R documentation
of 'SPACECAP-Package.Rd' etc.

July 9, 2014

`SPACECAP-package`	*A Program to Estimate Animal Abundance and Density using Bayesian Spatially-Explicit Capture-Recapture Models*

Description

SPACECAP is a user-friendly software package for estimating animal densities using closed model capture-recapture sampling based on photographic captures. This approach substantially deals with individual heterogeneity in capture probabilities resulting from the locations of traps relative to animal home range centres.

SPACECAP uses a Bayesian approach and Markov chain Monte Carlo simulation to generate samples from the posterior distribution of each parameter, as described by Royle et al (2009). This gives non-asymptotic inferences which are appropriate for small samples of capture data typical of photo-capture studies.

See Model and Priors for details of the model, Example files for the kind of data required, and SPACECAP for instructions on running the software.

For analysis of similar models using maximum likelihood methods, see Borchers and Efford (2008) and the **secr** package.

Details

Package:	SPACECAP
Type:	Package
Version:	1.1.0
Date:	2014-07-07
License:	GPL (>=2)
LazyLoad:	yes

Important changes to the output in version 1.1.0

The values for sigma, the scale parameter of the detection function, are now correctly reported. The units are those used for the trap and habitat pixel coordinates (usually meters).

Units for density are now animals per sq km, not animals per 100 sq km. The densities in the file 'pixeldensities_val_<time>.csv' are also in animals per sq km, not animals per pixel.

Analysis is much faster. Current version provided results at less than 50 per cent of the time taken in version 1.0.6 on some data sets.

Suggested Citation

PUBLICATION Arjun M. Gopalaswamy, Jeffrey A. Royle, James E. Hines, Pallavi Singh, Devcharan Jathanna, N. Samba Kumar and K. Ullas Karanth (2012). Program SPACECAP: software for estimating animal density using spatially explicit capture-recapture models. *Methods in Ecology and Evolution* 3(6): 1067-1072.

PACKAGE VERSION Arjun M. Gopalaswamy, Jeffrey A. Royle, Michael E. Meredith, Pallavi Singh, Devcharan Jathanna, N. Samba Kumar and K. Ullas Karanth (2014). SPACECAP: An R package for estimating animal density using spatially explicit capture-recapture models. Wildlife Conservation Society - India Program, Centre for Wildlife Studies, Bengaluru, India. Version 1.1.0.

The software could be cited as follows: "We used the software SPACECAP (Gopalaswamy et al. 2012) version 1.1.0 (Gopalaswamy et al. 2014) for the analysis".

Author(s)

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References

Borchers, D. L., and M. G. Efford. 2008. Spatially explicit maximum likelihood methods for capture-recapture studies. *Biometrics* 64:377-385.

Royle, J. A., K. U. Karanth, A. M. Gopalaswamy and N. S. Kumar. 2009. Bayesian inference in camera trapping studies for a class of spatial capture-recapture models. *Ecology* **90(11)**, 3233-3244.

SPACECAP	*Fits spatially-explicit capture recapture models*

Description

Function SPACECAP is the workhorse of the pkgSPACECAP package. It opens a Graphical User Interface (GUI) where the user selects the files containing the capture-recapture data, selects options for the model to run, and specifies the variables for the MCMC estimation. MCMC samples from the posterior distributions of the parameters are generated and saved as files, together with summary statistics and kernel density plots.

Usage

```
SPACECAP()
```

Details

Installing SPACECAP Version 1.1.0

You must have a recent version (R 2.15.3 or higher) of program R installed on your computer. If necessary, go to http://www.r-project.org/, select a mirror, then download and install R for your platform.

Launch R, and at the ">" prompt type

```
install.packages("SPACECAP")
```

and press Enter. SPACECAP must be upper case and in quotes. You will be asked to select a CRAN mirror and may need to confirm that R should create a personal library for your packages. **SPACE-CAP** depends on **coda**, and that should be installed automatically at the same time. You only need to install **SPACECAP** once.

SPACECAP stores its output in subfolders of R's working directory. You can set the working directory with the File > Change dir... option in the console or by typing setwd(choose.dir()) and browsing to the folder you want the output to go to.

To launch the **SPACECAP** GUI, you need to have R open, then at the ">" prompt enter

```
library(SPACECAP)
SPACECAP()
```

Note the empty parentheses () after SPACECAP in the second line.

You will not be able to work in the R Console while the the SPACECAP GUI is open. If you want to work in R while the analysis is running, you can open another instance of the R Console. You can even have several SPACECAP analyses running at the same time, by launching them from different R instances, and they will use different cores on a multicore computer.

SECR Analysis using SPACECAP

Running an SECR Analysis in **SPACECAP** involves four steps:

1. Setting up the input files
2. Selecting the appropriate model combination
3. Selecting the Markov chain Monte Carlo (MCMC) settings
4. Clicking "Run" on the main menu bar.

STEP 1: SETTING UP THE INPUT FILES FOR ANALYSIS

SPACECAP requires three input files:

1. Animal Capture File (Animal ID, trap ID, capture occasion)

2. Trap Deployment File (Trap ID, location and deployment record)

3. State-space File (the Potential Animal Home Range Center locations and habitat suitability indicator for these home range centers)

See the Example files page for more details and examples.

These three data files can be created using spreadsheet applications such as Microsoft EXCEL or LibreOffice Calc. They must be saved in ASCII comma separated format *(.csv)*, because **SPACECAP** can only read these types of input files.

INPUT FILE 1: Animal Capture Details

This is a table with 3 columns: Location Number, the Animal Identity Number and the Sampling Occasion number, in that order. Note that these are all "number" fields: use simple integer numbers.

Each individual captured should be given a unique identification number, ranging from 1 to n, where n is the total number of individuals included in this file. In the example below, the records have been sorted by ANIMAL_ID to facilitate checking that no numbers are missing.

Location Numbers must correspond to the numbers in the Trap Deployment file.

If only 6 animals were photo-captured and identified, the **INPUT FILE 1** for **SPACECAP** might look like this:

LOC_ID	ANIMAL_ID	SO
11	1	14
15	2	12
9	3	20
1	4	17
5	5	13
7	6	17
8	6	16

For example, the first row of data tells us that Animal ID no 1 was captured at Location ID 11 on the 14th sampling occasion.

The first row of the file must have the exact column headings as shown above, or it will not be recognized by **SPACECAP**.

INPUT FILE 2: Trap Deployment Details

The first column of this file has the Location Number. The next two columns have the X and Y coordinates of the trap location: see the example below. Use a projected coordinate system (ie, in meters, not degrees), such as UTM (Universal Transverse Mercator) or your national grid system.

After these first three columns, there is one column for each trapping occasion. Here, "1" means that a trap was operating at that location on that occasion, "0" means that no trap was operating. You do not have to have a trap at every location for the whole period. In particular, trap malfunction, theft, vandalism, etc. can be accounted for.

An example TRAP DEPLOYMENT DATA file is shown below. This file has 16 locations, but there were only 4 traps, which were moved between locations.

LOC_ID	X_Coord	Y_Coord	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	619303	1325966	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
2	624151	1325013	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
3	624722	1323864	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
4	621806	1322453	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
5	622451	1320137	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0
6	622599	1317937	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0
7	623179	1315941	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	625156	1315587	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0
9	626022	1314224	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0
10	627568	1315494	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0
11	619604	1324739	0	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	0	0
12	621478	1324515	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0
13	623317	1323989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
14	624406	1321603	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
15	624482	1320577	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
16	629229	1319793	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1

The table shows that the first four locations were operational during sampling occasions 1-5, except that the trap at location 3 was not working on occasion 4. No traps were operational at these sites

on occasions 6 to 20.

Again, the first row must have column headings as shown in the example above.

INPUT FILE 3: Potential Home Range Centers

This file contains the locations of possible home range centers for all the animals which might be detected by our traps. These are represented by a large number of equally spaced points or *pixels* in the form of a grid. This grid can be produced by GIS software such as ArcView or QGIS. See the figure on the Example files page.

To generate this file, you need to decide (1) the extent of the state space, (2) the size of the pixels, and (3) what habitat would be suitable as a home range center for your species.

The extent of the area covered by the file must be big enough to include the home ranges of animals with a reasonable probability of being captured. Under the Gaussian hazard model, animals with home range centers more than 3 or 4 times the detection function scale parameter, sigma, from the nearest trap have a negligable probability of being caught. For the negative exponential model we think 3-4x sigma should also be adequate but recommend checking this for specific data sets. Use a guestimate of the home range radius for a preliminary run, and check against the value of sigma produced (see **Things to check** below).

In principle, the state space cannot be too large, but in practice a large area will need a higher value for data augmentation (see below) and will run more slowly. Note that the estimate of density does not depend on the area of the state space, provided that is large enough.

Pixel size is related to home range size. For the animals captured, the software will estimate the location of the home range center, but has only pixel centers to choose from. This clearly would not work well if pixels were larger than home ranges. Pixel areas roughly (1/16) - (1/32) of a typical home range area would be appropriate.

Note the area of the pixel used, as that must be entered when running **SPACECAP** and a mistake there will result in a wrong answer for the density.

The potential home-range centers data file consists of a 3 column table. The first two columns are the X and Y coordinates (using the same coordinate system as the trap location file) of the center of each pixel in the state-space. The third column is a habitat suitability indicator, with "1" if the pixel centre lies within suitable habitat or with "0" otherwise. The first few rows of such a file is given below (the actual file will have thousands of rows):

X_COORD	Y_COORD	HABITAT
611734	1299581	1
612301.6	1299583	1
612869.2	1299585	0
613436.9	1299587	0
614004.5	1299589	0
614572.2	1299591	0
615139.8	1299593	0
615707.5	1299595	1
616275.1	1299597	1
616842.8	1299600	0
617410.4	1299602	1
617978.1	1299604	1
618545.7	1299606	1

Again, the column headings in the first row must be exactly as shown in the example.

Entering the file names in SPACECAP

The "Input Data" panel is the top left portion of the **SPACECAP** window. Use the Browse buttons to select each of the three input files in turn.

Enter the area of the pixels created for the potential home range centers file (in sq km) in the box below the file names.

Click on "OK" in the "Input Data" panel and check the frame at the bottom of the window for status or error messages. To edit your selection, just click on the "Edit" button and start the selection all over again.

STEP 2: SELECTING THE APPROPRIATE MODEL COMBINATION FOR ANALYSIS

The Model Definition panel of **SPACECAP** consists of a set of options to select an appropriate model combination for the Spatial-Capture Recapture Analysis. Model options that are "grayed out" are not available with the current version of **SPACECAP**.

The model choices are:

1. **Trap response present OR Trap response absent** The "Trap response present" option implements a local or "trap-specific" behavioral response under which the probability of encounter in a trap increases (or decreases) after initial capture in that specific location. This is in contrast to the conventional "global" behavioral response which implies a response to all traps everywhere after being caught once.

2. **Spatial Capture-Recapture OR Non-spatial Capture-Recapture** Select "Spatial Capture-Recapture" for running a spatially explicit capture-recapture analysis, or "Non-spatial Capture-Recapture" for running a conventional capture-recapture analysis (this is equivalent to the Null Model "M0" in non-spatial CR analysis)

Note that including a *location-specific* trap response in a *non-spatial* model may lead to spurious results, as the trap response coefficient will pick up the spatial structure in the data.

3. **Half Normal OR Negative Exponential**

See the discussion of detection functions on the Model and Priors help page. The half normal detection function is generally a good fit to the data. This has no effect for non-spatial analysis.

4. **Bernoulli (binary) OR Poisson encounter process** Currently the analysis is run with the Bernoulli encounter model in which the probability of success is derived as the probability of a positive response under a Poisson encounter rate model. This motivates use of the complementary log-log link which relates encounter probability to distance and other covariates.

After the model definition is complete, click on "OK" and check the frame at the bottom for status or error messages. To edit your selections, just click on the "Edit" button, change your model definition and click on "OK" again.

STEP 3: SETTING THE MARKOV-CHAIN MONTE CARLO (MCMC) PARAMETERS

SPACECAP uses a Markov-Chain Monte Carlo simulation algorithm written in R to estimate the parameters of the SECR models of Royle et al (2009). (Wikipedia has a short page on Markov chain Monte Carlo methods.) The relevant settings can be set in the MCMC simulation settings panel of **SPACECAP**.

No of iterations - This defines the total number of MCMC iterations for the analysis.

Burn-in - This defines the number of initial values to discard during the MCMC analysis. The Geweke diagnostic (see below) will indicate if this is adequate.

Thinning - This defines the proportion of iterations included in the output. If thinning = 10, only 1 in 10 of the iterations will be stored.

The number of values returned will be (iterations - burn-in) / thinning. The goodness-of-fit calculations are run for each value returned, and these are slow, so you should aim for about 10,000 values returned.

It is a good idea to do short runs to begin with (say 10,000 iterations with 5,000 burn-in) and do a much longer run to get your final results (at least 100,000 iterations with enough burn-in to give adequate Geweke statistics).

Data augmentation - This is the maximum number of uncaught animals in the whole state space, and sets an upper limit to the estimate of N for the MCMC run. If it is too low, the estimate of N and (hence the density) will be incorrect. On the other hand, the run time increases linearly with the data augmentation value. Try an initial value of 5 to 10 times the number of animals captured, and check the output (see the **Things to check** section below) and rerun with a higher value if necessary.

See the **Priors for N and psi** section of the Model and Priors page.

After the MCMC simulation values have been specified, click on "OK" and check the frame at the bottom for status or error messages. To edit these settings, just click on the "Edit" button, edit these values and click on "OK" again. You are now all set to start the analysis.

STEP 4: Running the analysis

Click on "Run" in the top menu bar. This will start the analysis and you will see a progress bar indicating the status of the analysis. Samples from the MCMC chain are reported in the bottom panel in the **SPACECAP** window and in the R Console.

Currently, an analysis of the example data set with the default model, 50,000 iterations, 20,000 burnin, thinning by 10, and data augmentation of 350 takes about 9.5 hours on a fast computer.

Results

The posterior density estimates along with standard errors appear as a table in the middle panel of the **SPACECAP** window and in the R Console when the analysis is complete. This table also reports estimates of parameters lam0, sigma, and psi. For a non-spatial analysis, sigma will be reported as NA. If the analysis was run with trap response present, beta, p1, and p2 are reported; the probability of capture (if trap to home range center distance is zero) = p1 before the first capture and p2 afterwards. With no behavioural response, these will be equal, and beta will be zero.

SPACECAP produces a number of files which you will find in a folder called "output_<timestamp>" in your working directory (use getwd() so see your working directory path):

info_<timestamp>.txt	a text file with background information and diagnostics.
param_val_<timestamp>.csv	the full MCMC chain for each parameter
summary_stats_<timestamp>.csv	summary statistics for each parameter
pixeldensities_val_<timestamp>.csv	estimates of density for each of the pixels in the potential home-range centers input
detectionFunction_<timestamp>.jpg	a plot of the detection function (spatial models)
density_lam0_<timestamp>.jpg	a density plot for the lam0 parameter
density_N_<timestamp>.jpg	a density plot for N
density_psi_<timestamp>.jpg	a density plot for psi
density_sigma_<timestamp>.jpg	a density plot for sigma (spatial models)
density_beta_<timestamp>.jpg	a density plot for beta (behavioural response models)

Things to check

Data augmentation: Check the density plot for psi; the right-hand tail should not get up to 1. The same applies to the density plot for N; the tail should not approach the upper limit of the prior. If it does, rerun the analysis with a higher value for data augmentation.

State-space extent: For spatial models, check the detection function plot and the detection probability for the smallest trap to state space edge distance. The detection probability for any animals with home ranges outside must be very small.

Convergence: The Geweke test (see `geweke.diag`) compares the means of the first 10% and the last 50% of the values in the chains. The z-scores are in the info file and should all be between -1.6 and +1.6. If not, rerun with a longer burn-in period.

Sample size: The values in the chain are not independent, and successive values are correlated. The effective sample size is the sample size adjusted for this autocorrelation (see `effectiveSize`). Effective sizes of several hundred are adequate for point estimates (mean or median), but many thousand are needed to get good estimates of the 95% HDI and to get smooth density curves. If necessary, run with more iterations (and higher thinning).

Model fit: Values of the Bayesian P-value (Royle et al. 2011) close to 0 or 1 imply that the model is inadequate. No simple solution to this, you will have to think of a better model!

Author(s)

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References

Geweke, J. 1992. Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. In: Bayesian Statistics, **4** (Bernardo, J. M. et al., Eds), 169-193. Oxford University Press.

Royle, J. A., K. U. Karanth, A. M. Gopalaswamy and N. S. Kumar. 2009. Bayesian inference in camera trapping studies for a class of spatial capture-recapture models. *Ecology* **90(11)**, 3233-3244.

Royle, J. A., M. Kery and J. Guelat. 2011. Spatial capture-recapture models for search-encounter data. *Methods in Ecology and Evolution* **2**:602-611.

Examples

```
SPACECAP()
```

| Model and Priors | *The* **SPACECAP** *model and prior distributions* |

Description

This page describes the model implemented by SPACECAP, its parameters and prior distributions. The model is described by Royle et al (2009).

The Spatial Capture-Recapture Model and its Parameters

The model considered in the current version of **SPACECAP** applies to binary observations y(i,j,k) for individual "i", trap "j" and sample occasion (e.g., night) "k". The model is a type of binary regression model, similar to logistic regression, in which

$$y(i, j, k) \; Bernoulli(p(i, j, k))$$

Here p(i, j, k) is the probability of detecting an individual "i", at trap "j" and sample occasion "k". The probability p(i,j,k) is then related to covariates of interest by applying a suitable transformation. In **SPACECAP** we make use of the complementary log-log link transformation. Thus, the simplest possible model (with no spatial component) is:

$$cloglog(p(i, j, k)) = b0$$

where b0 is a parameter to be estimated. The inverse of the cloglog transformation is:
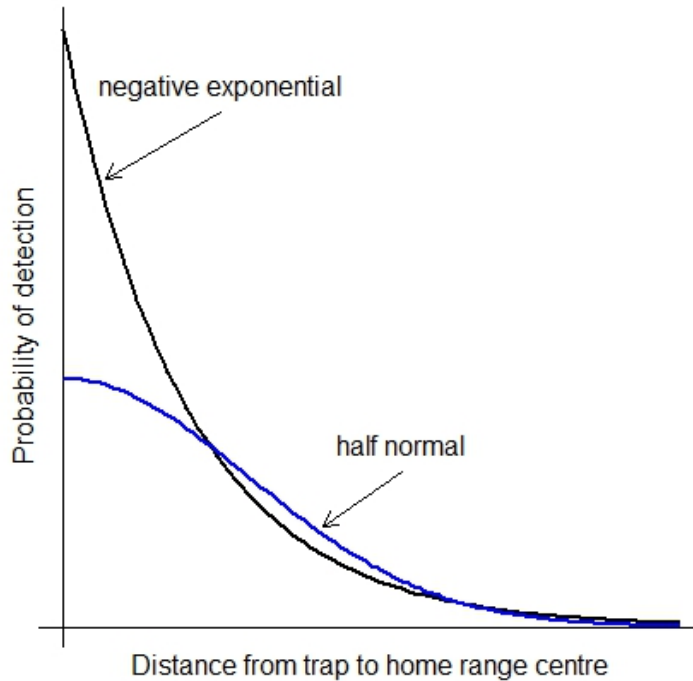
$$p(i, j, k) = 1 - exp(-exp(b0))$$

This particular function ('hazard model' in distance sampling) arises by considering the binary observations to be formally reduced from a Poisson encounter frequency model (see Royle et al 2009 for details). That is, p(i,j,k) is the Pr(at least 1 encounter in a trap) under the Poisson model.

Spatially-explicit models assume that the probability of detection decreases as the distance between the trap and the center of the animals home range increases:

$$cloglog(p(i, j, k)) = b0 + b2 * f[dist(s(i), u(j))]$$

where s(i) is the location of the home range centre and u(j) the location of the trap and b2 is a regression coefficient.

The Gaussian hazard detection function uses the squared distance between s(i) and u(i), and then b2 = -1/(2*sigma^2), where sigma is the usual scale parameter of the normal (Gaussian) distribution. **SPACECAP** can also fit a negative exponential hazard function using distance (not squared), when b2 = -1/sigma and sigma is the scale parameter of the negative exponential distribution. The difference in shape of the two functions is shown in the figure below:

The most general model that **SPACECAP** presently allows is a model in which

$$cloglog(p(i, j, k)) = b0 + b1 * x(i, j, k) + b2 * f[dist(s(i), u(j))]$$

In this expression x(i,j,k) is an indicator of previous capture of individual i in trap j. Thus "b1" is a measure of the behavioral response of an animal to a specific location, ie, it is attracted to or avoids a location where it was once detected, but does not respond to traps at other locations where it has not been detected (see Royle et al 2009 for more details).

The user provides a file of potential home range centers (see Example files). These constitute the *state space*, S, for the variable s(i). In **SPACECAP**, the parameter N is the number of home range centers located in S (see **Priors for N and psi** below).

Density, D = N/||S|| where ||S|| is the area of the state-space. The units for Density, D, are animals per sq km.

SPACECAP also reports several derived parameters:

lam0 = exp(b0), where b0 is the intercept of the regression, is the expected encounter rate of an individual whose home-range centre is exactly at the trap location.

beta = b1, is the regression coefficient that measures the behavioral response.

psi = the ratio of the number of animals actually present within S to the maximum allowable number (see next section).

Priors for N and psi

SPACECAP uses data augmentation (Royle et al 2007), whereby additional all-zero capture histories are appended to the data to represent animals not captured. Since the true number of animals present in the state space but not captured is unknown, a sufficiently large number of all-zero histories are added, some of which correspond to real uncaught animals and some to animals which are not available for capture ("phantoms").

N is the number of real animals in the space state; psi is the probability that an animal in the augmented data set is a real animal in the space state. The expected value of N is psi x M, where M is the total number of capture histories in the augmented data set.

psi has a uniform Beta(1, 1) prior.

The variable indicating whether a capture history refers to a real animal (z = 1) or a phantom (z = 0) is simulated as z ~ Bernoulli(psi), and N = sum(z). The uniform prior on psi translates into a discrete Uniform(0, M) prior on N.

This prior is intended to be uninformative, which requires that M » N. The user should check after an estimation run that the distribution of N does not approach M, or equivalently that psi does not approach 1, by inspecting the density plots generated (see **Things to check** on the SPACECAP page). We recommend that the value of M be set such that psi may be estimated to be between 0.2-0.8.

Priors for the coefficients in the linear predictor

All the coefficients in the linear predictor have improper flat priors on [-infty, infty] for a suitable transformation of the parameter.

The intercept is log(lam0), where lam0 is the expected number of captures of a single animal in a single trap on a single capture occasion, when the distance between the trap and the center of the animal's home range is zero. The flat prior on log(lam0) implies an uninformative scale prior on lam0;i.e. proportional to 1/lam0.

If a behavioral effect is included in the model, such that encounter rate for a specific animal and trap location changes after the first capture, an indicator variable is included in the linear predictor, with value 0 before the first capture and 1 thereafter. This coefficient, beta, has a flat prior.

For spatially explicit models, the encounter rate is assumed to decline as distance between trap and home range center increases. The distance variable in the linear predictor is either this distance (for a negative exponential detection function) or the squared distance (for a half-normal (Gaussian) detection function). The coefficient of this variable is either -1/sigma (negative exponential) or -1/(2*sigma^2) (half normal) where sigma is the usual scale parameter of the distribution. Sigma has a flat uniform [0,infty] prior.

Priors for location of home range centers

This has a uniform prior, ie, all pixels (potential home range centers) having good habitat as indicated in the input data have equal probability. (Pixels with bad habitat have zero probability of hosting a home range center.)

References

Royle, J. A., R. M. Dorazio, and W. A. Link. 2007. Analysis of multinomial models with unknown index using data augmentation. *Journal of Computational and Graphical Statistics* **16**:67-85.

Royle, J. A., K. U. Karanth, A. M. Gopalaswamy and N. S. Kumar. 2009. Bayesian inference in camera trapping studies for a class of spatial capture-recapture models. *Ecology* **90(11)**, 3233-3244.

Example files   *Example data files*

Description

The installation of **SPACECAP** includes a set of three example data files for a camera trap study of tigers. To find the location of the **SPACECAP** files, use

`find.package("SPACECAP")`

The data files are in the 'extdata' subdirectory. They are Comma Separated Variable (.csv) files which you can open in a text editor or in a spreadsheet program. Copy these files to a location outside the R library folder if you want to work with them.

The capture history file

This is called 'tigerCH.csv'. The columns are headed "LOC_ID", "ANIMAL_ID", and "SO", all in capitals and with underscores instead of spaces. **SPACECAP** will not accept capture history files without these exact column headings.

All the entries are simple integers. **SPACECAP** cannot work with alphabetical or alphanumeric IDs, so don't use "TIG02" or "RIVER21". There should be no missing values.

LOC_ID is the location number and must match the LOC_ID in the Trap Deployment file.

ANIMAL_ID identifies the individual animal captured. These must go from 1 to n, where n is the number of animals included in this file. There must be no gaps in the numbering; be careful if you decide to analyse a subset of your data and remove records before the period selected. This file is sorted by ANIMAL_ID to facilitate checking (though the order of the rows is not important for the analysis).

SO is the occasion number that the capture occured. Occasion numbers must correspond to the occasions in the Trap Deployment file.
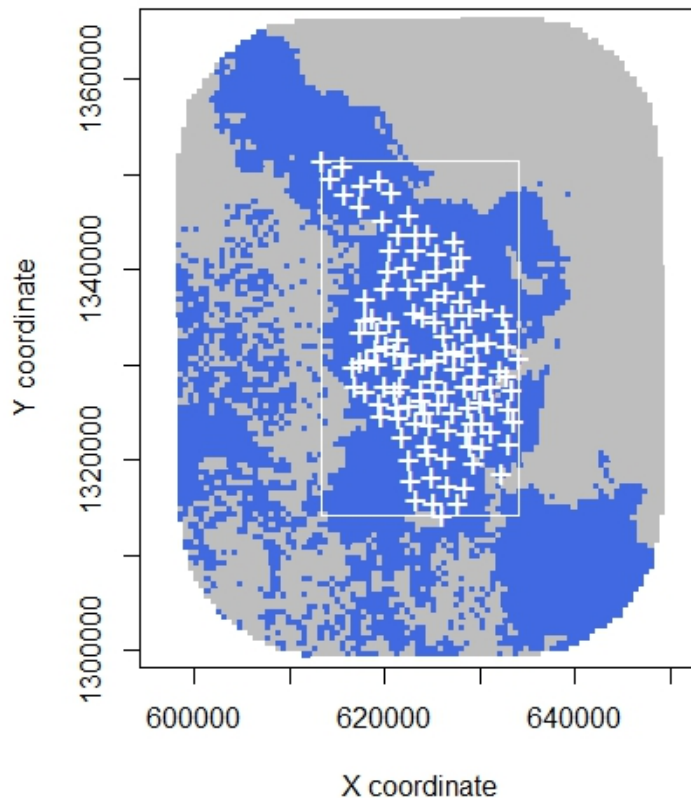
The trap deployment file

This is called 'tigerTraps.csv'. The first three columns are headed "LOC_ID", "X_COORD", and "Y_COORD" and the remaining columns are headed 1 to 48, as there were 48 capture occasions for this study. Your trap location file must have the same column headings.

LOC_ID is the location number and goes from 1 up to the total number of locations, with no gaps.

X_COORD and Y_COORD are the coordinates of the locations using the UTM (Universal Transverse Mercator) coordinate system. You can use any projected coordinate system using meters (but not latitude and longitude in degrees). The traps are shown by "+" symbols in the figure below.

Following these, there is one column for each trapping occasion. Here, "1" means that a trap was operating at that location on that occasion, "0" means that no trap was operating.

The potential home range centers file

This is called 'tigerHabitat.csv'. The columns are headed "X_COORD", "Y_COORD", and "HABITAT"; again these column headings are essential if the file is to be recognized by **SPACE-CAP**.

The file covers the whole area where animals captured in our traps could have their home range centers. In this case, it's an area extending 14km beyond the rectangle containing the traps - see the figure above. This area is represented by 9961 pixels, each with an area of 0.336 sq km.

The first two columns in the file give the coordinates of the center of each pixel, using the same coordinate system (UTM) as the trap locations.

The third column indicates whether the pixel has suitable habitat for the animal (1) or not (0). Pixels with suitable habitat are coloured blue in the figure above.

Analysing the example data

See the SPACECAP help page for instructions. Load the three example files and enter the pixel area (0.336 sq km). Choose your model and the number of iterations, burn-in and thinning. Data augmentation of 350 is adequate.

A run with the example data and the default model, with 50,000 iterations total, 20,000 burn-in, thinning by 10, and data augmentation of 350 took 9.5 hours on a modern desktop. Convergence was good and effective sample sizes 300 to 500. Data augmentation was adequate, and detection probability beyond the edge of the state space was less than 3E-13. The density estimate was 0.15 animals per sq km. Estimates of detection parameters were sigma = 2,020 m and lam0 = 0.015. More iterations would be needed to get reliable 95% credible intervals.

References

Royle, J. A., K. U. Karanth, A. M. Gopalaswamy and N. S. Kumar. 2009. Bayesian inference in camera trapping studies for a class of spatial capture-recapture models. *Ecology* **90(11)**, 3233-3244.

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