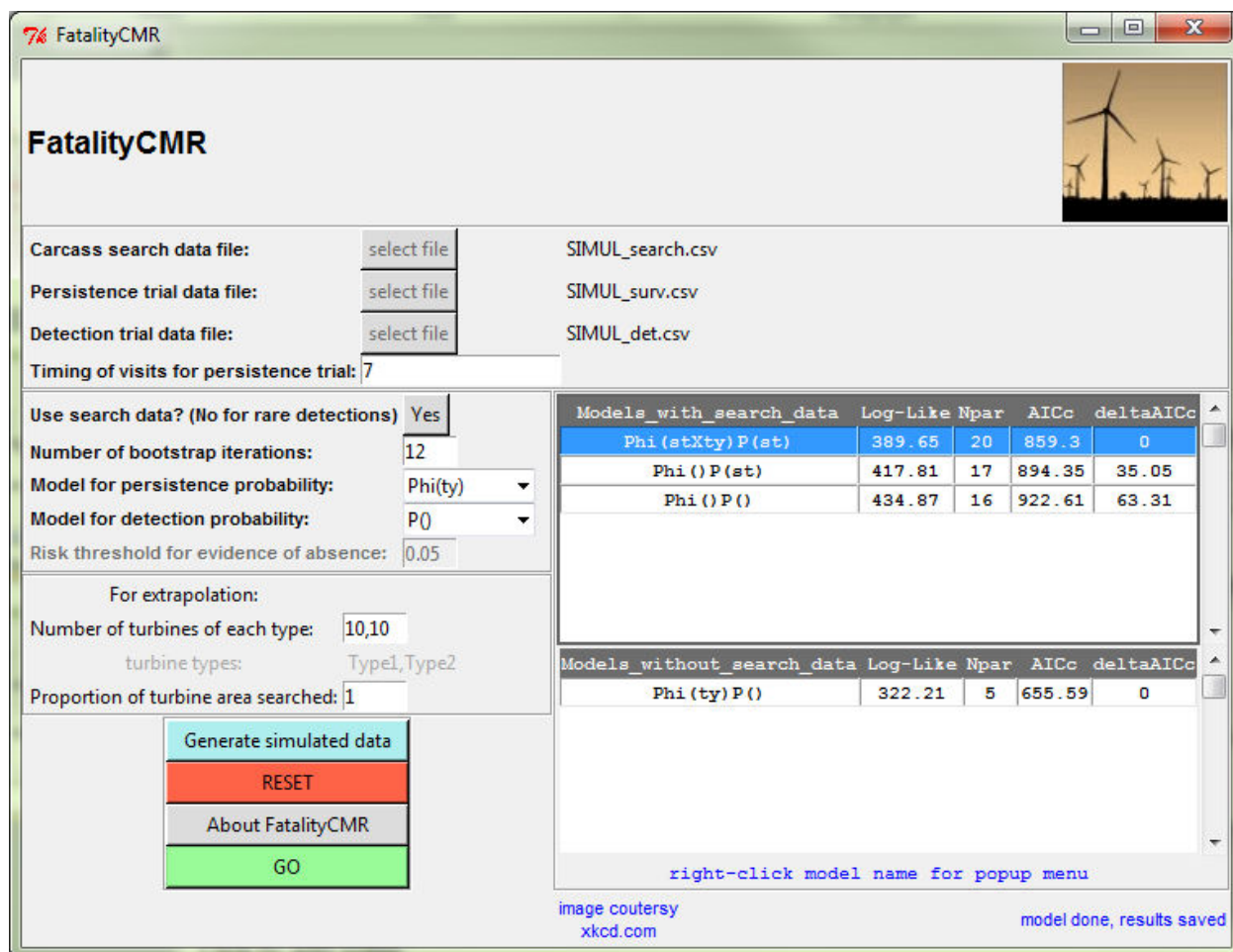


fatalityCMR – a capture-recapture software to correct raw counts of wildlife fatalities using trial experiments for carcass detection probability and persistence time

by Guillaume Péron, James E. Hines



FatalityCMR

Carcass search data file: SIMUL_search.csv

Persistence trial data file: SIMUL_surv.csv

Detection trial data file: SIMUL_det.csv

Timing of visits for persistence trial:

Use search data? (No for rare detections) Yes

Number of bootstrap iterations:

Model for persistence probability: ▼

Model for detection probability: ▼

Risk threshold for evidence of absence:

For extrapolation:

Number of turbines of each type:

turbine types:

Proportion of turbine area searched:

Models_with_search_data	Log-Like	Npar	AICc	deltaAICc
Phi(stXty) P(st)	389.65	20	859.3	0
Phi() P(st)	417.81	17	894.35	35.05
Phi() P()	434.87	16	922.61	63.31

Models_without_search_data	Log-Like	Npar	AICc	deltaAICc
Phi(ty) P()	322.21	5	655.59	0

right-click model name for popup menu

image coutersy xkcd.com model done, results saved

Preface

This report documents a user interface for the analysis of data resulting from carcass search and experimental trials in the context of the environmental assessment of wind farms. The interface was developed in R. The interface has been tested for accuracy using multiple datasets and the software offers the possibility to generate simulated data. If users find or suspect errors, please contact James E. Hines of the U.S. Geological Survey (USGS).

Every effort has been made by the USGS or the U.S. Government to ensure that the spreadsheet interface is error free; however, errors may exist in the spreadsheet interface. The distribution of the spreadsheets does not constitute any warranty by the USGS, and no responsibility is assumed by the USGS in connection therewith.

Contents

Preface.....	2
Contents	3
Figures.....	4
fatalityCMR – capture-recapture software to correct raw counts of wildlife fatalities using trial experiments for carcass detection probability and persistence time.....	5
Abstract	5
Introduction.....	6
Data structure	8
Carcass search data file.....	9
Persistence trial data file.....	10
Detection trial data file.....	11
Data simulation.....	12
Data analysis: Software options and interface.....	15
Timing of visits to planted carcasses for the persistence trial (4).....	17
Option of using search data or not (5)	17
Bootstrap variance computation (6).....	18
Biological effects acting on detection and persistence probabilities (7) and (8).....	18
Extrapolation to a larger area (10)	19
Model output and derived quantities.....	20

If using the search data	21
If not using the search data	23
About fatalityCMR	25
Utility	25
Acknowledgements.....	26
References Cited.....	26

Figures

Figure 1: Commands to open <code>fatalityCMR</code> from an R session once the necessary packages have been installed. Do not forget the double parenthesis when prompting <code>FCMR()</code>	9
Figure 2: Example of the formatting of the carcass search data file, viewed from Microsoft Excel.	11
Figure 3: Example of the formatting of the persistence trial data file, viewed from Microsoft Excel.	12
Figure 4: Example of the formatting of the detection trial data file, viewed from Microsoft Excel.	13
Figure 5: The data generation interface with default parameter values. This popup window appears after clicking on “Generate Simulated Data”.	16
Figure 6: The main interface window. 1: Data entry for the carcass search data. 2: Data entry for the persistence trial data. 3: Data entry for the detection trial data. 4: Data entry for the duration of the persistence trial (in days). 5: Option to use the carcass search data or not. If ‘No’ is selected then the software switches to ‘evidence of absence’ mode (see main text). 6: Number of	

replications in the parametric bootstrap for variance computation. 7 and 8: Model structure for persistence and detection probabilities, respectively. 9: Risk threshold for the ‘evidence of absence’ routine (see main text). This section activates only if the ‘No’ option is chosen at (5).

10: Parameters for the extrapolation to a larger area (e.g., whole wind farm). See main text. 11:

Button to enter the data simulation interface. 12: Reset button to erase all previously entered

data, as well as the results of previous analyses of these data. 13: “About button” for email

contact and reference. 14: “Go button” to launch the analysis once the data have been entered

and the correct options chosen. 15: Status bar with information printed in blue during

computation. This is also where tooltip info is displayed at the data entry stage. 16: Akaike

Information Criterion table with elements to compare model fit and parsimony. Right-click on

model names to access a menu and display either the text output file or the graph of carcass

distribution between turbine types. 17

Figure 7: Output file for models that use the carcass search data, viewed in Microsoft Windows

Notepad (partial view lacking data summary and model specification)..... 22

Figure 8: Output file for models that do not use carcass search data, viewed in Microsoft

Windows Notepad. The end of the output with the extrapolations to whole wind farm is omitted

from this view. 25

Figure 9: Popup windows that appears after clicking on ‘About FatalityCMR’ 26

fatalityCMR – capture-recapture software to correct raw counts of wildlife fatalities using trial experiments for carcass detection probability and persistence time

By Guillaume Péron, James E. Hines

Abstract

Many industrial and agricultural activities involve wildlife fatalities by collision, poisoning or other involuntary harvest: wind turbines, highway networks, utility networks, tall structures, pesticides, etc. Impacted wildlife may have official protection, including a requirement to monitor impacts. Carcass counts are often conducted to quantify the number of fatalities, but they need to be corrected for carcass persistence time (as influenced by removal by scavengers and decay) and detection probability (searcher efficiency). In this article we introduce new software that fits a superpopulation capture-recapture model to raw count data. It uses trial data to estimate detection and daily persistence probabilities. A recurrent issue is that fatalities of rare, protected species are infrequent, in which case the software offers the option to switch to an ‘evidence of absence’ mode based on binomial laws and the estimate of the probability of not finding a carcass. The software allows users to distinguish between different turbine types (e.g. different vegetation cover under turbines, or different technical properties), as well between two carcass age-classes or states, with transition between those classes (e.g. fresh and old). A data simulation feature may be used at the planning stage to optimize sampling design. Resulting mortality estimates can be used 1) to quantify the required amount of compensation, 2) inform mortality projections for proposed development sites, 3) inform decisions about management of existing sites, and 4) improve the design of carcass search protocols and trial experiments.

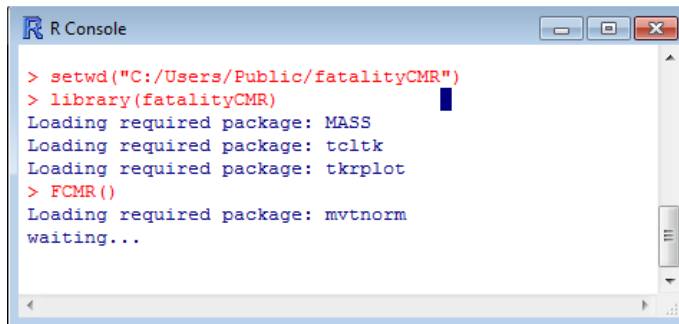
Introduction

The environmental impact of human activities is sometimes very direct, when human-made structures or molecules kill wildlife. Collisions with vehicles have for example been deemed a major limitation of turtle population growth in the US (Gibbs & Shriver 2002), and mortality by pesticide ingestion is claimed to reduce the abundance of several bird species (Mineau & Whiteside 2013). Recently, collisions with wind turbines have been identified as a significant threat to bird and bat species (Drewitt & Langston 2006; Bell & Smallwood 2010). A major concern for stakeholders is that some affected species benefit from official protection. For example, in the United States each and every death of a migratory bird caused by human activities is illegal in the absence of a permit (Migratory Bird Treaty Act of 1918). To assess the extent of the issue, it is often possible to directly document the “take” of protected species by searching for carcasses near the mortality source. However, the raw carcass counts represent minimum estimates of mortality. They need to be corrected for 1) persistence probability (loss of carcasses to scavengers, decay, weather and tide) and 2) detection probability (observers may miss some of the carcasses that are present during surveys) (Arnett *et al.* 2008; Smallwood *et al.* 2010; Huso 2011). In most cases, these probabilities are estimated using trial experiments, i.e., planting carcasses and monitoring their subsequent detection and fate. Trial experiments can also be based on ‘naturally-occurring’ carcasses.

We recently described a superpopulation capture-recapture approach (Crosbie & Manly 1985; Schwarz & Arnason 1996) that corrects for both persistence and detection (Péron *et al.* 2013). The method was developed with wind farms in mind, which will be reflected in the wording below, but can be applied to any type of wildlife fatality problem. In the present article we introduce software that allows implementation of our approach without extensive familiarity

with capture-recapture models or any programming language. The key feature that distinguishes the statistical modeling in this software from other fatality estimators (Bernardino *et al.* 2013) is the use of the capture-recapture modeling framework, which does not force strong assumptions about ‘bleed through’ (carcasses that persist undetected for multiple sampling occasions; Warren-Hicks *et al.* 2013). The software also accommodates differences among turbine ‘types’ and carcass ‘states’. Turbine types can account for different technologies or different vegetation cover, both factors known to affect persistence and/or detection probabilities (Smallwood 2013; Warren-Hicks *et al.* 2013). Turbines of different types can also exhibit different risk levels for wildlife (e.g. turbines located on a ridge top vs. turbines located on gentle slope; de Lucas *et al.* 2012). Carcass states account for the effect of decay or desiccation on detection and persistence probability, and thus for departures from the exponential distribution of time-to-removal and time-to-detection of the carcasses. A maximum of two states is allowed (e.g., fresh and dry, or intact and partially scavenged, etc.). There is currently little evidence about the impact of carcass ‘ageing’ on fatality estimation, and it is hoped that by making age-effects readily available in the estimation framework our software can help identify whether this variable (carcass state) should be routinely recorded and promote the adoption of common protocols for carcass age-determination. The software works from R (R-Development-Core-Team 2010) as function `FCMR()` in package `fatalityCMR`. `fatalityCMR` is freely available under GPL-2 license at http://www.mbr-pwrc.usgs.gov/software/fatalityCMR_2.0.3.zip. Substitute 2.0.2 instead of 2.0.3 if using R version 2 (instead of version 3). `fatalityCMR` relies on packages `tcltk`, `tkplot`, `mvtnorm`, and `MASS`, which are all readily available from the R-CRAN website <http://cran.r-project.org/> and will be automatically installed if not already present [the first session should be

run with administrator rights in this case]. The statistical modeling on which this software is based is detailed in Péron et al. (2013).



```

R Console
> setwd("C:/Users/Public/fatalityCMR")
> library(fatalityCMR)
Loading required package: MASS
Loading required package: tcltk
Loading required package: tkrplot
> FCMR()
Loading required package: mvtnorm
waiting...

```

Figure 1: Commands to open `fatalityCMR` from an R session once the necessary packages have been installed. Do not forget the double parenthesis when prompting `FCMR()`.

Data structure

`fatalityCMR` uses data on carcass searches, persistence trials, and detection trials to generate estimates of total fatalities. First, operators select a set of turbines and decide upon 1) a fixed area below each turbine, which they are going to search for carcasses, 2) a number T of sampling occasions and 3) the time intervals between these occasions. The software does not allow varying the protocol at different turbines; each turbine in the set has to be searched for carcasses at each occasion. Field technicians record the number of previously undetected carcasses, and, optionally, the type of turbine and the (dichotomous) age-class of the carcasses. No missing data (e.g., turbines that are not visited on a given occasion) are allowed. Second, the software requires data from persistence trials and detection trials. Persistence trials consist of regular checks of planted carcasses for a fixed number of days or until they disappear. This is the ‘persistence trial data’ hereafter. In detection trials, trial carcasses are placed throughout the survey area (or a portion of it) and investigators who are ignorant of the number and locations of carcasses search

the area and record how many trial carcasses are detected. This is the ‘detection trial data’ hereafter. The next three paragraphs describe how these three sets of data are formatted and entered into the software.

Carcass search data file

The carcass search data must be in a comma separated CSV file with specific formatting. The first line should contain specific headers, namely ‘State’, ‘ID’, ‘Type’, and ‘A1’, ‘A2’, ..., ‘AT’ where T is the number of sampling occasions (different searches). $T=12$ in Fig. 2. Headers are case-sensitive, so that entering a file with ‘type’ instead of ‘Type’ will trigger an error. ‘State’ is optional (see below). The second line must contain interval durations in days in columns ‘A1’, ‘A2’, ..., ‘AT-1’, where the number entered under ‘A1’ is the interval between sampling occasions 1 and 2, etc. The last cell, under ‘AT’, contains ‘NA’ since there is no interval following the last occasion. Then, starting in the third line of the file, enter one line per turbine and per carcass state (‘fresh’ and ‘old’ states). First enter as many lines as there are turbines in the study area. Under ‘ID’ enter the turbine ID numbers or any strings of characters to identify the turbines. Under ‘Type’ enter the turbine type; if there is no turbine type, enter the same string of characters throughout this column, e.g. ‘NoType’. Note that the exact same turbine type denominations must also be used in the persistence and detection trial data files. Under ‘State’ enter ‘fresh’ or any other appropriate name. Under ‘A1’, ‘A2’, ..., ‘AT’ enter the number of fresh carcasses found under each turbine at each sampling occasion. All turbines have to be searched at all sampling occasions; do not enter NA or 0 if the turbine was not searched. Then, enter a second series of lines (one per turbine). Under ‘State’ enter ‘dry’ or the name of the second state. Under ‘A1’, ‘A2’, ..., ‘AT’ enter the number of previously undetected carcasses that were assigned to the second age-class upon detection. If carcasses are not assigned to age

classes, then remove the ‘State’ column, and enter only one line per turbine. An example data file can be obtained using the data simulation capacity (see below).

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	State	ID	Type	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12		
2	NA	intdur	NA	2	2	2	2	2	2	2	2	2	2	2	2	NA	
3	fresh		1 Type1	0	0	0	1	0	1	0	1	0	2	0	2		
4	fresh		2 Type1	0	3	0	1	2	1	2	1	1	0	1	0		
5	fresh		3 Type1	2	1	0	0	1	1	0	0	0	0	0	0		
6	fresh		4 Type1	0	2	0	3	1	0	0	1	0	0	0	3		
7	fresh		5 Type1	0	1	0	0	1	1	0	0	0	0	0	1		
8	fresh		6 Type1	0	1	0	0	0	0	0	0	1	2	1	1		
9	fresh		7 Type1	0	1	1	0	2	1	1	1	0	0	0	0		
10	fresh		8 Type1	3	0	0	0	0	0	0	2	0	1	0	0		

Figure 2: Example of the formatting of the carcass search data file, viewed from Microsoft Excel.

Note: If different turbines are subjected to different search protocols (e.g., different time intervals, or different number of time occasions), you have to prepare one data file per type of search protocol and run separate analyses.

Persistence trial data file

All trial carcasses used in the persistence trial must be subjected to the same protocol; they must be checked for continued persistence on the same days; the software does allow different carcasses to be checked on different days, but the series of intervals between subsequent checks must be the same for all carcasses (e.g., daily checks for two weeks, or one check every two days for ten days). The persistence data file is also a comma-separated CSV file with specific formatting. The first line contains headers ‘State’, ‘Type’, ‘duration’, and ‘transition’, still case-specific. Below the header, there should be one line per trial carcass. Under ‘State’ enter the state of the carcass at the beginning of the trial. Under ‘Type’ enter the type of the turbine associated

with the trial carcass. Under ‘duration’ enter the persistence time in days. If the carcass is still present at the last visit, enter the duration of the persistence trial. Under ‘transition’ enter the time to transition, which is the last occasion at which the carcass was considered as in the first state. For example, if the carcass is checked on days 2,3,4,6,8,and 10, and on day 8 it is considered to have transitioned to the second state, then enter 6 under ‘transition’ for that carcass. If no transition is recorded, or if the carcass was already in the second state at the start of trial, enter ‘NA’ under ‘transition’. Any state \times type combination found in the carcass search data must also be represented in the persistence data file. An example persistence data file can be obtained using the data simulation capacity (see below).

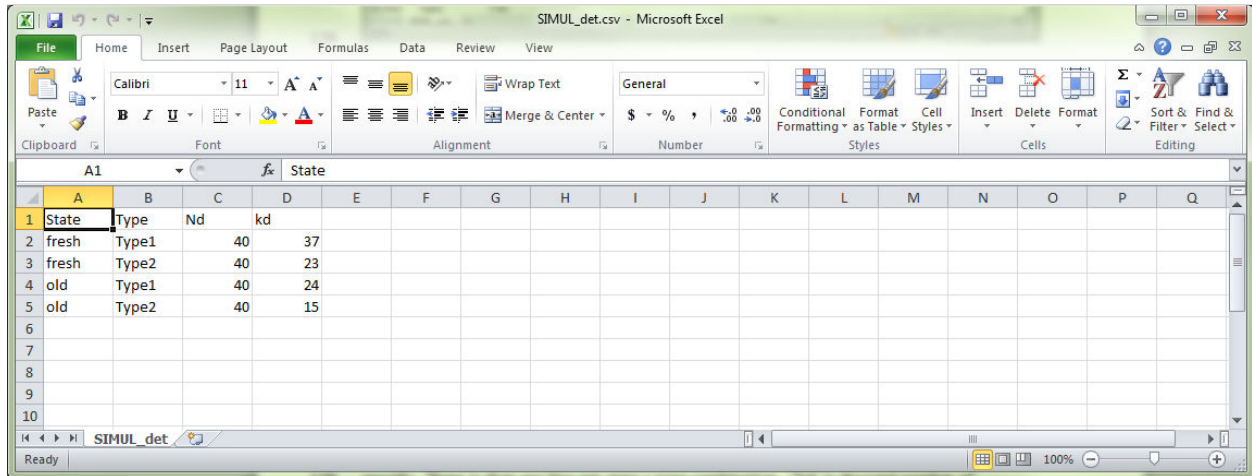
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	State	Type	duration	transition													
2	fresh	Type1	1	NA													
3	fresh	Type1	1	NA													
4	fresh	Type1	5	NA													
5	fresh	Type1	2	NA													
6	fresh	Type1	7	1													
7	fresh	Type1	7	7													
8	fresh	Type1	1	NA													
9	fresh	Type1	4	NA													
10	fresh	Type1	1	NA													

Figure 3: Example of the formatting of the persistence trial data file, viewed from Microsoft Excel.

Detection trial data file

The detection data file is also a comma separated CSV file with specific formatting. The first line contains headers ‘State’, ‘Type’, ‘Nd’, and ‘kd’, still case-specific. There should be one line per state \times type combination. ‘Nd’ is the total number of carcasses that were planted in this

combination. ‘kd’ is the number of those carcasses that were detected. Any state × type combination found in the carcass search data must also be represented in this file. An example data file can be obtained using the data simulation capacity (see below).



State	Type	Nd	kd
fresh	Type1	40	37
fresh	Type2	40	23
old	Type1	40	24
old	Type2	40	15

Figure 4: Example of the formatting of the detection trial data file, viewed from Microsoft Excel.

Note: The persistence and detection trial data files can be used for projects other than the one they originate from, under the assumption that persistence and/or detection probabilities are the same.

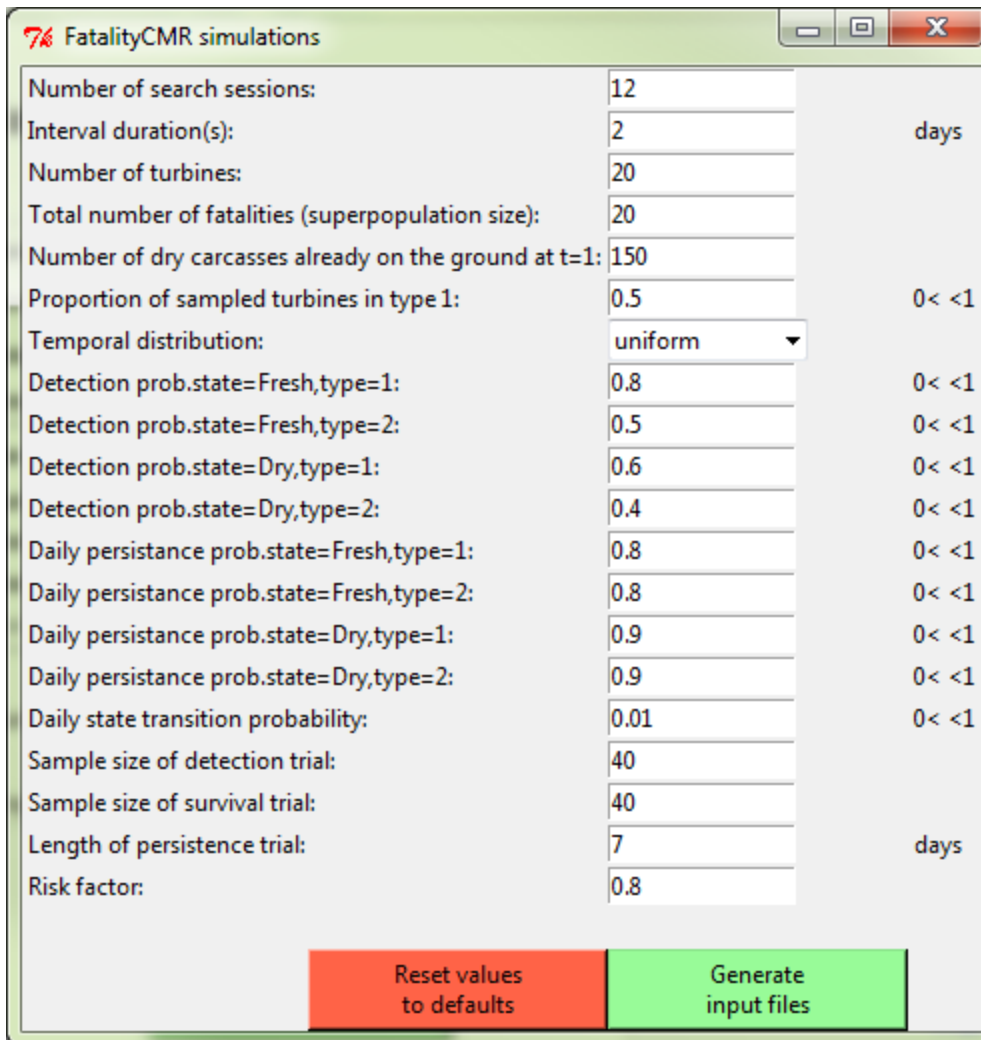
Data simulation

The software can generate datasets with two types of turbines and two carcass states. We review below the different parameters as they are designated in the data simulation window, which also serves as a review of model parameters (see Péron *et al.* 2013 for more details).

- Number of search sessions: the number of sampling occasions during which the area is searched for new carcasses.

- Interval duration(s): The duration in days between the successive sampling occasions. If fewer than $T-1$ numbers are entered (separated by a comma), then the interval duration is assumed fixed and only the first value is used.
- Number of turbines that are searched for carcasses
- Total number of fatalities (superpopulation size): The total number of carcasses that are available for detection during at least one of the sampling occasions, and that are not already dry at the first occasion.
- Number of dry carcasses already on the ground at $t=1$: The number of carcasses that are already dry at the first occasion.
- Proportion of sampled turbines in type 1: One minus this number indicates the proportion of sampled turbines in type 2.
- Temporal distribution: Choose either ‘uniform’ to fix the entry rate of new carcasses to a constant daily value, or ‘pulsed’ to mimic a pulsed phenology centered in the middle of the study period.
- Detection prob.state=Fresh,type=1: The detection probability of fresh carcasses under turbines of type 1.
- Detection prob.state=Fresh,type=2: The detection probability of fresh carcasses under turbines of type 2.
- Detection prob.state=Dry,type=1: The detection probability of dry carcasses under turbines of type 1.
- Detection prob.state=Dry,type=2: The detection probability of dry carcasses under turbines of type 2.

- Daily persistence prob.state=Fresh,type=1: The daily persistence probability of fresh carcasses under turbines of type 1.
- Daily persistence prob.state=Fresh,type=2: The daily persistence probability of fresh carcasses under turbines of type 2.
- Daily persistence prob.state=Dry,type=1: The daily persistence probability of dry carcasses under turbines of type 1.
- Daily persistence prob.state=Dry,type=2: The daily persistence probability of dry carcasses under turbines of type 2.
- Daily state transition probability: The daily probability that a fresh carcass becomes dry
- Sample size of detection trial: The number of carcasses of each type \times state combination that is used in the detection trial. If only one value is entered, it is considered to represent the number of carcasses used in each of the trial combinations, so that the total trial sample size is four times the entered value.
- Sample size of survival trial: The number of carcasses of each type \times state combination that is used (initially placed) in the survival trial. If only one value is entered, it is taken to represent the number of carcasses used in each of the trial combinations, so that the total trial sample size is four times the entered value.
- Length of persistence trial: The number of days each trial carcass is monitored for persistence
- Risk factor: The multiplication factor used to assign carcasses to one or the other turbine type. Risk factors below one indicate that type 1 is more dangerous (produces more dead birds), while risk factors above 1 indicate type 2 is more dangerous.



Parameter	Value	Unit/Constraint
Number of search sessions:	12	
Interval duration(s):	2	days
Number of turbines:	20	
Total number of fatalities (superpopulation size):	20	
Number of dry carcasses already on the ground at t=1:	150	
Proportion of sampled turbines in type 1:	0.5	0 < <1
Temporal distribution:	uniform	
Detection prob.state=Fresh,type=1:	0.8	0 < <1
Detection prob.state=Fresh,type=2:	0.5	0 < <1
Detection prob.state=Dry,type=1:	0.6	0 < <1
Detection prob.state=Dry,type=2:	0.4	0 < <1
Daily persistence prob.state=Fresh,type=1:	0.8	0 < <1
Daily persistence prob.state=Fresh,type=2:	0.8	0 < <1
Daily persistence prob.state=Dry,type=1:	0.9	0 < <1
Daily persistence prob.state=Dry,type=2:	0.9	0 < <1
Daily state transition probability:	0.01	0 < <1
Sample size of detection trial:	40	
Sample size of survival trial:	40	
Length of persistence trial:	7	days
Risk factor:	0.8	

Reset values to defaults Generate input files

Figure 5: The data generation interface with default parameter values. This popup window appears after clicking on “Generate Simulated Data”.

Data analysis: Software options and interface

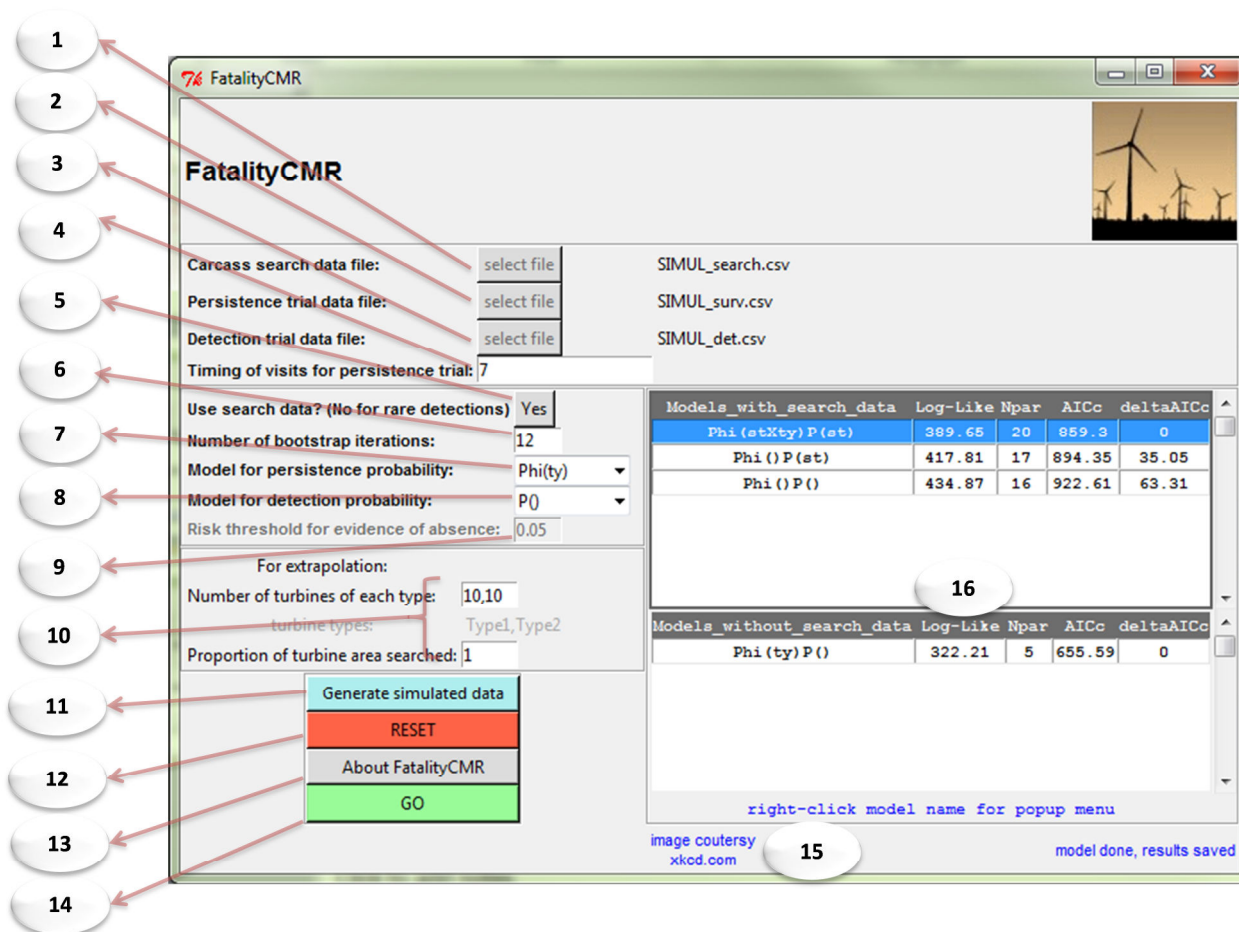


Figure 6: The main interface window. 1: Data entry for the carcass search data. 2: Data entry for the persistence trial data. 3: Data entry for the detection trial data. 4: Data entry for the duration of the persistence trial (in days). 5: Option to use the carcass search data or not. If 'No' is selected then the software switches to 'evidence of absence' mode (see main text). 6: Number of replications in the parametric bootstrap for variance computation. 7 and 8: Model structure for persistence and detection probabilities, respectively. 9: Risk threshold for the 'evidence of absence' routine (see main text). This section activates only if the 'No' option is chosen at (5). 10: Parameters for the extrapolation to a larger area (e.g., whole wind farm). See main text. 11: Button to enter the data simulation interface. 12: Reset button to erase all previously entered data, as well as the results of previous analyses of these data. 13: "About button" for email contact and reference. 14: "Go button" to launch the analysis once the data have been entered

and the correct options chosen. 15: Status bar with information printed in blue during computation. This is also where tooltip info is displayed at the data entry stage. 16: Akaike Information Criterion table with elements to compare model fit and parsimony. Right-click on model names to access a menu and display either the text output file or the graph of carcass distribution between turbine types.

Hereafter we review different options available to tailor the analysis. Numbers between brackets refer to the numbers in Fig. 6.

Timing of visits to planted carcasses for the persistence trial (4)

The software gives the option to either provide a single number in this space, which is interpreted as the duration of the entire trial, in days, with locations visited every day; or to enter a list of increasing integers, which are the days on which the locations were visited (e.g., 1,2,3,6,7 if trial carcasses were not checked on days 4 and 5 of a week-long trial, for example). Beware that there is no data checking for this feature. If the persistence trial data file (see above) indicates that a carcass was last recorded on a day that was not visited as per the timing of visits, there will not be an error message and this carcass will be considered as having persisted until the final day of the trial.

Option of using search data or not (5)

The total number of detected carcasses C may be small. In this case the standard capture-recapture procedure, or any estimation method that we know of, perform poorly. It is thereby recommended to choose the ‘No’ option if C is less than or equal to 5 carcasses. The procedure then relies on the estimate for P_0 , the probability that one carcass of unknown entry date is not detected. The estimate for P_0 depends only on the trial data and on the timing of the sampling

occasion; it does not make use of the result of the carcass searches. Under the assumption that each fatality event is independent of others, the software then computes two quantities. First, it provides the maximum number of carcasses that could have escaped detection, with a user-defined error risk α , i.e., N_{max} such that $\binom{N_{max}}{C} (1 - P_0)^C P_0^{N_{max}-C} = \alpha$. By default α is set to 0.05. Second, it computes an ad-hoc estimate of the number of fatalities, i.e., $\hat{N} = \sum_{n=C}^{\infty} [n \cdot \Pr(n|C)]$. In practice the summation is stopped as soon as $\Pr(n|C) = \binom{n}{C} (1 - P_0)^C P_0^{n-C}$ gets below 10^{-9} . Note that N_{max} will usually be larger than the true number of fatalities (depending on the value for α); N_{max} should be preferred over \hat{N} under the precautionary principle only (e.g., when enforcing that the take does not exceed a given threshold). The whole procedure can be referred to as the ‘evidence of absence’ routine (M. Huso, pers. comm.). We re-emphasize here that this procedure is designed for the case with very few detected carcasses only, and also that the “Yes” option should never be chosen if fewer than 5 carcasses have been found.

Bootstrap variance computation (6)

To compute standard error for some of the derived quantities the software performs a parametric bootstrap using the estimated variance-covariance of the parameters. The user can change the number of replications or set it to zero. In the bootstrap, the software generates parameter values from the multivariate normal distribution centered around the estimates; it computes derived quantities such as P_0 , and then estimate the standard deviation of the set of simulated values.

Biological effects acting on detection and persistence probabilities (7) and (8)

Detection and persistence probabilities may vary with turbine type or carcass state. You can choose among four pre-defined model structures for both persistence and detection probability:

constant probability, denoted by a blank; one parameter per turbine type, denoted by ‘ty’; state-specific probability, denoted by ‘st’; two-way interaction of type and state, denoted by ‘tyXst’. The effects are modeled on the logit scale. A “biological model” is then combinations of model structure for persistence and for detection. Biological models vary in their fit to the data. This fit and model parsimony are assessed using Akaike Information Criterion and associated metrics which (Burnham & Anderson 2002) are displayed in the model selection table (16). Estimates from the best ranking model should be considered as the most reliable.

Extrapolation to a larger area (10)

The software can perform simple extrapolations (cross multiplications) to extend the results from the search area to the whole wind farm. In the first space, the user may enter the total number of turbines of each type in the wind farm, separated by a comma. These numbers should include both the turbines selected for the surveys and those that were not monitored. If all turbines were searched, or if the total number is not known, leave this space blank. The parameter in the second space is a correction factor that accounts for unsearched areas within each turbine plot. This can represent inaccessible areas (dense vegetation cover, crag, water) or areas beyond the search radius. For example if it is known that $1-a=20\%$ of the carcasses fall beyond the search radius, and that $1-b=15\%$ of the area within the search radius could not be searched then the correction factor is $a*b = 0.68$. Note however that this correction factor assumes that inaccessible areas are distributed uniformly with respect to distance from the turbine pole; the correction should be amended if unsearchable areas are disproportionately close or far from the turbine pole. Smallwood (2013) reviews a lot of information available to compute a and b . If you want only the estimate of the number of carcasses that fell *within the search area*, simply enter the value 1 as the correction factor.

Model output and derived quantities

The software provides 1) a model comparison table in which the Akaike Information Criterion, corrected for small sample sizes, is used to compare the fit and parsimony of the different models (Burnham & Anderson 2002); 2) one text output file per model, with parameter estimates, derived quantities, data summary, and characteristics of the run; and 3) a graph displaying the observed distribution of carcasses between turbine types.

If using the search data

----- Parameter estimates (12 bootstrap replications)-----									
Entry probabilities:									
occasion	estimate	mean	BS	BS	std.dev				
1	0.0986	0.0908			0.0210				
2	0.1271	0.1327			0.0443				
3	0.0730	0.0699			0.0109				
4	0.1274	0.1283			0.0212				
5	0.0793	0.0730			0.0257				
6	0.0785	0.0823			0.0343				
7	0.0702	0.0799			0.0344				
8	0.0813	0.0785			0.0313				
9	0.0321	0.0380			0.0230				
10	0.0875	0.0929			0.0213				
11	0.0988	0.0954			0.0260				
12	0.0461	0.0384			0.0144				
Daily persistence/detection probability:									
persistence					detection				
	fresh		old		fresh		old		
	estimate	std.err	estimate	std.err	estimate	std.err	estimate	std.err	
Type1	0.8152	0.0171	0.8152	0.0171	0.7322	0.0321	0.7322	0.0321	
Type2	0.8152	0.0171	0.8152	0.0171	0.7322	0.0321	0.7322	0.0321	
Daily state transition probability: fresh to old									
	estimate	std.err							
	0.0247	0.0084							

FATALITY NUMBER:									

Carcasses within search area of 20 turbines out of 20									
Turbine	Detectable carcasses(N)				Corrected number(N*)				
	estimate	std.error	estimate	std.error	estimate	std.error	estimate	std.error	
1	5.0000	0.0000	5.4810	0.0528	5.4810	0.0528	5.4810	0.0528	
2	11.7549	0.2511	12.8866	0.3380	12.8866	0.3380	12.8866	0.3380	
3	9.1309	0.1454	10.0100	0.2259	10.0100	0.2259	10.0100	0.2259	
4	10.4233	0.2091	11.4269	0.2949	11.4269	0.2949	11.4269	0.2949	
5	10.6185	0.2272	11.6407	0.3065	11.6407	0.3065	11.6407	0.3065	
6	10.4233	0.2091	11.4269	0.2949	11.4269	0.2949	11.4269	0.2949	
7	13.0966	0.2985	14.3572	0.3866	14.3572	0.3866	14.3572	0.3866	
8	7.2099	0.1549	7.9041	0.2108	7.9041	0.2108	7.9041	0.2108	
9	17.0312	0.3319	18.6710	0.4705	18.6710	0.4705	18.6710	0.4705	
10	7.4019	0.1779	8.1144	0.2280	8.1144	0.2280	8.1144	0.2280	
11	5.0214	0.0391	5.5045	0.0734	5.5045	0.0734	5.5045	0.0734	
12	4.0310	0.0534	4.4188	0.0754	4.4188	0.0754	4.4188	0.0754	
13	3.0000	0.0000	3.2886	0.0317	3.2886	0.0317	3.2886	0.0317	
14	5.1254	0.1184	5.6188	0.1536	5.6188	0.1536	5.6188	0.1536	
15	2.0000	0.0000	2.1924	0.0211	2.1924	0.0211	2.1924	0.0211	
16	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
17	2.0000	0.0000	2.1924	0.0211	2.1924	0.0211	2.1924	0.0211	
18	5.1254	0.1184	5.6188	0.1536	5.6188	0.1536	5.6188	0.1536	
19	2.0000	0.0000	2.1924	0.0211	2.1924	0.0211	2.1924	0.0211	
20	2.0000	0.0000	2.1924	0.0211	2.1924	0.0211	2.1924	0.0211	
total									
Type1	111.6331	4.8146	122.3739	5.4426	122.3739	5.4426	122.3739	5.4426	
Type2	27.7580	0.6874	30.4278	0.7897	30.4278	0.7897	30.4278	0.7897	
already old at t=1 (D0):									
Type1	19.1549	0.8686							
Type2	1.3682	0.0620							

Extrapolation to whole wind farm (using N*):									
	from pooled data				from turbine-specific estimates				
	estimate	std.error	estimate	std.error	estimate	std.error	estimate	std.error	
	152.8017	5.4996	145.1378	0.9820	145.1378	0.9820	145.1378	0.9820	

Probability not to find a carcass given it is in survey area (P0):									
	estimate	std.err							
Type1	0.1175	0.0187							
Type2	0.1184	0.0188							

Between-turbine variance (corrected for sampling variance):									
24.4168	95% CI:	[14.0804 ; 52.198]							

Test for the effect of turbine type on fatality estimate:									
chi-squared(df= 1):	29.1081	P-value:	0						

- One entry probability value per sampling occasion

- One persistence and detection value for each turbine type × carcass state combination

- Daily transition probability between carcass states

- Turbine-specific estimated numbers of fatalities

- Estimated total number of fatalities, per turbine type
- Estimated number of 'old' carcasses at first sampling occasion

- Extrapolation to larger area

- Probability that a carcass is missed

- Variation between turbines

Figure 7: Output file for models that use the carcass search data, viewed in Microsoft Windows Notepad (partial view lacking data summary and model specification)

The central quantity to estimate is superpopulation size, i.e., the number of carcasses that were available for detection at least once during the period between the initial and final sampling occasions. This estimate is located under “Detectable carcasses (N)” in the output file. Turbine-specific estimates are computed by fixing persistence and detection parameters to their values obtained when using the pooled data, and running the model using only those carcasses found under the focal turbine. A correction is then performed for carcasses that enter and are removed by scavengers during the same interval and are thus never available for detection (see equation 8 in Péron *et al.* 2013). These corrected estimates are found under “Corrected number (N*)”. The extrapolated fatality numbers are located under “Extrapolation to whole wind farm”. They are computed using corrected estimates (N*). Two different extrapolations are performed. The first one uses the numbers estimated from the pooled data and corrects for the potential non-representative sampling of different turbines types. The second extrapolation uses the turbine-specific estimates and does not correct for the potential non-representative sampling of different turbines types. The standard error for the second extrapolation is computed using equation 5 in Skalski (1994). The probability of not finding a carcass of unknown entry date (P_0) is located under “Probability of not finding a carcass”. Note that this probability is conditional on the carcass being available for detection during at least one sampling occasion and within the search area. Last, the software provides two measures of between-turbine variation in the number of fatalities. The first measure is the variance in the turbine-specific fatality estimates, corrected for sampling error using equation 4.2 in Burnham *et al.* (1987). Note that if fatalities are rare, the algorithm often fails and displays NA for the variance estimate, indicating either that the variance is null or the sample too small. The 95% confidence interval is computed using the chi-squared distribution (Burnham *et al.* 1987). The second measure of between-turbine variation in

mortality is a chi-squared test for the effect of turbine type on fatality number. It tests whether the distribution of estimated fatalities deviates from that expected given the sampling stratification. There is also an option to display a graph of observed versus expected numbers of fatalities in different turbine types.

If not using the search data

The option to not use search data and base all inference on trial data plus timing of sampling occasions should only be chosen if few carcasses are detected. We thus included less information in the output to avoid small sample biases and errors. The key quantity to estimate is the probability of not finding a carcass that was available for detection in the search area during at least one sampling occasion (P_0). This quantity is located under “Probability of not finding a carcass (P0)” in the output file. It is computed for two different phenologies of carcass entry: uniform, i.e., a fixed daily probability that a fatality occurs, or pulsed, i.e., the carcass entry rate peaks in the middle of the study period. N_{max} (see “Option of using search data or not” above for definition of this notation) is located under “Maximum number of fatalities”, and \hat{N} is located under “Ad-hoc estimate of the number of fatalities”. Note that you have to sum values over the different turbine types to obtain the total estimated number of fatalities. The first set of values corresponds to carcasses within the search area. The second set of value corresponds to the values extrapolated using the correction factors (see “Extrapolation to a larger area” above).


```

carcassCMR ( version:2.0.2(2013-06-12) )                wed Sep 11 13:33:23 2013
----- Data summary -----
data filename: SIMUL_search.csv
surv filename: SIMUL_surv.csv
det filename: SIMUL_det.csv

Number of turbines of each type: 10 10
Duration of the persistence trial: 7 days

12 sampling occasions
20 sampled turbines out of a total of 20 turbines in the wind farm
Type1 : 10 sampled turbines
Type2 : 10 sampled turbines

Numbers of carcasses found:
by occasion: 1 0 1 2 3 0 0 0 0 2 5
by turbine : 1 1 1 0 1 2 1 1 1 2 0 0 0 0 1 0 1 0 1 0
Total      : 14

Persistence trial (duration: 7 days):
160 carcasses which persisted 4.75 days on average
Detection trial: 160 carcasses of which 98 were found

Model: Phi()P()without search data

Model Deviance= 305.3133
Number of estimated parameters: 4
Effective sample size: 40

----- Parameter estimates ( 12 bootstrap replications )-----
Daily persistence/detection probability:
              persistence                detection
      fresh      old      fresh      old
estimate std.err estimate std.err estimate std.err estimate std.err
Type1  0.8677  0.0194  0.8677  0.0194  0.6106  0.0341  0.6106  0.0341
Type2  0.8677  0.0194  0.8677  0.0194  0.6106  0.0341  0.6106  0.0341

Daily state transition probability: fresh to old
      estimate std.err
      0.0173  0.0136

-----
Probability of not finding a carcass given it is in surveyed area (P0):
-----
      Uniform entry rate Pulsed entry rate SE(unif) SE(pulse)
Type1          0.1653          0.1386  0.0241  0.0231
Type2          0.1653          0.1386  0.0241  0.0231
-----
Maximum number of fatalities (with risk threshold 0.05 )
-----
      Uniform entry rate Pulsed entry rate SE(unif) SE(pulse)
Type1        16.5329        15.8343  0.6448  0.5998
Type2         6.0420         5.7131  0.3018  0.2835
-----
Ad-hoc estimate of the number of fatalities
-----
      Uniform entry rate Pulsed entry rate SE(unif) SE(pulse)
Type1        15.3298        14.2970  0.9903  0.8753
Type2         4.2762         3.9656  0.3034  0.2671
-----
-----%%%%%%%%%%-----
Extrapolations to whole wind farm -----
-----
Maximum number of fatalities (with risk threshold 0.05 )
-----
      Uniform entry rate Pulsed entry rate SE(unif) SE(pulse)
Type1        16.5329        15.8343  0.6448  0.5998

```

Figure 8: Output file for models that do not use carcass search data, viewed in Microsoft Windows Notepad. The end of the output with the extrapolations to whole wind farm is omitted from this view.

About fatalityCMR

This displays the version number (2.0.3) and contact details for James E. Hines who is the maintainer of the software.

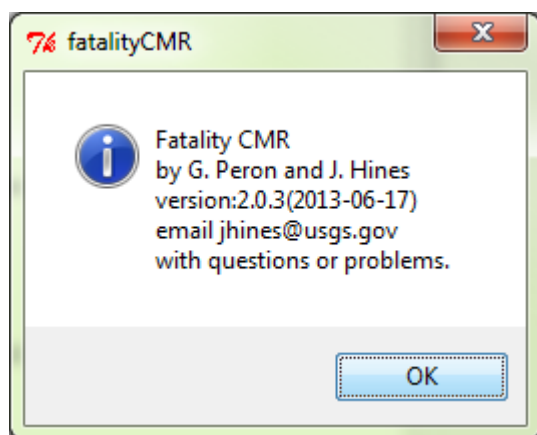


Figure 9: Popup windows that appears after clicking on 'About FatalityCMR'

Utility

We envision *fatalityCMR* being used for four primary purposes. First, fatality estimates can be used to quantify the level of required mitigation. For example, wind projects that kill eagles are often required to retrofit utility poles. Older utility poles cause eagle deaths by electrocution, and retrofitting them compensates for eagle deaths caused by the wind farm. Assuming a direct relationship between the number of retrofitted poles and the number of eagle deaths avoided, one can estimate the number of utility poles to retrofit. Second, proposed wind projects are often required to assess their potential impact on protected species as part of a permitting process. Predicting eagle take requires linking eagle use (measured in eagle-minutes in the U.S. Fish and Wildlife Service protocol) to eagle fatalities. In a Bayesian framework, this means updating the predictive model with new fatality estimates when those become available. Third, fatality

estimates from our software may be used adaptively to modify the operation of existing wind farms. For example, wind farms may have to alter or cease their operation once a threshold of take has been reached. Fatality estimates may be used to compare the risk to eagles of different operation modes, e.g., varying cut-off wind speeds, or times of day or year during which turbines are shut down. Fourth and last, our software, and specifically its data simulation capacity, can be used to design carcass search protocols and trial experiments (see Appendix). There is a tradeoff between field effort, cost, and expected precision of the fatality estimates (Péron *et al.* 2013). This tradeoff depends on the specifics of the wind project at stake, such as whether trial carcasses are easy to obtain or not, the remoteness or ease of access of the site, and the expected number of fatalities.

Acknowledgements

This work was supported by the U.S. Fish and Wildlife Service, and we thank B. Millsap and E. Bjerre for this support as well as guidance and useful discussions of carcass surveys. M. Huso and D. Dalthorp offered eventually important insight into the evidence of absence routine. Matt J. Clement made useful suggestions about an earlier version of this manual. We also thank James D. Nichols, William L. Kendall, Kimberley A. Peters and David S. Mizrahi.

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