U-CARE 2.2 User's Manual

(Utilities–CApture-REcapture)

Version 2.2, September 2005

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To be cited as :
CHOQUET, R., REBOULET, A.M., LEBRETON, J.D., GIMENEZ, O., PRADEL, R. (2005). U-CARE 2.2 User's Manual. CEFE, Montpellier, France. (http://ftp.cefe.cnrs.fr/biom/Soft-CR/).

1. Introduction

U-CARE is a computer program that deals with the first steps of the analyses of capture-recapture data, namely the preparation of the data set and the assessment of the fit of a general model (Cormack-Jolly-Seber and variants for single-state data; Jolly-Move and variants for multistate data). First, U-CARE offers some tools for selecting a subset of the data, such as a particular range of years, and for recoding, such as pooling two states into one. It also switches the data between different formats, including the MARK format (with some restrictions, see section 3.1), and prepares some summary formats like the m-array. Once a final decision about which data are to be analyzed has been made, the next step should be the assessment of the fit of a general model. U-CARE implements the current state of the art in goodness-of-fit testing for both single- and multi-state data sets. In its previous versions, U-CARE provided goodness-of-fit tests for single-state models only. The tests of the multistate JollyMoVe model (Pradel, Wintrebert and Gimenez, 2003) have been incorporated in the current 2.2 version.

The present manual is divided into three main parts. Chapter 2 “How to begin?” guides the beginner through some usual steps based on a simple example. Chapter 3 explains the “data manipulation” procedures and chapters 4 and 5 the “goodness-of-fit tests” procedures for respectively single-state and multistate models.

2. How to begin ?

2.1. **Installation**

The latest version of U-CARE can be freely downloaded from the following address: http://ftp.cefe.cnrs.fr/biom/Soft-CR/**.** At the time this manual is written, this is version 2.2. To install U-CARE on your computer:

a) Download and unzip file U_CARE_2_2_1.zip which contains:
U-CARE Version 2.2, the required MATLAB 7 ® dynamic libraries, this manual and the example files ED.INP and HESTBECK.RH.

b) Go to the directory that contains the unzipped files and execute Setup.exe.

c) If MATLAB is installed on your computer, you may have to edit the $PATH environment variable for U-CARE to run properly: you must ensure that the path of the newly installed libraries appears before the path of MATLAB itself. Beware that the $PATH variable is a sensitive element of your computer system. Hence, you may want to get the assistance of some knowledgeable computer person. Here is an example:

Select **Start > Settings > Control Panel > System > Advanced > Environment Variables**. Then, select the **Path** variable in the bottom list and click **Edit**.

The **path** variable contains a long line. Something like:

C:%SystemRoot%\system32;%SystemRoot%;%SystemRoot%\System32\Wbem;C:\MATLAB701\bin\win32;**C:\Program Files\MathWorks\MATLAB Component Runtime\v72\runtime\win32;**

You must move the MATLAB runtime libraries path (in bold) ahead of that of MATLAB ® itself like this:

C:%SystemRoot%\system32;%SystemRoot%;%SystemRoot%\System32\Wbem;**C:\Program Files\MathWorks\MATLAB Component Runtime\v72\runtime\win32;**C:\MATLAB701\bin\win32;

d) Double-click on U_CAREV2_2_1.exe to start the program.

2.2. **Starting with an example**

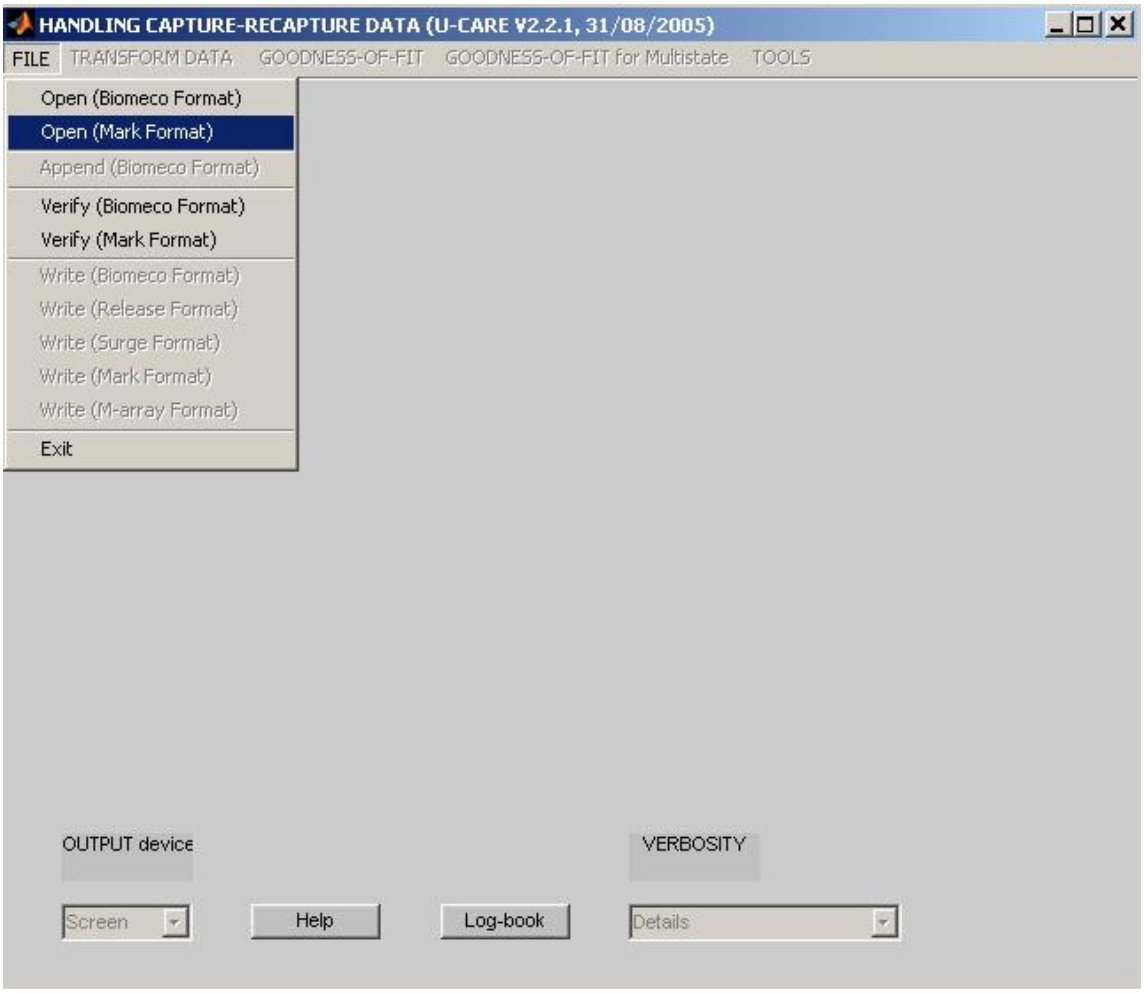


Fig.1: Available options in the menu upon entry in U-CARE.

The executable is named **U_CAREV2_2_1.exe**. Double-click on this file to launch U-CARE. You are now presented with the window of figure 1 where only the FILE option of the menu bar at the top is active. Click on it. The pull-down menu associated has 2 active items for entering data in one of two formats (BIOMECO and MARK with some restrictions, see section 3.1 for details). In case of doubt, it is possible to verify the validity of a file format (items starting with 'Verify'). Here we will directly open the file **ED.INP** in MARK entry format (Fig.2). Select the option *"Open (Mark Format)"*, then the file **ED.INP**. This file contains data from a classical study of a European dipper population. There are 294 ringed birds in total, one individual per line.

```
1111110   1 0 ;
1111100   0 1 ;
1111000   1 0 ;
1111000   0 1 ;
1101110   0 1 ;
1100000   1 0 ;
1100000   1 0 ;
1100000   1 0 ;
1100000   1 0 ;
…..
```

Fig. 2: Entry format for the European dipper example data set. The encounter histories are followed by the frequencies of individuals having this particular encounter history in each of two groups (males then females). Here, there is one individual per line.

MARK format provides for individual covariates, such as weight, given as supplementary columns at the end of each row. These columns cannot easily be distinguished from the group columns (male/female for instance) which precede them. Hence, U-CARE needs to know how many covariate columns are present in the data set and asks for their number. Validate the default 0 for no covariate in the European dipper data set. After you have hit the ENTER key, U-CARE displays a short information summary of the data in its main window. The beginning of the data set is also shown in a separate window: histories followed by the capture frequencies by group. Here, the last two columns are for males and females respectively (Fig.3). Also, all the main menu items are now activated.

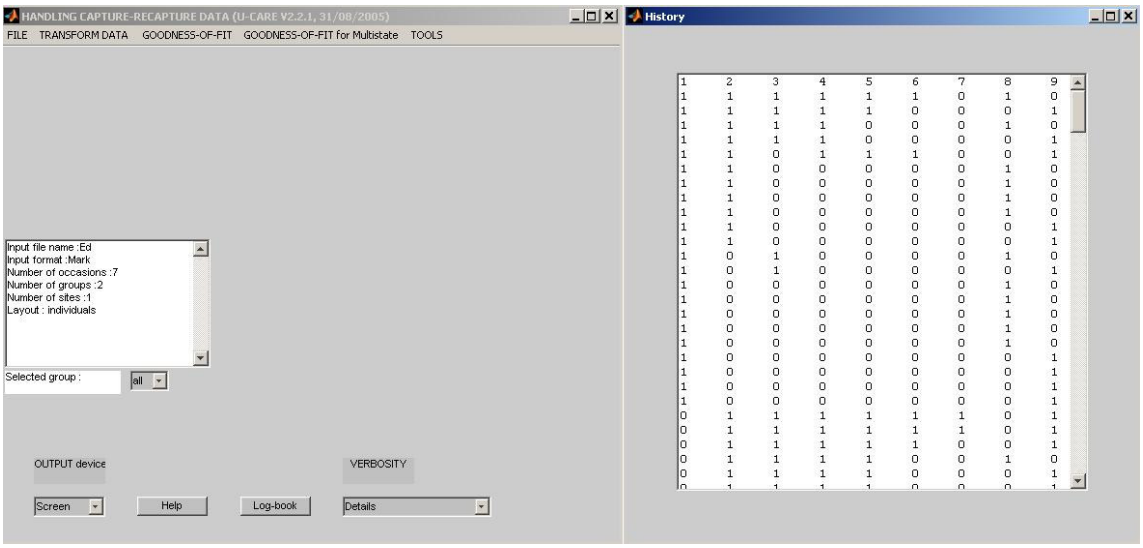


Fig.3: Program U-CARE once the data have been loaded.

The main menu has five items which fall into three main categories of treatments:
1) input-output into several file formats (item FILE),
2) manipulation and transformation of data (item TRANSFORM DATA) and
3) fit assessment (item GOODNESS-OF-FIT for single-state data and item "GOODNESS-OF-FIT for multistate" for multistate data).
The item TOOLS contains some additional statistical tools that may prove useful.

To get more familiar with the program, we will now go through some basic manipulations and data treatments.

2.3. **Goodness of fit test with two groups**

A visual inspection of the data may be a first approach to understanding it. However, the raw data is lengthy and its features difficult to grasp. A more compact form is obtained by summarizing the data by encounter histories. To do that, in the menu *"Transform Data"*, select the option *"encounter histories layout"*. The display changes in the secondary window. The encounter histories are now sorted and followed by the total number of males and females within each encounter history (fig.4). Some encounter histories appear to be more frequent than others but we can move a step ahead and get a still more compact and readable picture of

the data called the m-array. The m-array displays the numbers of individuals released at each occasion followed by the numbers of them next reencountered at each date.

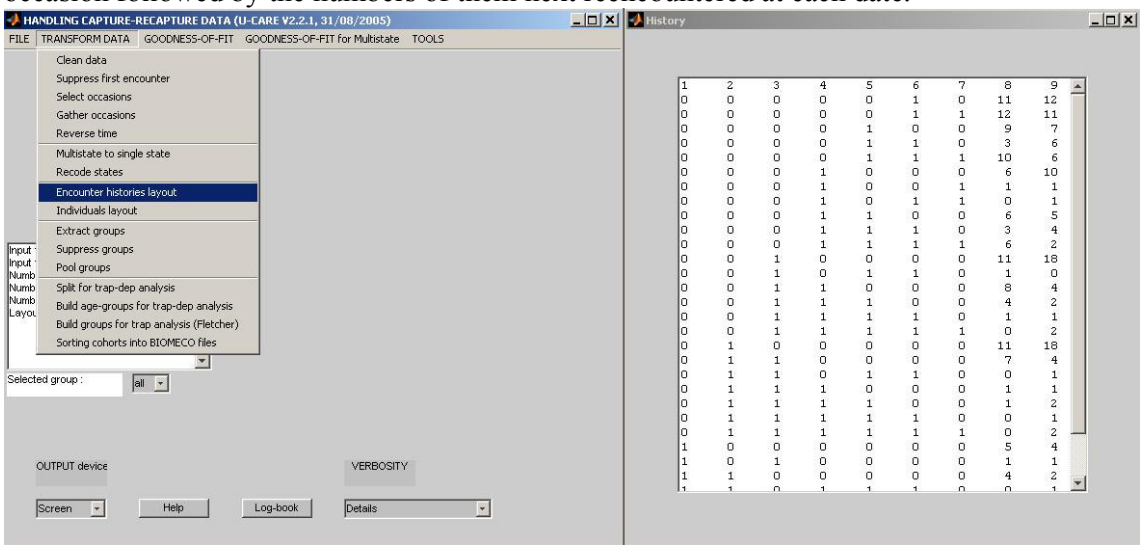


Fig.4: European dipper data set in the encounter histories layout.

To obtain the m-array for each of the two predefined categorical groups (males and females), first change *"Selected group"* to *"all"* (indeed, this should be the default). Then select the option *"M-ARRAY"* in the menu *"TOOLS"*. Two m-arrays should appear in the secondary window (fig.5).

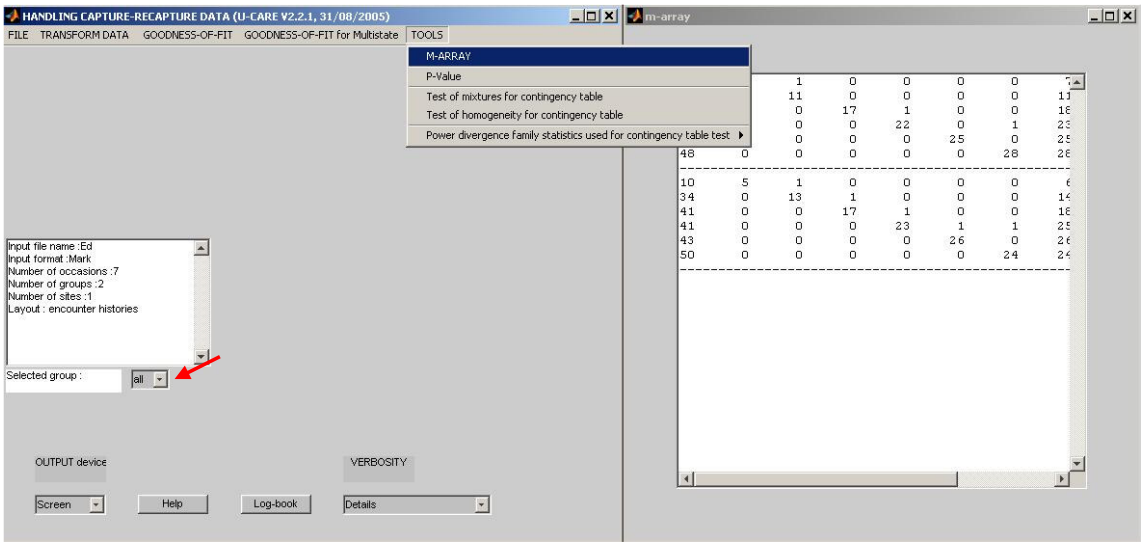


Fig.5: m-array by sex for the European dipper data set

	Ri	*mij*					*ri*
		2	*3*	*4*	*5*	*6*	*7*	
1	12	6	1	0	0	0	0	7
2	26		11	0	0	0	0	11
3	37			17	1	0	0	18
4	39				22	0	1	23
5	45					25	0	25
6	48						28	28

1 10	5	1	0	0	0	0	6
2 34		13	1	0	0	0	14
3 41			17	1	0	0	18
4 41				23	1	1	25
5 43					26	0	26
6 50						24	24

Fig.6: Description of the European dipper m-array. The numbers in italics on the left are the occasions *i*. R_i is the number released at occasion *i*. m_{ij} is the number released at occasion *i* next reencountered at occasion *j*. r_i is the total reencountered among the R_i originally released at occasion *i*. There are two m-arrays: one for the males, one for the females.

The compact form of the m-array provides a fairly good insight into the data. The high values on the main diagonal show that most releases are followed almost immediately by a reencounter. This indicates that encounter probabilities are high. In contrast, the ratios r/R tend to be close to 0.5, indicating a fairly moderate probability of survival. In this context, the first reencounter at occasion 7 only of 2 individuals (one male, one female) released at occasion 4, appears suspicious. These individuals may be differing from the others, reflecting thus some heterogeneity in the data. However, because only two individuals are concerned, the influence of such a limited heterogeneity on estimates and model selection is expected to be negligible. The purpose of Goodness-Of-Fit testing is to decide whether such departures are significant or not and to check systematically the basic assumptions of the classical capture-recapture models.

To run an overall GOF test for the two European dipper sex groups, select the option *"Sum of TESTs over groups"* of the menu *"GOODNESS-OF-FIT"*. The results appear in the secondary window as below:

```
Global TEST, number of groups =2
df =21
Quadratic Chi2 =21.3376
        ->P-level=0.4385
N(0,1) statistic for transient(>0) =-0.075728
        ->P-level, two-sided test =0.93964
        ->P-level, one-sided test for transience =0.53018
N(0,1) signed statistic for trap-dependence =-1.581
        ->P-level, two-sided test =0.11388
```

The statistical approaches used in U-CARE for single-state data are explained in more detail in Chapter 4. The results indicate that the CJS model by sex group is acceptable. Hence, model selection may start safely from model (φ_{t*s}, p_{t*s}). The specific and more powerful tests of transience and trap-dependence appearing in the results window are described in sections 4.3 and 4.5 respectively.

2.4. **Goodness of fit test on pooled data**

U-CARE makes it possible to pool categorical groups. For this, the encounter histories layout (rather than the individuals layout) must be selected first. Thus, select in the menu *"Transform data"* the option *"encounter histories layout"*. A window appears (see Figure 7), type the phrase "{1 2}" and click OK to pool the two groups into one.

Fig. 7: The phrase "{1 2}" pools the first and the second groups to one group.

Then you can use the same GOF procedures as above. The overall m-array for pooled data is simply the sum of the sex-specific m-arrays obtained in section 2.3:

	Ri			mij			ri
1	22	11	2	0	0	0	13
2	60		24	1	0	0	25
3	78			34	2	0	36
4	80				45	1	2	48
5	88					51	0	51
6	98						52	52

After the sex groups have been pooled, one may test the fit of model (φ_t, p_t) instead of (φ_{t*s}, p_{t*s}). The overall GOF results show that the CJS model not accounting for sex is also acceptable.

Global TEST, number of groups =1
df =12
Quadratic Chi2 =14.108
->P-level=0.29387
N(0,1) statistic for transient(>0) =-0.054287
->P-level, two-sided test =0.95671
->P-level, one-sided test for transience =0.52165
N(0,1) signed statistic for trap-dependence =-1.5381
->P-level, two-sided test =0.12402

Remark: *When there are several groups as in this example, it is recommended to conduct GOF tests separately for each group, and to test for group effects in a more detailed way through model selection.*

The various tests illustrated here are explained in more detail in Chapter 4.

3. Data manipulation

3.1. **Data format**

- Two data formats are supported for input in U-CARE. The first format is the **BIOMECO** format :

```
n k+g
name1
name2
e11 e12  ....      e1k   eff11 … eff1g
         ....
         ....
         ....
         ....
en1 en2  ....      enk   effn1 … effng
```

'*k*' is the number of encounter occasions, '*g*' the number of predefined groups and '*n*' the number of histories. *k*+*g* is in effect the total number of columns in the file. The strings 'name1' and 'name2' are the names of two optional files containing the labels for the rows and columns respectively. The dummy name '$' can be used if you do not wish to provide specific labels. e_{ij} is 0 if the individual was not encountered at occasion *j* or *v* if it was encountered in state *v*. The set of values (e_{i1} e_{i2} .... e_{ik}) is called an encounter history and the associated vector eff_i. is the number of animals in each group with history *i*. Note also that in the BIOMECO format, U-CARE tries to estimate the number of groups by itself and prompts the user for validation. This estimation may be wrong and may have to be modified.
Important: To specify that an individual has been removed at its last encounter (e.g. lost on capture) a negative number is put for the size of the encounter history. For instance, "010010 -1" means that the animal was removed at occasion 5.

- Alternatively, the input data file could be in the following restricted **MARK** format :

```
e11e12  ....      e1k   eff11 … eff1g;
        ....
        ....
        ....
        ....
en1en2  ....      enk   effn1 … effng;
```

The program prompts for the number of columns containing individual covariates. By default, this value is zero (i.e., no individual covariates). If individual covariates are specified then the corresponding columns will be skipped because data manipulation with individual covariates is not supported at present. Restrictions to the MARK format are:

- Two frequencies must be separated by one and only one space.

- There must be no tab characters anywhere in the file.

- Comments are not supported.

If this is not the case, the program will be unable to read the data properly and will abort.

Data read in one of these two formats may be saved in the other or in one of three additional formats. All of these formats may also be used to save data after transformations (see section 3.2). The additional formats are:

- The **RELEASE** format :

The RELEASE format (Burnham et al. 1987) is similar to the MARK format but in addition contains commands for the number of occasions and the number of groups. An example follows. This format is used with program RELEASE that does goodness-of-fit testing for single-state data sets.

```
PROC TITLE EXAMPLE RELEASE INPUT FILE;
PROC CHMATRIX OCCASIONS=12 GROUPS=3;
000000000011 0 0 1 ;
101111100000 0 1 1 ;
…
110000000000 0 1 1 ;
111111100110 0 1 1 ;
GLABEL(1)=GROUP1;
GLABEL(2)=GROUP2;
GLABEL(3)=GROUP3;
PROC STOP;
```

- The **SURGE** format :

The SURGE format is a compact representation of single-state data, enabling fast model fitting to single-state data in program SURGE (Pradel et al., 1991).

```
k-1
b1      b2  b3                ....       bk-1
a12 a13               ....      a1k
a23                ....      a2k
…
ai,i+1 ....      aik
…
ak-1,k
c11    c12 c13          ....      c1k-1
c22 c23          ....      c2k-1
…
ci,i    ....      cik-1
…
ck-1,k-1
d11    d12 d13          ....      d1k-1
d22 d23          ....      d2k-1
…
di,i    ....      dik-1
…
dk-1,k-1
```

There are as many SURGE output files as groups '*g*'. '*k*' is the number of encounter occasions. 'b_i' is the number of animals marked at occasion *i*. 'a_{ij}' is the number of animals marked at occasion *i* seen at occasion *j*. 'c_{ij}' is the number of animals marked at occasion *i* seen for the last time at occasion *j*. 'd_{ij}' is the number of animals marked at occasion *i*

censored at occasion *j* (i.e., removed at time of capture, for instance through death while marking).

- The **m-array** format :

The m-array format is another compact representation of the data, usable with single-state and multistate data alike (see figure 6 in section 2.3 for details). '*s*' is the number of states.

```
k  s
R1  m12  m13                 ....       m1k
R2  m23                  ....       m2k
…
Rk-1  mk-1k
```

There are as many m-array files as groups. For multi-state data, 'R_i' are vectors of size '*s*' and 'm_{ij}' are matrices of size *s* x *s*.

3.2. **Data manipulations**

With U-CARE, you can read a file in one of the two entry formats (see 3.1), conduct one or several transformations, and store the transformed data in one of 5 output formats. The original file is not modified unless you decide to overwrite it.

A. Basic data transformations:

- *"Clean data"*: removes empty histories (that only contain zeroes) and histories with no individual.

- *"Suppress first encounter"*: changes the first non-zero of each history into a zero. For example, the history 0100200 becomes 0000200 after transformation.

- *"Select occasions"*: selects occasions to keep (deletes the others). The occasions to keep are listed separated by one space or a comma and enclosed by braces like in "{1,3,4,6}". This option also supports more elaborate lists of occasions: for instance, consecutive occasions can be specified with the first and the last separated by a colon, such as in "{2:6}" for all occasions 2, 3 ,4, 5 and 6. Regularly spaced occasions can be specified with the additional indication of a step such as in "{2:2:6}", which is equivalent to "{2 4 6}". For those knowledgeable, this is MATLAB ® syntax. More details can be found in section 3.3.

- *"Gather occasions"* (single state only): gathers "a" occasions together. Every "a" columns are replaced with a single column containing the number of times the individual has been encountered during the entire period. This is sometime needed when there are numerous or regularly stepped occasions. Most time, it is followed by a *"multistate to single state"* transformation (see below).

- *"Reverse time"*: reverses each encounter history. For instance, history 0210100 becomes 0010120. Reversing time is not allowed when there are right-censored animals in the data set (i.e., at least one encounter history with negative numbers of individuals).

B. Recoding:

- *"Multistate to single state"*: All states are collapsed to one state. For instance, the history 0200300 becomes 0100100.

- *"Recode states":* This is more elaborate. It exchanges any state code for any other state code. For instance, changing state 2 to state 3 and state 3 to state 2 transforms history 0200300 into 0300200.

C. Layouts:

- *"Encounter histories layout":* This layout has one row per encounter history. Replicate encounter histories are pooled and their frequencies added. Note however that a history with a negative frequency is in effect a different history and is treated as such. For example:

0100100 5		
0100100 3	will become	0100100 8
0100100 –1		0100100 –1

- *"Individuals layout":* In this layout, each individual is put on a separate line. All frequencies are then 1 or -1. This may be useful to incorporate newly acquired individual covariates.

D. Managing predefined groups:

- *"Extract groups"*: retains only a range of consecutive groups. You have to enter the first and the last group numbers in the range. To select non consecutive groups, consider the next option.

- *"Suppress groups":* removes one or several consecutive groups entirely. To eliminate non consecutive groups, the operation may be repeated. For instance, to eliminate groups 1 and 3, you may first eliminate group 3, then group 1. If you do it the other way, beware that group 3 will have been renumbered 2 meanwhile.

- *"Pool groups"*: the most powerful tool for managing groups. New groups are created by merging ancient groups. A list of ancient groups separated by spaces defines a new group. The new groups are themselves enclosed between braces and separated by semi-colons. For instance, the syntax '{1 2}; {3}' will be used for putting the former groups 1 and 2 into the new group 1 while former group 3 stands by itself as new group 2. A formal definition of the syntax for lists can be found in section 3.3. a former group that does not appear in a list is effectively removed.

E. Advanced treatments:

- *"Split for trap-dep analysis".* To fit models with encounter probabilities dependent on the time elapsed since last encounter (trap-dependent models in the sense of Pradel, 1993), data must be presented in a special way. This process is made automatic with this option of U-CARE. After running this option, a model with an age effect on encounter probabilities is in effect a model with trap-dependent encounter probabilities (see Pradel

1993 for details). In effect, this option stops an encounter history each time an animal is encountered and starts another encounter history from this point. For example, history "0300120 5" will be replaced with the three histories "0300100 -5", "0000120 -5" and "0000020 5". If the frequency is negative then the last history will not be present: for example, history "0300120 -5" will be replaced with the two histories "0300100 -5" and "0000120 -5".

- *"Build age-groups for trap-dep analysis"*. The previous option does not keep track of the time elapsed since the first encounter. Yet, this information is needed if age is to be incorporated in the model. This more elaborate option dispatches the new encounter histories among groups based on the time elapsed since the first encounter. For instance, history "0300120 5" is replaced with "0300100 -5 0 0 0 0 0 0", "0000120 0 0 0 -5 0 0 0" and "0000010 0 0 0 0 5 0 0". Suppose that the animals in the data set are first encountered at birth, then the new group 4 would correspond to encounter histories starting when the animal is 3 years old.

- *"Build groups for trap analysis (Fletcher)"*. This option is to be used with data coming from a robust design experiment. The encounter history retains only the primary periods but the total number of encounters during the secondary periods making up a primary period is encoded as a state. For instance, the history 0102300 has 7 primary periods and the animal was encountered once during primary period 2, twice during primary period 4 and three times during primary period 5. This option splits the encounter histories and dispatches the new encounter histories among groups based on the number of encounters during the terminating primary period. For instance, the history 0102300 5 will be split into the two histories 0101000 0 -5 0 and 0001100 0 0 5. Note that the resulting data is single-state. (Fletcher 1994)

- *"Sorting cohorts into BIOMECO files"*: Sometimes the individuals have been marked during their birth year, which thus appears as their first encounter; but the analysis focuses on the adult life starting at the first reencounter. This option removes the initial encounter in each encounter history but retains the cohort by dispatching the resulting encounter histories among several BIOMECO files, one for each cohort (i.e. year of birth). In this way, it remains possible to account for age in the models. With *k* occasions, there are potentially *k*-1 cohorts numbered 1 to *k*-1. The BIOMECO file name for cohort *i* is of the form 'name*i*.rh'. The program prompts the user to provide the string 'name'.

3.3. **How to define a list?**

"m n l p" refers to the four elements m n l p

"m: n" refers to the consecutive elements from m to n

"m: b: n" refers to nonconsecutive elements between m and n, starting at m and with b as a step value (m, m+b, m+2b…).

3.4. **Options for goodness of fit tests.**

The aim of this section is not to describe the tests themselves (this is done in chapters 4 and 5), but to describe the options for running these tests. These options regard the input data to be analyzed and the output results to be produced. But before describing these options, you need

to know that this is the first version that incorporates multistate goodness-of-fit (GOF) tests. It is somewhat transitory as it retains the 'old' single-state GOF test as a separate item in the main menu. Because single-state GOF tests can be retrieved as a particular case of the new multistate GOF tests, we plan to remove them eventually. Therefore, we have decided to not implement in the single-state section the new options being added (such as new verbosity levels). What follows may thus be relevant only to the multistate GOF tests.

Before running GOF tests, you can decide:

- to run the tests on just one group or on all groups;
- to get more or less output details;
- to direct the output to a file or only to the screen.

By default, GOF tests are carried out on all groups. To carry them out on just one group, select the group you want in the list next to *"Selected group"*

By default, reasonably detailed results are displayed in the secondary window on the right of the main window. However, under 'Verbosity' you can ask for more details. The options 'No details' and 'Details' (the default) are synonymous at the moment. They provide chi-square statistics, degrees of freedom and P-values for the test components as well as for the test itself. The option 'Details with contingency tables' additionally provides the contingency tables on which the test components are based. Eventually, you may pick 'Full details' to get also the contingency tables previous to any pooling and the table of expected numbers.

By default, the outputs are directed only to the screen. However, under 'Output device', you may select 'Single step file' or 'New global file' to save the results in text files. The difference between the two is that with 'Single step file' each test will be saved in a different file while they will all go in the same file with 'New global file'.

4. Goodness-of-fit tests for single-state data.

The main goal of program U-CARE is to conduct goodness-of-fit tests and hence, to identify an appropriate umbrella model from which to start model selection. The classical software for single-state GOF testing is program RELEASE (Burnham et al., 1987), a version of which is implemented in program MARK (White and Burnham, 1999). Program U-CARE contains the same tests for single state, but with a slightly different strategy for pooling sparse contingency tables; hence, the results may slightly differ from those obtained by RELEASE. In addition, U-CARE contains more specific tests for a more detailed diagnosis of the data with respect to several models. Specifically, it contains "directional" tests for transience (Pradel et al., 1997) and trap-dependence (trap-happiness or trap shyness; Pradel, 1993).
U_CARE version 2.2 contains also up to date multistate tests with a decomposition of the tests into several components similar to those existing for single state (Pradel et al., to appear in Animal Biodiversity and Conservation) (see chapter 5).
Forthcoming versions of U-CARE will incorporate further specialized tests and appropriate treatment for sparse data together with recommendations on which model should be used as a starting point in model selection.

4.1. **An intuitive presentation**

In single-state capture-recapture theory, optimal goodness-of-fit tests are readily available for three main models:

- the Cormack-Jolly-Seber (CJS) model denoted ϕ_t,p_t (see Lebreton et al., 1992),
- the 'transient' version of the CJS model denoted ϕ_{a2*t},p_t (see Pradel et al,. 1997),
- the version of the CJS model with immediate trap-dependence on capture denoted ϕ_t,p_{m*t} (see Pradel, 1993).

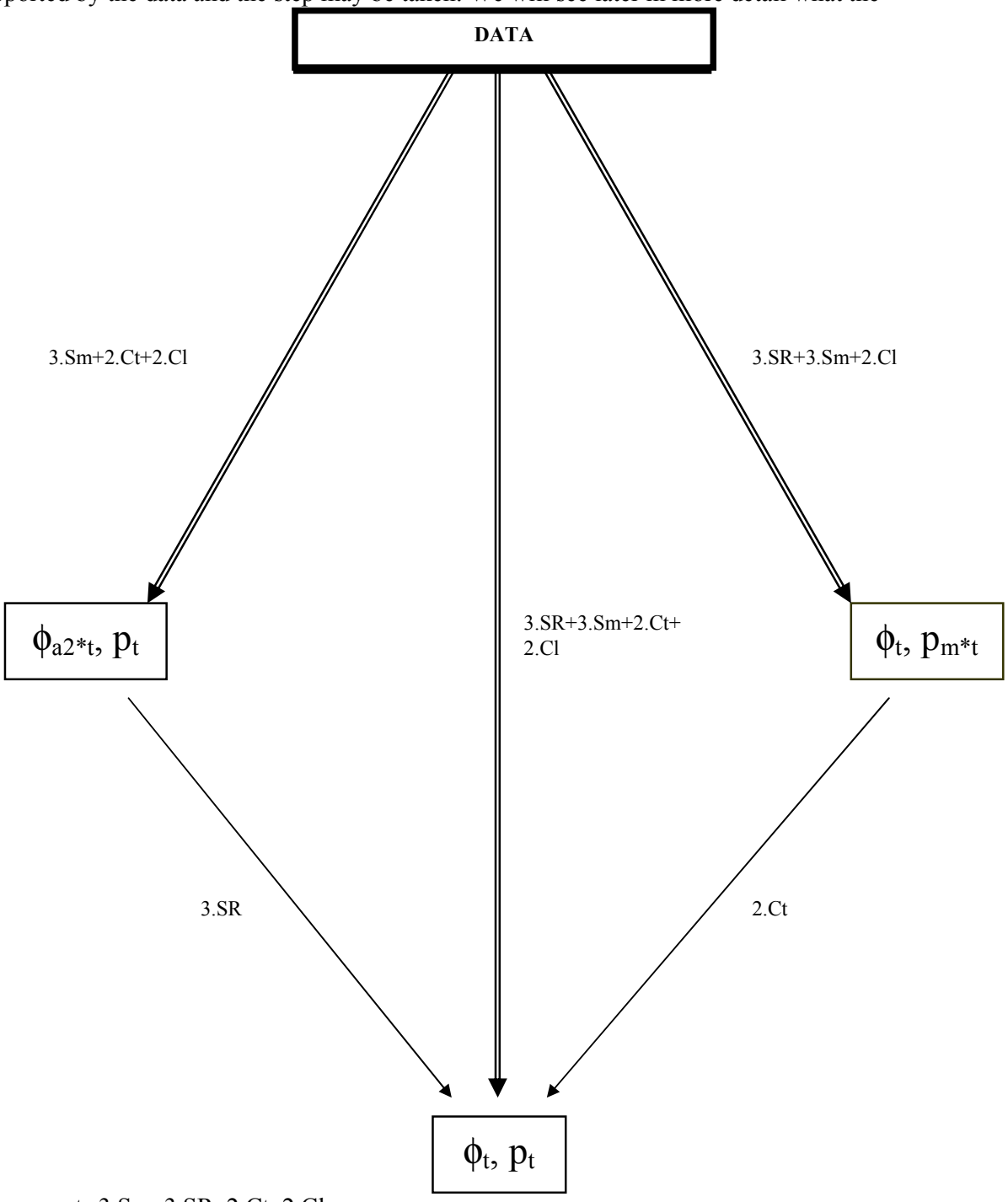
Model ϕ_t,p_t makes the assumption that survival and encounter probabilities are solely time-dependent. It is the most restrictive of the three as it does not permit survival to differ between newly marked and previously marked animals like ϕ_{a2*t},p_t, or encounter probability to differ between animals encountered at the previous occasion and those not encountered like ϕ_t,p_{m*t}. In fact, ϕ_t,p_t is nested within each of the two other models. Models ϕ_t,p_{m*t} and ϕ_{a2*t},p_t are themselves unrelated, each making an assumption that the other does not (see figure 8).

As a consequence of this hierarchy, the goodness-of-fit test of ϕ_t,p_t involves more components (more assumptions need to be checked) than the goodness-of-fit tests of ϕ_t,p_{m*t} or ϕ_{a2*t},p_t. Actually, the goodness-of-fit test of ϕ_t,p_t can be decomposed into two steps according to two different paths:

- the goodness-of-fit test of ϕ_{a2*t},p_t (3.Sm+2.Ct+2.Cl) plus the test of ϕ_t,p_t against ϕ_{a2*t},p_t (3.SR).

- the goodness-of-fit test of ϕ_t,p_{m*t} (3.SR+2.Sm+2.Cl) plus the test of ϕ_t,p_t against ϕ_t,p_{m*t} (3.Ct).

Figure 8 illustrates these considerations. Each arrow points toward further assumptions. If the associated test is significant (which can be visualised as the arrow being too 'long', and viewed as 'the assumptions cannot be stretched that much'), the additional assumptions should be rejected. If it is not significant (the arrow is short), the additional assumptions are supported by the data and the step may be taken. We will see later in more detail what the



components 3.Sm, 3.SR, 2.Ct, 2.Cl are.

4.2. **A more formal presentation**

A comprehensive view of ***capture-recapture survival models*** is given by Lebreton et al. (1992) to which the reader is referred for an introduction to what follows. A key assumption of capture-recapture survival models is the independence of individuals, which leads to multinomial distributions for the number of individuals in the various capture-recapture histories. As a consequence, if a model describes correctly the data, the residual variation should just reflect multinomial variability. Any systematic source of variation having been taken into account in the model structure, such a model is said to fit the data.

To examine biological questions, one selects one or several models within a set of biologically plausible models, e.g., by use of AIC (Akaike's information criterion). AIC is calculated as the deviance of a model plus twice the number of identifiable parameters (Burnham et al. 1998). It is critical for valid model selection that the set of models considered includes at least one model that fits the data. If not, the results will be biased and unreliable.

Starting from a plausible model with potential effects to be examined and checking its fit is thus the first step in capture-recapture analysis (Lebreton et al., 1992). Optimal goodness-of-fit tests of the assumptions inherent in the time-dependent CJS model are based on a classical partitioning of the likelihood according to sufficient statistics (Pollock et al., 1985). This partitioning of the likelihood, for sufficient statistics T is:

$$P(\text{data}/\text{ parameters}) = P(\text{data}/T) \times P(T/\text{parameters})$$

The second term, P(T/parameters), viewed as a likelihood, is a function of the parameters and serves to estimate the parameters in software such as SURGE (Pradel et al., 1991; Reboulet et al., 1999) or MARK (White et al., 1999). The term P(data/T) does not depend on the parameters; it contains the factorial terms of multinomial probabilities and corresponds to hypergeometric distributions. The compatibility of the data with these distributions is tested in turn, asymptotically, by contingency table chi-squared tests. These tests, organized into several interpretable components by partitioning P(data/T), are implemented in program JOLLY (Pollock et al., 1990) and, in a slightly more detailed way, in program RELEASE (Burnham et al., 1987). RELEASE is also available within MARK (White and Burnham 1999) as a menu option.

The purpose of U-CARE is to provide improved versions of these general goodness-of-fit tests to capture-recapture survival models and to add more specialized tests in a user-friendly way.

The terminology used is that of Burnham et al. (1987) as implemented previously in RELEASE and slightly extended to a more detailed partitioning (see Pradel, 1993). The overall test is composed of TEST 3.SR+TEST 3.SM+TEST 2.CT+TEST 2.CL and tests the goodness-of-fit of the CJS model (Φ_t, p_t). If one or several components are significant, the goodness-of-fit of several alternative models can be checked by ignoring some of these components (Table 1; see also Lebreton et al., 2000). The meaning of these tests is explained below in detail.

If it is decided that lack of fit of a model to the data is due to overdispersion rather than structural failure of the model (Lebreton et al. 1992), a correction factor $\hat{c}$ may be computed. This can be done based on the values of goodness-of-fit tests given by U-CARE.

Table 1: Scenarios for goodness-of-fit tests for capture-recapture models from the CJS family. The table shows possible results of the GOF tests and suggested courses of action.

Test components used	Results	Umbrella model	Remarks
TEST 3.SR + TEST 3.SM + TEST 2.CT + TEST 2.CL	non significant	(Φ_t, p_t)	CJS model
TEST 3.SM + TEST 2.CT + TEST 2.CL	non significant	(Φ_{a2*t}, p_t)	Brownie et al., 1983 Pradel et al., 1997
TEST 3.SR + TEST 3.SM + TEST 2.CL	non significant	(Φ_t, p_{t*m})	identifiability problems (Pradel, 1993) ;
Any of the combination above	significant	start from corresponding model with over-dispersion coefficient	check that the individual estimates of over-dispersion per component are even

4.3. **TEST 3.SR and associated tests**

4.3.1. Basic statistical theory for TEST 3.SR # i

TEST 3.SR component # *i* is based on the contingency table, noted TABLE 3.SR(i), given in Table 2.

Table 2: The 2x2 table TABLE 3.SR(i) based on the individuals encountered at occasion *i* that serves as a basis of TEST 3.SR component # *i*

	Seen later	Never seen again	Total
Never seen before ("new" or "newly marked")	$\mathbf{o_{11}}$	$\mathbf{o_{12}}$	$\mathbf{o_{1.}}$
Seen before ("old" or "already marked")	$\mathbf{o_{21}}$	$\mathbf{o_{22}}$	$\mathbf{o_{2.}}$
Total	$\mathbf{o_{.1}}$	$\mathbf{o_{.2}}$	$\mathbf{o_{..}}$ (total number seen on occasion *i*)

The null hypothesis being tested is
H_0(i) : *there is no difference in the probability of being later reencountered between "new" and "old" individuals encountered at occasion i.*

The basic test is then a χ^2 test of homogeneity of TABLE 3.SR(i), based on the expected numbers given in Table 3.

Table 3: Expected numbers under $H_0(i)$ for the 2x2 table TABLE 3.SR(i) (see text for details)

	Seen later	Never seen again	Total
Never seen before ("new" or "newly marked")	$e_{11} = o_{.1}x o_{1.} / o_{..}$	$e_{12} = o_{.2}x o_{1.} / o_{..}$	$o_{1.}$
Seen before ("old" or "already marked")	$e_{21} = o_{.1}x o_{2.} / o_{..}$	$e_{22} = o_{.2}x o_{2.} / o_{..}$	$o_{2.}$
Total	$o_{.1}$	$o_{.2}$	$o_{..}$

The usual χ^2 statistic is obtained as:

$X^2(i) = \Sigma(\mathbf{o_{jk}}-\mathbf{e_{jk}})^2/\mathbf{e_{jk}}$

and under $H_0(i)$ follows asymptotically a χ^2 distribution with 1 degree of freedom. All the information in TEST 3.SR is derived from this basic setting. "Asymptotically" corresponds to the usual requirement that the expected values $\mathbf{e_{jk}}$ must be over some threshold, commonly taken as equal to 2 (Reference ?).

When one or several marginal numbers $\mathbf{o_{.k}}$ and/or $\mathbf{o_{j.}}$ in TABLE 3.SR(i) are equal to 0, one or several expected numbers $\mathbf{e_{jk}}$ will be equal to zero, and $X^2(i)$ cannot be calculated. Such components will appear as equal to 0 with 0 degree of freedom.

The general alternative hypothesis to $H_0(i)$ is simply:
$H_1(i)$: *there is a difference in the probability of being later reencountered between "new" and "old" individuals encountered at occasion i.*

Under $H_1(i)$, $X^2(i)$ follows asymptotically a non-central χ^2 distribution, with a non-centrality factor depending on the numbers of old and new individuals expected to be later reencountered.

Alternatively, *and in a totally equivalent way*, one may use the signed-square root of the chi-squared statistic to test for $H_1(i)$ against $H_0(i)$:

$z(i) = \text{sign}(\mathbf{o_{21}}-\mathbf{e_{21}}) * X(i)$

Under $H_0(i)$, z(i) follows asymptotically a standardized normal distribution N(0,1). Under $H_1(i)$, z(i) follows asymptotically a standardized normal distribution $N(\mu_i,1)$, where μ_i depends on the numbers of old and new individuals expected to be later reencountered.

However, frequently newly marked individuals consist in part of transient individuals (Pradel et al. 1997). In this case the alternative hypothesis of interest is:
$HT_1(i)$: *among individuals encountered at occasion i, the "new" individuals tend to be less reencountered later than the "old" individuals*.

This will be also the case when animals are marked at a same age (e.g., as immature) and survival in the first age class is smaller than later on, a common pattern of age-dependent survival. Under $H_1(i)$, z(i) follows then asymptotically a standardized normal distribution $N(\mu_i,1)$, *where μ_i is negative* since the expected value of $\mathbf{o_{21}}$ will be lower than $\mathbf{o_{.1}}\ \mathbf{o_{2.}}/\ \mathbf{o_{..}}$. In U-CARE, this test is made on $\mathbf{o_{21}}$ like in program RELEASE (in this case, *μ_i is positive).*

4.3.2. Basic statistical theory for TEST 3.SR

One overall hypothesis inherent in the CJS model is the combination of the null hypotheses $H_0(i)$ above :

H_0 : *there is no difference in the probability of being later reencountered between the "new" and "old" individuals*

The overall statistic $X^2 = \Sigma\ X^2(i)$ under H_0 follows a χ^2 distribution, with *k* degrees of freedom, where *k* is the number of components.
Under H_1 : *there is a difference in the probability of being later reencountered between the "new" and "old" individuals*, X^2 follows asymptotically a non-central χ^2 distribution with *k* degrees of freedom and a non-centrality parameter depending on the numbers of old and new individuals expected to be later reencountered. Thus, X^2 is an omnibus statistic for testing for any departure from H_0.

However, as mentioned above, i.e., due to transience or age-dependence, the alternative hypothesis of interest is frequently :

HT_1 : *the "new" individuals tend to be less reencountered later than the "old" individuals*.

In this situation, X^2 is not optimal anymore to test for HT_1 against H_0. A more powerful statistic, leading to what one may call for the sake of brevity a "directional test", is obtained by combining the statistics z(i) which will tend to be all positive under HT_1. In fact under H_0, Σ z(i) follows a normal distribution N(0,k), and under H_1 or HT_1, a normal distribution $N(\Sigma\mu_i, k)$. In practice, one may better use:

$z = \Sigma\ z(i) / \sqrt{k}$, with distribution N(0,1) under H_0 and $N(\Sigma\mu_i / \sqrt{k}, 1)$ under HT_1.

Z has no interest to test for H_1 against H_0 since the μ_i can be either positive or negative under H_1 and make $\Sigma\mu_i$ close to 0. However, under HT_1, all the μ_i will be positive, and Z ensures maximal power to test for HT_1 against H_0. The convergence of z to a normal distribution will be very good even for a moderate value of *k*. It is also recommended to use a one-sided test to test for H_0 against HT_1 : the 0.05 level for z will be then 1.67 (rather than 1.96).

4.3.3. Sparseness

Many of the 2x2 tables used in the above tests will be sparse, i.e., have low expected numbers. The asymptotic $\chi^2(1)$ distribution for either χ^2 (i) or G^2 is then inadequate. As soon as there is as least one cell with low expected values in a contingency table, U-CARE uses the Fisher exact test . Then the chi² statistic is back-calculated as the value of a $\chi^2(1)$ distribution that leads to the corresponding P-value. When summing the resulting statistics, one obtains overall chi² tests that are reasonably protected against sparse data.

The P-value of $X^2(i)$ obtained using the Cochran correction is also given. Haber (1983) conducted a large simulation study and compared several approaches to X^2 tests for sparse 2x2 contingency tables. He concluded that the Cochran correction was the most adequate in a majority of cases. We are presently investigating further options to handle sparse data.

4.3.4. Implementation in U-CARE

The items in the output of TEST 3.SR in U-CARE are listed and explained in Table 4. An example of results for Black-headed Gull data (Reference ??) is given in Table 5.

Table 4: Items in the output of TEST 3.SR in U-CARE and their meaning

Item	Meaning	Comments
component	component number	encounter occasion used as reference (range : 2 to *K*-1)
df	degrees of freedom	since all tables are 2 x 2 must be 1, or 0 when one of the margin terms is 0.
z	signed square root of the χ^2 statistic : $z(i) = \text{sign}(o_{21}-e_{21}) * X(i)$ o_{11}	follows a N(0,1) distribution under $H_0(i)$, shifted to negative or positive values under $H_1(i)$, shifted to positive values under $HT_1(i)$
LOR	Log odds-ratio $\text{Ln}\ (o'_{11}o'_{22}/o'_{12}o'_{21})$ With $o'_{jk}=o_{jk} + 0.5$ (Gart's correction, see Agresti, 1999)	Expected value is 0 under $H_0(i)$, differs from 0 under $H_1(i)$, is positive under $HT_1(i)$
S.E.LOR	$\text{Sqrt}(1/o'_{11}+1/o'_{22}+1/o'_{12}+1/o'_{21})$	Standard error of the LOR under H_0.
chi2	the χ^2 statistic $X^2(i)$	asymptotically follows a $\chi^2(1)$ distribution under $H_0(i)$, and a non-central $\chi^2(1)$ distribution under $H_1(i)$
G2	The G-test version of the chi2 statistic	Follows asymptotically a $\chi^2(1)$ distribution under $H_0(i)$, and a non-central $\chi^2(1)$ distribution under $H_1(i)$
low nrs	"low numbers" : Flag for sparseness in this component	The number of expected values e_{ij} which are smaller than 2.
P(chi2)	P-level of the X^2 statistic	Based on the asymptotic $\chi^2(1)$ distribution if there are no low expected values , and on the Fisher's exact test if otherwise
P(Cochran)	P-level of the X^2 statistic	Based on the Cochran correction for sparseness (Haber, 1983)
P(G2)	P-level of the G^2 statistic	Based on the asymptotic $\chi^2(1)$ distribution if there are no low expected values, and on the Fisher exact test otherwise

U-CARE gives then a set of overall results for TEST 3.SR detailed below:

Item	Meaning	Further comments
N(0,1) statistic for transient(>0)	Compound statistic $z = \Sigma z(i)/\sqrt{k}$	follows a N(0,1) distribution under H_0, shifted to positive values under HT_1
P-level, two-sided test	P-level of	Tests for an excess or a

	the above statistic	lack of newly marked individuals that are never seen again
P-level, one-sided test for transience	One-sided version of the P-level	Tests for an excess of newly marked individuals that are never seen again ("transience")
Log-Odds-Ratio (LOR)	Compound LOR statistic	follows a Normal distribution under H_0, shifted to positive values under HT_1
N(0,1) LOR statistic for transience (>0)	Standardized Compound LOR statistic	follows a N(0,1) distribution under H_0, shifted to positive values under HT_1 Asymptotically equivalent to the statistic z above
P-level, two-sided test	P-level of the above statistic	Tests for an excess or a lack of newly marked never seen again
P-level, one-sided test for transience	One-sided version of the P-level	Tests for an excess of newly marked never seen again ("transience")
df	Degrees of freedom of the overall TEST 3.SR statistics	Ignores tables with one or several marginal numbers equal to 0
Quadratic Chi2	Quadratic chi2 statistic for Test3.Sr	Corrected for sparseness (see 4.3.3)
P-level	P-level of the above statistic	
G2	G test version of Test3.Sr	Corrected for sparseness (see 4.3.3)
P-level	P-level of the above statistic	

Table 5: TEST 3.SR results for Black-headed Gull data.

```
TEST 3.SR, group =1
component   df      z        LOR    S.E.LOR   chi2      G2
     2       1    0.00    -1.10     1.71     0.00     0.00
     3       1    0.00     0.00     1.75     0.00     0.00
     4       1    0.00    -0.68     1.67     0.00     0.00
     5       1    2.11     1.59     0.82     4.44     4.46
     6       1    0.23     0.16     0.78     0.05     0.05
     7       1    0.64     0.40     0.64     0.41     0.41
     8       1    1.90     1.06     0.58     3.62     3.62
     9       1    1.52     0.65     0.43     2.32     2.29
    10       1    2.53     0.95     0.38     6.39     6.15
    11       1    0.75     0.32     0.42     0.56     0.55
    12       1    1.61     0.89     0.56     2.60     2.52
    13       1   -0.09    -0.02     0.50     0.01     0.01
    14       1    1.54     0.71     0.46     2.37     2.35
    15       1    0.75     0.34     0.45     0.57     0.57
    16       1    0.62     0.32     0.50     0.38     0.37
    17       1    1.29     0.72     0.57     1.66     1.63
    18       1    2.11     1.17     0.56     4.45     3.99
component   df    low nrs P(chi2) P(Cochran) P(G2)
     2       1    2.00     1.00     1.00     1.00
     3       1    2.00     1.00     1.00     1.00
     4       1    2.00     1.00     1.00     1.00
     5       1    0.00     0.04     0.05     0.03
     6       1    0.00     0.82     1.00     0.81
     7       1    0.00     0.52     0.74     0.52
     8       1    0.00     0.06     0.09     0.06
     9       1    0.00     0.13     0.18     0.13
    10       1    0.00     0.01     0.02     0.01
    11       1    0.00     0.45     0.51     0.46
    12       1    0.00     0.11     0.15     0.11
    13       1    0.00     0.93     1.00     0.93
    14       1    0.00     0.12     0.16     0.13
    15       1    0.00     0.45     0.49     0.45
    16       1    0.00     0.54     0.60     0.54
    17       1    0.00     0.20     0.24     0.20
    18       1    0.00     0.03     0.05     0.05
================================================
N(0,1) statistic for transient(>0) =4.2476
      P-level, two-sided test =2.1603e-005
      P-level, one-sided test for transience =1.0802e-005
Log-Odds-Ratio (LOR) =1.8129
N(0,1) standardized LOR statistic for transience (>0) =2.0596
      P-level, two-sided test =0.039432
      P-level, one-sided test for transience =0.019716
Overall test df =17
Quadratic Chi2 =29.8277
      P-level =0.027615
G2 =28.9891
      P-level =0.034627
```

4.4. **TEST 3.Sm**

TEST 3.Sm component # *i* is based on the contingency table, noted TABLE 3.Sm(i), shown in Table 6.

Table 6: The 2xn table TABLE 3.Sm(i) based on the individuals encountered at occasion *i* that will be seen again. This table serves as the basis for the TEST 3.Sm component # *i*.

	Encountered at *i*+1	....	Encountered at *k*	TOTAL
Never seen before ("new" or "newly marked")	$o_{1\ i+1}$	....	$o_{1\ k}$	$o_{1.}$
Seen before ("old" or "already marked")	$o_{2\ i+1}$	....	o_{2k}	$o_{2.}$
TOTAL	$o_{.i+1}$	....	$o_{.k}$	$o_{..}$ (total number seen on occasion *i* that will be seen again)

The null hypothesis being tested is:
$H_0(i)$: *there is no difference in the expected time of first reencounter between the "new" and "old" individuals encountered at occasion i and seen again at least once.*

The basic test is then a χ^2 test of homogeneity of TABLE 3.Sm(i). To date, this test has received no simple interpretation.

As soon as there is as least one low expected value in the contingency table, U-CARE uses a pooling algorithm and eventually resorts to the Fisher exact test when the table shrunk to size 2x2 has still some low expected values. Then the chi² statistic is back-calculated as the value of a $\chi^2(1)$ distribution yielding the corresponding P-value. When summing the resulting statistics, one obtains overall chi² tests that are reasonably protected against sparse data. From the p-values obtained, the $X^2(i)$ and $G^2(i)$ values are back-calculated from the value of the $\chi^2(1)$ distribution leading to the corresponding P-values. This ensures as much as possible good distributional properties of the overall X^2 and G^2 statistics, which is obtained by summing the components. The results given by U-CARE are as follows:

`df`	Degrees of freedom of the overall TEST 3.Sm statistics	Ignores tables with one or several marginal numbers equal to 0
`Quadratic Chi2`	Quadratic chi2 statistic for Test3.Sm	Corrected for sparseness (see 4.3.3)
`P-level`	P-level of the above statistic	
`G2`	G test version of Test3.Sm	Corrected for sparseness (see 4.3.3)
`P-level`	P-level of the above statistic	

4.5. **TEST 2.CT and associated tests**

4.5.1. Basic statistical theory for Test2.CT # i

Like TEST 3.SR#*i*, TEST 2.CT # *i* is based on a 2 x 2 contingency table. Statistical developments are thus quite parallel and are explained here again for the sake of completeness.

TEST 2.CT component # *i* is based on the contingency table, noted TABLE 2.Ct(i), given in Table 7.

Table 7: The 2 x 2 table TABLE 2.CT(i) based on the individuals encountered before (or at) occasion *i* and after (or at) occasion *i*+1 – and thus known to be alive at both *i* and *i*+1, - which serves as a basis of TEST 2.CT component # *i*

	Reencountered at *i*+1	Reencountered later	TOTAL
Not encountered at *i*	$\mathbf{o_{11}}$	$\mathbf{o_{12}}$	$\mathbf{o_{1.}}$
Encountered at *i*	$\mathbf{o_{21}}$	$\mathbf{o_{22}}$	$\mathbf{o_{2.}}$
TOTAL	$\mathbf{o_{.1}}$	$\mathbf{o_{.2}}$	$\mathbf{o_{..}}$ (total number known to be alive at both *i* and *i*+1)

The null hypothesis being tested is

$H_0(i)$: *there is no difference in the probability of being reencountered at i+1 between those encountered and not encountered at occasion i conditional on presence at both occasions.*

The basic test is then a χ^2 test of homogeneity of TABLE 2.CT(i), based on the expected numbers given in Table 8.

Table 8: Expected numbers under $H_0(i)$ for the 2x2 table TABLE 2.CT(i) (see text)

	Encountered at *i*+1	Not encountered at *i*+1	TOTAL
Not encountered at *i*	$\mathbf{e_{11} = o_{.1x}o_{1.}/ o_{..}}$	$\mathbf{e_{12} = o_{.2x}o_{1.}/ o_{..}}$	$\mathbf{o_{1.}}$
Encountered at *i*	$\mathbf{e_{21} = o_{.1x}o_{2.}/ o_{..}}$	$\mathbf{e_{22} = o_{.2x}o_{2.}/ o_{..}}$	$\mathbf{o_{2.}}$
TOTAL	$\mathbf{o_{.1}}$	$\mathbf{o_{.2}}$	$\mathbf{o_{..}}$

The usual χ^2 statistic is:

$$X^2(i) = \Sigma(\mathbf{o_{jk}}-\mathbf{e_{jk}})^2/\mathbf{e_{jk}}$$

Under $H_0(i)$, it follows asymptotically a χ^2 distribution with 1 degree of freedom. All the information in TEST 2.CT is derived from this basic setting. "Asymptotically" corresponds to the usual requirement that the expected numbers $\mathbf{e_{jk}}$ be greater than some threshold, commonly taken as equal to 2 (Reference).

When one or several marginal numbers $\mathbf{o_{.k}}$ and/or $\mathbf{o_{j.}}$ in TABLE 2.CT(i) are equal to 0, one or several expected numbers $\mathbf{e_{jk}}$ will be equal to zero, and $X^2(i)$ cannot be calculated. Such components will appear as equal to 0 with 0 degree of freedom.

The general alternative hypothesis to $H_0(i)$ is simply:

$H_1(i)$: *there is a difference in the probability of being reencountered at i+1 between those encountered and not encountered at occasion i conditional on presence at both occasions.*

Under $H_1(i)$, $X^2(i)$ asymptotically follows a non-central χ^2 distribution, with a non-centrality parameter depending on the numbers of observed and not observed at *i* individuals expected to be reencountered at *i*+1.

Alternatively, *and in an equivalent way*, one may use the signed-square root of the chi-squared statistic to test for $H_1(i)$ against $H_0(i)$:

$z(i) = \text{sign}(\mathbf{o_{11}}-\mathbf{e_{11}}) * X(i)$

Under $H_0(i)$, z(i) asymptotically follows a standardized normal distribution N(0,1). Under $H_1(i)$, z(i) asymptotically follows a standardized normal distribution $N(\mu_i,1)$, where μ_i depends on the numbers of observed and not observed at *i* individuals expected to be reencountered at *i*+1.

However, a frequent case in capture recapture is that individuals encountered at *i* tend to avoid (trap-shy individuals) or seek (trap-happy individuals) the traps at *i*+1 (Pradel, 1993). In this case the alternative hypothesis of interest is:

$HT_1(i)$: *among individuals alive at both occasions i and i+1, those encountered at i tend to be less (if trap-shy) or more (if trap-happy) reencountered at i+1*.

For a given experiment it may be possible to specify whether animals are more likely to be trap-shy or trap-happy. For instance, trap-happiness is expected when baited traps are used. Under $H_1(i)$ z(i) then asymptotically follows a standardized normal distribution $N(\mu_i,1)$, *where μ_i is negative (resp. positive)* in case of trap-happiness (resp. trap-shyness) since the expected value of $\mathbf{o_{11}}$ will be smaller (resp. greater) than $\mathbf{o_{.1}\, o_{1.}/\, o_{..}}$.

4.5.2. Basic statistical theory for Test2.CT

Test2.CT uses data structures very similar to Test3.Sr. Thus, we here largely repeat previous material. The presentation below is given for the sake of clarity.

One overall hypothesis inherent in the CJS model is the combination of the null hypotheses $H_0(i)$ above :

H_0 : *there is no difference in the probability of being reencountered between the animals encountered and not encountered at the previous occasion conditional on presence at both occasions*

The overall statistic $X^2 = \Sigma\, X^2(i)$ follows under H_0 a χ^2 distribution, with *k* degrees of freedom, where *k* is the number of components.

Under H_1 : *there is a difference in the probability of being reencountered between the animals encountered and not encountered at the previous occasion conditional on presence at both*

occasions, X^2 asymptotically follows a non-central χ^2 distribution with *k* degrees of freedom and a non-centrality parameter that depends on the numbers of individuals observed and not observed at the previous occasion expected to be reencountered. X^2 is thus an omnibus statistic for testing for any departure from H_0 in the CJS model.

However, as mentioned above the alternative hypothesis of interest is frequently :

HT_1 : *among individuals alive at two successive occasions, those encountered on the first occasion tend to be either less (trap-shyness) or more (trap-happiness) reencountered at the second occasion*.

In this situation, X^2 is not optimal anymore as a test for HT_1 against H_0. A more powerful statistic, leading to what one may call a "directional test", is obtained by combining the statistics z(i), which will tend to be positive (trap-happiness) or negative (trap-shyness) under HT_1. In fact under H_0, Σ z(i) follows a normal distribution N(0,k), and under H_1 or HT_1, a normal distribution $N(\Sigma\mu_i, k)$. In practice, one may better use:

$z = \Sigma z(i) / \sqrt{k}$, with distribution N(0,1) under H_0 a and $N(\Sigma\mu_i / \sqrt{k}, 1)$ under HT_1.

z is not useful as a test statistic for H_1 against H_0 since the μ_i can be either positive or negative under H_1 and yield $\Sigma\mu_i$ close to 0. However, under HT_1, all the μ_i will be positive (trap-happiness) or negative (trap-shyness), and Z ensures maximal power to test for HT_1 against H_0. The convergence of z to a normal distribution will be very good even for a moderate value of *k*. It is also recommended to use a one-sided test to test for H_0 against HT_1 : the 0.05 level for z will be then 1.67 (rather than 1.96).

4.5.3. Sparseness

Sparse data are treated as in TEST 3.SR (see 4.3.3).

4.5.4. Implementation in U-CARE

Table 9: Items in the output of TEST 2.CT in U-CARE and their meaning

Item	Meaning	Comments
`component`	component number	encounter occasion used as reference (range : 2 to *K*-1)
`df`	degrees of freedom	since all tables are 2 x 2 must be 1, or 0 when one of the margins is empty
`z`	signed square root of the χ^2 statistic : $z(i) = sign(o_{11}-e_{11}) * X(i)$	follows a N(0,1) distribution under $H_0(i)$, shifted to negative or positive values under $H_1(i)$, shifted to positive (trap-happiness) or negative (trap-shyness) values under $HT_1(i)$
`LOR`	Log odds-ratio $Ln(o'_{11}o'_{22}/o'_{12}o'_{21})$ With $o'_{jk} = o'_{jk} + 0.5$ Gart's correction (Agresti 1999)	Expected value is 0 under $H_0(i)$, differs from 0 under $H_1(i)$, is positive or negative under $HT_1(i)$
`S.E.LOR`	$Sqrt(1/o'_{11}+1/o'_{22}+1/o'_{12}+1/o'_{21})$	Standard error of the LOR under H_0.

`chi2`	the χ^2 statistic $X^2(i)$	asymptotically follows a $\chi^2(1)$ distribution under $H_0(i)$, and a non-central $\chi^2(1)$ distribution under $H_1(i)$
`G2`	The G-test version of the chi2 statistic	asymptotically follows a $\chi^2(1)$ distribution under $H_0(i)$, and a non-central $\chi^2(1)$ distribution under $H_1(i)$
`low nrs`	"low numbers" : Flag for sparseness in this component	The number of expected values e_{ij} that are smaller than 2.
`P(chi2)`	P-level of the X^2 statistic	Based on the asymptotic $\chi^2(1)$ distribution
`P(Cochran)`	P-level of the X^2 statistic	Based on Cochran correction for sparseness (Haber 1983)
`P(G2)`	P-level of the G^2 statistic	Based on the asymptotic $\chi^2(1)$ distribution

U-CARE gives then a set of overall results detailed below:

Item	Meaning	Further comments
N(0,1) signed statistic for trap-dependence	Compound statistic $z = \Sigma z(i)/\sqrt{k}$	follows a N(0,1) distribution under H_0, shifted to positive or negative values under HT_1
Trap-happiness <0 trap-shyness >0	Indicates type of trap dependence according to the sign of z	
P-level, two-sided test	P-level of the above statistic	Tests for Trap-happiness or trap-shyness
Logit(p*)-logit(p)	Mean difference in logit between encounter probability immediately after release (p*) and later on (p)	Deduced from LOR. Positive if trap-happiness, negative if trap shyness.
N(0,1) LOR statistic for trap-dependence	Standardized compound LOR statistic	Compares logit(p*)-logit(p) to 0
Trap-happiness <0 trap-shyness >0	Indicates type of trap dependence according to the sign of the statistic	
P-level, two-sided test	P-level of the above statistic	Tests for trap-dependence. Asymptotically equivalent to the statistic z above
df	Degrees of freedom of the overall TEST 2.CT statistics	Skips tables with one or several marginal numbers equal to 0
Quadratic Chi2	Quadratic chi2 statistic for TEST 2.CT	Corrected for sparseness (see 4.3.3)
P-level	P-level of the above statistic	
G2	G test version of TEST 2.CT	Corrected for sparseness (see 4.3.3)
P-level	P-level of the above statistic	

4.6. **TEST 2.CL**

TEST 2.CL component # *i* is based on the contingency table, noted TABLE 2.CL(i), shown in Table 10.

Table 10: The 2xn table TABLE 2.CL(i) based on the individuals encountered before (or at) occasion *i* and after (or at) occasion *i*+2 – and thus known to be alive at both *i* and *i*+1, - which serves as a basis of TEST 2.CL component # *i*

	Next encountered at *i*+2	....	Next encountered at *k*	
Not encountered at *i*	$o_{1\ i+2}$	....	o_{1k}	$o_{1.}$
Encountered at *i*	$o_{2\ i+2}$	....	o_{2k}	$o_{2.}$
	$o_{.i+2}$	....	$o_{.k}$	$o_{..}$ (total number not encountered at *i*+1 known to be alive at both *i* and *i*+2)

The null hypothesis being tested is

$H_0(i)$: *there is no difference in the expected time of next reencounter between the individuals encountered and not encountered at occasion i conditional on presence at both occasions i and i+2.*

The basic test is then a χ^2 test of homogeneity of TABLE 2.CL(i), based on the expected numbers given in Table 11.

Table 11: Expected numbers under $H_0(i)$ for the 2xn table TABLE 2.CL(i) (see text)

	Next encountered at *i*+2	....	Next encountered at *k*	
Not encountered at *i*	$e_{1\ i+2} = o_{.i+2x}o_{1.}/o_{..}$	....	$e_{1k} = o_{.kx}o_{1.}/o_{..}$	$o_{1.}$
Encountered at *i*	$e_{2\ i+2} = o_{.i+2x}o_{2.}/o_{..}$	....	$e_{2k} = o_{.kx}o_{2.}/o_{..}$	$o_{2.}$
	$o_{.i+2}$	....	$o_{.k}$	$o_{..}$

The usual χ^2 statistic:

$$X^2(i) = \Sigma(o_{jk}-e_{jk})^2/e_{jk}$$

Under $H_0(i)$ it asymptotically follows a χ^2 distribution with *k-i-2* degrees of freedom. All the information in TEST 2.CL is derived from this basic setting. "Asymptotically" refers to the usual requirement that the expected values e_{jk} be greater than some threshold, which commonly taken as equal to 2 (Reference)

To date, this test has received no simple interpretation.

5. Goodness-of-fit tests for multistate data.

The option 'GOODNESS-OF-FIT for Multistate' of the main menu of U-CARE opens onto the goodness-of-fit test (Pradel et al. 2003) of the JollyMove (JMV) model (Brownie et al. 1993) for multistate data. Multistate models allow for transitions between states (denoted ψ), survival probabilities (F) and encounter probabilities (p). In the JMV model,

- transitions vary by state of departure, state of arrival and time interval (ψ_{f*to*t} in the notations of Choquet et al. 2004),
- survival probabilities vary by state of departure and time interval (F_{f*t}),
- encounter probabilities vary by previous state, current state and date (p_{f*to*t}).

This model is more general than the better-known multistate conditional Arnason-Schwarz (CAS) model in that the later does not allow encounter probabilities to vary by previous state. The Arnason-Schwarz model was described first and may be considered as more 'natural' than the JMV model. However, there is currently no optimal GOF test available for the CAS model. When there is just one state, both the JMV and the CAS models reduce to the single-state CJS model.

The GOF test of the JMV model thus serves for multistate data the same purpose as the GOF test of the CJS model for single-state data. There are indeed many similarities between the two and especially in the way they are implemented in U-CARE version 2.2. There are also some profound differences but these are not immediately visible to the user. We follow here a presentation that parallels that of the CJS GOF test of chapter 4. It is advisable to read this chapter first.

5.1. **An intuitive presentation**

The theory for multistate GOF tests is not as advanced as that for single-state GOF tests. We present here the state of the art and make some recommendations where the theory is still in progress. At present, optimal goodness-of-fit tests are available for two main models:

- the JollyMove (JMV) model denoted ψ_{f*to*t}, F_{f*t}, p_{f*to*t} (Brownie et al, 1993),
- the 'transient' version of the JMV model denoted ψ_{f*to*t}, $F_{\mathbf{a2}*f*t}$, p_{f*to*t} (Pradel et al,. to appear).

Model JMV assumes that survival, transition and encounter probabilities are solely time- and state-dependent. Model ψ_{f*to*t}, $F_{\mathbf{a2}*f*t}$, p_{f*to*t} additionally allows survival to differ between newly marked and previously marked animals. JMV is thus nested within ψ_{f*to*t}, F_{a2*f*t}, p_{f*to*t} (see figure 9).

As a consequence of this hierarchy, the goodness-of-fit test of JMV involves one more component (this component tests the additional assumption of no difference in survival between newly marked and previously marked animals) than the goodness-of-fit test of ψ_{f*to*t}, F_{a2*f*t}, p_{f*to*t}. The goodness-of-fit test of JMV can thus be decomposed into two steps: the goodness-of-fit test of ψ_{f*to*t}, F_{a2*f*t}, p_{f*to*t} (sum of the components WBWA, 3G.Sm, M.ITEC and M.LTEC described below) plus the test of JMV against ψ_{f*to*t}, F_{a2*f*t}, p_{f*to*t} (3G.SR).

Figure 9 illustrates these considerations. Each arrow points toward further assumptions. If the associated test is significant (which can be visualised as the arrow being too 'long', and viewed as 'the assumptions cannot be stretched that far'), the additional assumptions should be rejected. If it is not significant (the arrow is short), the additional assumptions are supported by the data and the step may be taken. We will see later what the components WBWA, 3G.SR, 3G.Sm, M.ITEC and M.LTEC are.

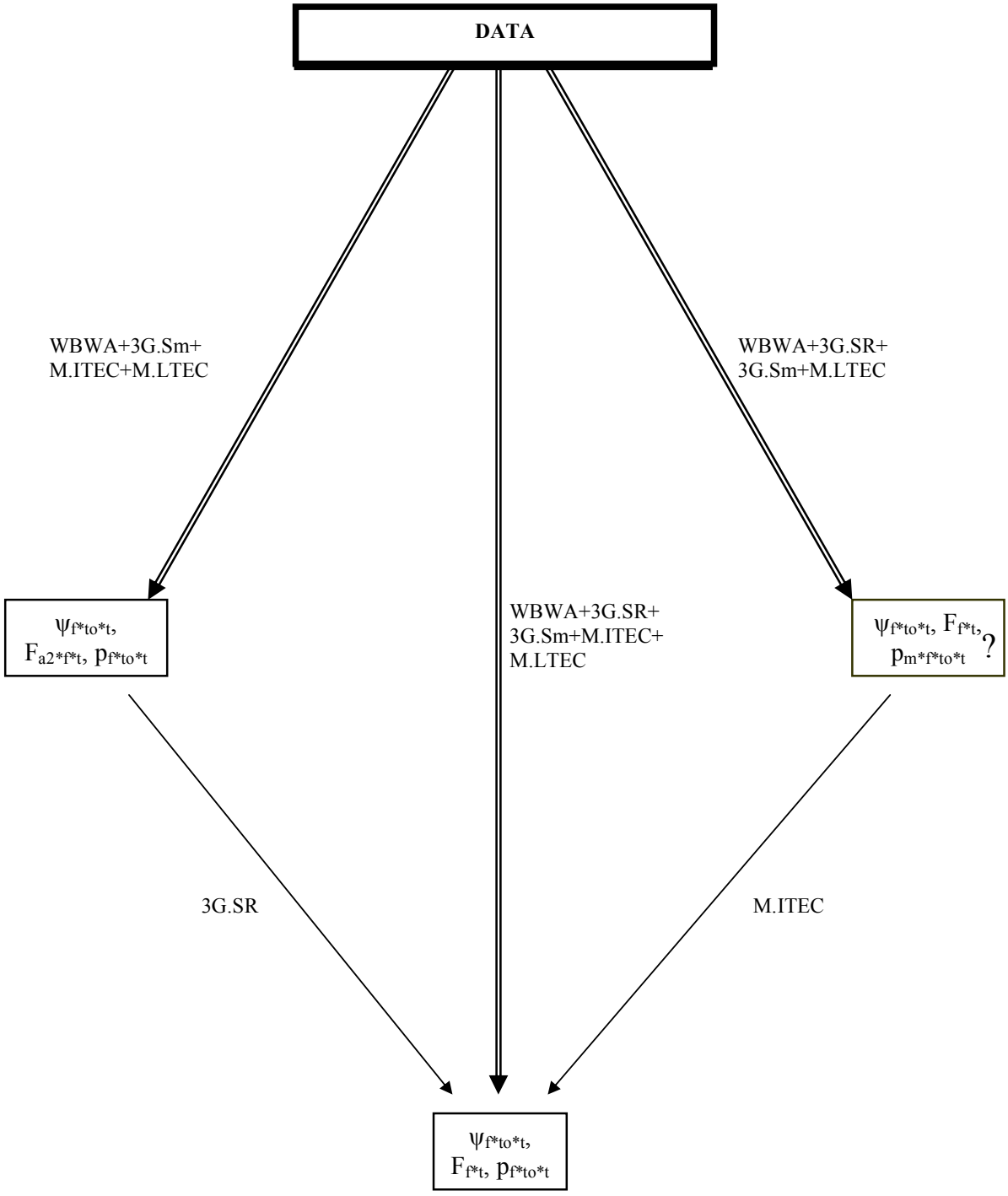


Figure 9: The reference models, their connections and associated tests, for multistate capture-recapture data (the JMV family). Model ψ_{f*to*t}, F_{f*t}, $p_{\mathbf{m}*f*to*t}$ generalizes model JMV (ψ_{f*to*t}, F_{f*t}, p_{f*to*t}) by allowing different encounter probabilities if animals have been encountered at the last occasion. M.ITEC is a component test that targets such an Immediate Trap Effect on Capture. It is suspected but not yet formally established that the generalization of JMV associated to M.ITEC is ψ_{f*to*t}, F_{f*t}, $p_{m*f*to*t}$.

Further, it is interesting to note that one of the component tests, M.ITEC was designed to detect an Immediate Trap Effect on Capture, i.e. a temporal change in catchability following capture. This component is thus the equivalent of TEST 2.CT for single-state data to which it reduces when there is just one state. It is likely, but not yet formally established, that leaving out this component yields the optimal GOF test of model ψ_{f*to*t}, F_{f*t}, $p_{\mathbf{m}*f*to*t}$, a generalization of JMV where encounter probabilities may differ for animals which were caught at the previous occasion. This model reduces to the trap-dependent single-state model (Φ_t, p_{t*m}) when there is just one state. With this, the parallel between single-state and multistate GOF tests would be complete (see Table 12 and 13).

Table 12: Equivalence of single-state and multistate goodness-of-fit component tests. When multistate goodness-of-fit tests are applied to single-state data, one component collapses; the others are exactly equivalent to single-state components as indicated below. In practice, different rules of handling sparse data may lead to somewhat different numerical results.

TEST WBWA	collapses
TEST 3G.SR	TEST 3.SR
TEST 3G.SM	TEST 3.SM
TEST M.ITEC	TEST 2.CT
TEST M.LTEC	TEST 2.CL

Table 13: Scenarios for goodness-of-fit tests for capture-recapture models from the JMV family. The table shows possible results of the GOF test and suggested courses of action.

Test components used	Results	Umbrella model	Remarks
TEST WBWA+ TEST 3G.SR + TEST 3G.SM + TEST M.ITEC + TEST M.LTEC	non significant	(ψ_{f*to*t}, F_{f*t}, p_{f*to*t})	JMV model
TEST WBWA + TEST 3G.SM + TEST M.ITEC + TEST M.LTEC	non significant	(ψ_{f*to*t}, F_{a2*f*t}, p_{f*to*t})	Pradel et al., to appear
TEST WBWA+TEST 3G.SR + TEST 3G.SM + TEST M.LTEC	non significant	*(ψ_{f*to*t}, F_{f*t}, $p_{m*f*to*t}$) ?*	to be confirmed
TEST 3G.SR + TEST 3G.SM + TEST M.ITEC + TEST M.LTEC	non significant	no exact corresponding model identified. A	The memory models *do not belong* to the family of multistate

		memory model should be used (see Hestbeck et al. 1991; Brownie et al. 1993; Pradel 2005)	models. They are currently under development and software is available to fit only a limited number of them (program MEMNON). You may consider using an overdispersion factor (see next item).
Any of the combination above	significant	start from corresponding model with over-dispersion coefficient	check that the individual estimates of over-dispersion are even

5.2. **TEST WBWA (Where Before vs. Where After)**

TEST WBWA subcomponent (i,l) is based on the contingency table, noted TABLE WBWA(i,l), given in Table 14.

Table 14: The sxs table TABLE WBWA(i,l) based on the individuals encountered at occasion *i* in state *l* that serves as a basis of TEST WBWA(i,l).

	next encountered in state 1		next encountered in state *s*	Total
last encountered in state 1	$\mathbf{o_{11}}$	…	$\mathbf{o_{1s}}$	$\mathbf{o_{1.}}$
	…	…	…	
last encountered in state *s*	$\mathbf{o_{s1}}$	…	$\mathbf{o_{ss}}$	$\mathbf{o_{s.}}$
Total	$\mathbf{o_{.1}}$		$\mathbf{o_{.s}}$	$\mathbf{o_{..}}$ (total number seen on occasion *i* in state *l* that have been seen previously and will be seen again)

The null hypothesis being tested is

$H_0(i,l)$: *there is no difference in the expected state of next reencounter among the individuals previously encountered in the different states.*

The basic test is then a χ^2 test of homogeneity of TABLE WBWA(i,l), based on the expected numbers given in Table 15.

Table 15: Expected numbers under $H_0(i,l)$ for the sxs table TABLE WBWA(i,l) (see text)

	next encountered in state 1	....	next encountered in state *s*	
last encountered in state 1	$\mathbf{e_{11} = o_{.1}o_{1.}/o_{..}}$	**....**	$\mathbf{e_{1s} = o_{.s}o_{1.}/o_{..}}$	$\mathbf{o_{1.}}$
	…	**…**	**…**	
last encountered in state *s*	$\mathbf{e_{s1} = o_{.1}o_{s.}/o_{..}}$	**....**	$\mathbf{e_{ss} = o_{.s}o_{s.}/o_{..}}$	$\mathbf{o_{s.}}$
	$\mathbf{o_{.1}}$	**....**	$\mathbf{o_{.s}}$	$\mathbf{o_{..}}$ (total number seen on occasion *i* in state *l* that have been seen previously and will be seen again)

The usual χ^2 statistic is obtained as:

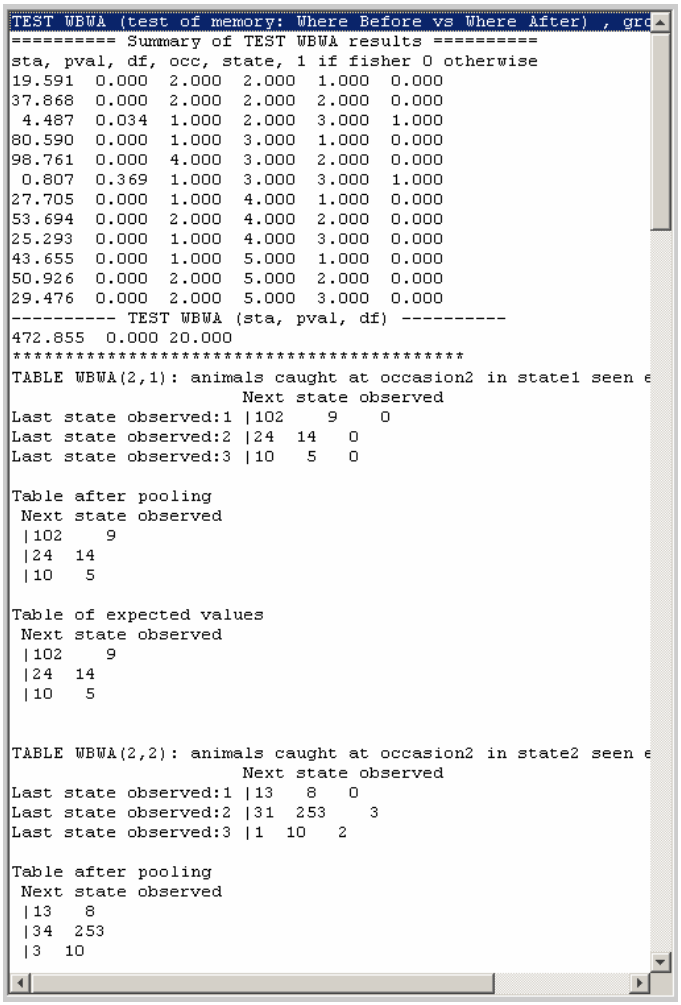
$$X^2(i) = \Sigma(\mathbf{o_{jk}}-\mathbf{e_{jk}})^2/\mathbf{e_{jk}}$$

and under $H_0(i,l)$ follows asymptotically a χ^2 distribution. All the information in TEST WBWA(i,l) is derived from this basic setting. "Asymptotically" corresponds to the usual requirement that the expected values $\mathbf{e_{jk}}$ must be over some threshold, commonly taken as equal to 2 (Reference ?). Some automatic pooling rules are implemented in U-CARE to avoid as much as possible low expected numbers.

Table 16: Items in the output of TEST WBWA in U-CARE and their meaning. The following items are given for each subcomponent defined by an occasion *i* and a state *l*. This is followed by the items *sta, pval* and *df* for the overall test.

Item	Meaning	Comments
`sta`	the χ^2 statistic $X^2(i,l)$	asymptotically follows a χ^2 distribution under $H_0(i,l)$, and a non-central χ^2 distribution under $H_1(i,l)$
`pval`	P-level of the X^2 statistic	Based on the asymptotic χ^2 distribution if there are no low expected values, and on the Fisher's exact test otherwise.
`df`	degrees of freedom	
`occ`	encounter occasion *i*	range : 2 to *K*-1
`state`	site or state of encounter *l*	
`1 if Fisher`	index of the test used	is 0 if the asymptotic $\chi^2(1)$ distribution is used; 1 if the statistic is back-calculated based on the P-level of the Fisher exact test.

Table 17: TEST WBWA results for Canada goose data with the verbosity level 'full details'.



5.3. **TEST 3G.SR and associated tests**

5.3.1. Basic statistical theory for TEST 3G.SR(i,l)

TEST 3G.SR subcomponent (i,l) is based on the contingency table, noted TABLE 3G.SR(i,l), given in Table 18.

Table 18: The 2x2 table TABLE 3G.SR(i,l) based on the individuals encountered at occasion *i* in state *l* that serves as a basis of TEST 3G.SR(i,l).

	Seen later	Never seen again	Total
Never seen before ("new" or "newly marked")	$\mathbf{o_{11}}$	$\mathbf{o_{12}}$	$\mathbf{o_{1.}}$
Seen before ("old" or "already marked")	$\mathbf{o_{21}}$	$\mathbf{o_{22}}$	$\mathbf{o_{2.}}$
Total	$\mathbf{o_{.1}}$	$\mathbf{o_{.2}}$	$\mathbf{o_{..}}$ (total number seen on occasion *i* in state *l*)

The null hypothesis being tested is

$H_0(i,l)$: *there is no difference in the probability of being later reencountered between "new" and "old" individuals encountered at occasion* i *in state* l.

The basic test is then a χ^2 test of homogeneity of TABLE 3G.SR(i,l), based on the expected numbers given in Table 19.

Table 19: Expected numbers under $H_0(i,l)$ for the 2x2 table TABLE 3G.SR(i,l) (see text for details)

	Seen later	Never seen again	Total
Never seen before ("new" or "newly marked")	$e_{11} = o_{.1}xo_{1.}/ o_{..}$	$e_{12} = o_{.2}xo_{1.}/ o_{..}$	$o_{1.}$
Seen before ("old" or "already marked")	$e_{21} = o_{.1}xo_{2.}/ o_{..}$	$e_{22} = o_{.2}xo_{2.}/ o_{..}$	$o_{2.}$
Total	$o_{.1}$	$o_{.2}$	$o_{..}$

The usual χ^2 statistic is obtained as:

$X^2(i) = \Sigma(\mathbf{o_{jk}}-\mathbf{e_{jk}})^2/\mathbf{e_{jk}}$

and under $H_0(i,l)$ follows asymptotically a χ^2 distribution with 1 degree of freedom. All the information in TEST 3G.SR(i,l) is derived from this basic setting. "Asymptotically" corresponds to the usual requirement that the expected values $\mathbf{e_{jk}}$ must be over some threshold, commonly taken as equal to 2 (Reference ?).

When one or several marginal numbers $\mathbf{o_{.k}}$ and/or $\mathbf{o_{j.}}$ in TABLE 3G.SR(i,l) are equal to 0, one or several expected numbers $\mathbf{e_{jk}}$ will be equal to zero, and $X^2(i,l)$ cannot be calculated. Such components will appear as equal to 0 with 0 degree of freedom.

The general alternative hypothesis to $H_0(i,l)$ is simply:
$H_1(i,l)$: *there is a difference in the probability of being later reencountered between "new" and "old" individuals encountered at occasion* i *in state* l.

Under $H_1(i,l)$, $X^2(i,l)$ follows asymptotically a non-central χ^2 distribution, with a non-centrality factor depending on the numbers of old and new individuals expected to be later reencountered.

5.3.2. Basic statistical theory for TEST 3G.SR

One overall hypothesis inherent in the CJS model is the combination of the null hypotheses $H_0(i,l)$ above :

H_0 : *there is no difference in the probability of being later reencountered between the "new" and "old" individuals*

The overall statistic $X^2 = \Sigma\ X^2(i,l)$ under H_0 follows a χ^2 distribution, with *k* degrees of freedom, where *k* is the number of components.
Under H_1 : *there is a difference in the probability of being later reencountered between the "new" and "old" individuals*, X^2 follows asymptotically a non-central χ^2 distribution with *k* degrees of freedom and a non-centrality parameter depending on the numbers of old and new individuals expected to be later reencountered. Thus, X^2 is an omnibus statistic for testing for any departure from H_0.

However, as mentioned above, i.e., due to transience or age-dependence, the alternative hypothesis of interest is frequently:

HT_1 : *the "new" individuals tend to be less reencountered later than the "old" individuals*.

In this situation, X^2 is not optimal anymore to test for HT_1 against H_0.

5.3.3. Sparseness

Many of the 2x2 tables used in the above tests will be sparse, i.e., have low expected numbers. The asymptotic $\chi^2(1)$ distribution for either $\chi^2(i,l)$ is then inadequate. As soon as there is at least one cell with low expected values in a contingency table, U-CARE uses the Fisher exact test. Then the χ^2 statistic is back-calculated as the value of a $\chi^2(1)$ distribution that leads to the corresponding P-value. When summing the resulting statistics, one obtains overall χ^2 tests that are reasonably protected against sparse data.

5.3.4. Implementation in U-CARE

The items in the output of TEST 3G.SR in U-CARE are listed and explained in Table 20. An example of results for Canada goose data (Hestbeck et al. 1991) is given in Table 21. Below the tests themselves, the contingency tables TABLE 3G.SR(i,l) on which they are based are displayed if the verbosity level selected was 'details with contingency table' or 'full details'. The level 'full details' also displays the tables of expected values (see table 21).

Table 20: Items in the output of TEST 3G.SR in U-CARE and their meaning. The following items are given for each subcomponent defined by an occasion *i* and a state *l*. They are followed by the items *sta, pval* and *df* for the overall test.

Item	Meaning	Comments
`sta`	the χ^2 statistic $X^2(i,l)$	asymptotically follows a $\chi^2(1)$ distribution under $H_0(i,l)$, and a non-central $\chi^2(1)$ distribution under $H_1(i,l)$
`pval`	P-level of the X^2 statistic	Based on the asymptotic $\chi^2(1)$ distribution if there are no low expected values, and on the Fisher's exact test otherwise
`df`	degrees of freedom	since all tables are 2x2 must be 1, or 0 when one of the margin terms is 0.
`occ`	encounter occasion *i*	range : 2 to *K*-1
`state`	site or state of encounter *l*	
`1 if Fisher`	index of the test used	is 0 if the asymptotic $\chi^2(1)$ distribution is used; 1 if the statistic is back-calculated based on the P-level of the Fisher exact test.

Table 21: TEST 3G.SR results for Canada goose data with the verbosity level set to 'full details'.

```
TEST 3G.SR (test of transience), group =1
========== Summary of TEST 3G.SR results ==========
sta, pval, df, occ, state, 1 if fisher 0 otherwise
 0.004  0.950  1.000  2.000  1.000  0.000
 0.000  0.987  1.000  2.000  2.000  0.000
 8.130  0.004  1.000  2.000  3.000  0.000
11.394  0.001  1.000  3.000  1.000  0.000
 2.708  0.100  1.000  3.000  2.000  0.000
33.459  0.000  1.000  3.000  3.000  0.000
10.608  0.001  1.000  4.000  1.000  0.000
 0.353  0.552  1.000  4.000  2.000  0.000
10.168  0.001  1.000  4.000  3.000  0.000
11.013  0.001  1.000  5.000  1.000  0.000
 0.129  0.719  1.000  5.000  2.000  0.000
29.785  0.000  1.000  5.000  3.000  0.000
---------- TEST 3G.SR (sta, pval, df) ----------
117.753  0.000 12.000
****************************************
TABLE 3G.SR(2,1): animals caught at occasion2 in state1 seen
     Seen again - Never seen again
New  |814  920
Old  |164  184

Table of expected values
     Seen again - Never seen again
New  |814.5303      919.4697
Old  |163.4697      184.5303

TABLE 3G.SR(2,2): animals caught at occasion2 in state2 seen
     Seen again - Never seen again
New  |1432  1769
Old  |321  396

Table of expected values
     Seen again - Never seen again
New  |1432.1983      1768.8017
Old  |320.8017      396.1983

TABLE 3G.SR(2,3): animals caught at occasion2 in state3 seen
     Seen again - Never seen again
New  |402  623
Old  |41  32

Table of expected values
     Seen again - Never seen again
New  |413.5474      611.4526
Old  |29.4526      43.5474
```

5.4. **TEST 3G.Sm**

TEST 3G.Sm component (i,l) is actually a catch-all composite test that gather what remains of the GOF test after the other components have been isolated. It is based on several contingency tables of three types, noted TABLE 3G.Sm(i,l).a, TABLE 3G.Sm(i,l).b and TABLE 3G.Sm(i,l).c shown in Tables 22, 23 and 24 respectively.

Table 22: The 2x(k-i)s table TABLE 3G.Sm(i,l).a based on the individuals encountered at occasion *i* in state *l* that will be seen again. This table serves as the basis for TEST 3G.Sm(i,l).a.

	Encountered at *i*+1 in state 1	Encountered at *i*+1 in state 2	....	Encountered at *k* in state *s*	TOTAL
Never seen before ("new" or "newly marked")	$o_{1,(i+1,1)}$	$o_{1,(i+1,2)}$	....	$o_{1,(k,s)}$	$o_{1.}$
Seen before ("old" or "already marked")	$o_{2,(i+1,1)}$	$o_{2,(i+1,2)}$	....	$o_{2,(k,s)}$	$o_{2.}$

TOTAL	$o_{., (i+1,1)}$	$o_{., (i+1,2)}$	....	$o_{., (k,s)}$	$o_{..}$ (total number seen on occasion *i* in state *l* that will be seen again)

Table 23: The sx2 table TABLE 3G.Sm(i,l).b based on the individuals encountered at occasion *i* in state *l* that have been seen before. This table serves as the basis for TEST 3G.Sm(i,l).b.

	seen again	not seen again	TOTAL
last seen in state 1	$o_{1, 1}$	$o_{1, 2}$	$o_{1.}$
…	…	…	…
last seen in state *s*	$o_{s, 1}$	$o_{s, 2}$	$o_{2.}$
TOTAL	$o_{., 1}$	$o_{., 2}$	$o_{..}$ (total number seen on occasion *i* in state *l* that have been seen before)

Table 24: The sx(k-i) table TABLE 3G.Sm(i,l).c(j) based on the individuals encountered at occasion *i* in state *l* that have been seen before and will be seen again in state *j*. This table serves as the basis for TEST 3G.Sm(i,l).c(j). There are *s* such tables (*j*=1… *s*).

	Encountered at *i*+1 in state *j*	....	Encountered at *k* in state *j*	TOTAL
last seen in state 1	$o_{1, (i+1)}$	....	$o_{1, k}$	$o_{1.}$
…	…	…	…	…
last seen in state *s*	$o_{s, (i+1)}$	....	$o_{s, k}$	$o_{s.}$
TOTAL	$o_{., (i+1)}$	....	$o_{., k}$	$o_{..}$ (total number seen on occasion *i* in state *l* that have been seen before and will be seen again in state *j*)

The null hypothesis being tested is the conjunction of H_0(i,l).a, H_0(i,l).b and H_0(i,l).c.

H_0(i,l).a : *there is no difference in the expected time and state of first reencounter between the "new" and "old" individuals encountered at occasion* i *in state* l *and seen again at least once.*

H_0(i,l).b : *there is no difference in the probability of being later reencountered between the individuals encountered at occasion* i *in state* l *that have been encountered earlier based on their state of most recent encounter.*

H_0(i,l).c is itself the conjunction of the *s* hypotheses H_0(i,l).c(j), *j*=1… *s*.

H_0(i,l).c(j) : *there is no difference in the expected time of first reencounter between the individuals encountered at occasion* i *in state* l *that have been encountered earlier and will be next reencountered in state* j *based on their state of most recent encounter.*

Each individual hypothesis leads to a χ^2 test of homogeneity of its associated contingency table. To date, these tests have received no simple interpretation.

As soon as there is as least one low expected value in a contingency table, U-CARE uses the Fisher exact test. Then the χ^2 statistic is back-calculated as the value of a $\chi^2(1)$ distribution yielding the corresponding P-value. When summing the resulting statistics, one obtains overall χ^2 tests that are reasonably protected against sparse data. This ensures as much as possible good distributional properties of the overall X^2 and G^2 statistics, which is obtained by summing the components. The results given by U-CARE are as follows.

Table 25: Items in the output of TEST 3G.Sm in U-CARE and their meaning. The following items are given for each subcomponent defined by an occasion *i* and a state *l*. They are followed by the items *sta, pval* and *df* for the overall test.

Item	Meaning	Comments
`sta`	the χ^2 statistic $X^2(i,l)$	asymptotically follows a $\chi^2(1)$ distribution under $H_0(i,l)$, and a non-central $\chi^2(1)$ distribution under $H_1(i,l)$
`pval`	P-level of the X^2 statistic	Based on the asymptotic $\chi^2(1)$ distribution if there are no low expected values, and on the Fisher's exact test otherwise
`df`	degrees of freedom	since all tables are 2x2 must be 1, or 0 when one of the margin terms is 0.
`occ`	encounter occasion *i*	range : 2 to *K*-1
`state`	site or state of encounter *l*	
`1 if Fisher`	index of the test used	is 0 if the asymptotic $\chi^2(1)$ distribution is used; 1 if the statistic is back-calculated based on the P-level of the Fisher exact test.

Table 26: TEST 3G.Sm results for Canada goose data with the verbosity level set to 'details with contingency tables'.

```
TEST 3G.Sm (composite test), group =1
========== Summary of TEST 3G.Sm results ==========
sta, pval, df, occ, state, 1 if fisher 0 otherwise
23.913  0.047 14.000  2.000  1.000  1.000
24.810  0.073 16.000  2.000  2.000  1.000
11.232  0.189  8.000  2.000  3.000  1.000
36.521  0.001 14.000  3.000  1.000  1.000
21.365  0.210 17.000  3.000  2.000  0.000
23.073  0.010 10.000  3.000  3.000  1.000
55.339  0.000  8.000  4.000  1.000  1.000
17.172  0.103 11.000  4.000  2.000  1.000
45.089  0.000 10.000  4.000  3.000  0.000
 9.062  0.028  3.000  5.000  1.000  0.000
 5.974  0.201  4.000  5.000  2.000  0.000
29.218  0.000  4.000  5.000  3.000  0.000
---------- TEST 3G.Sm (sta, pval, df) ----------
302.769  0.000119.000
****************************************
TABLE 3G.Sm(2,1).a: animals caught at occasion2 in state1 see
Table after pooling
New  |390  124  122   64   46   35   18   15
Old  |101   10   27    7    5    7    3    4

TABLE 3G.Sm(2,1).a: X2(7)=18.138, P=0.011363

TABLE 3G.Sm(2,1).b: animals caught at occasion2 in state1 and
Table after pooling
 |111  128
 |38  47
 |15   9

TABLE 3G.Sm(2,1).b: X2(2)=2.521, P=0.28351

TABLE 3G.Sm(2,1).c(1): animals caught at occasion2 in state1
Table after pooling
 |75  27
 |19   5
 |7  3

TABLE 3G.Sm(2,1).c(1): X2(2)=0.42576, P=0.80825

TABLE 3G.Sm(2,1).c(2): animals caught at occasion2 in state1
Table after pooling
 |4  4  5  1
 |6  3  2  3

TABLE 3G.Sm(2,1).c(2): X2(3)=2.8286, P=0.41882
```

Table 27: TEST 3G.Sm results for Canada goose data with the verbosity level set to 'full details'.

```
TEST 3G.Sm (composite test), group =1
========== Summary of TEST 3G.Sm results ==========
sta, pval, df, occ, state, 1 if fisher 0 otherwise
23.913  0.047 14.000  2.000  1.000  1.000
24.810  0.073 16.000  2.000  2.000  1.000
11.232  0.189  8.000  2.000  3.000  1.000
36.521  0.001 14.000  3.000  1.000  1.000
21.365  0.210 17.000  3.000  2.000  0.000
23.073  0.010 10.000  3.000  3.000  1.000
55.339  0.000  8.000  4.000  1.000  1.000
17.172  0.103 11.000  4.000  2.000  1.000
45.089  0.000 10.000  4.000  3.000  0.000
 9.062  0.028  3.000  5.000  1.000  0.000
 5.974  0.201  4.000  5.000  2.000  0.000
29.218  0.000  4.000  5.000  3.000  0.000
---------- TEST 3G.Sm (sta, pval, df) ----------
302.769  0.000119.000
****************************************
TABLE 3G.Sm(2,1).a: animals caught at occasion2 in state1 se
      Next encounter depending from date and state
New  |390  124    0  122   64    3   46   35    3   18    9
Old  |101   10    0   27    7    0    5    7    0    3    4

Table after pooling
New  |390  124  122   64   46   35   18   15
Old  |101   10   27    7    5    7    3    4

Table of expected values
New  |408.6646      111.5297      124.0143      59.09407
Old  |82.3354      22.4703      24.9857      11.9059      8.

TABLE 3G.Sm(2,1).a: X2(7)=18.138, P=0.011363

TABLE 3G.Sm(2,1).b: animals caught at occasion2 in state1 an
                     Seen again - Never seen again
Last state observed :1 |111  128
Last state observed :2 |38  47
Last state observed :3 |15   9

Table after pooling
 |111  128
 |38  47
 |15   9

Table of expected values
 |112.6322      126.3678
 |40.0575      44.9425
 |11.3103      12.6897
```

5.5. **TEST M.ITEC and associated tests**

5.5.1. Basic statistical theory for TEST M.ITEC component i

TEST M.ITEC component *i* is based on the 2sx2s contingency table, noted TABLE M.ITEC(i), given in Table 28.

Table 28: The *2s* x *2s* table TABLE M.ITEC(i) based on the individuals encountered before (or at) occasion *i* and after (or at) occasion *i*+1 – and thus known to be alive at both *i* and *i*+1 – which serves as a basis of TEST M.ITEC component *i*.

		immediately reencountered				later reencountered			
		in state 1	in state 2	…	in state *s*	in state 1	…	in state *s*	TOTAL
previously released	in state 1	o_{11}	o_{12}	…	o_{1s}	$o_{1,s+1}$	…	$o_{1,2s}$	$o_{1.}$
	in state 2	o_{21}	o_{22}	…	o_{2s}	$o_{2,s+1}$	…	$o_{2,2s}$	$o_{2.}$

	…	…	…	…	…	…	…	…	…
	in state *s*	o_{s1}	o_{s2}		o_{ss}	$o_{s,\,s+1}$		$o_{s,\,2s}$	$o_{s.}$
currently released	in state 1	$o_{s+1,\,1}$	$o_{s+1,\,2}$	…	$o_{s+1,\,s}$	$o_{s+1,\,s+1}$	…	$o_{s+1,\,2s}$	$o_{s+1,\,.}$
	in state 2	$o_{s+2,\,1}$	$o_{s+2,\,2}$		$o_{s+2,\,s}$	$o_{s+2,\,s+1}$		$o_{s+2,\,2s}$	$o_{s+2,\,.}$
	…	…	…	…	…	…	…	…	…
	in state *s*	$o_{2s,\,1}$	$o_{2s,\,2}$		$o_{2s,\,s}$	$o_{2s,\,s+1}$		$o_{2s,\,2s}$	$o_{2s,\,.}$
	TOTAL	$o_{.1}$	$o_{.2}$	…	$o_{.s}$	$o_{.,\,s+1}$	…	$o_{.,\,2s}$	$o_{..}$ (total number known to be alive at both *i* and *i*+1)

The null hypothesis being tested is

H_0(i) : *there is no difference in the probabilities of being reencountered in the different states at* i+*1 between the animals in the same state at occasion* i *whether encountered or not encountered at this date, conditional on presence at both occasions.*

The basic test *cannot be a test of homogeneity* of TABLE M.ITEC(i) because the exact state of the animals not encountered at *i* remains unknown. Rather, one tests whether each category of not encountered at *i* animals is consistent with being a mixture of animals encountered at *i* in the different states. The corresponding model is detailed in table 29. The cell probabilities for the animals not encountered at *i* are linear combinations of the cell probabilities for the animals encountered at *i*. The test proceeds by estimating the cell probabilities π_{ij}, *i*=1… *s*, *j*=1… 2*s* and the mixture coefficients γ_{ij}, *i*=1… *s*, *j*=1… *s* by maximum likelihood using a Newton-Raphson algorithm from the MATLAB library. Then, expected values for numbers in the different cells can be calculated and compared to observed values.

Table 29: The cell probabilities of the mixture model underlying TEST M.ITEC(i). The mixture coefficients γ_{ij} and the cell probabilities π_{ij} are unknown parameters.

		immediately reencountered				later reencountered			
		in state 1	in state 2	…	in state *s*	in state 1	…	in state *s*	TOTAL
previously released	in state 1	$\Sigma\gamma_{1j}\pi_{j1}$	$\Sigma\gamma_{1j}\pi_{j2}$	…	$\Sigma\gamma_{1j}\pi_{js}$	$\Sigma\gamma_{1j}\pi_{j,\,s+1}$	…	$\Sigma\gamma_{1j}\pi_{j,\,2s}$	
	in state 2	$\Sigma\gamma_{2j}\pi_{j1}$	$\Sigma\gamma_{2j}\pi_{j2}$	…	$\Sigma\gamma_{2j}\pi_{js}$	$\Sigma\gamma_{2j}\pi_{j,\,s+1}$	…	$\Sigma\gamma_{2j}\pi_{j,\,2s}$	
	…	…	…	…	…	…	…	…	
	in state *s*	$\Sigma\gamma_{sj}\pi_{j1}$	$\Sigma\gamma_{sj}\pi_{j2}$	…	$\Sigma\gamma_{sj}\pi_{js}$	$\Sigma\gamma_{sj}\pi_{j,\,s+1}$	…	$\Sigma\gamma_{sj}\pi_{j,\,2s}$	
currently released	in state 1	π_{11}	π_{12}	…	π_{1s}	$\pi_{1,\,s+1}$	…	$\pi_{1,\,2s}$	**1**
	in state 2	π_{21}	π_{22}	…	π_{2s}	$\pi_{2,\,s+1}$	…	$\pi_{2,\,2s}$	**1**

	…	…	…	…	…	…	…	…	…
	in state *s*	π_{s1}	π_{s2}		π_{ss}	$\pi_{s,\,s+1}$		$\pi_{s,\,2s}$	**1**

The usual χ^2 statistic for the comparison of expected and observed numbers is then computed:

$X^2(i) = \Sigma(\mathbf{o_{jk}}-\mathbf{e_{jk}})^2/\mathbf{e_{jk}}$

Under $H_0(i)$, it follows asymptotically a χ^2 distribution with s^2 degrees of freedom. All the information in TEST M.ITEC(i) is derived from this basic setting. "Asymptotically" is not as well defined here as for tests of homogeneity. The pooling algorithm in U-CARE strives to meet the usual requirement that the expected numbers $\mathbf{e_{jk}}$ be greater than the common threshold of 2 (Reference). However, this is not always possible (see 5.5.3).

The general alternative hypothesis to $H_0(i)$ is simply:

$H_1(i)$: *there is a difference in the probabilities of being reencountered in the different states at* i+*1 between the animals encountered and not encountered at occasion* i *in the same state conditional on presence at both occasions.*

Under $H_1(i)$, $X^2(i)$ asymptotically follows a non-central χ^2 distribution, with a non-centrality parameter depending on the numbers expected in the different cells of the table.

5.5.2. Basic statistical theory for TEST M.ITEC

One overall hypothesis inherent in the CJS model is the combination of the null hypotheses $H_0(i)$ above :

H_0 : *there is no difference in the probabilities of being reencountered in the different states between the animals encountered and not encountered at the previous occasion then in the same state, conditional on presence at both occasions*

The overall statistic $X^2 = \Sigma\, X^2(i)$ follows under H_0 a χ^2 distribution, with s^2k degrees of freedom, where *k* is the number of components.

Under H_1 : *there is a difference in the probability of being reencountered in the different states between the animals encountered and not encountered at the previous occasion in the same state conditional on presence at both occasions*, X^2 asymptotically follows a non-central χ^2 distribution with s^2k degrees of freedom and a non-centrality parameter that depends on the numbers expected in the different cells of the tables. X^2 is thus an omnibus statistic for testing for any departure from H_0 in the JMV model.

5.5.3. Sparseness

U-CARE treats sparse data by pooling rows and columns in an appropriate manner in order to reach expected values that are all above the threshold of 2. It should be noted that the rows pertaining to the animals currently encountered cannot be pooled with other rows or among themselves. It is no more allowed to pool an "immediately reencountered" column with a "later reencountered" column although it is possible to pool within each category. All other combinations are possible.

The pooling algorithm will nonetheless stop short of reducing the number of degrees of freedom to below 1. Often, low expected numbers will remain. Unfortunately, there is currently no exact test available for TEST M.ITEC and for mixture tests in general. Hence, it is advisable to check that the number of low expected values is 0 (see the output in the next section for this item) for each table, especially if one or several tables yield extremely high statistics. To check that the asymptotic distribution is reasonably approached by an individual test, one can compare the X^2 and the G^2 statistics associated to this test; they should be reasonably close and at least of the same order of magnitude. In case of a strong discrepancy, we advise to favor the G^2 value which is much less sensitive to low expected numbers and should therefore be much lower. It is also possible simply to ignore the problematic components and to recalculate the overall test without them.

5.5.4. Implementation in U-CARE

Table 30: Items in the output of TEST M.ITEC in U-CARE and their meaning. The following items are given for each subcomponent, one per occasion. They are followed by the items *sta, pval* and *df* for the overall test.

Item	Meaning	Comments
`sta`	the χ^2 statistic $X^2(i)$	asymptotically follows a $\chi^2(df)$ distribution under $H_0(i)$. and a non-central $\chi^2(df)$ distribution under $H_1(i)$
`pval`	P-level of the X^2 statistic	Based on the asymptotic $\chi^2(df)$ distribution
`df`	degrees of freedom	$1 \leq df \leq 2s$ depending on the amount of pooling, or 0 when the original table is degenerate.
`occ`	encounter occasion *i*	range : 2 to *K*-2
`low numbers`	flag for sparseness	The number of expected values e_{ij} that are smaller than 2.

Table 31: TEST M.ITEC results for Canada goose data with the verbosity level set to 'full details'.

```
TEST M.ITEC (test of immediate trap-dependance), group =1
========== Summary of TEST M.ITEC results ==========
chi2, p(chi2), g2, p(g2), df, occ, low numbers
14.267  0.113 14.151  0.117  9.000  2.000  3.000
30.838  0.000 30.422  0.000  9.000  3.000  0.000
23.119  0.006 23.269  0.006  9.000  4.000  1.000
---------- TEST M.ITEC (chi2, p(chi2), g2, p(g2), df) ----------
68.225  0.000 67.842  0.000 27.000
*****************************************
TABLE M.ITEC(2): animals known to be alive at both2 and3
                        Seen immediately - Next seen later
Previously released in state :1 |36  18   0  24  13   1
Previously released in state :2 |36  158    2   32  146    5
Previously released in state :3 |11  30  18   5  23  16
Currently released in state :1 |491  134    0  221  126    6
Currently released in state :2 |159  869   15  122  573   15
Currently released in state :3 |14  101  158   16   77   77

Table after pooling
                     Seen immediately - Next seen later
Previously released |36  18   0  24  13   1
Previously released |36  158    2   32  146    5
Previously released |11  30  18   5  23  16
Currently released |491  134    0  221  126    6
Currently released |159  869   15  122  573   15
Currently released |14  101  158   16   77   77

Table of expected values
                    Seen immediately - Next seen later
Previously released |40.6452      17.0034     0.103029      19.1866      14.4264     0.635336
Previously released |38.54675      179.4349      2.923187      28.74443      125.7982      3.55259
Previously released |9.9206      30.1708      21.9953      6.73001      22.3814      11.8019
Currently released |486.6576      134.446     0.02209422      225.2611      125.2631      6.350159
Currently released |156.9863      848.0266      13.93373      124.6389      592.828      16.58649
Currently released |14.21857      100.9194      154.0475      15.43956      77.30161      81.07337
```

5.6. **TEST M.LTEC**

TEST M.LTEC component *i* is based on the contingency table, noted TABLE M.LTEC(i), shown in Table 32.

Table 32: The *2s* x *s*(*k*-*i*-1) table TABLE M.LTEC(i) based on the individuals not encountered at *i*+1 encountered before (or at) occasion *i* and after (or at) occasion *i*+2 – and thus known to be alive at both *i* and *i*+2 – which serves as a basis of TEST M.LTEC component *i*.

		next reencountered at *i*+2			…	next reencountered at *k*			
		in state 1	…	in state *s*	…	in state 1	…	in state *s*	TOTAL
previously released	in state 1	o_{11}	…	o_{1s}	…	$o_{1,\,s(k-i-2)+1}$	…	$o_{1,\,s(k-i-1)}$	$o_{1.}$
	in state 2	o_{21}	…	o_{2s}	…	$o_{2,\,s(k-i-2)+1}$	…	$o_{2,\,s(k-i-1)}$	$o_{2.}$
	…	…	…	…	…	…	…	…	…
	in state *s*	o_{s1}		o_{ss}		$o_{s,\,s(k-i-2)+1}$		$o_{s,\,s(k-i-1)}$	$o_{s.}$
currently released	in state 1	$o_{s+1,\,1}$	…	$o_{s+1,\,s}$	…	$o_{s+1,\,s(k-i-2)+1}$	…	$o_{s+1,\,s(k-i-1)}$	$o_{s+1,\,.}$
	in state 2	$o_{s+2,\,1}$		$o_{s+2,\,s}$		$o_{s+2,\,s(k-i-2)+1}$		$o_{s+2,\,s(k-i-1)}$	$o_{s+2,\,.}$
	…	…	…	…	…	…	…	…	…
	in state *s*	$o_{2s,\,1}$		$o_{2s,\,s}$		$o_{2s,\,s(k-i-2)+1}$		$o_{2s,\,s(k-i-1)}$	$o_{2s,\,.}$
	TOTAL	$o_{.1}$	…	$o_{.s}$	…	$o_{.,\,s(k-i-2)+1}$	…	$o_{.,\,s(k-i-1)}$	$o_{..}$ (total number not encountered at *i*+1 known to be alive at both *i* and *i*+2)

The null hypothesis being tested is

H_0(i) : *there is no difference in the expected time and state of next reencounter between the individuals in the same state at occasion* i *that were not encountered at occasion* i+*1 whether encountered or not encountered at occasion* i *conditional on presence at both occasions* i *and* i+*2.*

For the same reason as TEST M.ITEC, TEST M.LTEC(i) *is not a test of homogeneity* of TABLE M.LTEC(i) (see 5.5). Again, one tests whether each category of not encountered at *i* animals is consistent with being a mixture of animals encountered at *i* in the different states. The corresponding model is detailed in table 33. The cell probabilities for the animals not encountered at *i* are linear combinations of the cell probabilities for the animals encountered at *i*. The test proceeds by estimating the cell probabilities π_{ij}, *i*=1… *s*, *j*=1… 2*s* and the mixture coefficients γ_{ij}, *i*=1… *s*, *j*=1… *s* by maximum likelihood using a Newton-Raphson

algorithm from the MATLAB library. Then, expected values for numbers in the different cells can be calculated and compared to observed values.

Table 33: The cell probabilities of the mixture model underlying TEST M.LTEC(i). The mixture coefficients γ_{ij} and the cell probabilities π_{ij} are unknown parameters.

		next reencountered at i+2			…	next reencountered at k			
		in state 1	…	in state s	…	in state 1	…	in state s	TOTAL
previously released	in state 1	$\Sigma\gamma_{1j}\pi_{j1}$	…	$\Sigma\gamma_{1j}\pi_{j2}$	…	$\Sigma\gamma_{1j}\pi_{j,\,s(k-i-2)+1}$	…	$\Sigma\gamma_{1j}\pi_{j,\,s(k-i-1)}$	
	in state 2	$\Sigma\gamma_{2j}\pi_{j1}$	…	$\Sigma\gamma_{2j}\pi_{j2}$	…	$\Sigma\gamma_{2j}\pi_{j,\,s(k-i-2)+1}$	…	$\Sigma\gamma_{2j}\pi_{j,\,s(k-i-1)}$	
	…	…	…	…	…	…	…	…	
	in state s	$\Sigma\gamma_{sj}\pi_{j1}$		$\Sigma\gamma_{sj}\pi_{j2}$		$\Sigma\gamma_{sj}\pi_{j,\,s(k-i-2)+1}$		$\Sigma\gamma_{sj}\pi_{j,\,s(k-i-1)}$	
currently released	in state 1	π_{11}	…	π_{1s}	…	$\pi_{1,\,s(k-i-2)+1}$	…	$\pi_{1,\,s(k-i-1)}$	**1**
	in state 2	π_{21}		π_{2s}		$\pi_{2,\,s(k-i-2)+1}$		$\pi_{2,\,s(k-i-1)}$	**1**
	…	…	…	…	…	…	…	…	…
	in state s	π_{s1}		π_{ss}		$\pi_{s,\,s(k-i-2)+1}$		$\pi_{s,\,s(k-i-1)}$	**1**

The usual χ^2 statistic for the comparison of expected and observed numbers is then computed:

$$X^2(i) = \Sigma(\mathbf{o_{jk}}-\mathbf{e_{jk}})^2/\mathbf{e_{jk}}$$

Under $H_0(i)$, it follows asymptotically a χ^2 distribution with $s^2(k\text{-}i\text{-}2)$ degrees of freedom. All the information in TEST M.ITEC(i) is derived from this basic setting. "Asymptotically" is not as well defined here as for tests of homogeneity. The pooling algorithm in U-CARE strives to meet the usual requirement that the expected numbers $\mathbf{e_{jk}}$ be greater than the common threshold of 2 (Reference). However, this is not always possible (see 5.5.3).

The general alternative hypothesis to $H_0(i)$ is simply:

$H_1(i)$: *there is a difference in the expected time and state of next reencounter between the individuals in the same state at occasion* i *that were not encountered at occasion* i+*1 whether encountered or not encountered at occasion* i *conditional on presence at both occasions* i *and* i+*2.*

Under $H_1(i)$, $X^2(i)$ asymptotically follows a non-central χ^2 distribution, with a non-centrality parameter depending on the numbers expected in the different cells of the table.

To date, this test has received no simple interpretation.

The treatment of sparseness and the implementation in U-CARE are exactly as for TEST M.ITEC (see section 5.5).

Table 34: TEST M.LTEC results for Canada goose data with the verbosity level set to 'full details'.

```
TEST M.LTEC, group =1
========== Summary of TEST M.LTEC results ==========
chi2, p(chi2), g2, p(g2), df, occ, low numbers
14.103  0.168 13.168  0.214 10.000  2.000  2.000
 6.885  0.649  7.366  0.599  9.000  3.000  3.000
---------- TEST M.LTEC (chi2, p(chi2), g2, p(g2), df) ----------
20.988  0.337 20.534  0.363 19.000
*****************************************
TABLE M.LTEC(2): animals not encountered at3 known to be alive at both2 and4
                     Next re-encounter depending on date and state
Previously released in state :1 |13   6   0   6   5   1   5   2   0
Previously released in state :2 |22  92   3   7  32   2   3  22   0
Previously released in state :3 |3  10  10   0   8   3   2   5   3
Currently released in state :1 |149   71    3   51   42    3   21   13    0
Currently released in state :2 |63  335   10   41  164    3   18   74    2
Currently released in state :3 |8  47  48   7  16  18   1  14  11

                     Next re-encounter depending on date and state
Previously released |22  92   3   7  32   2   3  22
Previously released |16  16  10   6  13   7   7   7
Currently released |149   71    3   51   42    3   21   13
Currently released |63  335   10   41  164    5   18   74
Currently released |8  47  48   7  16  29   1  14

                     Next re-encounter depending on date and state
Previously released |18.7884      85.4263      3.27344      10.2839      39.5363       1.8186      4.55893      19.3
Previously released |18.8547      20.4899      10.2858      7.37219      9.95895      6.49629      3.16799      5.37
Currently released |146.926      69.37547      2.986358      49.67801      43.35137      3.031876      24.15672
Currently released |65.65034      340.6852      9.796784      37.96299      157.137      5.129918      16.79261
Currently released |7.77865      45.0205      47.6584      6.70501      17.0182      29.5238      1.32312      14.97

TABLE M.LTEC(3): animals not encountered at4 known to be alive at both3 and5
                     Next re-encounter depending on date and state
Previously released in state :1 |57  47   4  26  15   0
Previously released in state :2 |48  196    5   21   96    2
Previously released in state :3 |7  24  21   3  19  14
Currently released in state :1 |150  116    5   52   46    2
Currently released in state :2 |53  325   14   29  146    6
Currently released in state :3 |11  27  39   1  21  26

                     Next re-encounter depending on date and state
Previously released |57  47   4  26  15   0
Previously released |48  196    5   21   96    2
Previously released |7  24  21   3  19  14
Currently released |150  116    5   52   46    2
Currently released |53  325   14   29  146    6
Currently released |11  27  39   1  21  26
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