RDSURVIV

User's Manual

by

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Introduction

Program RDSURVIV (**R**obust-**D**esign-**SURVIV**al analysis) computes parameter estimates of survival and capture probability and temporary emigration using models described in "Estimating Temporary Emigration using Capture-recapture Data with Pollock's Robust" (Kendall et. al., 1997). Actually, RDSURVIV is a specially modified version of Dr. G. White's program SURVIV (White, 1983) which incorporates the robust-design models. With this program and it's companion program, CNVRDSRV, users are able to get parameter estimates for these complex models from capture-history data without having to specify the cell probabilities.

This program/method should be used in cases where a significant portion of the sampled population is unavailable for capture during some of the sampling periods. Ignoring the situation by using standard open model Jolly-Seber analysis will result in biased estimates of population size and capture probability. For example, if the trapping area only allows the capture of breeders, then the animals which are non-breeders in a particular sample are "temporary emigrants" for that sample since their probability of capture is zero.

RDSURVIV is intended to be used in a situation where the sampling experiment consists of a combination of both "closed" and "open" model design. Under the "closed" part of the design, animals are captured, tagged and released repeatedly over a short period of time. It is called "closed" because it is assumed that the samples are taken over such a short period of time that the population is "closed" to any type of additions or deletions to the population (ie., the population size is fixed). Under the "open" part of the design, the "closed" type samples are repeated after a period of time long enough to allow additions and deletions to the population. In the program and documentation, samples taken during the "open" part of the experiment are called "primary" or "major" sampling periods. Sampling occasions within the primary periods where the population is assumed closed are

called "secondary" or "minor" sampling periods. An example of this design is one where small mammals are captured on the first five days of each month for ten months. Each day would be a secondary period, and each group of five days of the month would be considered a primary period. We would expect that there would be almost no change in the population over the five days of the secondary periods, but there would be changes between months (primary periods).

Output from RDSURVIV includes survival probability estimates, capture probability estimates, estimates of the proportion of temporary emigrants, goodness-of-fit tests, and likelihood-ratio tests. Estimates may be computed under the "Markovian temporary emigration" models or the "Random temporary emigration" models. The Markovian models assume that probability of an animal temporarily emigrating depends on weather the animal was a temporary emigrant in the previous sampling occasion. "Random emigration models assume that the probability of an animal temporarily emigrating does not depend on weather the animal was a temporary emigrant in the previous sampling occasion.

By default, several models are generated. The names of the models are combinations of the names used by program CAPTURE for closed models, and a commonly used scheme for open models used by programs MARK and SURGE.

Input to RDSURVIV consists of statements which define the capture data and statements defining the selected model structure. The format of the input file is the same as for program SURVIV except that no cell probabilities need be given. The statements defining the data consist of 2 parts. The first part consists of a summary of the secondary period data, and the second part consists of the data summarized by primary period. The format of the primary-period summary is what has been commonly referred to as an m_{ij} array or Leslie method-B Table.

M_{ij} array

	next recaptured in		
number released	2	3	4
R_1	m_{12}	m_{13}	m_{14}
R_2		m_{23}	m_{24}
R_3			m_{34}

R_i denotes the number of animals released in major period *i*,

m_{ij} denotes the number of animals recaptured in major period *j* which were last caught in major period *i*

The secondary-period data consists of a stratification of the major-period data by secondary-period capture-history with one modification: Instead of using the total number of animals released in the primary period, the number of unmarked animals released is used. So, the secondary period data should be in the following format:

$COHORT=u_1;$
$X_{11..1}:;$
$X_{11..0}:;$
:
:
$X_{00..1}:;$
$COHORT=m_{12};$
$X_{11..1}:;$
$X_{11..0}:;$
:
:
$X_{00..1}:;$
$COHORT=m_{13};$
$X_{11..1}:;$
$X_{11..0}:;$
:
:
$X_{00..1}:;$
:
:

where u_i represents the number of unmarked animals which were caught and released in primary period *i*, and

X_i represents the number of animals with capture-history *i*.

The secondary-period data is followed by the primary-period data (which is the m_{ij} array) in the following format:

$COHORT=R_1;$
$m_{12}:;$
$m_{13}:;$
$m_{14}:;$
$COHORT=R_2;$
$m_{23}:;$
$m_{24}:;$
$COHORT=R_3;$
$m_{34}:;$

the number of animals captured and released in each time-period and stratum, and the number next recaptured in each subsequent time-period and stratum. Statements which set parameters equal to other parameters define model structure.

Although RDSURVIV eliminates the need for specifying cell probabilities, the job of summarizing capture-history records and defining model structure can be very complicated and can lead to errors. Program CNVRDSRV was created to automate this process. CNVRDSRV reads as input the capture-history records and produces all of the statements necessary to run program RDSURVIV under the

"Markovian emigration" or "Random emigration" model sets described above.

Using CNVRDSRV

To run CNVRDSRV, type the following command at the DOS prompt:

CNVRDSRV caphisfile n k_1 k_2 k_3 ... k_n

Where *n* is the number of primary time periods, and

k_i is the number of secondary time periods per primary time period.

CNVRDSRV will print a summary of movements and create a file called CNVRDSRV.OUT containing a summary of the data and the statements defining the desired models.

Here is a portion of a sample input file containing capture-history records which can be converted to RDSURVIV input by program CNVRDSRV:

```
000 000 000 100        33
000 000 000 101        22
000 000 000 110        22
000 000 000 111        15
000 000 001 000        62
000 000 001 001         9
000 000 001 010         9
000 000 001 011         6
000 000 001 100         9
000 000 001 101         6
000 000 001 110         6
000 000 001 111         4
000 000 010 000        62
000 000 010 001         9
000 000 010 010         9
000 000 010 011         6
000 000 010 100         9
000 000 010 101         6
000 000 010 110         6
```

In this example, there are 4 primary periods and 3 secondary periods per primary period for a total of 12 capture occasions. Also, the capture-histories are summarized with the last number in the line indicating the number of animals which had each particular capture-history. Note that the spaces seperating the zeros and ones in the capture-history are ignored by the program and are only there to make it easier to check the data.

From the first record in this file, you can see that 33 animals were captured on the first secondary period of primary period 4. 22 animals were captured on the first and third secondary period of primary period 4.

The output file created by CNVRDSRV which can be input to RDSURVIV should look something like this:

```
PROC TITLE ;
PROC MODEL NPAR=32 ADDCELL;
COHORT=19584 /* u(1) */;
1575:  /* 111 */;
2407:  /* 110 */;
2407:  /* 101 */;
3596:  /* 100 */;
2407:  /* 011 */;
3596:  /* 010 */;
COHORT=2406 /* u(2) */;
201:  /* 111 */;
295:  /* 110 */;
295:  /* 101 */;
440:  /* 100 */;
295:  /* 011 */;
440:  /* 010 */;
COHORT=8818 /* m(1,2) */;
694:  /* 111 */;
1086:  /* 110 */;
1086:  /* 101 */;
1622:  /* 100 */;
1086:  /* 011 */;
1622:  /* 010 */;
COHORT=605 /* u(3) */;
50:  /* 111 */;
74:  /* 110 */;
74:  /* 101 */;
111:  /* 100 */;
74:  /* 011 */;
111:  /* 010 */;
COHORT=2223 /* m(1,3) */;
183:  /* 111 */;
274:  /* 110 */;
274:  /* 101 */;
406:  /* 100 */;
274:  /* 011 */;
406:  /* 010 */;
COHORT=5009 /* m(2,3) */;
383:  /* 111 */;
617:  /* 110 */;
617:  /* 101 */;
925:  /* 100 */;
617:  /* 011 */;
925:  /* 010 */;
COHORT=180 /* u(4) */;
15:  /* 111 */;
22:  /* 110 */;
22:  /* 101 */;
33:  /* 100 */;
22:  /* 011 */;
33:  /* 010 */;
COHORT=664 /* m(1,4) */;
```

```
55:  /* 111 */;
82:  /* 110 */;
82:  /* 101 */;
121:  /* 100 */;
82:  /* 011 */;
121:  /* 010 */;
COHORT=1287 /* m(2,4) */;
108:  /* 111 */;
160:  /* 110 */;
160:  /* 101 */;
233:  /* 100 */;
160:  /* 011 */;
233:  /* 010 */;
COHORT=3483 /* m(3,4) */;
258:  /* 111 */;
433:  /* 110 */;
433:  /* 101 */;
642:  /* 100 */;
433:  /* 011 */;
642:  /* 010 */;
COHORT=19584   /* R(1)  */;
8818:  /*  m(1,2)  */;
2223:  /*  m(1,3)  */;
664:  /*  m(1,4)  */;
COHORT=11224   /* R(2)  */;
5009:  /*  m(2,3)  */;
1287:  /*  m(2,4)  */;
COHORT=7837   /* R(3)  */;
3483:  /*  m(3,4)  */;
LABELS;
S(1)=p(1,1);
S(2)=p(1,2);
S(3)=p(1,3);
S(4)=c(1,2);
S(5)=c(1,3);
S(6)=p(2,1);
S(7)=p(2,2);
S(8)=p(2,3);
S(9)=c(2,2);
S(10)=c(2,3);
S(11)=p(3,1);
S(12)=p(3,2);
S(13)=p(3,3);
S(14)=c(3,2);
S(15)=c(3,3);
S(16)=p(4,1);
S(17)=p(4,2);
S(18)=p(4,3);
S(19)=c(4,2);
S(20)=c(4,3);
S(21)=PHI(1);
S(22)=PHI(2);
S(23)=PHI(3);
S(24)=GAM'(2);
S(25)=GAM'(3);
S(26)=GAM'(4);
S(27)=GAM(3);
S(28)=GAM(4);
S(29)=THETA(1);
S(30)=THETA(2);
S(31)=THETA(3);
S(32)=THETA(4);
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(0)Sng;
CONSTRAINTS;
S(2)=S(1) /* p(1,2)=p(1,1) */;
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S(3)=S(1) /* p(1,3)=p(1,1) */;
S(4)=S(1) /* c(1,2)=p(1,1) */;
S(5)=S(1) /* c(1,3)=p(1,1) */;
S(7)=S(6) /* p(2,2)=p(2,1) */;
S(8)=S(6) /* p(2,3)=p(2,1) */;
S(9)=S(6) /* c(2,2)=p(2,1) */;
S(10)=S(6) /* c(2,3)=p(2,1) */;
S(12)=S(11) /* p(3,2)=p(3,1) */;
S(13)=S(11) /* p(3,3)=p(3,1) */;
S(14)=S(11) /* c(3,2)=p(3,1) */;
S(15)=S(11) /* c(3,3)=p(3,1) */;
S(17)=S(16) /* p(4,2)=p(4,1) */;
S(18)=S(16) /* p(4,3)=p(4,1) */;
S(19)=S(16) /* c(4,2)=p(4,1) */;
S(20)=S(16) /* c(4,3)=p(4,1) */;
S(22)=S(21) /* PHI(2)=PHI(1) */;
S(23)=S(21) /* PHI(3)=PHI(1) */;
S(24)=0 /* GAM'(2)=0 -> no emigration */;
S(25)=0 /* GAM'(3)=0 -> no emigration */;
S(26)=0 /* GAM'(4)=0 -> no emigration */;
S(27)=0 /* GAM(3)=0 -> no emigration */;
S(28)=0 /* GAM(4)=0 -> no emigration */;
S(29)=1 /* THETA(1) not used in this model */;
S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(b)Sng;
INITIAL; RETAIN=A; CONSTRAINTS;
S(2)=S(1) /* p(1,2)=p(1,1) */;
S(3)=S(1) /* p(1,3)=p(1,1) */;
S(5)=S(4) /* c(1,2)=c(1,1) */;
S(7)=S(6) /* p(2,2)=p(2,1) */;
S(8)=S(6) /* p(2,3)=p(2,1) */;
S(10)=S(9) /* c(2,2)=c(2,1) */;
S(12)=S(11) /* p(3,2)=p(3,1) */;
S(13)=S(11) /* p(3,3)=p(3,1) */;
S(15)=S(14) /* c(3,2)=c(3,1) */;
S(17)=S(16) /* p(4,2)=p(4,1) */;
S(18)=S(16) /* p(4,3)=p(4,1) */;
S(20)=S(19) /* c(4,2)=c(4,1) */;
S(24)=0 /* GAM'(2)=0 -> no emigration */;
S(25)=0 /* GAM'(3)=0 -> no emigration */;
S(26)=0 /* GAM'(4)=0 -> no emigration */;
S(27)=0 /* GAM(3)=0 -> no emigration */;
S(28)=0 /* GAM(4)=0 -> no emigration */;
S(29)=1 /* THETA(1) not used in this model */;
S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(t)Stng;
INITIAL; RETAIN=A; CONSTRAINTS;
S(4)=S(2) /* c(1,2)=c(1,2) */;
S(5)=S(3) /* c(1,3)=c(1,3) */;
S(9)=S(7) /* c(2,2)=c(2,2) */;
S(10)=S(8) /* c(2,3)=c(2,3) */;
S(14)=S(12) /* c(3,2)=c(3,2) */;
S(15)=S(13) /* c(3,3)=c(3,3) */;
S(19)=S(17) /* c(4,2)=c(4,2) */;
S(20)=S(18) /* c(4,3)=c(4,3) */;
S(24)=0 /* GAM'(2)=0 -> no emigration */;
S(25)=0 /* GAM'(3)=0 -> no emigration */;
S(26)=0 /* GAM'(4)=0 -> no emigration */;
S(27)=0 /* GAM(3)=0 -> no emigration */;
S(28)=0 /* GAM(4)=0 -> no emigration */;
S(29)=1 /* THETA(1) not used in this model */;
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S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(bt)Stng;
INITIAL; RETAIN=A;
S(32)=1;
S(31)=1;
S(30)=1;
S(29)=1;
CONSTRAINTS;
S(4)=-1 /* c(1,2)=-1 -> c(1,2)=p(1,2)**THETA(1) */;
S(5)=-1 /* c(1,3)=-1 -> c(1,3)=p(1,3)**THETA(1) */;
S(9)=-1 /* c(2,2)=-1 -> c(2,2)=p(2,2)**THETA(2) */;
S(10)=-1 /* c(2,3)=-1 -> c(2,3)=p(2,3)**THETA(2) */;
S(14)=-1 /* c(3,2)=-1 -> c(3,2)=p(3,2)**THETA(3) */;
S(15)=-1 /* c(3,3)=-1 -> c(3,3)=p(3,3)**THETA(3) */;
S(19)=-1 /* c(4,2)=-1 -> c(4,2)=p(4,2)**THETA(4) */;
S(20)=-1 /* c(4,3)=-1 -> c(4,3)=p(4,3)**THETA(4) */;
S(24)=0 /* GAM'(2)=0 -> no emigration */;
S(25)=0 /* GAM'(3)=0 -> no emigration */;
S(26)=0 /* GAM'(4)=0 -> no emigration */;
S(27)=0 /* GAM(3)=0 -> no emigration */;
S(28)=0 /* GAM(4)=0 -> no emigration */;
S(29)<20 /* THETA(1) not used in this model */;
S(30)<20 /* THETA(2) not used in this model */;
S(31)<20 /* THETA(3) not used in this model */;
S(32)<20 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(0)Sgr;
CONSTRAINTS;
S(2)=S(1) /* p(1,2)=p(1,1) */;
S(3)=S(1) /* p(1,3)=p(1,1) */;
S(4)=S(1) /* c(1,2)=p(1,1) */;
S(5)=S(1) /* c(1,3)=p(1,1) */;
S(7)=S(6) /* p(2,2)=p(2,1) */;
S(8)=S(6) /* p(2,3)=p(2,1) */;
S(9)=S(6) /* c(2,2)=p(2,1) */;
S(10)=S(6) /* c(2,3)=p(2,1) */;
S(12)=S(11) /* p(3,2)=p(3,1) */;
S(13)=S(11) /* p(3,3)=p(3,1) */;
S(14)=S(11) /* c(3,2)=p(3,1) */;
S(15)=S(11) /* c(3,3)=p(3,1) */;
S(17)=S(16) /* p(4,2)=p(4,1) */;
S(18)=S(16) /* p(4,3)=p(4,1) */;
S(19)=S(16) /* c(4,2)=p(4,1) */;
S(20)=S(16) /* c(4,3)=p(4,1) */;
S(25)=S(24) /* GAM'(3)=GAM'(2) */;
S(26)=S(24) /* GAM'(4)=GAM'(2) */;
S(27)=S(24) /* GAM(3)=GAM'(2)  */;
S(28)=S(24) /* GAM(4)=GAM'(2)  */;
S(29)=1 /* THETA(1) not used in this model */;
S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(0)Sgm;
CONSTRAINTS;
S(2)=S(1) /* p(1,2)=p(1,1) */;
S(3)=S(1) /* p(1,3)=p(1,1) */;
S(4)=S(1) /* c(1,2)=p(1,1) */;
S(5)=S(1) /* c(1,3)=p(1,1) */;
S(7)=S(6) /* p(2,2)=p(2,1) */;
S(8)=S(6) /* p(2,3)=p(2,1) */;
S(9)=S(6) /* c(2,2)=p(2,1) */;
S(10)=S(6) /* c(2,3)=p(2,1) */;
S(12)=S(11) /* p(3,2)=p(3,1) */;
S(13)=S(11) /* p(3,3)=p(3,1) */;
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S(14)=S(11) /* c(3,2)=p(3,1) */;
S(15)=S(11) /* c(3,3)=p(3,1) */;
S(17)=S(16) /* p(4,2)=p(4,1) */;
S(18)=S(16) /* p(4,3)=p(4,1) */;
S(19)=S(16) /* c(4,2)=p(4,1) */;
S(20)=S(16) /* c(4,3)=p(4,1) */;
S(25)=S(24) /* GAM'(3)=GAM'(2) */;
S(26)=S(24) /* GAM'(4)=GAM'(2) */;
S(28)=S(27) /* GAM(4)=GAM(3) */;
S(29)=1 /* THETA(1) not used in this model */;
S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(b)Sgr;
INITIAL; RETAIN=A; CONSTRAINTS;
S(2)=S(1) /* p(1,2)=p(1,1) */;
S(3)=S(1) /* p(1,3)=p(1,1) */;
S(5)=S(4) /* c(1,3)=p(1,1) */;
S(7)=S(6) /* p(2,2)=p(2,1) */;
S(8)=S(6) /* p(2,3)=p(2,1) */;
S(10)=S(9) /* c(2,3)=p(2,1) */;
S(12)=S(11) /* p(3,2)=p(3,1) */;
S(13)=S(11) /* p(3,3)=p(3,1) */;
S(15)=S(14) /* c(3,3)=p(3,1) */;
S(17)=S(16) /* p(4,2)=p(4,1) */;
S(18)=S(16) /* p(4,3)=p(4,1) */;
S(20)=S(19) /* c(4,3)=p(4,1) */;
S(25)=S(24) /* GAM'(3)=GAM'(2) */;
S(26)=S(24) /* GAM'(4)=GAM'(2) */;
S(27)=S(24) /* GAM(3)=GAM'(2)  */;
S(28)=S(24) /* GAM(4)=GAM'(2)  */;
S(29)=1 /* THETA(1) not used in this model */;
S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(b)Sgm;
INITIAL; RETAIN=A; CONSTRAINTS;
S(2)=S(1) /* p(1,2)=p(1,1) */;
S(3)=S(1) /* p(1,3)=p(1,1) */;
S(5)=S(4) /* c(1,3)=p(1,1) */;
S(7)=S(6) /* p(2,2)=p(2,1) */;
S(8)=S(6) /* p(2,3)=p(2,1) */;
S(10)=S(9) /* c(2,3)=p(2,1) */;
S(12)=S(11) /* p(3,2)=p(3,1) */;
S(13)=S(11) /* p(3,3)=p(3,1) */;
S(15)=S(14) /* c(3,3)=p(3,1) */;
S(17)=S(16) /* p(4,2)=p(4,1) */;
S(18)=S(16) /* p(4,3)=p(4,1) */;
S(20)=S(19) /* c(4,3)=p(4,1) */;
S(25)=S(24) /* GAM'(3)=GAM'(2) */;
S(26)=S(24) /* GAM'(4)=GAM'(2) */;
S(28)=S(27) /* GAM(4)=GAM(3)  */;
S(29)=1 /* THETA(1) not used in this model */;
S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(t)Sgr(t);
INITIAL; RETAIN=A; CONSTRAINTS;
S(4)=S(2) /* c(1,2)=c(1,2) */;
S(5)=S(3) /* c(1,3)=c(1,3) */;
S(9)=S(7) /* c(2,2)=c(2,2) */;
S(10)=S(8) /* c(2,3)=c(2,3) */;
S(14)=S(12) /* c(3,2)=c(3,2) */;
S(15)=S(13) /* c(3,3)=c(3,3) */;
S(19)=S(17) /* c(4,2)=c(4,2) */;
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S(20)=S(18) /* c(4,3)=c(4,3) */;
S(26)=S(25) /* GAM'(last-1)=GAM'(last) */;
S(27)=S(25) /* GAM(3)=GAM'(3) */;
S(28)=S(25) /* GAM(4)=GAM'(3) */;
S(29)=1 /* THETA(1) not used in this model */;
S(30)=1 /* THETA(2) not used in this model */;
S(31)=1 /* THETA(3) not used in this model */;
S(32)=1 /* THETA(4) not used in this model */;
PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(bt)Sgr(t);
INITIAL; RETAIN=A;
S(32)=1;
S(31)=1;
S(30)=1;
S(29)=1;
CONSTRAINTS;
S(4)=-1 /* c(1,2)=-1 -> c(1,2)=p(1,2)**THETA(1) */;
S(5)=-1 /* c(1,3)=-1 -> c(1,3)=p(1,3)**THETA(1) */;
S(9)=-1 /* c(2,2)=-1 -> c(2,2)=p(2,2)**THETA(2) */;
S(10)=-1 /* c(2,3)=-1 -> c(2,3)=p(2,3)**THETA(2) */;
S(14)=-1 /* c(3,2)=-1 -> c(3,2)=p(3,2)**THETA(3) */;
S(15)=-1 /* c(3,3)=-1 -> c(3,3)=p(3,3)**THETA(3) */;
S(19)=-1 /* c(4,2)=-1 -> c(4,2)=p(4,2)**THETA(4) */;
S(20)=-1 /* c(4,3)=-1 -> c(4,3)=p(4,3)**THETA(4) */;
S(26)=S(25) /* GAM'(last-1)=GAM'(last) */;
S(27)=S(25) /* GAM(3)=GAM'(3) */;
S(28)=S(25) /* GAM(4)=GAM'(3) */;
S(29)<20 /* THETA(1) used to compute c(1,j) */;
S(30)<20 /* THETA(2) used to compute c(2,j) */;
S(31)<20 /* THETA(3) used to compute c(3,j) */;
S(32)<20 /* THETA(4) used to compute c(4,j) */;
PROC TEST; PROC STOP;
```

This file is an ASCII text file which can be edited with any editor or word-processor (If using a word-processor, be sure to save as ASCII text file - not the default). When the file is created by CNVRDSRV, you may edit it to enter a title, or proceed to run the analysis with RDSURVIV.

The following section describes the statements in the file produced by CNVRDSRV.

The title statement is used to identify the data used in the analysis. You may enter any string you like as long as it is enclosed by single quote marks (') and the statement ends with a semicolon (;). In the file, any text enclosed by the characters "/*" and "*/" are comments. CNVRDSRV inserts comments to make the file easy to read.

The model definition statements start with "PROC MODEL NPAR=32 ADDCELL;" and end with "3483: /* m(3,4) */;". The "NPAR=32" indicates the maximum number of parameters (estimated or fixed) in any of the following models. In this example there are 20 (5x4) capture probabilities, 3 survival rate parameters, and 9 temporary emigration probability parameters, giving 32 parameters.

The "COHORT=" statements and the statements that follow contain the summarized data as described above. By looking at the commented text next to the numbers, you can easily see that 19584 animals were captured in primary period 1. Of those 19584 captured as unmarked in primary period 1, 1575 were captured in all three secondary periods. 2407 animals were captured in the first two but not the third secondary period. RDSURVIV computes the number captured in only the last secondary period by subtracting the sum of the other six numbers from the total cohort size (19584).

The next "COHORT=" statement indicates that 2406 animals were caught for the first time in primary period 2 (u(2)=unmarked in 2). 201 of those animals were caught in all three secondary periods. etc.

The m(1,2) in the comments of the next "COHORT=" statement indicates that those 8818 animals were captured in primary period 2, and were last caught in primary period 1. 694 of those animals were caught in all three secondary periods of primary period 2.

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 capture probability parameters are *p* and *c*, where p(i,j) is the probability of capture for unmarked animals in secondary period *j* of primary period *i*, and c(i,j) is the probability of capture for previously caught animals in secondary period *j* of primary period *i*. The survival rate parameters are PHI(i), for i=1 to k primary periods. The parameter GAM'(i) is the probability of an animal being a temporary emigrant given that it was not a temporary emigrant in the previous primary period (i-1). The parameter, GAM(i), is the probability of an animal being a temporary emigrant given that it was a temporary emigrant in the previous primary period (i-1).

By defining the parameters this way, we are able to generate estimates with various assumptions about capture probability and temporary emigration. Under the most general model using these parameters, it is not possible to compute time-specific capture probabilities for both unmarked and marked animals. As a compromise, we can generate a model where capture probabilities are time-specific, but the capture probabilities for marked animals is a function of capture probabilities for unmarked, see Burnham. (So they are different, but not independent.)

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.

The statements following the "CONSTRAINTS" statement describe each model in terms of the most general model. In model "M(0)Sng", the capture probabilities are constant within secondary periods, survival rates are assumed to be constant across primary periods, and there is no temporary emigration (ng is an abbreviation for no gamma). The "M(0)" part of the model name comes from the naming convention used by program CAPTURE for closed model capture-recapture analysis. In this model, capture probabilities are constant over time (secondary periods) and are the same for unmarked and marked individuals. The statement which sets p(1,2)=p(1,1) indicates that the capture probability in the second secondary period of the first primary period is the same as the capture probability in the first secondary period of the first primary period. Similarly for p(1,3)=p(1,1), c(1,2)=p(1,1) and c(1,3)=p(1,1).

The constant survival rate for this model is achieved by setting the second and third survival rates equal to the first survival rate (PHI(2)=PHI(1), PHI(3)=PHI(1)).To indicate that there is no temporary emigration, all GAM' and GAM parameters are set equal to zero (probability of being a temporary emigrant is zero regardless of status in the previous period).

In this model, the parameter THETA is not used, so it is set to 1.0. The THETA parameters are only used when capture probabilities are time-specific and different for unmarked and marked animals (see model M(bt) below).

The next model is defined starting with the next "PROC ESTIMATE" statement. This model is the same as the first model except that capture probabilities for unmarked animals are different than those of marked animals. The name for this model, M(b), indicates that there is a behavior effect on capture probabilities, but no time effect. So, capture probabilities are constant over time (within a primary period), but different for previously captured animals. Looking at the constraints for this model, this becomes evident. The p(1,2) and p(1,3) is set equal to p(1,1) as before, but c(1,2) is set equal to c(1,1), not p(1,1). This means that for the first primary period there are two distinct capture probability parameters: p(1,1) - capture probability for unmarked animals, and c(1,1) - capture probability for marked animals.

The next "PROC ESTIMATE" statement defines a model where capture-probability is time-specific within primary periods, but the same for unmarked and marked animals. As in the previous models, survival rates are assumed constant over primary periods and there is no temporary emigration.

Rather than detail every model, the following table summarizes the models initially created by CNVRDSRV:

Model	capture probability assumptions	Survival rate assumptions	Temporary emigration assumptions
M(0)Sng	capture probability constant over secondary periods	Survival constant over primary periods	No gamma - No temporary emigration
M(b)Sng	behavior effect on capture probability - different for marked and unmarked animals	Survival constant over primary periods	No gamma - No temporary emigration
M(t)Stng	time effect - different capture probabilities for each secondary period.	time effect - Survival varies over t	No temporary emigration
M(bt)Stng	behavior and time effect	time effect	No temporary emigration
M(0)SGr	constant	constant	Gamma random - temporary emigration not dependant on previous emigration status
M(0)SGm	constant	constant	Gamma Markovian - temporary emigration dependant on previous emigration status
M(b)SGr	behavior effect	constant	Gamma random - temporary emigration not dependant on previous emigration status
M(b)SGm	behavior effect	constant	Gamma Markovian

M(t)SGr(t)	time effect	constant	Gamma random, with time effect
M(bt)SGr(t	behavior and time effect	constant	Gamma random, with time effect

The "PROC TEST;" statement causes RDSURVIV to print tables of statistics used for comparison of the models. "PROC STOP;" causes RDSURVIV to stop execution even if more statements follow. An option to the "PROC TEST" statement allows you to save the AIC values from each of the models in a file. The file can then be sorted and used on later analysis so that models from earlier runs can be compared to models from later runs.

RDSURVIV

To run RDSURVIV, type "RDSURVIV" at a DOS command prompt. If using Windows, open an MSDOS widow and type "RDSURVIV". RDSURVIV 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] [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 CNVRDSRV and is called CNVRDSRV.OUT unless it has been renamed. A full pathname may be used to indicate a file in a different directory. If this item is omitted, RDSURVIV expects the input from the keyboard. (Cntl-Break will abort the program).

If "l=out_file" is specified, output from RDSURVIV 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, RDSURVIV will print a header and the title in the output file after every n lines. The default value for n is 60.

The "noecho" option causes RDSURVIV 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 RDSURVIV, enter the following at the above prompt:

i=cnvRDSRV.out l=sample.out lines=9999

The output produced by RDSURVIV 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 RDSURVIV on the sample data file listed previously:

```
RDsurviv - Robust Design Survival Rate Estimation
  3-Apr-97      14:22:52         RDsurviv 1.0        Oct, 1996       Page  001
                    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
- - - - - -
      Dimension limitations for this run:
        Maximum number of parameters              256
        Maximum number of cohorts                  64
        Maximum number of classes within a cohort  64
        Maximum number of models for PROC TEST     20
      If your problem needs larger dimensions, reset the values
      in the MODELC include file and recompile the program.

  Date       Modifications
  ---------  ------------------------------------------------------------
  March, 90  NORMALIZE option for PROC MODEL to normalize cell probabilities.
  March, 90  ADDCELL option for PROC MODEL to add cell with 1 - sum of cells.
  March, 90  NOBINCOF option for PROC ESTIMATE to not add bin. coef. to like.

  INPUT --- PROC TITLE ;

     CPU time in seconds for last procedure was    0.00

  INPUT --- PROC MODEL NPAR=32 ADDCELL;

  INPUT ---    COHORT=19584 /* u(1) */;
  INPUT ---       1575:  /* 111 */;
  INPUT ---       2407:  /* 110 */;
  INPUT ---       2407:  /* 101 */;
  INPUT ---       3596:  /* 100 */;
  INPUT ---       2407:  /* 011 */;
  INPUT ---       3596:  /* 010 */;

  INPUT ---    COHORT=2406 /* u(2) */;
  INPUT ---       201:  /* 111 */;
  INPUT ---       295:  /* 110 */;
  INPUT ---       295:  /* 101 */;
  INPUT ---       440:  /* 100 */;
  INPUT ---       295:  /* 011 */;
  INPUT ---       440:  /* 010 */;

  INPUT ---    COHORT=8818 /* m(1,2) */;
  INPUT ---       694:  /* 111 */;
  INPUT ---       1086:  /* 110 */;
  INPUT ---       1086:  /* 101 */;
  INPUT ---       1622:  /* 100 */;
  INPUT ---       1086:  /* 011 */;
  INPUT ---       1622:  /* 010 */;

  INPUT ---    COHORT=605 /* u(3) */;
  INPUT ---       50:  /* 111 */;
  INPUT ---       74:  /* 110 */;
  INPUT ---       74:  /* 101 */;
  INPUT ---       111:  /* 100 */;
  INPUT ---       74:  /* 011 */;
  INPUT ---       111:  /* 010 */;

  INPUT ---    COHORT=2223 /* m(1,3) */;
  INPUT ---       183:  /* 111 */;
  INPUT ---       274:  /* 110 */;
  INPUT ---       274:  /* 101 */;
  INPUT ---       406:  /* 100 */;
  INPUT ---       274:  /* 011 */;
  INPUT ---       406:  /* 010 */;

  INPUT ---    COHORT=5009 /* m(2,3) */;
  INPUT ---       383:  /* 111 */;
  INPUT ---       617:  /* 110 */;
  INPUT ---       617:  /* 101 */;
  INPUT ---       925:  /* 100 */;
  INPUT ---       617:  /* 011 */;
  INPUT ---       925:  /* 010 */;
```

```
INPUT ---    COHORT=180 /* u(4) */;
INPUT ---       15:  /* 111 */;
INPUT ---       22:  /* 110 */;
INPUT ---       22:  /* 101 */;
INPUT ---       33:  /* 100 */;
INPUT ---       22:  /* 011 */;
INPUT ---       33:  /* 010 */;

INPUT ---    COHORT=664 /* m(1,4) */;
INPUT ---       55:  /* 111 */;
INPUT ---       82:  /* 110 */;
INPUT ---       82:  /* 101 */;
INPUT ---       121:  /* 100 */;
INPUT ---       82:  /* 011 */;
INPUT ---       121:  /* 010 */;

INPUT ---    COHORT=1287 /* m(2,4) */;
INPUT ---       108:  /* 111 */;
INPUT ---       160:  /* 110 */;
INPUT ---       160:  /* 101 */;
INPUT ---       233:  /* 100 */;
INPUT ---       160:  /* 011 */;
INPUT ---       233:  /* 010 */;

INPUT ---    COHORT=3483 /* m(3,4) */;
INPUT ---       258:  /* 111 */;
INPUT ---       433:  /* 110 */;
INPUT ---       433:  /* 101 */;
INPUT ---       642:  /* 100 */;
INPUT ---       433:  /* 011 */;
INPUT ---       642:  /* 010 */;

INPUT ---    COHORT=19584   /* R(1)  */;
INPUT ---       8818:  /*  m(1,2)  */;
INPUT ---       2223:  /*  m(1,3)  */;
INPUT ---       664:  /*  m(1,4)  */;

INPUT ---    COHORT=11224   /* R(2)  */;
INPUT ---       5009:  /*  m(2,3)  */;
INPUT ---       1287:  /*  m(2,4)  */;

INPUT ---    COHORT=7837   /* R(3)  */;
INPUT ---       3483:  /*  m(3,4)  */;

INPUT ---    LABELS;
INPUT ---       S(1)=p(1,1);
INPUT ---       S(2)=p(1,2);
INPUT ---       S(3)=p(1,3);
INPUT ---       S(4)=c(1,2);
INPUT ---       S(5)=c(1,3);
INPUT ---       S(6)=p(2,1);
INPUT ---       S(7)=p(2,2);
INPUT ---       S(8)=p(2,3);
INPUT ---       S(9)=c(2,2);
INPUT ---       S(10)=c(2,3);
INPUT ---       S(11)=p(3,1);
INPUT ---       S(12)=p(3,2);
INPUT ---       S(13)=p(3,3);
INPUT ---       S(14)=c(3,2);
INPUT ---       S(15)=c(3,3);
INPUT ---       S(16)=p(4,1);
INPUT ---       S(17)=p(4,2);
INPUT ---       S(18)=p(4,3);
INPUT ---       S(19)=c(4,2);
INPUT ---       S(20)=c(4,3);
INPUT ---       S(21)=PHI(1);
INPUT ---       S(22)=PHI(2);
INPUT ---       S(23)=PHI(3);
INPUT ---       S(24)=GAM'(2);
INPUT ---       S(25)=GAM'(3);
INPUT ---       S(26)=GAM'(4);
INPUT ---       S(27)=GAM(3);
INPUT ---       S(28)=GAM(4);
INPUT ---       S(29)=THETA(1);
INPUT ---       S(30)=THETA(2);
INPUT ---       S(31)=THETA(3);
INPUT ---       S(32)=THETA(4);

   CPU time in seconds for last procedure was    0.11
```

The next part of the output lists the parameter estimates and goodness-of-fit test statistics for model "M(0)Sng". The "Number of parameters in model" is the value in the "PROC MODEL NPAR=32" statement. Since capture probabilities are constant over secondary periods, survival rates are constant across primary periods and there is no temporary emigration, there are 5 unique parameters in the model (1 survival probabilities and 4 capture probabilities).

```
INPUT --- PROC ESTIMATE MAXFN=32000 NOVAR NAME=M(0)Sng;

INPUT ---    CONSTRAINTS;
INPUT ---       S(2)=S(1) /* p(1,2)=p(1,1) */;
INPUT ---       S(3)=S(1) /* p(1,3)=p(1,1) */;
INPUT ---       S(4)=S(1) /* c(1,2)=p(1,1) */;
INPUT ---       S(5)=S(1) /* c(1,3)=p(1,1) */;
INPUT ---       S(7)=S(6) /* p(2,2)=p(2,1) */;
INPUT ---       S(8)=S(6) /* p(2,3)=p(2,1) */;
INPUT ---       S(9)=S(6) /* c(2,2)=p(2,1) */;
INPUT ---       S(10)=S(6) /* c(2,3)=p(2,1) */;
INPUT ---       S(12)=S(11) /* p(3,2)=p(3,1) */;
INPUT ---       S(13)=S(11) /* p(3,3)=p(3,1) */;
INPUT ---       S(14)=S(11) /* c(3,2)=p(3,1) */;
INPUT ---       S(15)=S(11) /* c(3,3)=p(3,1) */;
INPUT ---       S(17)=S(16) /* p(4,2)=p(4,1) */;
INPUT ---       S(18)=S(16) /* p(4,3)=p(4,1) */;
INPUT ---       S(19)=S(16) /* c(4,2)=p(4,1) */;
INPUT ---       S(20)=S(16) /* c(4,3)=p(4,1) */;
INPUT ---       S(22)=S(21) /* PHI(2)=PHI(1) */;
INPUT ---       S(23)=S(21) /* PHI(3)=PHI(1) */;
INPUT ---       S(24)=0 /* GAM'(2)=0 -> no emigration */;
INPUT ---       S(25)=0 /* GAM'(3)=0 -> no emigration */;
INPUT ---       S(26)=0 /* GAM'(4)=0 -> no emigration */;
INPUT ---       S(27)=0 /* GAM(3)=0 -> no emigration */;
INPUT ---       S(28)=0 /* GAM(4)=0 -> no emigration */;
INPUT ---       S(29)=1 /* THETA(1) not used in this model */;
INPUT ---       S(30)=1 /* THETA(2) not used in this model */;
INPUT ---       S(31)=1 /* THETA(3) not used in this model */;
INPUT ---       S(32)=1 /* THETA(4) not used in this model */;

    Number of parameters in model  =  32

    Number of parameters set equal =  18

    Number of parameters fixed     =   9

    Number of parameters estimated =   5
```

Before the estimates are printed, RDSURVIV prints the final value of the function determined by the optimization routine and error-code. If the error-code is not zero, an error or warning message is printed indicating a problem with the data. This may happen when the data are sparse and some parameters are inestimable.

```
     Final function value 122537.95     (Error Return =   0)

   Number of significant digits       8

   Number of function evaluations   134
```

Below are the estimates from the first model. The numbers in the far left column are the parameter numbers. The second column of numbers is the unique parameter number. Parameters with the same unique parameter number are all considered the same parameter. Since all capture-probabilities in the first primary period were assumed equal for this model, the first five parameters have the same unique parameter number. Also, since survival was assumed constant over time, all the survival parameters, PHI, have the same unique parameter number. Parameters with a negative parameter number are parameters which were not used (estimated) in the model (GAM', GAM, THETA in this model).

Results for model M(0)SNG

				95% Confidence Interval	
I	Parameter	S(I)	Standard Error	Lower	Upper
1	1 p(1,1)	0.399390	0.267126E-02	0.394154	0.404626
2	1 p(1,2)	0.399390	0.267126E-02	0.394154	0.404626
3	1 p(1,3)	0.399390	0.267126E-02	0.394154	0.404626
4	1 c(1,2)	0.399390	0.267126E-02	0.394154	0.404626
5	1 c(1,3)	0.399390	0.267126E-02	0.394154	0.404626
6	2 p(2,1)	0.344949	0.250767E-02	0.340034	0.349864
7	2 p(2,2)	0.344949	0.250767E-02	0.340034	0.349864
8	2 p(2,3)	0.344949	0.250767E-02	0.340034	0.349864
9	2 c(2,2)	0.344949	0.250767E-02	0.340034	0.349864
10	2 c(2,3)	0.344949	0.250767E-02	0.340034	0.349864
11	3 p(3,1)	0.349472	0.304342E-02	0.343507	0.355437
12	3 p(3,2)	0.349472	0.304342E-02	0.343507	0.355437
13	3 p(3,3)	0.349472	0.304342E-02	0.343507	0.355437
14	3 c(3,2)	0.349472	0.304342E-02	0.343507	0.355437
15	3 c(3,3)	0.349472	0.304342E-02	0.343507	0.355437
16	4 p(4,1)	0.378037	0.424166E-02	0.369724	0.386351
17	4 p(4,2)	0.378037	0.424166E-02	0.369724	0.386351
18	4 p(4,3)	0.378037	0.424166E-02	0.369724	0.386351
19	4 c(4,2)	0.378037	0.424166E-02	0.369724	0.386351
20	4 c(4,3)	0.378037	0.424166E-02	0.369724	0.386351
21	5 PHI(1)	0.670951	0.262664E-02	0.665803	0.676099
22	5 PHI(2)	0.670951	0.262664E-02	0.665803	0.676099
23	5 PHI(3)	0.670951	0.262664E-02	0.665803	0.676099
24	-24 GAM'(2)	0.000000E+00	0.000000E+00	0.000000E+00	0.000000E+00
25	-25 GAM'(3)	0.000000E+00	0.000000E+00	0.000000E+00	0.000000E+00
26	-26 GAM'(4)	0.000000E+00	0.000000E+00	0.000000E+00	0.000000E+00
27	-27 GAM(3)	0.000000E+00	0.000000E+00	0.000000E+00	0.000000E+00
28	-28 GAM(4)	0.000000E+00	0.000000E+00	0.000000E+00	0.000000E+00
29	-29 THETA(1)	1.00000	0.000000E+00	1.00000	1.00000
30	-30 THETA(2)	1.00000	0.000000E+00	1.00000	1.00000
31	-31 THETA(3)	1.00000	0.000000E+00	1.00000	1.00000
32	-32 THETA(4)	1.00000	0.000000E+00	1.00000	1.00000

Following the parameter estimate table is the goodness-of-fit test for the model. Hopefully, it is self-explanatory. (The entire table is not included here to conserve paper.)

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	1575	1592.732	0.197	0 < P < 1
1	2	2407	2395.178	0.058	0 < P < 1
1	3	2407	2395.178	0.058	0 < P < 1
1	4	3596	3601.911	0.010	0 < P < 1
1	5	2407	2395.178	0.058	0 < P < 1
1	6	3596	3601.911	0.010	0 < P < 1
1	7	3596	3601.911	0.010	0 < P < 1
1	Cohort df=	6		0.402	P = 0.9988
2	1	201	137.366	29.479	0 < P < 1
2	2	295	260.854	4.470	0 < P < 1
2	3	295	260.854	4.470	0 < P < 1
2	4	440	495.357	6.186	0 < P < 1
2	5	295	260.854	4.470	0 < P < 1
2	6	440	495.357	6.186	0 < P < 1
2	7	440	495.357	6.186	0 < P < 1
2	Cohort df=	6		61.446	P = 0.0000
3	1	694	503.445	72.125	0 < P < 1
3	2	1086	956.032	17.668	0 < P < 1
3	3	1086	956.032	17.668	0 < P < 1
3	4	1622	1815.486	20.621	0 < P < 1
3	5	1086	956.032	17.668	0 < P < 1
3	6	1622	1815.486	20.621	0 < P < 1
3	7	1622	1815.486	20.621	0 < P < 1

```
3 Cohort df=  6                  186.993   P = 0.0000
4      1        50      35.631      5.794   0 < P < 1
4      2        74      66.326      0.888   0 < P < 1
4      3        74      66.326      0.888   0 < P < 1
```

Hardware Considerations

RDSURVIV is available for IBM-compatible PC's running Windows 3.1, 95 or NT, DOS, or OS/2. The source code for RDSURVIV is available for anyone using another operating system (unix, Macintosh)..

Software Availability

Program RDSURVIV is available via the world-wide-web at:

www.mbr-pwrc.usgs.gov/software.html

or via anonymous ftp at:

pandion.er.usgs.gov

or from the author - send blank diskette to:

Jim Hines

Patuxent Wildlife Research Center

11510 American Holly Dr. #201

Laurel, MD 20708-4017 USA

Software Installation

To install RDSURVIV 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 RDSURVIV programs onto the hard disk of a PC:

c:> **mkdir \RDSrv**

c:> **cd \RDSrv**

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

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