MSSRVRCV

User's Manual

By

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Introduction

Program MSSRVRCV (Multi-State SuRVival and ReCoVery analysis) computes parameter estimates of survival, state transition, recovery, and capture probability using the model structure of Kendall et al. (*Ecology*, in review). MSSRVRCV is a generalization of program MSSURVIV (Brownie et al. 1993), and allows the use of state specific band recoveries in addition to usual recapture/resighting data to estimate demographic parameters. As such, the estimation routine consists of a specially modified version of Dr. G. White's program SURVIV (White, 1983). With program MSSRVRCV and its companion program, CNVMSRCV, users are able to get parameter estimates without having to specify cell probabilities.

MSSRVRCV is intended for the case in which one is interested in transition probabilities between stratum in addition to the usual parameters of interest such as survival, recovery, or capture probability. The strata can be defined as any discrete category to which captured animals can be assigned at any given time. For example, strata may be based on such factors as location or individual variables such as breeding status or weight class. An added advantage of MSSRVRCV over MSSURVIV is that information from band recoveries, which are often "free," can be entered into the modeling framework, and will generally increase the precision on resulting parameter estimates. However, because the model structure requires knowledge about the state in which an individual is recovered, we anticipate that the use of this program will be most relevant to cases in which "stratum" refers to a physical location. Note that it is not currently possible to produce parameter estimates using the "Non-Markovian/memory" models (Brownie et al. 1993) using MSSRVRCV.

Output from MSSRVRCV includes survival probability estimates (PHI), transition probability estimates from sampling period to sampling period (PSI), transition probability estimates from sampling period to recovery period (TAU), capture probability estimates (P), recovery probability estimates (F or LAM), goodness-of-fit tests and AIC values. Unlike program MSSURVIV, no default models are produced by program MSSRVRCV. Instead, users must manipulate parameter index matrices (PIMs) in the same manner as in program MARK (White and Burnham 1999) to specify details of the model structure. An excellent instruction manual for program MARK which details how PIMs work is provided in Evan Cooch's "Program Mark: A Gentle Introduction" which can be found online at http://www.phidot.org/software/mark/docs/book.

The experimental situation to which this program applies is one in which animals are initially marked with a unique tag, and released. This process is repeated for each of the sampling periods. Information used to assign the animal to the proper stratum (e.g. weight, age, location, etc.) is recorded for each capture of an animal, and is also recorded for each band recovery reported between formal sampling periods. Using these data, the encounter-history of each animal is generated consisting of codes indicating the status of the animal at each capture period and in each recovery period. Details of the correct data format are provided below.

Like programs SURVIV and MSSURVIV, MSSRVRCV consists of statements defining the data and statements defining the model structure. Although MSSRVRCV 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 CNVMSRCV was created to automate this process. CNVMSRCV reads as input the encounter-history records and produces all of the statements necessary to run program MSSRVRCV.

<u>Data Format</u>

The correct data format for using CNVMSRCV consists of summarized records of unique encounter histories delimited by carriage returns. For each encounter history record, a given line will consist of a capture history (directly comparable to the type used in MSSURVIV), followed by a space, followed by a lower case letter to designate group status, followed by a space, followed by a number reflecting the sampling period after which the individuals sharing the encounter history were recovered (or is left blank if these individuals were not recovered), followed by a space, followed by the strata in which these individuals were recovered, followed by a space, followed by the number of individuals sharing this unique encounter history.

Capture History – The capture history contains stratum-specific records of captures during sampling periods. For each sampling period in the study, an individual is assigned an indicator corresponding to the state in which it was captured, if it was captured during that period. If the individual was not captured, it is assigned a '0' for that period. By convention, upper case letters are usually used for capture state. For example, in a study in which there are 3 possible strata, A, B, and C, would usually be used for capture states. For more information on

capture histories, see the user manual for program MSSURVIV.

Group Status – A lowercase letter, starting with 'a' is used to designate group status. For example, if one wanted to compare a general model with sex stratification on parameters to a model in which demographic parameters were set equal across sexes, it would be necessary to use 2 groups. This could be accomplished, for instance, by setting the group status of males to 'a' and the group status of females to 'b' (or *vice versa*).

Recovery Strata – By convention, sequential numbers are usually used to designate recovery strata. This helps distinguish them from recaptures. Thus, if there are 3 possible recovery strata, we would usually use '1', '2', and '3' rather than 'A', 'B', and 'C.'

For example, the encounter history

0A0B00 a 5 1 2

would indicate that the individuals sharing this capture history were first caught during the second sampling period in stratum A, not caught during the third sampling period, caught in stratum B in the fourth sampling period, then were recovered between the fifth and sixth sampling periods in recovery stratum 1. There were 2 such individuals that shared this unique encounter history and they belonged to group 'a'. Likewise, the entry

A0000C b 23

Indicates that 23 individuals in group 'b' were first caught in stratum A in sample period 1, but were not seen again until the sixth and final sampling period, in which they were caught in stratum C. These individuals were never recovered.

Using CNVMSRCV

To start program CNVMSRCV, simply double click on its icon, or type 'cnvmsrcv' at the DOS prompt. This will open a windows based graphical user interface (see Figure 1). In the edit box for "Recapture Strata Codes," type all codes used in your capture histories with no spaces (e.g. ABC for a study with three capture strata). In the "Recovery Strata Codes" edit box, type all recovery strata codes with no spaces (e.g. 12 for a study with two recovery strata). Select which type of recovery parameterization you would like to use by toggling the 'Brownie' or 'Seber' switches in the 'Parameterization option' box (see subsequent sections for more on recovery parameterizations). Next, pull down the File menu at the top of your screen and select "Input File." This will allow you to browse for your encounter history file on your desktop and will directly cut and paste the contents of your input file into the conversion program. Next, pull down the File menu, and select or create an "Output File". When this is to your satisfaction, pull down the "Run" menu and select "Convert."

Figure 1. CNVMSRCV graphical user interface.

🐂 cnymsrcy	
File Run Quit	
Recapture Strata Codes: ABC Recovery Strata Codes: 12	Parameterization option
Input file:	
Output file:cnvmsrcv.out	

For example, consider the following encounter history file for 1 group, 3 sampling periods, and 2 recapture and recovery strata:

A00 a 1 2 1 A00 a 14 ABO a 2 AAO a 10 AAO a 2 1 2 AOB a 1 B00 a 15 BAO a 3 BBB a 5 BBO a 12 BB0 a 2 2 3 BB0 a 3 2 1 0A0 a 13 0AB a 5 0AA a 1 2 3 0AA a 10 0B0 a 19 0B0 a 2 1 1 0B0 a 2 2 4 0BA a 1

0BB a 3 00A a 14 00A a 3 1 2 00B a 13 00B a 3 2 2

In this example there are 2 recapture strata (A and B), and 2 recovery strata (1 and 2). To apply CNVMSRCV to this data set, 'AB' would be entered in the 'Recapture Strata Codes' edit box and '12' would be entered in the 'Recovery Strata Codes' edit box. Using the 'Convert' command after the input and output files have been specified (recovery parameterization was left as the default Brownie 'f') produces a MSSRVRCV input file with contents

```
proc title 'data=C:\Conn\mult recov\mssrvrcv\mssrvrcv\example.inp';
proc model npar=121 addcell nyrs=3 nstrat=2 nrstrat=2 ngrps=1;
REM LIVE RECAPS YEAR (1);
cohort=30.;12.:;2.:;0.:;1.:;
cohort=39.;3.:;21.:;0.:;0.:;
REM LIVE RECAPS YEAR (2);
cohort=46.;13.:;5.:;
cohort=51.;1.:;8.:;
REM DEAD RECOVERIES YEAR (1);
cohort=15.;0.:;1.:;0.:;0.:;0.:;0.:;
cohort=15.;0.:;0.:;0.:;0.:;0.:;
REM DEAD RECOVERIES YEAR (2);
cohort=28.;2.:;0.:;0.:;0.:;
cohort=42.;1.:;7.:;0.:;1.:;
REM DEAD RECOVERIES YEAR (3);
cohort=30.;2.:;0.:;
cohort=29.;0.:;2.:;
PROC ESTIMATE NOVAR maxfn=32001 NSIG=6 NAME=MOD1;
PIM;
PHI-U;
1 1;
1;
PHI-A;
1 1;
1;
PHI-B;
1 1;
1;
MOV-UA;
0 0;
0;
MOV-UB;
0 0;
0;
MOV-AU;
0 0;
0;
MOV-AB;
2 2;
2;
MOV-BU;
0 0;
0;
```

MOV-BA; 3 3; 3; P-A; 4 4; 4; P-B; 5 5; 5; F-1; 6 6 6; 6 6; 6; F-2; 777; 77; 7; TAU-U1; 0 0 0; 0 0; 0; TAU-U2; 0 0 0; 0 0; 0; TAU-A1; -2 -2 -2; -2 -2; -2; TAU-A2; 8 8 8; 8 8; 8; TAU-B1; 9 9 9; 99; 9; TAU-B2; -2 -2 -2; -2 -2; -2; DESIGN MATRIX IDENTITY ROWS=9 COLS=9; INITIAL; .9 .1 .1 .3 .3 .05 .05 .1 .1; FIXED; -2; PROC STOP;

Understanding and Manipulating the MSSRVRCV Input File

For the most part, the m_{ij} arrays and command lines in the above should be familiar to users of MSSURVIV. However, some new developments have been included in MSSRVRCV that deserve explanation. Also, the initial model structure produced by CNVMSRCV needs to be manipulated by the user. See the user's manual to MSSURVIV at <u>http://www.mbr-pwrc.usgs.gov/software.html</u> for explanations of statements and options not covered here, as well as details about using design matrices.

Cohorts, m_{ij} arrays, and losses on capture – The structure to cohorts under 'LIVE RECAPS' is identical to that used in MSSURVIV. For each sampling period in which there is a possibility of future recapture, the total number of individuals released in a given state is specified following a 'cohort=' statement. On the same line, the number of those individuals later seen in any state is specified. The total number of individuals released in other states is listed on consecutive lines.

For example, from the above MSSRVRCV input file, releases in sampling period 1 and subsequent recaptures are specified as

```
REM LIVE RECAPS YEAR (1);
cohort=30.;12.:;2.:;0.:;1.:;
cohort=39.;3.:;21.:;0.:;0.:;
```

A total of 30 individuals were released in state A in sampling period 1. 12 of these individuals were next seen in state A at sampling period 2, two were next seen in state B at sampling period 2, zero were next seen in state A in sampling period 3, and one was seen in state B in sampling period 3. Likewise, 39 individuals were released in state B in sampling period 1. Of these, 3 were next seen in state A in sampling period 2, 21 were next seen in state B in sampling period 2, and 0 were next seen alive after that.

The structure to cohorts in '*DEAD RECOVERIES*' is analogous, with the difference that cohort sizes for dead recoveries are reduced by the total number ever seen alive again. This adaptation is necessary to get the multinomial probability structure to work out correctly (the cell probabilities for dead recoveries are also adjusted by the probability of never being seen alive again within the estimation routine).

Because the conversion program CNVMSRCV does not currently allow for losses on capture, the user of MSSRVRCV will need to manually subtract the total number of losses on capture by year and state from their respective cohort size in the MSSRVRCV input file. For instance, in the above example, if there were 3 losses on capture in state A at sampling period 1, and 4 losses in state B at sampling period 1, then the cohort sizes for *LIVE RECAPS* would become 30-3=27 for state A, and 39-4=35 for state B. Similarly the cohort sizes for *DEAD RECOVERIES* in sample period 1 would change to 12 and 11, respectively.

Multiple groups – In the case of multiple groups, complete summaries of the data will be stacked on top of each other. Likewise, complete sets of PIMs will be stacked on top of each other with group 'a' having the first set of PIMs, group 'b' the second set of PIMs and so on. It is advantageous to manually add a group indicator to each PIM if there are multiple groups present to eliminate mistakes. This is especially important if using the MATLAB based PIM editor. For instance, if group 'a' was males and group 'b' was females, one might change the PIM title 'PHI-U;' to 'PHI-U-MALES;', etc. Do not use spaces when attaching group indicators to PIM titles, and be sure to keep the original PIM title as the first part of your new title (e.g. do not use a title like 'MALES-PHI-U').

PIM structure, unobservable states, and constraints – While CNVMSRCV conveniently automates the process of turning encounter histories into sufficient statistics, only a basic format

for PIMs is produced, and the user is left to edit the PIMs to produce model structure. This can be done manually with a text editor, or with the MATLAB based PIM editor mentioned previously. If you choose to edit PIMs manually, be sure to change the 'npar=' statement in the second line of the input file to reflect the total number of parameters you wish to estimate. Likewise, if you are using an "identity" design matrix, change 'ROWS=' and 'COLS=' to the total number of parameters to be estimated.

In editing PIMs, parameters that the user wishes to estimate should receive positive numerical values. This is done in the same fashion as program MARK (White and Burnham 1999). In addition, all non-positive numbers are reserved for use in constraining parameters equal to constants. In particular, putting a '0' in a PIM will set that value to 0. Putting a '-1' in a PIM constrains the parameter associated with that entry to be 1. Additional parameters can be fixed to constants by inserting consecutive negative numbers in the PIMs, starting with -2, then -3, etc. For each such negative number, program MSSRVRCV will "look" for values to fix these entries to under the 'FIXED;' card at the end of the input file (see completed input file below for an example).

In addition to the number of strata specified by the user, program CNVMSRCV will produce PIMs for an unobservable state U. Individuals can move to stratum U and are subject to mortality, but cannot be recaptured in that state. However, all individuals are assumed to be available for recovery. See Kendall et al. (*in review*) for further details on estimation issues regarding the unobservable state. If no unobservable state is desired, simply change all entries for PIMs containing the unobservable state to '0'.

Numerical problems can sometimes arise in estimating transition probabilities to recovery areas because one of the transition probabilities must be obtained by subtraction for each stratum. A default solution to this problem is not obvious, and so to resolve this problem flexibility is allowed in specifying which TAU transition probabilities are to be obtained by subtraction. In practice, it is usually desirable to make this the largest transition probability. For each source state, the user must specify this state transition by fixing all parameters within the group to a negative number using the procedure outlined above (see the completed input file below for an example).

Recovery Parameterization – Program MSSRVRCV allows two parameterizations of recovery rate. One is the *f* parameterization of recovery rate used by Brownie *et al.* 1985. The other is the so-called "Seber" parameterization, where recovery rate is equal to (1-S)*lambda (Seber 1970). For more on issues involving these two possible parameterizations, see Kendall *et al.* (in review).

The conversion program CNVMSRCV allows the user to specify which recovery parameterization they would like to use. MSSRVRCV input files differ in a few places depending upon which such parameterization is selected. For the "Seber" parameterization, the keyword 'RCVOPT' must occur somewhere in the line following the 'proc model' card. Secondly, since the Seber parameterization requires an extra survival rate [because of the (1-S) following the final release], an extra parameter is added to all 'PHI' PIMs. Finally, the PIM name for recovery parameters must start with 'F' under the Brownie parameterization, and

'LAM' under the Seber parameterization. If these differences are not consistent, the user will receive an error message when trying to run MSSRVRCV.

Initial values of parameters – Like MSSURVIV, the user is required to assign all parameters initial values. This is done by listing the initial values for parameter 1, parameter 2, etc. following the 'INITIAL' card near the end of the input file. If initial values parameters are close to their true values, the time for numerical optimization will be shorter. Generally, convergence will occur more often if initial guesses for values of parameters are low than if they are high relative to their true values. If more than one line is needed, be sure to indent all lines one space following the first line of initial values. A semicolon is needed after the last line of initial values.

Running MSSRVRCV

To run MSSRVRCV on a PC, open a DOS window and change to the directory that mssrvrcv.exe is kept in. At the command line, type

echo i=<input file path and name> l=<output file path and name> | mssrvrcv

Results from MSSRVRCV will be stored in your output file, and should be interpreted (along with error messages) in the same fashion as MSSURVIV. See the user's manual for MSSURVIV for more information.

Completed Sample Input Files:

The following are examples of completed sample input files:

f parameterization:

```
proc title 'mssrvrcv exp value data- combined recap/resight probs';
proc model npar=32 addcell nyrs=4 nstrat=2 nrstrat=2 ngrps=1;
REM LIVE RECAPS YEAR (1);
cohort=100;56.32:;14.08:;4.5281:;2.2303:;0.38215:;0.26666:;
cohort=100;7.04:;63.36:;1.2165:;5.5419:;0.15961:;0.4892:;
REM LIVE RECAPS YEAR (2);
cohort=100;57.024:;13.376:;4.643:;2.1154:;
cohort=100;7.744:;62.656:;1.3314:;5.427:;
REM LIVE RECAPS YEAR (3);
cohort=100;57.728:;12.672:;
cohort=100;8.448:;61.952:;
REM DEAD RECOVERIES YEAR (1);
cohort=22.193;7:;3:;0.5914:;0.36864:;0.051453:;0.040707:;0.0045883:;0.004259:;
cohort=22.193;2.5:;7.5:;0.2755:;0.6845:;0.02933:;0.06284:;0.003101:;0.005746:;
REM DEAD RECOVERIES YEAR (2);
cohort=22.8416;7.1:;2.9:;0.60182:;0.35818:;0.052221:;0.039939:;
cohort=22.8416;2.4:;7.6:;0.27254:;0.68746:;0.030093:;0.062067:;
REM DEAD RECOVERIES YEAR (3);
cohort=29.6;7.2:;2.8:;0.60653:;0.35347:;
cohort=29.6;2.3:;7.7:;0.27725:;0.68275:;
REM DEAD RECOVERIES YEAR (4);
```

<pre>cohort=100;7.2:;2.8:; cohort=100;2.3:;7.7:;</pre>
PROC ESTIMATE maxfn=32001 NSIG=6 NAME=MOD1;
PIM;
PHI-U;
0 0 0; 0 0;
0;
PHI-A;
1 2 3;
2 3; 3;
PHI-B;
4 5 6;
5 6;
6; MOV-UA;
0 0 0;
0 0;
0; NOL UD
MOV-UB; 0 0 0;
0 0;
0;
MOV-AU; 0 0 0;
0 0;
0;
MOV-AB;
7 8 9; 8 9;
9;
MOV-BU;
0 0 0; 0 0;
0;
MOV-BA;
10 11 12;
11 12; 12;
P-A;
13 14 15;
14 15;
15; P-B;
16 17 18;
17 18;
18; F-1;
19 20 21 22;
20 21 22;
21 22; 22;
E-2;
23 24 25 26;
24 25 26;
25 26;

```
26;
TAU-U1;
0 0 0 0;
0 0 0;
0 0;
0;
TAU-U2;
0 0 0 0;
0 0 0;
0 0;
0;
TAU-A1;
27 28 29 29;
28 29 29;
29 29;
29;
TAU-A2;
-2 -2 -2 -2;
   -2 -2 -2;
      -2 -2;
         -2;
TAU-B1;
30 31 32 32;
31 32 32;
32 32;
32;
TAU-B2;
-2 -2 -2 -2;
   -2 -2 -2;
      -2 -2;
         -2;
DESIGN MATRIX IDENTITY ROWS=32 COLS=32;
INITIAL;
.8 .8 .8 .8 .8 .2 .19 .18 .1 .11 .12
 .88 .88 .88 .88 .88
 .1 .1 .1 .1 .1 .1 .1 .7 .71 .72 .25 .24 .23;
FIXED;
-9;
PROC STOP;
```

"Seber" parameterization:

```
proc title 'mssrvrcv exp value data- combined recap/resight probs';
proc model npar=32 addcell rcvopt nyrs=4 nstrat=2 nrstrat=2 ngrps=1;
REM LIVE RECAPS YEAR (1);
cohort=100;56.32:;14.08:;4.5281:;2.2303:;0.38215:;0.26666:;
cohort=100;7.04:;63.36:;1.2165:;5.5419:;0.15961:;0.4892:;
REM LIVE RECAPS YEAR (2);
cohort=100;57.024:;13.376:;4.643:;2.1154:;
cohort=100;7.744:;62.656:;1.3314:;5.427:;
REM LIVE RECAPS YEAR (3);
cohort=100;57.728:;12.672:;
cohort=100;8.448:;61.952:;
REM DEAD RECOVERIES YEAR (1);
cohort=22.193;7:;3:;0.5914:;0.36864:;0.051453:;0.040707:;0.0045883:;0.004259:;
```

```
cohort=22.193;2.5:;7.5:;0.2755:;0.6845:;0.02933:;0.06284:;0.003101:;0.005746:;
REM DEAD RECOVERIES YEAR (2);
cohort=22.8416;7.1:;2.9:;0.60182:;0.35818:;0.052221:;0.039939:;
cohort=22.8416;2.4:;7.6:;0.27254:;0.68746:;0.030093:;0.062067:;
REM DEAD RECOVERIES YEAR (3);
cohort=29.6;7.2:;2.8:;0.60653:;0.35347:;
cohort=29.6;2.3:;7.7:;0.27725:;0.68275:;
REM DEAD RECOVERIES YEAR (4);
cohort=100;7.2:;2.8:;
cohort=100;2.3:;7.7:;
PROC ESTIMATE maxfn=32001 NSIG=6 NAME=MOD1;
PIM;
PHI-U;
0 0 0 0;
  0 0 0;
    0 0;
     0;
PHI-A;
1 2 3 3;
  2 3 3;
    3 3;
      3;
PHI-B;
4 5 6 6;
  5 6 6;
    6 6;
     6;
MOV-UA;
0 0 0;
  0 0;
    0;
MOV-UB;
0 0 0;
 0 0;
   0;
MOV-AU;
0 0 0;
 0 0;
   0;
MOV-AB;
789;
  8 9;
    9;
MOV-BU;
0 0 0;
  0 0;
   0;
MOV-BA;
10 11 12;
11 12;
12;
P-A;
13 14 15;
14 15;
15;
P-B;
16 17 18;
```

```
17 18;
18;
LAM-1;
19 20 21 22;
 20 21 22;
   21 22;
     22;
LAM-2;
23 24 25 26;
24 25 26;
25 26;
26;
TAU-U1;
0 0 0 0;
0 0 0;
0 0;
0;
TAU-U2;
0 0 0 0;
0 0 0;
0 0;
0;
TAU-A1;
27 28 29 29;
28 29 29;
29 29;
29;
TAU-A2;
-2 -2 -2 -2;
   -2 -2 -2;
      -2 -2;
         -2;
TAU-B1;
30 31 32 32;
31 32 32;
32 32;
32;
TAU-B2;
-2 -2 -2 -2;
   -2 -2 -2;
      -2 -2;
         -2;
DESIGN MATRIX IDENTITY ROWS=32 COLS=32;
INITIAL;
.8 .8 .8 .8 .8 .2 .19 .18 .1 .11 .12
.88 .88 .88 .88 .88
.1 .1 .1 .1 .1 .1 .1 .7 .71 .72 .25 .24 .23;
FIXED;
-9;
PROC STOP;
```

Sources

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