



TMSURVIV

User's Manual

by

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Introduction

Program TMSURVIV (**Transient-Model-SURVIV**al analysis) computes parameter estimates of survival and capture probability and proportions of "residents" under the Jolly-Seber models described in "Capture-Recapture Survival Models Taking Account of Transients" (Pradel et. al., 1997). Actually, TMSURVIV is a specially modified version of Dr. G. White's program SURVIV (White, 1983) which incorporates the transient models. With this program and it's companion program, CNVTMSRV, users are able to get parameter estimates for these complex models from capture-history data without having to specify the cell probabilities.

TMSURVIV is intended to be used in a situation where the sampling area includes animals which pass through the area and are not part of the "resident" population. .

Output from TMSURVIV includes survival probability estimates, capture probability estimates, estimates of the proportion of residents, goodness-of-fit tests, and likelihood-ratio tests.

By default, models are generated for standard Jolly-Seber models (where all animals are assumed to be residents), and transient models (a portion of the population is transient and only available for capture in one sample). The model names signify the structure of the model. Each model name is in the form "S.P.G." where "S" stands for survival, "P" stands for capture probability, and "G" stands for "gamma (proportion of residents)". If S,P, or G are followed by a "t", then the corresponding parameter is "time-dependent". If there is no "G" in the name, then all animals are assumed to be residents (proportion of residents = 1.0), which is equivalent to the Jolly-Seber models.

Since program TMSURVIV is a generalization of program JOLLY, the conversion/model generation program (CNVTMSRV) will read input files designed for program JOLLY. Input consists of capture-histories for each animal, preceded by statements defining the specifics of the data (title, number of periods, interval lengths).

Using CNVTMSRV

To run CNVTMSRV, type CNVTMSRV at the DOS prompt and respond to the program prompts. When the program is run, you are prompted for the name of the file(s) containing the capture-histories. Analysis on groups of animals may be performed by separating the capture-histories into different files. CNVTMSRV will prompt for each input file and a 1-character identifier (eg. M for male, F for female) until 'END' is entered for the input file.

Here is the output file created by CNVTMSRV which can be input to TMSURVIV:

```
PROC TITLE 'Lazuli bunting data from DESIGN & ANAL. METH... Burhnam et al.';
PROC MODEL NPAR=21 ADDCELL;
COHORT= 168 /* unmarked in 1 */;
31.; 4.; 0.; 1.; 0.; 0.; 0.;
COHORT= 31 /* marked in 2 */;
7.; 4.; 0.; 0.; 0.; 0.;
COHORT= 367 /* unmarked in 2 */;
12.; 10.; 4.; 1.; 0.; 1.;
COHORT= 23 /* marked in 3 */;
12.; 0.; 1.; 0.; 0.;
COHORT= 65 /* unmarked in 3 */;
8.; 3.; 0.; 0.; 0.;
COHORT= 34 /* marked in 4 */;
16.; 3.; 0.; 0.;
COHORT= 230 /* unmarked in 4 */;
25.; 3.; 3.; 1.;
COHORT= 49 /* marked in 5 */;
20.; 0.; 0.;
COHORT= 255 /* unmarked in 5 */;
38.; 13.; 1.;
COHORT= 66 /* marked in 6 */;
28.; 2.;
COHORT= 256 /* unmarked in 6 */;
39.; 7.;
COHORT= 83 /* marked in 7 */;
30.;
COHORT= 240 /* unmarked in 7 */;
46.;
LABELS;
S(1)=PHI(1);
S(2)=PHI(2);
S(3)=PHI(3);
S(4)=PHI(4);
S(5)=PHI(5);
S(6)=PHI(6);
S(7)=PHI(7);
S(8)=p(2);
S(9)=p(3);
S(10)=p(4);
S(11)=p(5);
S(12)=p(6);
S(13)=p(7);
S(14)=p(8);
S(15)=gamma(1);
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S(16)=gamma(2);
S(17)=gamma(3);
S(18)=gamma(4);
S(19)=gamma(5);
S(20)=gamma(6);
S(21)=gamma(7);
PROC ESTIMATE NOVAR MAXFN=32000 NAME=SP; CONSTRAINTS;
S(2)=S(1);
S(3)=S(1);
S(4)=S(1);
S(5)=S(1);
S(6)=S(1);
S(7)=S(1);
S(9)=S(8);
S(10)=S(8);
S(11)=S(8);
S(12)=S(8);
S(13)=S(8);
S(14)=S(8);
S(15)=1;
S(16)=1;
S(17)=1;
S(18)=1;
S(19)=1;
S(20)=1;
S(21)=1;
PROC ESTIMATE NOVAR MAXFN=32000 NAME=SPG; CONSTRAINTS;
S(2)=S(1);
S(3)=S(1);
S(4)=S(1);
S(5)=S(1);
S(6)=S(1);
S(7)=S(1);
S(9)=S(8);
S(10)=S(8);
S(11)=S(8);
S(12)=S(8);
S(13)=S(8);
S(14)=S(8);
S(16)=S(15);
S(17)=S(15);
S(18)=S(15);
S(19)=S(15);
S(20)=S(15);
S(21)=S(15);
PROC ESTIMATE NOVAR MAXFN=32000 NAME=StPt; CONSTRAINTS;
S(16)=1;
S(17)=1;
S(18)=1;
S(19)=1;
S(20)=1;
S(21)=1;
PROC ESTIMATE NOVAR MAXFN=1 NAME=StPtGt; CONSTRAINTS;
S(14)=1;
S(15)=1;
initial;
s(1)=0.588756 ;
s(2)=0.480049 ;
s(3)=0.727235 ;
s(4)=0.601595 ;
s(5)=0.608575 ;
s(6)=0.501442 ;
s(7)=0.349755 ;
s(8)=0.313413 ;
s(9)=0.454870 ;

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```
s(10)=0.655431 ;
s(11)=0.688543 ;
s(12)=0.629337 ;
s(13)=0.737137 ;
s(16)=0.168890 ;
s(17)=0.214131 ;
s(18)=0.286596 ;
s(19)=0.364735 ;
s(20)=0.453364 ;
s(21)=0.562283 ;
PROC TEST; PROC STOP;
```

The output file, CNVTMSRV.OUT, contains a title statement, statements to define the input data, label definitions, statements to describe models, a test statement and a stop statement.

The title statement is used to identify the data used in the analysis.

The model definition statements start with "PROC MODEL NPAR=21 ADDCELL;" and end with "COHORT=240;". The "NPAR=21" indicates the maximum number of parameters (estimated or fixed) in any of the following models. In this example there are 7 survival rate parameters, 7 capture probability parameters, and 7 residency parameters.

Following the data are the labels for each of the parameters. Internally, the parameters are called "S(1), S(2), ... S(NPAR)". The labels relate these internal parameters to meaningful labels for these models. The survival parameters are labelled PHI, followed by time period in parenthesis. The capture-probability parameters are labelled "p", and the residency parameters are labelled "gamma". If more than one group was input, the label will have a 1-character identifier tacked onto the end to indicate the group.

After the label definitions come the model definitions for each model. Each model starts with a "PROC ESTIMATE" statement. Options on the "PROC ESTIMATE" statement include "NOVAR" which inhibits printing of the variance-covariance matrix, the number of significant digits, "NSIG" (i.e., number of digits following the decimal point which do not change at the end of the iterative process), the maximum number of function evaluations, "MAXFN", and the name of the model. If the variance-covariance matrix of parameter estimates is desired, delete the string "NOVAR" using a text editor.

CNVTMSRV produces the model definitions from most restrictive (model "SP") to most general (model "StPtGt"). The reason for this is that the most restrictive model has the fewest estimable parameters and converges more easily. Final estimates from this model can then be input as starting values to more general models. If more than one group was entered in CNVTMSRV, a series of additional models is produced which assumes the data came from only one group (eg. 1SP, 1StPtGt,...).

The statements following the "CONSTRAINTS" statement describe each model in terms of the most general model. In model "SP", the survival and capture probabilities are assumed to be constant across time, so the survival probabilities for time period two and three are set equal to the survival

probabilities for time period one. The capture probabilities are also assumed constant over time, so the capture probabilities for time periods 3 and 4 are set equal to the capture probabilities for time period 2. These equalities must be specified in terms of parameter number which can be obtained from the labels section.

The sequence of statements starting with "PROC ESTIMATE ... NAME=SPG" cause TMSURVIV to produce estimates under the model with constant survival and capture probabilities and a constant proportion of residents.

The sequence of statements starting with "PROC ESTIMATE ... NAME=StP" cause TMSURVIV to produce estimates under the model with time-specific survival probabilities and constant capture probabilities (equivalent to model "B" in JOLLY).

The "PROC TEST;" statement causes TMSURVIV to print tables of statistics used for comparison of the models. "PROC STOP;" causes TMSURVIV to stop execution even if more statements follow.

TMSURVIV

TMSURVIV prompts for one line of input to specify the name of the input and output files and command line options. When the program is run, the following prompt appears:

Enter command line parameters [i=in_file] [l=out_file]

[lines=n] [compile run] [noecho]:

At this prompt, any or all of the items enclosed in brackets may be specified. If "i=in_file" is specified, the input will be read from the file "in_file". Usually, this is the file created by CNVTMSRV and is called CNVTMSRV.OUT unless it has been renamed. A full pathname may be used to indicate a different directory. If this item is omitted, TMSURVIV expects the input from the keyboard. (Cntrl-Break will abort the program).

If "l=out_file" is specified, output from TMSURVIV will be directed to the file "out_file". The default output file is the CRT screen. To direct output directly to the printer, use "l=lpt1".

If "lines=n" is included, TMSURVIV will print a header and the title in the output file after every n lines. The default value for n is 60.

If "compile run" is included, TMSURVIV will only check the input file for errors and not perform any analysis. This option is used in SURVIV to create the estimation routine and is not needed in TMSURVIV.

The "noecho" option causes TMSURVIV to suppress printing of the input data. This option is useful when there are several runs of models on the same data and you would like to conserve paper, but at least one run should contain a listing of the data to check for "typos".

To run the sample data file with TMSURVIV, enter the following at the above prompt:

i=cnvtmlsr.v out l=sample.out lines=9999

The output produced by TMSURVIV contains a listing of the input data, estimates of the parameters under each model, a goodness-of-fit test for each model, an AIC statistic for each model, and between model tests. The following output was created using TMSURVIV on the sample data file listed previously:

SURVIV - Survival Rate Estimation with User Specified Cell Probabilities
2-Sep-97 15:47:55 Version 1.4(OS/2) June, 1991 Page 001

INPUT --- PROC TITLE 'Lazuli bunting data from DESIGN & ANAL. METH...
INPUT --- Burhnam et al.';

CPU time in seconds for last procedure was 0.00

INPUT --- PROC MODEL NPAR=21 ADDCELL;
INPUT --- COHORT= 168 /* unmarked in 1 */;
INPUT --- 31;;4;;0;;1;;0;;0;;0;;
INPUT --- COHORT= 31 /* marked in 2 */;
INPUT --- 7;;4;;0;;0;;0;;0;;
INPUT --- COHORT= 367 /* unmarked in 2 */;
INPUT --- 12;;10;;4;;1;;0;;1;;
INPUT --- COHORT= 23 /* marked in 3 */;
INPUT --- 12;;0;;1;;0;;0;;
INPUT --- COHORT= 65 /* unmarked in 3 */;
INPUT --- 8;;3;;0;;0;;0;;
INPUT --- COHORT= 34 /* marked in 4 */;
INPUT --- 16;;3;;0;;0;;
INPUT --- COHORT= 230 /* unmarked in 4 */;
INPUT --- 25;;3;;3;;1;;
INPUT --- COHORT= 49 /* marked in 5 */;
INPUT --- 20;;0;;0;;
INPUT --- COHORT= 255 /* unmarked in 5 */;
INPUT --- 38;;13;;1;;
INPUT --- COHORT= 66 /* marked in 6 */;
INPUT --- 28;;2;;
INPUT --- COHORT= 256 /* unmarked in 6 */;
INPUT --- 39;;7;;
INPUT --- COHORT= 83 /* marked in 7 */;
INPUT --- 30;;
INPUT --- COHORT= 240 /* unmarked in 7 */;
INPUT --- 46;;

INPUT --- PROC ESTIMATE NOVAR MAXFN=32000 NAME=SP;

Number of parameters in model = 21

Number of parameters set equal = 12

Number of parameters fixed = 7

Number of parameters estimated = 2

Final function value 1133.1718 (Error Return = 0)

Number of significant digits 7

Number of function evaluations 45

I	Parameter	S(I)	Standard Error	95% Confidence Interval	
				Lower	Upper
1	1 PHI(1)	0.379861	0.200672E-01	0.340529	0.419193
2	1 PHI(2)	0.379861	0.200672E-01	0.340529	0.419193
3	1 PHI(3)	0.379861	0.200672E-01	0.340529	0.419193
4	1 PHI(4)	0.379861	0.200672E-01	0.340529	0.419193
5	1 PHI(5)	0.379861	0.200672E-01	0.340529	0.419193
6	1 PHI(6)	0.379861	0.200672E-01	0.340529	0.419193
7	1 PHI(7)	0.379861	0.200672E-01	0.340529	0.419193
8	2 p(2)	0.432594	0.327044E-01	0.368494	0.496695
9	2 p(3)	0.432594	0.327044E-01	0.368494	0.496695
10	2 p(4)	0.432594	0.327044E-01	0.368494	0.496695
11	2 p(5)	0.432594	0.327044E-01	0.368494	0.496695
12	2 p(6)	0.432594	0.327044E-01	0.368494	0.496695
13	2 p(7)	0.432594	0.327044E-01	0.368494	0.496695
14	2 p(8)	0.432594	0.327044E-01	0.368494	0.496695
15	-15 gamma(1)	1.000000	0.000000E+00	1.000000	1.000000
16	-16 gamma(2)	1.000000	0.000000E+00	1.000000	1.000000
17	-17 gamma(3)	1.000000	0.000000E+00	1.000000	1.000000
18	-18 gamma(4)	1.000000	0.000000E+00	1.000000	1.000000
19	-19 gamma(5)	1.000000	0.000000E+00	1.000000	1.000000
20	-20 gamma(6)	1.000000	0.000000E+00	1.000000	1.000000
21	-21 gamma(7)	1.000000	0.000000E+00	1.000000	1.000000

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	31	27.607	0.417	0 < P < 1
1	2	4	5.950	0.639	0 < P < 1
1	3	0	1.282	1.282	0 < P < 1
1	4	1	0.276	1.894	0 < P < 1
1	5	0	0.060	0.060	0 < P < 1
1	6	0	0.013	0.013	0 < P < 1
1	7	0	0.003	0.003	0 < P < 1
1	8	132	132.809	0.005	0 < P < 1
1	Cohort	df= 2		1.303	P = 0.5214
2	1	7	5.094	0.713	0 < P < 1
2	2	4	1.098	7.670	0 < P < 1
2	3	0	0.237	0.237	0 < P < 1
2	4	0	0.051	0.051	0 < P < 1
2	5	0	0.011	0.011	0 < P < 1
2	6	0	0.002	0.002	0 < P < 1
2	7	20	24.507	0.829	0 < P < 1
2	Cohort	df= 1		3.957	P = 0.0467
3	1	12	60.308	38.695	0 < P < 1
3	2	10	12.998	0.692	0 < P < 1
3	3	4	2.802	0.513	0 < P < 1
3	4	1	0.604	0.260	0 < P < 1
3	5	0	0.130	0.130	0 < P < 1
3	6	1	0.028	33.676	0 < P < 1
3	7	339	290.130	8.232	0 < P < 1
3	Cohort	df= 3		49.284	P = 0.0000
4	1	12	3.779	17.880	0 < P < 1
4	2	0	0.815	0.815	0 < P < 1
4	3	1	0.176	3.871	0 < P < 1
4	4	0	0.038	0.038	0 < P < 1
4	5	0	0.008	0.008	0 < P < 1
4	6	10	18.184	3.684	0 < P < 1
4	Cohort	df= 1		17.593	P = 0.0000
5	1	8	10.681	0.673	0 < P < 1
5	2	3	2.302	0.212	0 < P < 1
5	3	0	0.496	0.496	0 < P < 1
5	4	0	0.107	0.107	0 < P < 1
5	5	0	0.023	0.023	0 < P < 1

5	6	54	51.390	0.133	0 < P < 1
5 Cohort	df=	2		0.807	P = 0.6679
6	1	16	5.587	19.407	0 < P < 1
6	2	3	1.204	2.678	0 < P < 1
6	3	0	0.260	0.260	0 < P < 1
6	4	0	0.056	0.056	0 < P < 1
6	5	15	26.893	5.260	0 < P < 1
6 Cohort	df=	1		25.163	P = 0.0000
7	1	25	37.795	4.332	0 < P < 1
7	2	3	8.146	3.251	0 < P < 1
7	3	3	1.756	0.882	0 < P < 1
7	4	1	0.378	1.021	0 < P < 1
7	5	198	181.925	1.420	0 < P < 1
7 Cohort	df=	3		10.634	P = 0.0139
8	1	20	8.052	17.729	0 < P < 1
8	2	0	1.735	1.735	0 < P < 1
8	3	0	0.374	0.374	0 < P < 1
8	4	29	38.838	2.492	0 < P < 1
8 Cohort	df=	2		22.331	P = 0.0000
9	1	38	41.903	0.364	0 < P < 1
9	2	13	9.032	1.744	0 < P < 1
9	3	1	1.947	0.460	0 < P < 1
9	4	203	202.119	0.004	0 < P < 1
9 Cohort	df=	2		1.199	P = 0.5490
10	1	28	10.846	27.134	0 < P < 1
10	2	2	2.338	0.049	0 < P < 1
10	3	36	52.817	5.355	0 < P < 1
10 Cohort	df=	2		32.537	P = 0.0000
11	1	39	42.067	0.224	0 < P < 1
11	2	7	9.067	0.471	0 < P < 1
11	3	210	204.866	0.129	0 < P < 1
11 Cohort	df=	2		0.824	P = 0.6625
12	1	30	13.639	19.626	0 < P < 1
12	2	53	69.361	3.859	0 < P < 1
12 Cohort	df=	1		23.485	P = 0.0000
13	1	46	39.438	1.092	0 < P < 1
13	2	194	200.562	0.215	0 < P < 1
13 Cohort	df=	1		1.306	P = 0.2530

@@ 1 0 0 47 207.123 21 190.424 -157.121 318.242

G Total (Degrees of freedom = 47) 207.123
Pr(Larger Chi-square) = 0.0000
With pooling, Degrees of freedom = 21 Pearson Chi-square = 190.424
Pr(Larger Chi-square) = 0.0000
Log-likelihood = -157.12123 Akaike Information Criterion = 318.24245

CPU time in seconds for last procedure was 0.03

INPUT --- PROC ESTIMATE NOVAR MAXFN=32000 NAME=SPG;

Number of parameters in model = 21

Number of parameters set equal = 18

Number of parameters fixed = 0

Number of parameters estimated = 3

Final function value 1081.9256 (Error Return = 0)

Number of significant digits 8

Number of function evaluations 71

95% Confidence Interval

I	Parameter	S(I)	Standard Error	Lower	Upper
1	1 PHI(1)	0.586343	0.291084E-01	0.529291	0.643396
2	1 PHI(2)	0.586343	0.291084E-01	0.529291	0.643396
3	1 PHI(3)	0.586343	0.291084E-01	0.529291	0.643396
4	1 PHI(4)	0.586343	0.291084E-01	0.529291	0.643396
5	1 PHI(5)	0.586343	0.291084E-01	0.529291	0.643396
6	1 PHI(6)	0.586343	0.291084E-01	0.529291	0.643396
7	1 PHI(7)	0.586343	0.291084E-01	0.529291	0.643396
8	2 p(2)	0.617879	0.328420E-01	0.553509	0.682250
9	2 p(3)	0.617879	0.328420E-01	0.553509	0.682250
10	2 p(4)	0.617879	0.328420E-01	0.553509	0.682250
11	2 p(5)	0.617879	0.328420E-01	0.553509	0.682250
12	2 p(6)	0.617879	0.328420E-01	0.553509	0.682250
13	2 p(7)	0.617879	0.328420E-01	0.553509	0.682250
14	2 p(8)	0.617879	0.328420E-01	0.553509	0.682250
15	3 gamma(1)	0.354799	0.316262E-01	0.292812	0.416786
16	3 gamma(2)	0.354799	0.316262E-01	0.292812	0.416786
17	3 gamma(3)	0.354799	0.316262E-01	0.292812	0.416786
18	3 gamma(4)	0.354799	0.316262E-01	0.292812	0.416786
19	3 gamma(5)	0.354799	0.316262E-01	0.292812	0.416786
20	3 gamma(6)	0.354799	0.316262E-01	0.292812	0.416786
21	3 gamma(7)	0.354799	0.316262E-01	0.292812	0.416786

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	31	21.595	4.096	0 < P < 1
1	2	4	4.838	0.145	0 < P < 1
1	3	0	1.084	1.084	0 < P < 1
1	4	1	0.243	2.360	0 < P < 1
1	5	0	0.054	0.054	0 < P < 1
1	6	0	0.012	0.012	0 < P < 1
1	7	0	0.003	0.003	0 < P < 1
1	8	132	140.171	0.476	0 < P < 1
1	Cohort	df= 2		4.817	P = 0.0899
2	1	7	11.231	1.594	0 < P < 1
2	2	4	2.516	0.875	0 < P < 1
2	3	0	0.564	0.564	0 < P < 1
2	4	0	0.126	0.126	0 < P < 1
2	5	0	0.028	0.028	0 < P < 1
2	6	0	0.006	0.006	0 < P < 1
2	7	20	16.528	0.729	0 < P < 1
2	Cohort	df= 2		2.501	P = 0.2864
3	1	12	47.174	26.227	0 < P < 1
3	2	10	10.570	0.031	0 < P < 1
3	3	4	2.368	1.124	0 < P < 1
3	4	1	0.531	0.415	0 < P < 1
3	5	0	0.119	0.119	0 < P < 1
3	6	1	0.027	35.570	0 < P < 1
3	7	339	306.212	3.511	0 < P < 1
3	Cohort	df= 3		32.638	P = 0.0000
4	1	12	8.333	1.614	0 < P < 1
4	2	0	1.867	1.867	0 < P < 1
4	3	1	0.418	0.809	0 < P < 1
4	4	0	0.094	0.094	0 < P < 1
4	5	0	0.021	0.021	0 < P < 1
4	6	10	12.267	0.419	0 < P < 1
4	Cohort	df= 2		2.850	P = 0.2405
5	1	8	8.355	0.015	0 < P < 1
5	2	3	1.872	0.680	0 < P < 1
5	3	0	0.419	0.419	0 < P < 1
5	4	0	0.094	0.094	0 < P < 1
5	5	0	0.021	0.021	0 < P < 1
5	6	54	54.238	0.001	0 < P < 1
5	Cohort	df= 2		0.163	P = 0.9219

6	1	16	12.318	1.101	0 < P < 1
6	2	3	2.760	0.021	0 < P < 1
6	3	0	0.618	0.618	0 < P < 1
6	4	0	0.139	0.139	0 < P < 1
6	5	15	18.165	0.552	0 < P < 1
6	Cohort df= 2			1.728	P = 0.4214
7	1	25	29.564	0.705	0 < P < 1
7	2	3	6.624	1.983	0 < P < 1
7	3	3	1.484	1.548	0 < P < 1
7	4	1	0.333	1.340	0 < P < 1
7	5	198	191.995	0.188	0 < P < 1
7	Cohort df= 2			1.138	P = 0.5660
8	1	20	17.752	0.285	0 < P < 1
8	2	0	3.977	3.977	0 < P < 1
8	3	0	0.891	0.891	0 < P < 1
8	4	29	26.379	0.260	0 < P < 1
8	Cohort df= 2			5.414	P = 0.0668
9	1	38	32.778	0.832	0 < P < 1
9	2	13	7.344	4.356	0 < P < 1
9	3	1	1.645	0.253	0 < P < 1
9	4	203	213.233	0.491	0 < P < 1
9	Cohort df= 2			4.116	P = 0.1277
10	1	28	23.911	0.699	0 < P < 1
10	2	2	5.357	2.104	0 < P < 1
10	3	36	36.732	0.015	0 < P < 1
10	Cohort df= 2			2.818	P = 0.2444
11	1	39	32.906	1.128	0 < P < 1
11	2	7	7.373	0.019	0 < P < 1
11	3	210	215.721	0.152	0 < P < 1
11	Cohort df= 2			1.299	P = 0.5223
12	1	30	30.070	0.000	0 < P < 1
12	2	53	52.930	0.000	0 < P < 1
12	Cohort df= 1			0.000	P = 0.9872
13	1	46	30.850	7.440	0 < P < 1
13	2	194	209.150	1.097	0 < P < 1
13	Cohort df= 1			8.538	P = 0.0035

@@ 2 0 0 46 104.630 22 68.0196 -105.875 217.750

G Total (Degrees of freedom = 46) 104.630

Pr(Larger Chi-square) = 0.0000

With pooling, Degrees of freedom = 22 Pearson Chi-square = 68.020

Pr(Larger Chi-square) = 0.0000

Log-likelihood = -105.87508 Akaike Information Criterion = 217.75016

CPU time in seconds for last procedure was 0.05

INPUT --- PROC ESTIMATE NOVAR MAXFN=32000 NAME=StPt;

Number of parameters in model = 21

Number of parameters set equal = 0

Number of parameters fixed = 8

Number of parameters estimated = 13

Final function value 1097.6643 (Error Return = 0)

Number of significant digits 6

I	Parameter	S(I)	Standard Error	95% Confidence Interval	
				Lower	Upper
1	1 PHI(1)	0.488248	0.142347	0.209248	0.767248
2	2 PHI(2)	0.222704	0.492480E-01	0.126178	0.319231
3	3 PHI(3)	0.551159	0.128118	0.300047	0.802270
4	4 PHI(4)	0.323701	0.548025E-01	0.216288	0.431114
5	5 PHI(5)	0.408204	0.589237E-01	0.292714	0.523695
6	6 PHI(6)	0.332919	0.442633E-01	0.246163	0.419675
7	7 PHI(7)	0.235294	0.236021E-01	0.189034	0.281554
8	8 p(2)	0.377931	0.118809	0.145065	0.610797
9	9 p(3)	0.230000	0.617062E-01	0.109056	0.350944
10	10 p(4)	0.373868	0.863731E-01	0.204577	0.543159
11	11 p(5)	0.471658	0.818681E-01	0.311196	0.632119
12	12 p(6)	0.450512	0.690642E-01	0.315146	0.585878
13	13 p(7)	0.619403	0.765506E-01	0.469364	0.769442
14	-14 p(8)	1.00000	0.000000E+00	1.00000	1.00000
15	-15 gamma(1)	1.00000	0.000000E+00	1.00000	1.00000
16	-16 gamma(2)	1.00000	0.000000E+00	1.00000	1.00000
17	-17 gamma(3)	1.00000	0.000000E+00	1.00000	1.00000
18	-18 gamma(4)	1.00000	0.000000E+00	1.00000	1.00000
19	-19 gamma(5)	1.00000	0.000000E+00	1.00000	1.00000
20	-20 gamma(6)	1.00000	0.000000E+00	1.00000	1.00000
21	-21 gamma(7)	1.00000	0.000000E+00	1.00000	1.00000

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	31	31.000	0.000	0 < P < 1
1	2	4	2.614	0.735	0 < P < 1
1	3	0	1.803	1.803	0 < P < 1
1	4	1	0.461	0.630	0 < P < 1
1	5	0	0.095	0.095	0 < P < 1
1	6	0	0.024	0.024	0 < P < 1
1	7	0	0.003	0.003	0 < P < 1
1	8	132	132.000	0.000	0 < P < 1
1	Cohort df=	3		1.541	P = 0.6729
2	1	7	1.588	18.447	0 < P < 1
2	2	4	1.095	7.702	0 < P < 1
2	3	0	0.280	0.280	0 < P < 1
2	4	0	0.058	0.058	0 < P < 1
2	5	0	0.015	0.015	0 < P < 1
2	6	0	0.002	0.002	0 < P < 1
2	7	20	27.962	2.267	0 < P < 1
2	Cohort df=	1		23.138	P = 0.0000
3	1	12	18.798	2.459	0 < P < 1
3	2	10	12.968	0.679	0 < P < 1
3	3	4	3.316	0.141	0 < P < 1
3	4	1	0.683	0.147	0 < P < 1
3	5	0	0.172	0.172	0 < P < 1
3	6	1	0.025	38.284	0 < P < 1
3	7	339	331.038	0.192	0 < P < 1
3	Cohort df=	3		4.106	P = 0.2503
4	1	12	4.739	11.123	0 < P < 1
4	2	0	1.212	1.212	0 < P < 1
4	3	1	0.250	2.255	0 < P < 1
4	4	0	0.063	0.063	0 < P < 1
4	5	0	0.009	0.009	0 < P < 1
4	6	10	16.727	2.706	0 < P < 1
4	Cohort df=	1		9.920	P = 0.0016
5	1	8	13.394	2.172	0 < P < 1
5	2	3	3.425	0.053	0 < P < 1
5	3	0	0.706	0.706	0 < P < 1
5	4	0	0.177	0.177	0 < P < 1

5	5	0	0.026	0.026	0 < P < 1
5	6	54	47.273	0.957	0 < P < 1
5 Cohort	df=	2		3.540	P = 0.1703
6	1	16	5.191	22.507	0 < P < 1
6	2	3	1.069	3.486	0 < P < 1
6	3	0	0.269	0.269	0 < P < 1
6	4	0	0.039	0.039	0 < P < 1
6	5	15	27.432	5.634	0 < P < 1
6 Cohort	df=	1		29.164	P = 0.0000
7	1	25	35.115	2.914	0 < P < 1
7	2	3	7.234	2.478	0 < P < 1
7	3	3	1.819	0.766	0 < P < 1
7	4	1	0.263	2.065	0 < P < 1
7	5	198	185.568	0.833	0 < P < 1
7 Cohort	df=	3		7.990	P = 0.0462
8	1	20	9.011	13.401	0 < P < 1
8	2	0	2.266	2.266	0 < P < 1
8	3	0	0.328	0.328	0 < P < 1
8	4	29	37.395	1.885	0 < P < 1
8 Cohort	df=	2		17.879	P = 0.0001
9	1	38	46.895	1.687	0 < P < 1
9	2	13	11.795	0.123	0 < P < 1
9	3	1	1.705	0.292	0 < P < 1
9	4	203	194.605	0.362	0 < P < 1
9 Cohort	df=	2		2.068	P = 0.3556
10	1	28	13.610	15.215	0 < P < 1
10	2	2	1.968	0.001	0 < P < 1
10	3	36	50.422	4.125	0 < P < 1
10 Cohort	df=	1		17.478	P = 0.0000
11	1	39	52.790	3.602	0 < P < 1
11	2	7	7.632	0.052	0 < P < 1
11	3	210	195.578	1.064	0 < P < 1
11 Cohort	df=	2		4.718	P = 0.0945
12	1	30	19.529	5.614	0 < P < 1
12	2	53	63.471	1.727	0 < P < 1
12 Cohort	df=	1		7.341	P = 0.0067
13	1	46	56.471	1.941	0 < P < 1
13	2	194	183.529	0.597	0 < P < 1
13 Cohort	df=	1		2.539	P = 0.1111

@@ 3 0 0 36 136.108 10 131.422 -121.614 269.228

G Total (Degrees of freedom = 36) 136.108

Pr(Larger Chi-square) = 0.0000

With pooling, Degrees of freedom = 10 Pearson Chi-square = 131.422

Pr(Larger Chi-square) = 0.0000

Log-likelihood = -121.61377

Akaike Information Criterion = 269.22754

CPU time in seconds for last procedure was 0.14

INPUT --- PROC ESTIMATE NOVAR MAXFN=32000 NAME=StPtGt;

Number of parameters in model = 21

Number of parameters set equal = 0

Number of parameters fixed = 2

Number of parameters estimated = 19

Final function value 1050.5491 (Error Return = 0)

Number of significant digits 6

I	Parameter	S(I)	Standard Error	95% Confidence Interval	
				Lower	Upper
1	1 PHI(1)	0.268398	0.498914E-01	0.170611	0.366185
2	2 PHI(2)	0.485112	0.131254	0.227854	0.742369
3	3 PHI(3)	0.674294	0.132072	0.415433	0.933156
4	4 PHI(4)	0.728724	0.128546	0.476773	0.980675
5	5 PHI(5)	0.517647	0.956648E-01	0.330144	0.705150
6	6 PHI(6)	0.555981	0.831053E-01	0.393094	0.718867
7	7 PHI(7)	0.361446	0.527329E-01	0.258089	0.464802
8	8 p(2)	0.687500	0.115878	0.460379	0.914621
9	9 p(3)	0.382353	0.833418E-01	0.219003	0.545703
10	10 p(4)	0.633333	0.879815E-01	0.460890	0.805777
11	11 p(5)	0.606061	0.850581E-01	0.439347	0.772775
12	12 p(6)	0.612245	0.696055E-01	0.475818	0.748672
13	13 p(7)	0.714286	0.697071E-01	0.577660	0.850912
14	-20 p(8)	1.00000	0.000000E+00	1.00000	1.00000
15	-21 gamma(1)	1.00000	0.000000E+00	1.00000	1.00000
16	16 gamma(2)	0.215011	0.650886E-01	0.874375E-01	0.342585
17	17 gamma(3)	0.299408	0.988362E-01	0.105689	0.493127
18	18 gamma(4)	0.248970	0.557393E-01	0.139721	0.358219
19	19 gamma(5)	0.499608	0.105866	0.292110	0.707106
20	14 gamma(6)	0.395313	0.750206E-01	0.248272	0.542353
21	15 gamma(7)	0.530278	0.104530	0.325399	0.735157

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	31	31.000	0.000	0 < P < 1
1	2	4	2.614	0.735	0 < P < 1
1	3	0	1.803	1.803	0 < P < 1
1	4	1	0.461	0.630	0 < P < 1
1	5	0	0.095	0.095	0 < P < 1
1	6	0	0.024	0.024	0 < P < 1
1	7	0	0.003	0.003	0 < P < 1
1	8	132	132.000	0.000	0 < P < 1
1	Cohort	df= 3		1.541	P = 0.6729
2	1	7	5.750	0.272	0 < P < 1
2	2	4	3.967	0.000	0 < P < 1
2	3	0	1.014	1.014	0 < P < 1
2	4	0	0.209	0.209	0 < P < 1
2	5	0	0.053	0.053	0 < P < 1
2	6	0	0.008	0.008	0 < P < 1
2	7	20	20.000	0.000	0 < P < 1
2	Cohort	df= 2		0.569	P = 0.7523
3	1	12	14.636	0.475	0 < P < 1
3	2	10	10.097	0.001	0 < P < 1
3	3	4	2.582	0.779	0 < P < 1
3	4	1	0.532	0.412	0 < P < 1
3	5	0	0.134	0.134	0 < P < 1
3	6	1	0.019	49.727	0 < P < 1
3	7	339	339.000	0.000	0 < P < 1
3	Cohort	df= 3		2.763	P = 0.4296
4	1	12	9.822	0.483	0 < P < 1
4	2	0	2.511	2.511	0 < P < 1
4	3	1	0.517	0.450	0 < P < 1
4	4	0	0.130	0.130	0 < P < 1
4	5	0	0.019	0.019	0 < P < 1
4	6	10	10.000	0.000	0 < P < 1
4	Cohort	df= 2		1.975	P = 0.3724
5	1	8	8.311	0.012	0 < P < 1
5	2	3	2.125	0.360	0 < P < 1
5	3	0	0.438	0.438	0 < P < 1
5	4	0	0.110	0.110	0 < P < 1

```

5      5      0      0.016      0.016      0 < P < 1
5      6      54      54.000      0.000      0 < P < 1
5 Cohort df= 2      0.048      P = 0.9765
6      1      16      15.016      0.064      0 < P < 1
6      2      3      3.093      0.003      0 < P < 1
6      3      0      0.778      0.778      0 < P < 1
6      4      0      0.112      0.112      0 < P < 1
6      5      15      15.000      0.000      0 < P < 1
6 Cohort df= 2      0.307      P = 0.8575
7      1      25      25.290      0.003      0 < P < 1
7      2      3      5.210      0.937      0 < P < 1
7      3      3      1.310      2.179      0 < P < 1
7      4      1      0.189      3.468      0 < P < 1
7      5      198      198.000      0.000      0 < P < 1
7 Cohort df= 2      0.016      P = 0.9921
8      1      20      15.529      1.287      0 < P < 1
8      2      0      3.906      3.906      0 < P < 1
8      3      0      0.565      0.565      0 < P < 1
8      4      29      29.000      0.000      0 < P < 1
8 Cohort df= 2      5.758      P = 0.0562
9      1      38      40.376      0.140      0 < P < 1
9      2      13      10.155      0.797      0 < P < 1
9      3      1      1.468      0.149      0 < P < 1
9      4      203      203.000      0.000      0 < P < 1
9 Cohort df= 2      0.626      P = 0.7313
10     1      28      26.211      0.122      0 < P < 1
10     2      2      3.789      0.845      0 < P < 1
10     3      36      36.000      0.000      0 < P < 1
10 Cohort df= 2      0.967      P = 0.6166
11     1      39      40.189      0.035      0 < P < 1
11     2      7      5.811      0.243      0 < P < 1
11     3      210      210.000      0.000      0 < P < 1
11 Cohort df= 2      0.279      P = 0.8699
12     1      30      30.000      0.000      0 < P < 1
12     2      53      53.000      0.000      0 < P < 1
12 Cohort df= 1      0.000      P = 1.0000
13     1      46      46.000      0.000      0 < P < 1
13     2      194      194.000      0.000      0 < P < 1
13 Cohort df= 1      0.000      P = 1.0000

```

```

@@ 4 0 0 30 41.8773 7 14.8486 -74.4986 186.997

```

```

G Total (Degrees of freedom = 30) 41.877
Pr(Larger Chi-square) = 0.0733
With pooling, Degrees of freedom = 7 Pearson Chi-square = 14.849
Pr(Larger Chi-square) = 0.0380

```

```

Log-likelihood = -74.498573 Akaike Information Criterion = 186.99715

```

```

CPU time in seconds for last procedure was 0.21

```

```

INPUT --- PROC TEST;

```

Submodel	Name	Log-likelihood	NDF	Akaike Inf. Criter.	G-O-F
1	SP	-157.12123	47	318.24245	0.0000
2	SPG	-105.87508	46	217.75016	0.0000
3	STPT	-121.61377	36	269.22754	0.0000
4	STPTGT	-74.498573	30	186.99715	0.0733

```

Likelihood Ratio Tests Between Models

```

General Submodel	Reduced Submodel	Chi-square	Degrees Freedom	Pr(Larger Chi-square)
------------------	------------------	------------	-----------------	-----------------------

SPG	SP	102.492	1	0.0000
STPT	SP	71.015	11	0.0000
STPTGT	SP	165.245	17	0.0000
STPT	SPG	0.000	10	1.0000
STPTGT	SPG	62.753	16	0.0000
STPTGT	STPT	94.230	6	0.0000

* * WARNING * * Sequence of models reinitialized to zero.

CPU time in seconds for last procedure was 0.00

INPUT --- PROC STOP;

CPU time in minutes for this job was 0.01

E X E C U T I O N S U C C E S S F U L

Hardware Considerations

The program has also been compiled for DOS and Windows95.

Software Installation

To install TMSURVIV on a PC simply make a sub-directory to contain the programs and copy the files from the floppy disk. The disk contains the executable program file, so no compilation is necessary unless you wish to alter the dimensions. Here are the commands to install the TMSURVIV programs onto the hard disk of a PC:

c:> **mkdir tmsrv**

c:> **cd tmsrv**

c:> **xcopy a:.* /s**

To install TMSURVIV on other computers, a FORTRAN compiler will be required. The files must first be transferred to disk on the computer, then compiled and linked into an executable program file. A "make" file is included which will create the executable program file from the source files if the target computer has the make utility (as most Unix systems do). If the target computer doesn't have a make utility, a "batch" file is included to compile all of the routines. Most likely, the make file or batch file will have to be edited to reflect the names of the compiler and linker on the target system.

Literature Cited

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Pollock, K.H., J.D. Nichols, C. Brownie, and J.E. Hines. 1990. Statistical inference for capture-recapture experiments. *Wildlife Monographs* 107. 97pp.

White, G.C. 1983. Numerical estimation of survival rates from band-recovery and biotelemetry data. *The Journal of Wildlife Management* 47:716-728.

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