correct for 0 or all dead during a time interval. *)
164
165         pexp=Table[(pexpinit[[i]]-pcont[[i]])/(1-pcont[[i]]),{i,m}];
166         c=Table[If[j<=i,1,0],{i,m},{j,m}];
167         up2=c.pexp;
168         up3=Table[If[up2[[i]]<=0,(0.5)/(nexp+1),up2[[i]]],{i,m}];
169         up=Table[If[up3[[i]]>=1.,(dexp[[i]]+0.5)/(nexp+1.),up3[[i]]],{i,m}];

170         (* Calculate the standard error for each residual for calculating
171            standardized residuals. *)

172         dexp2=Table[If[j3>1,dexp[[j3]]-dexp[[j3-1]],dexp[[j3]]],{j3,m}];
173         seresid=Sqrt[up*(1-up)/(nexp-dexp2)];

174         (* Use the regression equation to calculate predicted probit for
175            each time interval or dosage *)

176         tz=a+b*t;

177         (* Calculate the predicted proportion kill at each x depending on
178            the transformation used *)

179         If[trany == "probit",tp=Map[CDF[ndist,#]&,tz]];
180         If[trany == "logit",tp=Exp[tz]/(1+Exp[tz])];
181         If[trany == "gompertz",tp=1-Exp[-Exp[tz]]];

182         (* Calculate the probit corresponding to the observed proportion
183            kill. *)

184         Do[If[trany != "probit",Goto[other]];
185         y=Map[Quantile[ndist,#]&,up];
186         uz=Table[y[[i]],{i,m}];
187         Goto[endtrans];
188         Label[other];
189         If[trany != "logit",Goto[gomp],uz=Table[Log[up[[i]]/
190            (1-up[[i]])],{i,m}];
191         Goto[endtrans];
192         Label[gomp];
193         uz=Table[Log[-Log[1-up[[i]]]],{i,m}];
194         Label[endtrans];,{i2,1}];

195         (* Calculate residuals for proportion kill and probits. Residuals
196            are calculated as observed minus predicted. *)

197         pres=up2-tp;
198         zres=uz-tz;

199         (* Calculate standardized residual for proportion kill. *)

200         stdresid=pres/seresid;

201         (* Convert log(time) to time, if necessary. *)

202         If[tranx=="yes",t=10^t];

203         (* If residuals are very small, set it equal to 0.0000 so that
204            scientific notation will not be used and the data can be easily

```

```

205         imported into a graphics package. The point will essentially look
206         like 0 in a graph, no matter how much smaller than 0.0001 it is. *)

207     presout2=Table[If[pres[[i]]>0. && pres[[i]]<0.00005,0.0000,pres[[i]]],
208       {i,inc}];
209     zresout2=Table[If[zres[[i]]>0. && zres[[i]]<0.00005,0.0000,zres[[i]]],
210       {i,inc}];
211     sresout2=Table[If[stdresid[[i]]>0. && stdresid[[i]]<0.00005,0.0000,
212       stdresid[[i]]],{i,inc}];
213     presout=Table[If[presout2[[i]]<0. && presout2[[i]]>-0.00005,0.0000,
214       presout2[[i]]],{i,inc}];
215     zresout=Table[If[zresout2[[i]]<0. && zresout2[[i]]>-0.00005,0.0000,
216       zresout2[[i]]],{i,inc}];
217     sresout=Table[If[sresout2[[i]]<0. && sresout2[[i]]>-0.00005,0.0000,
218       sresout2[[i]]],{i,inc}];

219     (* Write output for proportion kill to file. *)

220     Write[out,"This section of the output contains the observed proportion"]
221     ;
222     Write[out,"killed, the proportion killed backtransformed from"];
223     Write[out,"predictions using the regression equation, the residual"];
224     Write[out,"(observed minus predicted) proportion killed, and the"];
225     Write[out,"standardized residual (residuals divided by their standard"];
226     Write[out,"errors)."];
227     WriteString[out," \n\n"];
228     Write[out,"Time or Dose      Untransformed Proportion Killed      Residual
229     Std. Residual\n"];
230     Write[out,"
231               Observed      Predicted\n"];
231     Do[Write[out,PaddedForm[SequenceForm["      ",t[[i]],"      ",
232       up2[[i]],"      ",tp[[i]],"      ",presout[[i]],"
233       ",sresout[[i]]],{8,4}]],{i,m}];

234     (* Write output for probits to file. *)

235     WriteString[out," \n\n"];
236     Write[out,"This section of the output contains the probit
237     corresponding"];
238     Write[out,"to the observed, corrected proportion killed; the probit"];
239     Write[out,"predicted using the regression equation; and the residual"];
240     Write[out,"(observed minus predicted) probits.\n\n"];
241     Write[out,"      Time or Dose      Transformed Proportion Killed      Residual
242     "];
243     Write[out,"
244               Observed      Predicted\n"];
244     Do[Write[out,PaddedForm[SequenceForm["      ",t[[i]],"      ",
245       uz[[i]],"      ",tz[[i]],"      ",zresout[[i]]],{8,4}]],{i,m}];

246     Label[no];
247     ,{i5,1}}

248     (* This section does the backtransformation at specified intervals. *)

249     (* Calculate number of time intervals or dosages *)

250     inc=((intend-intstart)/ints)+1;

251     (* Set up a vector containing the time intervals or dosages (x) *)

252     x=Table[i,{i,intstart,intend,ints}];

253     (* Apply log10 transformation to time, if applicable. *)

254     If[tranx=="yes",logx=Log[10,x] //N];

255     (* Use the regression equation to calculate predicted y for each time

```

```

256         interval or dosage *)

257     If[tranx=="yes",y=a+b*logx];
258     If[tranx=="no",y=a+b*x];

259     (* Calculate the proportion kill at each x depending on the
260        transformation used *)

261     If[trany == "probit",p=Map[CDF[ndist,#]&,y]];
262     If[trany == "logit",p=Exp[y]/(1+Exp[y])];
263     If[trany == "gompertz",p=1-Exp[-Exp[y]]];

264     (* If p is very small set it equal to 0.0001 so that scientific
265        notation will not be used and the data can be easily imported
266        into a graphics package. The point will essentially look like
267        0 in a graph, no matter how much smaller than 0.0001 it is. *)

268     pout=Table[If[p[[i]]<0.0001,0.0001,p[[i]]],{i,inc}];

269     If[trany == "probit",title="  Probit"];
270     If[trany == "logit",title="  Logit"];
271     If[trany == "gompertz",title="Gompertz"];

272     (* Write data to output file. *)

273     WriteString[out," \n\n"];
274     WriteString[out,"Backtransformed output from the regression equation"];
275     WriteString[out," \n\n"];
276     Write[out,"      Time or Dose","      ",title,"      Prop. Kill\n"];
277     Do[Write[out,PaddedForm[SequenceForm[x[[i]],"      ",
278        y[[i]],"      ",pout[[i]]],{14,4}]],{i,inc}];

279     (* Graph output data and write to file. *)

280     (* Plot obs. vs. pred. % kill *)

281     Needs["Graphics`Graphics`"]
282     g1=ListPlot[Table[{t[[i]],up2[[i]]},{i,m}],DisplayFunction ->Identity]
283     g2=ListPlot[Table[{x[[i]],pout[[i]]},{i,inc}],PlotJoined->True,
284     DisplayFunction ->Identity]
285     Show[g1,g2,Frame->True,PlotLabel->"Observed and Calculated Proportion
286     kill vs Time", DisplayFunction->$DisplayFunction,AxesOrigin->{0,0}]

287     (* Plot residual % kill vs. time *)

288     g3=ListPlot[Table[{t[[i]],presout[[i]]},{i,m}],DisplayFunction
289     ->Identity]
290     Show[g3,Frame->True,PlotLabel->"Residual of proportion kill vs
291     time",DisplayFunction->$DisplayFunction,AxesOrigin->{0,0}]

292     (* Plot standardized residual % kill vs. time *)

293     g4=ListPlot[Table[{t[[i]],sresout[[i]]},{i,m}],DisplayFunction
294     ->Identity]
295     Show[g4,Frame->True,PlotLabel->"Standardized residual of proportion kill
296     vs time",DisplayFunction->$DisplayFunction,AxesOrigin->{0,0}]

297     (* Plot observed and predicted probits vs. time *)

298     g5=ListPlot[Table[{t[[i]],uz[[i]]},{i,m}],DisplayFunction
299     ->Identity]
300     g6=ListPlot[Table[{x[[i]],y[[i]]},{i,inc}],PlotJoined->True,
301     DisplayFunction ->Identity]
302     Show[g5,g6,Frame->True,PlotLabel->"Observed and Calculated Probits
303     vs Time",DisplayFunction->$DisplayFunction,AxesOrigin->{0,0}]

```

```
304      (* Plot residual probits vs. time *)
305      g7=ListPlot[Table[{t[[i]],zresout[[i]]},{i,m}],DisplayFunction
306      ->Identity]
307      Show[g7,Frame->True,PlotLabel->"Residual probits vs
308      time",DisplayFunction->$DisplayFunction,AxesOrigin->{0,0}]
309      Close[out]
```

APPENDIX II - PROGRAM OUTPUT

1 probit - backtransformed data
 2 S. granarius on wheat
 3 Malathion - 7 mg/kg - Table 1

4 Input data:

5 Starting time or dose = 3
 6 Ending time or dose = 21
 7 Size of intervals = 1
 8 Logarithmic transformation of time or dose = no
 9 Transformation = probit
 10 Intercept = -1.807
 11 Slope = 0.112272
 12 Residuals desired = yes
 13

14 Input data for calculating residuals:

15 Number of time intervals = 6
 16 Number dead in controls = {0, 0, 0, 0, 0, 0}
 17 Number dead in treatments = {6, 12.5, 14.25, 19, 44, 72}
 18 Time intervals = {3, 6, 7, 10, 14, 21}
 19 Number of controls = 100
 20 Number treated = 100
 21

22 This section of the output contains the observed proportion
 23 killed, the proportion killed backtransformed from
 24 predictions using the regression equation, the residual
 25 (observed minus predicted) proportion killed, and the
 26 standardized residual (residuals divided by their standard
 27 errors).
 28

29	Time or Dose	Untransformed Proportion Killed	Residual	Std. Residual
30		Observed Predicted		
31	3.0000	0.0600 0.0708	-0.0108	-0.4391
32	6.0000	0.1250 0.1285	-0.0035	-0.1032
33	7.0000	0.1425 0.1536	-0.0111	-0.3149
34	10.0000	0.1900 0.2469	-0.0569	-1.4155
35	14.0000	0.4400 0.4070	0.0330	0.5752
36	21.0000	0.7200 0.7091	0.0109	0.2063
37				

38 This section of the output contains the probit corresponding
 39 to the observed, corrected proportion killed; the probit
 40 predicted using the regression equation; and the residual
 41 (observed minus predicted) probits.

42	Time or Dose	Transformed Proportion Killed	Residual
43		Observed Predicted	
44	3.0000	-1.5548 -1.4702	-0.0846
45	6.0000	-1.1503 -1.1334	-0.0170
46	7.0000	-1.0692 -1.0211	-0.0481
47	10.0000	-0.8779 -0.6843	-0.1936
48	14.0000	-0.1510 -0.2352	0.0842
49	21.0000	0.5828 0.5507	0.0321

50

51 Backtransformed output from the regression equation

52	Time or Dose	Probit	Prop. Kill
53	3.0000	-1.4702	0.0708
54	4.0000	-1.3579	0.0872
55	5.0000	-1.2456	0.1064
56	6.0000	-1.1334	0.1285
57	7.0000	-1.0211	0.1536
58	8.0000	-0.9088	0.1817
59	9.0000	-0.7966	0.2129
60	10.0000	-0.6843	0.2469
61	11.0000	-0.5720	0.2837
62	12.0000	-0.4597	0.3229
63	13.0000	-0.3475	0.3641
64	14.0000	-0.2352	0.4070
65	15.0000	-0.1229	0.4511
66	16.0000	-0.0106	0.4958
67	17.0000	0.1016	0.5405
68	18.0000	0.2139	0.5847
69	19.0000	0.3262	0.6279
70	20.0000	0.4384	0.6695
71	21.0000	0.5507	0.7091

Footnotes

Names of products are included for the benefit of the reader and do not imply endorsement or preferential treatment by USDA.