



## **THE GENERAL MODEL (Hypotheses 1-5)**

The multievent framework distinguishes the events, coded in the capture histories, from the states, which must be inferred. For the analyses performed, the events are:

- 0- stork not observed in a particular occasion
- 1- stork observed foraging in a ricefield
- 2- stork observed foraging at a dump

and the underlying biological states are:

- R1- Resident stork specialised in ricefields
- R2- Resident stork specialised in dumps
- R3- Resident generalist stork
- I1- Immigrant stork specialised in ricefields
- I2- Immigrant stork specialised in dumps
- I3- Immigrant generalist stork
- D - Dead stork

A multievent model use three kinds of parameters: the initial state probabilities, the transition probabilities, and the event probabilities (conditional on the underlying states).

The initial state probabilities correspond in our model to the proportions of newly encountered individuals belonging to the states R1, R2, R3, I1, I2 and I3. We decompose the initial state probabilities in two steps: the first step (residency status assignment) corresponds to the probability that a newly encountered individual is a resident “R” ( $\pi$ ) or an immigrant “I” ( $1 - \pi$ ). This parameter is group specific ( $g$ ) and fixed to 1 for group 1 (known residents) and to 0 for group 2 (known immigrants).

$$\text{Residency Status} = \begin{matrix} & \text{R} & \text{I} \\ \begin{pmatrix} \pi_g & 1 - \pi_g \end{pmatrix} \end{matrix}$$

The second step corresponds to the foraging strategy adopted by the individual. The corresponding probabilities denoted by  $\beta$  are conditional on the residency status (R=residents; I=immigrants), thus allowing different compositions in terms of foraging strategies between residents (R1, R2 and R3) and immigrants (I1, I2 and I3).

$$\text{Foraging Strategy} = \begin{matrix} & \text{R1} & \text{R2} & \text{R3} & & \text{I1} & \text{I2} & \text{I3} \\ \begin{matrix} \text{R} \\ \text{I} \end{matrix} \begin{pmatrix} \beta_1 & \beta_2 & 1 - \beta_1 - \beta_2 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_3 & \beta_4 & 1 - \beta_3 - \beta_4 \end{pmatrix} \end{matrix}$$

Multievent models as implemented in the software E-SURGE that we used provide for transition between states. The only meaningful transition would have been death. However, given the short duration of our study relative to the white stork life span we assumed no mortality. Hence, the traditional survival probability of capture-recapture models is not a parameter of interest in our models and it will be fixed to 1 in the IVFV step (see below). However, the inclusion of this parameter in the model is necessary in the E-SURGE implementation and could be useful in those situations in which survival ( $\phi$ ) may be lower than 1.

$$\text{Survival} = \begin{matrix} & \text{R1} & \text{R2} & \text{R3} & \text{I1} & \text{I2} & \text{I3} & \text{D} \\ \begin{matrix} \text{R1} \\ \text{R2} \\ \text{R3} \\ \text{I1} \\ \text{I2} \\ \text{I3} \\ \text{D} \end{matrix} \begin{pmatrix} \phi & 0 & 0 & 0 & 0 & 0 & 1 - \phi \\ 0 & \phi & 0 & 0 & 0 & 0 & 1 - \phi \\ 0 & 0 & \phi & 0 & 0 & 0 & 1 - \phi \\ 0 & 0 & 0 & \phi & 0 & 0 & 1 - \phi \\ 0 & 0 & 0 & 0 & \phi & 0 & 1 - \phi \\ 0 & 0 & 0 & 0 & 0 & \phi & 1 - \phi \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix} \end{matrix}$$

The event probabilities relate the observations coded in the capture histories to the underlying biological states. A matrix form with the conditioning state in rows and the event in columns is a particularly handy presentation. The event probabilities are decomposed in two steps: the first step corresponds to the state-specific probabilities of foraging in ricefields ( $\alpha_i$ ) and dumps ( $1 - \alpha_i$ ).

$$\text{Foraging} = \begin{matrix} R1 \\ R2 \\ R3 \\ I1 \\ I2 \\ I3 \\ D \end{matrix} \begin{matrix} \text{Ricefields} & \text{Dumps} \\ \left( \begin{array}{cc} \alpha_1 & 1 - \alpha_1 \\ \alpha_2 & 1 - \alpha_2 \\ \alpha_3 & 1 - \alpha_3 \\ \alpha_4 & 1 - \alpha_3 \\ \alpha_5 & 1 - \alpha_5 \\ \alpha_6 & 1 - \alpha_6 \\ 1 & 0 \end{array} \right) \end{matrix}$$

Note that foraging probabilities in ricefields for dead individuals (inexistent in this case) were arbitrarily considered to be 1.

The second step involves time (t) and foraging-habitat-specific (ricefields “ $p_1$ ” and dumps “ $p_2$ ”) probabilities of resighting ( $p$ ).

$$\text{Resighting} = \begin{matrix} & & 0 & 1 & 2 \\ \text{Ricefields} & \left( \begin{array}{ccc} 1 - p_{1t} & p_{1t} & 0 \\ 1 - p_{2t} & 0 & p_{2t} \end{array} \right) \\ \text{Dumps} & & & & \end{matrix}$$

### **THE SIMPLIFIED MODEL FOR KNOWN-AGE RESIDENTS (Hypotheses 6-7)**

This simplified model considers the same events:

- 0- stork not observed in a particular occasion
- 1- stork observed foraging in a ricefield

2- stork observed foraging at a dump

and two underlying biological states, the second one, unused, being required by the software:

R- Resident known-age stork

D- Dead bird

As every individual in this data set is a known-age resident stork, all initial state probabilities are trivially 1 and this kind of parameter is not used here.

R

Residency Status = 1

Again, survival probability(  $\phi$  ) is not a parameter of interest and it will be fixed to 1 in the IVFV step (see below).

$$Survival = \begin{matrix} & R & D \\ \begin{matrix} R \\ D \end{matrix} & \begin{pmatrix} \phi & 1-\phi \\ 0 & 1 \end{pmatrix} \end{matrix}$$

As in the previous model, the first step in event probabilities includes the probability of foraging at ricefields and dumps, now being only estimated for residents.

$$Foraging = \begin{matrix} & \text{Ricefields} & \text{Dumps} \\ \begin{matrix} R \\ D \end{matrix} & \begin{pmatrix} \alpha & 1-\alpha \\ 1 & 0 \end{pmatrix} \end{matrix}$$

Similarly to the previous model, the second step considers the same structure of time (t) and foraging-habitat-specific (ricefields and dumps) probabilities of resighting ( $p$ ).

$$Resighting = \begin{matrix} & & 0 & 1 & 2 \\ \begin{matrix} \text{Ricefields} \\ \text{Dumps} \end{matrix} & \begin{pmatrix} 1-p_{1t} & p_{1t} & 0 \\ 1-p_{2t} & 0 & p_{2t} \end{pmatrix} \end{matrix}$$

## **THE MODEL SELECTION PROCEDURE**

Models corresponding to the different biological hypotheses proposed can be built and fitted to the data using the program E-SURGE 1.7. Model selection is based on the Akaike's Information Criterion (AIC). Based on previous analyses and knowledge of the species and the study area, all models consider:

- Survival probabilities of 1.
- Resighting probabilities varying between ricefields and dumps and over days. Additionally, we fixed resighting probabilities to zero in those habitats and days in which there were no fieldwork visits.

## **IMPLEMENTATION OF MODELS IN E-SURGE**

We present here how to implement the models done during the analyses (hypotheses 1-7) using program E-SURGE 1.7.1.

E-SURGE can be downloaded at <http://www.cefe.cnrs.fr/biom/logiciels.htm>. It can read in data in a no-frill MARK format (files ".inp"); i.e. data with no comments, no tabulations, no letters in the capture histories (only digits are allowed). Data files used for this study are provided in supplementary information Supplements SD1 and SD2.

After opening a new session and reading in the data (two first items of the bar menu), the numbers of states considered (seven for hypotheses 1-5 and two for hypotheses 6-7) and age classes considered (one), have to be specified through the 'Modify' button.

It is then possible to go through the four steps represented by the coloured buttons at the bottom left.

**Specifying the patterns (tool GEPAT)**

This stage roughs out the model by specifying the probabilities presented above that will not be used (impossible initial states, transitions, or events)– code '-' (minus sign) –and those that will be calculated from others (because they are the last of a set of exclusive complementary options)– code '\*'. Pattern files for models of hypotheses 1- 5 and 6 -7 are provided in Supporting Information SP1 and SP2, respectively (file extension must be changed to “.pat”).

**Specifying the effects (tool GEMACO)**

Here we detail the definition used for each model. See program manual for a detailed description of GEMACO syntax.

<b>Model</b>	<b>IS step 1</b>	<b>IS step 2</b>	<b>Transition</b>	<b>Event, step 1</b>	<b>Event, step 2</b>
Hypothesis 1	i	i	i	i	resight
Hypothesis 2	i	i	i	i	resight
Hypothesis 3	g	i	i	f(1 2 3,4 5 6)	resight
Hypothesis 4	i	to(1 4,2 5)	i	f(1 4,2 5,3,6)	resight
Hypothesis 5	g	to	i	f(1 4,2 5,3,6)	resight
Hypothesis 6			i	i	resight
Hypothesis 7			i	i+xind(1)	resight

“i” constrains all parameters to be equal

“g” indicates between-groups differences

“f” indicates row and “to” indicates column. Numbers separated by a space indicate those rows/columns in which parameters are equal and numbers separated by a comma those rows/columns in which parameters differ.

“i+xind(1)” indicates an individual covariate effect

“resight” is a shortcut used for specifying resighting probabilities. The syntax of this shortcut is:

```
firste+nexte. [[to(2) .t(2,6,7,8,9,14,16,20,21,22,23,27,28,29,30,34,35,36,37,41,42,43,44,45,49,50,51,55,56,57,58,62,63,64,65,71,72,76,77,78) ]+[to(3) .t(15,17,20,23,27,28,29,35,36,37,38,42,43,44,45,49,50,51,52,55,56,57,59,62,63,65,66,70,71,72,73,76,77,78,80) ]]+others
```

Here, we distinguish the initial encounter probability (firste) from the subsequent probabilities (nexte) of resighting birds in the different foraging areas (to(2) and to(3), for ricefields and dumps, respectively) which are allowed to vary over days in which visits to the study area were carried out (t). The remaining time occasions correspond to those days without fieldwork visits (others) in which resighting probabilities will be fixed to zero in the IVFV step.

By the button “CALL GEMACO” model constraints are loaded.

### **Setting some parameter values (tool IVFV)**

For all the models (Hypothesis 1-7), the single survival probability must be set to 1. The first event probability in the second step is the probability of encounter at the time of marking, it must be set to 1. The last event probability is the probability of encountering a stork when no fieldwork was carried out; it has to be set to 0.

Additional parameters must be fixed on models Hypothesis 1-5. See below:

Model	Initial State step 1	Initial State step 2	Event, step 1
Hypothesis 1	$\pi = 0$	$(\beta_1 = \beta_2 = \beta_3 = \beta_4) = 0$	$(\alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = \alpha_5 = \alpha_6) = 0.5$
Hypothesis 2	$\pi = 0$	$(\beta_1 = \beta_2 = \beta_3 = \beta_4) = 0$	
Hypothesis 3	$\pi$ (group 1) = 1 $\pi$ (group 2) = 0	$(\beta_1 = \beta_2 = \beta_3 = \beta_4) = 0$	
Hypothesis 4	$\pi = 0$		$(\alpha_1 = \alpha_4) = 1$ $(\alpha_2 = \alpha_5) = 0$
Hypothesis 5	$\pi$ (group 1) = 1 $\pi$ (group 2) = 0		$(\alpha_1 = \alpha_4) = 1$ $(\alpha_2 = \alpha_5) = 0$

### **Advanced Numerical Options**

To avoid problems associated with local minima, which are common with multistate and multievent models in general, use the option multiple random in E-SURGE. We ran each model ten times with different initial parameter values.

### **Run**

The models can now be run.

Once the model was run, we used the tool “retrieve model” and we ran it again to ensure convergence to the lowest deviance.

\*\*\* Warning. Current limitation of the output of models including individual covariates is that the rank of the model is only available across Hessian (less accurate than with the numerical CMF approach). Consequently, we corrected the rank of the model proposed by E-SURGE by adding

one parameter (that corresponding to the slope) to those estimated by the constant model (model 6). In addition, standard errors are only available for mathematical parameters; mean estimates should be transformed to the real scale (inverse logit transformation) and SE of age-related foraging probabilities should be calculated using the delta-method (see program E-SURGE Help: Slides Fixed effects with individual Covariates with E-SURGE). We provide below the R code for inverse logit transformation and SE calculation:

```

IndCov<-function(int,slope,X,VCV){
  A<-1/(1+exp(-(int+slope*X)))
  U<-matrix(c(A*(1-A),X*A*(1-A)),2,1)
  varA<-t(U)%*%VCV%*%U
  return(varA)
}
X<-seq(0.1,2,by=0.1)
res<-rep(0,length(X))
int<-0.709827858
slope<-1.326272145
vari<-0.1384601                ## intercept variance##
covis<-(-0.15111164)          ## intercept-slope covariance##
vars<-0.23261706              ## slope variance ##
covsi<-(-0.15111164)         ## intercept-slope covariance ##
VCV<-matrix(c(vari,covis,covsi,vars),2,2)
for(i in 1:length(X)){
  res[i]<-IndCov(int,slope,X[i],VCV)      #var(A) ##
}
estimateREAL<-matrix(A,20,1)
seREAL<-matrix(res^0.5,20,1)
##parameter values for covariate values ranging from 0.1 to 2 (1 to 20 years old)##
estimateREAL

```

## SE of parameter values for covariate values ranging from 0.1 to 2 (1 to 20 years old)##  
seREAL

### **Testing model robustness**

An additional analysis not considering uncertain individuals (i.e., removing encounter histories corresponding to group 3) was performed to test the robustness of the model. Model definition and parameter fixing was the same as that presented above. In this case no parameter was estimated in IS (step 1) because only individuals of certain residence status were considered. Using this alternative approach, estimates on the proportion of resident and immigrant storks belonging to each foraging strategy (R1, R2, R3, I1, I2 and I3) were the same as those estimated with the full dataset, only resulting in slightly wider confidence limits (differences in parameter CI limits ranged from 0 to 0.04), thus confirming the robustness of the model.