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U-CARE: Utilities for performing goodness of fit tests and manipulating Capture–REcapture data

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Abstract: In any statistical analysis, assessing the goodness of fit of a model to the data is crucial to avoid drawing incorrect conclusions. U-CARE is a computer application that deals with the mandatory first steps of the analyses of capture-recapture data: 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 multi-state data). U-CARE implements the current state of the art in goodness-of-fit testing by incorporating components aimed at detecting the most likely departures from assumptions (Pradel et al. 2003), (Pradel et al. 2005). It is a free and stand-alone application for Windows.

Keywords: Arnason-Schwarz model, Contingency tables, Directional tests, Memory model, Overdispersion coefficient, Test of multinomial mixture, Test WBWA, Test 3G.SR, Test M.ITEC, Transient, Trap-dependence.

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50 The estimation and comparison of demographic rates in animal and plant populations (Lebreton et
51 al. 1992), (Gregg and Kery 2006) is currently based on following marked individuals over time and
52 possibly space and analyzing the resulting data with adequate statistical models. Such models, in
53 which individuals may move among states (such as geographical sites or breeding statuses) over
54 discrete time periods, must account for the non-exhaustive detection of individuals. These so-called
55 capture-recapture models are still evolving (Pradel et al. 2005). In their current form, they are based
56 on two key assumptions.

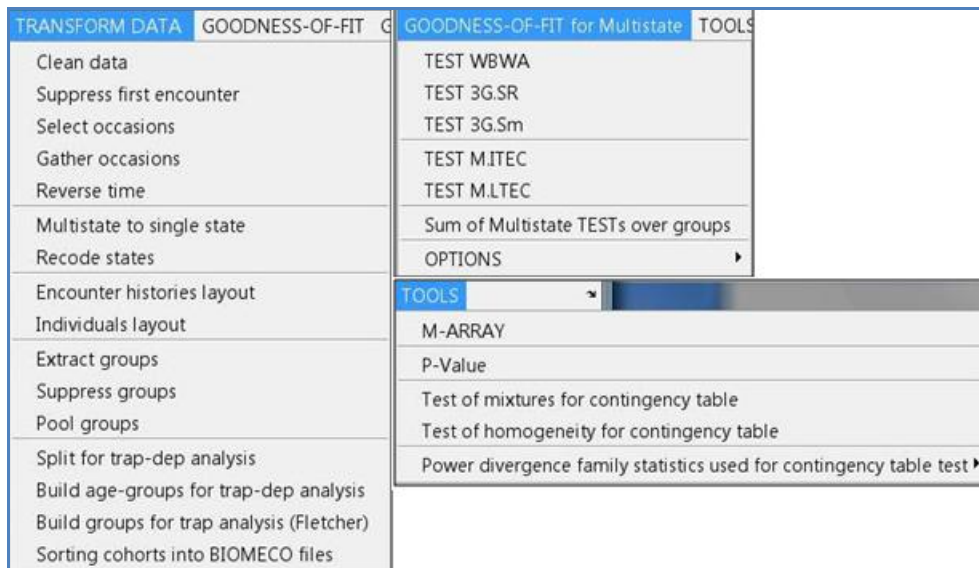
- 57 1) The individuals are assumed to be independent,
58 2) Within the history of each individual, the successive pairs of each release associated with its
59 subsequent reencounter (if any) are assumed to be independent (Burnham 1991).

60 While fitting multi-state capture-recapture models can now be carried out without much difficulty
61 with a variety of computer software applications (M-SURGE (Choquet et al. 2004 #340), E-SURGE
62 (Rouan et al., Choquet et al. 2008) or MARK (White and Burnham 1999) for a frequentist approach,
63 MARK for Bayesian inference), the examination of the above mentioned assumptions can be done in
64 an optimal way (Pradel et al. 2003) only with program U-CARE. And yet this step is critical. For
65 instance, if a major structural effect such as the presence of transient individuals on the study site is
66 overlooked, survival will be severely underestimated. More generally, spurious effects will often be
67 detected if no model fits the data. This is best seen when considering how model selection proceeds.
68 In the frequentist paradigm, model selection is generally based on the Akaike information criterion
69 (AIC, see (Burnham and Anderson 2002)). The AIC is equal to the deviance plus two times the number
70 of estimable parameters. In presence of lack of fit, the deviance tends to be inflated, thus leading to
71 the selection of over-parameterized models and potentially to erroneous biological conclusions.
72 Moreover, the estimate of precision of the Maximum Likelihood Estimators (MLE) will be overly
73 optimistic. The consequences of lack-of-fit are thus too deleterious to be ignored.

74 A preliminary assessment of Goodness-Of-Fit (GOF) is thus a crucial prerequisite, just as in any
75 statistical analysis (D'Agostino and Stephens 1986). Unlike in regression, residuals are not easily
76 available in CR to check the validity of a model. Furthermore, the omnibus approach to goodness-of-
77 fit testing that consists of comparing expected vs. observed sufficient statistics is impractical due to
78 the sparseness of the data. A specific approach was developed (reviewed in Pradel et al. 2003). By
79 making this approach available in an easy-to-use software application, we aim at encouraging
80 practitioners to assess the validity of their assumptions. Sound model selection, i.e. preceded by
81 appropriate GOF assessment, is indeed becoming more and more common in the literature (e.g.
82 (Henaux et al. 2007), (Jenouvrier et al. 2008)) but it is still far from being systematic. We describe
83 here the main features of program U-CARE. More details on tests and tools can be found in the user's
84 manual (Choquet et al. 2005).

85 U-CARE (<<http://purl.oclc.org/NET/U-CARE>>) is a free, easy-to-use, stand-alone, menu-driven
 86 computer application for Windows, with a set of options for managing data and GOF tests
 87 capabilities for both single-state and multi-state capture-recapture models (see Figure 1). The two
 88 kinds of test are presented as the sum of components examining different aspects of the data
 89 through a range of contingency tables. This structure guides the choice of an appropriate model. For
 90 instance, if the only significant subcomponent of the multistate goodness-of-fit test is TEST 3G.SR, a
 91 two age-class structure for survival should be used (Pradel et al. 1995), while, if this is TEST
 92 WhereBeforeWhereAfter (WBWA), a memory model is recommended (Pradel et al. 2003). Due to
 93 historical reasons, biological relevance is particularly furthered for single-state data through the
 94 computation of directional tests. We briefly examine hereafter the following four aspects of data
 95 analysis for which U-CARE can be very useful:

- 96 1) How to prepare the data?
- 97 2) How to detect overdispersion?
- 98 3) How to correct for overdispersion?
- 99 4) How to conduct specific tests?



100
 101 **Figure 1 : U-CARE has 5 menus showing utilities for input-output of capture-recapture files (FILE menu), manipulation of**
 102 **data (TRANSFORM DATA menu), goodness-of-fit testing for single-state (GOODNESS OF FIT menu) and multi-state**
 103 **(GOODNESS OF FIT FOR MULTI-STATE menu) data and various additional tools (TOOLS menu). Three of them are shown.**

- 104 1) How to prepare the data?

105 First, the menu TRANSFORM DATA offers some tools for selecting a data subset, such as a particular
 106 range of years or some groups (e.g. males or females, 'ringed as young' or 'ringed as adults'), and for
 107 recoding data, such as pooling states, groups or years. Among other features, the menu FILE makes it
 108 possible to convert data between two main formats (Biomeco (Lebreton and Roux 1989) and Mark
 109 (White and Burnham 1999)).

- 110 2) How to detect overdispersion?

111 When the data are ready, the next step should be the assessment of the fit of a general model to the
 112 data at hand. For single-state data, the classical model is the model with time dependent only
 113 parameters (Cormack-Jolly-Seber) (CJS); for multistate data, this is a time and state dependent model
 114 (Arnason-Schwarz) (AS). For both of them, the probability of the encounter history of each individual

115 is calculated conditional on its first capture. Optimal goodness of fit tests of the assumptions
 116 inherent in the CJS or the JMV model, this last being a slight generalization of the AS model, are then
 117 derived based on the classical partitioning, according to sufficient statistics T, of the likelihood
 118 $P(\text{data}/\text{parameters})$:

119
$$P(\text{data}/\text{parameters})=P(\text{data}/T) \times P(T/\text{parameters}).$$

120 The compatibility of the data with the hypergeometric distributions in $P(\text{data}/T)$ are tested
 121 asymptotically by contingency table chi-squared tests. These tests are organized into several
 122 interpretable components by further partitioning $P(\text{data}/T)$ (Pradel et al. 2005). If systematic
 123 departures from the general model can be ruled out, lack of fit may result from the lack of
 124 independence among individuals (the two members of a pair, social groups, a contagious disease...
 125 Then, the value of the Pearson statistic is much larger than the residual degrees of freedom. One
 126 simple measure for overdispersion is \hat{c} defined as the ratio of the Pearson statistic X^2 by its number
 127 of degrees of freedom df

128
$$\hat{c} = \frac{\chi X^2}{df}$$

129 This ratio can be calculated for each component individually or overall. Although there is no clear cut
 130 decision rule to decide that an observed lack of fit results solely from overdispersion, a reasonable
 131 rule of thumb is: the \hat{c} ratio is greater than 1 for all components, and there is no component for
 132 which the \hat{c} ratio greatly exceeds the others. This procedure, although not perfect, works generally
 133 well as long as the overall ratio does not exceed 3, sometimes 5 (Burnham and Anderson 2002 -
 134 numéro de page?); if it does, an important factor has likely been left out of the model and should be
 135 identified. On the other hand, small structural effects that result in an overall \hat{c} between 1 and 3 can
 136 without much damage be assimilated to overdispersion and treated as noise (see below for how to
 137 do this in practice).

138 To illustrate these general ideas, we will now treat the example of the study of movements of
 139 Canada geese *Branta canadensis* between three wintering regions, Mid-Atlantic, Chesapeake and
 140 Carolinas, between 1984 and 1989 (Hestbeck et al. 1991).

141
 142 The option 'GOODNESS-OF-FIT for Multi-state' of the main menu of U-CARE opens onto the
 143 goodness-of-fit test of the JollyMove (JMV) model (Brownie et al. 1993). Multi-state models
 144 (Hestbeck et al. 1991) allow for transitions between states (the wintering sites for the geese),
 145 survival probabilities and encounter probabilities. In the JMV model, transitions vary by state of
 146 departure, state of arrival and time interval. Survival probabilities vary by state of departure and time
 147 interval. Encounter probabilities vary by previous state, current state and date. This model, in
 148 contrast with the better-known Arnason-Schwarz (AS) model, allows encounter probabilities to vary
 149 by previous state. However, there is currently no optimal GOF test available for the AS model.
 150 Program U-CARE contains specific tests for transience (Test 3G.SR, null hypothesis H0: 'There is no
 151 difference in the probability of being later reencountered between "new" and "old" individuals
 152 encountered simultaneously. '), trap-dependence (Test M.ITEC, H0(i): 'There is no difference in the
 153 probabilities of being reencountered in the different states at i+1 between the animals in the same
 154 state at occasion i whether encountered or not encountered at this date, conditional on presence at
 155 both occasions. '), and memory (Test WBWA H0: 'There is no difference in the expected state of next
 156 reencounter among individuals previously encountered in the different states'). The \hat{c} ratio for the
 157 JMV model is computed from these three main components plus two complementary tests 3G.SM
 158 and M.LTEC (Pradel et al. 2005).

159
$$\hat{c} = \frac{\chi X_{WBWA}^2 + \chi X_{aG.SR}^2 + \chi X_{aG.SM}^2 + \chi X_{M.ITEC}^2 + \chi X_{M.LTEC}^2}{df_{WBWA} + df_{aG.SR} + df_{aG.SM} + df_{M.ITEC} + df_{M.LTEC}}$$

160 If we were to consider that the lack of fit is due solely to overdispersion, the overall \hat{c} ratio for the
 161 geese would be:

162
$$\hat{c} = \frac{472.8 + 117.7 + 302.7 + 68.2 + 21.9}{20 + 12 + 119 + 27 + 19} = 5$$

163 However, the \hat{c} ratio relative to the WBWA component is huge: 23.6 (see Figure 2)!

164

TEST WBWA (test of memory: Where Before vs Where After) , group =1						
===== Summary of TEST WBWA results =====						
sta	pval	df	occ	state	1 if fisher	0 otherwise
19.591	0.000	2.000	2.000	1.000	0.000	
37.868	0.000	2.000	2.000	2.000	0.000	
4.487	0.034	1.000	2.000	3.000	1.000	
80.590	0.000	1.000	3.000	1.000	0.000	
98.761	0.000	4.000	3.000	2.000	0.000	
0.807	0.369	1.000	3.000	3.000	1.000	
27.705	0.000	1.000	4.000	1.000	0.000	
53.694	0.000	2.000	4.000	2.000	0.000	
25.293	0.000	1.000	4.000	3.000	0.000	
43.655	0.000	1.000	5.000	1.000	0.000	
50.926	0.000	2.000	5.000	2.000	0.000	
29.476	0.000	2.000	5.000	3.000	0.000	
----- TEST WBWA (sta, pval, df) -----						
472.855	0.000	20.000				

165

166 **Figure 2 Details of Test WBWA for the Canada goose (*Branta Canadensis*) data from U-CARE. The Pearson statistic (*sta*) is**
 167 **calculated per occasion and state. The \hat{c} ratio is 23.6. This suggests strong memory effects in accordance with the overall**
 168 **p-value (*pval*).**

169

170 3) How to correct for overdispersion?

171 Given the large value of the overall \hat{c} ratio obtained for the Canada geese, we must try and \hat{c} find a
 172 more general model that takes into account the effects unveiled by the GOF test: \hat{c} \hat{c} the strong
 173 memory effect and a transient effect. The \hat{c} ratio of Test 3G.SR is indeed 9.8. A model studied in
 174 (Rouan et al.) combines these two effects. After discarding the components corresponding to the
 175 effects incorporated in this model (memory: component WBWA; transience: component 3G.SR), the
 176 new \hat{c} ratio is

177
$$\hat{c} = \frac{302.7 + 68.2 + 21.9}{119 + 27 + 19} = 2.4,$$

178 This value is typical of large data sets with several thousands of individuals where individual
 179 differences inherent in any animal population are inevitably detected. This ratio can be used as a
 180 variance inflation factor for the model of Rouan and derived models. There is an option in M-SURGE,
 181 E-SURGE and MARK to introduce this factor. The impact of the correction factor \hat{c} is null on
 182 parameter estimates, but estimated (co)variances are multiplied by \hat{c} , widths of the Wald-CI-
 183 intervals are $\sqrt{\hat{c}}$ times larger and the deviance is divided by \hat{c} . This in turn affects model selection
 184 where the AIC is replaced with the QAIC (Burnham and Anderson 2002). This procedure of identifying
 185 a starting model is valid more generally and should be pursued until an acceptable value for the \hat{c}
 186 ratio is reached. \hat{c}

187 4) How to conduct more specific tests?

188 U-CARE provides details that may give some additional information, notably the tables of observed
 189 and expected numbers. For example, Figure 3 shows that newly marked individuals are less
 190 recaptured than previously marked individuals at occasion 5 on sites 1 and 3 but not 2. This is a
 191 general pattern over all occasions which suggests that transients may be absent from the central site
 192 2. A more specific model could be considered. For an application to seasonal data, see ((Gauthier et

193 al. 2001)). U-CARE also gives directional tests (REF) focusing more closely on the detection of
194 transience and trap-dependence.

TABLE 3G.SR(5,1): animals caught at occasion5 in state1 seen earlier and later.	
Seen again - Never seen again	
New	93 317
Old	279 602
Table of expected values	
Seen again - Never seen again	
New	118.141 291.859
Old	253.859 627.141
TABLE 3G.SR(5,2): animals caught at occasion5 in state2 seen earlier and later.	
Seen again - Never seen again	
New	297 748
Old	512 1330
Table of expected values	
Seen again - Never seen again	
New	292.8317 752.1683
Old	516.16834 1325.8317
TABLE 3G.SR(5,3): animals caught at occasion5 in state3 seen earlier and later.	
Seen again - Never seen again	
New	157 504
Old	134 197
Table of expected values	
Seen again - Never seen again	
New	193.9022 467.0978
Old	97.09778 233.9022

195

196 **Figure 3 Tables of expected and observed values for Test 3G.SR at occasion 5 for sites 1, 2, 3**

197 Eventually, the option 'TOOLS' contains some specific tools, not easily found, like the ability to test
198 for mixtures of multinomial in a contingency table (Pradel et al. 2003), with an improved algorithm.

199 To cite U-CARE or acknowledge its use, cite this Software Note as follows, substituting the version of
200 the application that you used for "Version 2.3":

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202 for performing goodness of fit tests and manipulating Capture-REcapture data. *Ecography* ? : ?-?.
203 (Version 2.3)

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205

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