Setting up data for analysis with secr

Gather SCR data

SCR surveys use detectors at fixed locations to record the presence of individually identifiable animals at those locations. Detectors can be camera-traps, hair snares and dung surveys, live-captures, or acoustic detectors.

Set up data

The R package `secr` provides methods for estimating animal density from SCR data under many different conditions. This sheet summarizes getting your data into the format `secr` wants.

Analyze data

Once the data has been set up, use it to build SCR models and extract results on animal density and abundance, detectability, and important covariates.

(1) Make the detector/trap file

Each line of `trapfile` contains the location of each detector (e.g. camera), plus any extra information about that detector.

TrapID	X	Y	Effort	/	tri	temp
A1	0	0	10 20	/	0.6	25
A2	5	0	10 19	/	0.9	23
A3	0	5	0 20	/	0.8	31

1 **TrapID**, **X**, and **Y** must be specified in the order given. **X** and **Y** must be in UTM coordinates.

2 **Effort** records number of days each detector recorded for (optional). One value per occasion, separated by white space

3 A column of "/" indicates everything all columns the right of this column contain covariates (optional, only use if covariates used).

4 Other variables record values of any covariates at the traps (optional).

Trap-specific variables only needed if detection function parameters vary across traps (`g0, lambda0, sigma`).

If using multiple sessions (see below), need one file per session.

Save as a .csv or .txt file to read into R later.

Sessions

A **session** is a sampling block that is treated as **independent.**

Can be spatial (arrays far apart enough that no animals are detected on both) or temporal.

```
ch <- read.capthist(
  captfile="ch.csv",
  trapfile =
  c("sess1.csv",
  "sess2.csv")
my_mask <-
 make.mask(traps(ch))
```

Session ID is in `captfile`, one trap file per session, and `make.mask` works as before (traps object is now a list).

Detector types

"**multi**" - animals can be detected at most once across all detectors in each occasion.

"**proximity**" - animals can be detected at most once at each detector in each occasion.

"**count**" - animals can be detected any number of times at each detector in each occasion.

See `?detector` for others.

(2) Make the capture history file

Each line of `capthist` contains one detection, with ID variables recordings information about that detection.

Session	Animal	Occasion	TrapID
1	z001	1	A2
1	z174	2	A1
1	z024	1	A1

1 Each detection is recorded as a **session** identifier, **animal** identifier, **occasion** identifier.

2 Each detection includes a detector identifier, either as **trapID** (as above) or as X- and Y-coordinates (replace **trapID** with two columns **X**, and **Y)**

If you only use one session or occasion, include a column of 1's (the columns must appear in `capthist`).

Save as a .csv or .txt file to read into R later.

(5) Add mask covariates

Mask covariates are used to model density (`D`), not detection parameters (`g0, lambda0, sigma`).

Adding covariates from a dataframe

```
covariates(my_mask) <-
 data.frame(elevation =
 c(0,110,80,30), temp =
 c(25,26,36,37)
```

can also add covariates before `read.mask` as in the bottom box in (4)

Adding covariates from a spatial data source

Assumes you have covariates stored in a spatial data source, which can be e.g. an ESRI polygon shapefile, SpatialPolygonsDataFrame, SpatialGridDataFrame (called `spdata` below)

```
addCovariates(object = ch,
 spatialdata = spdata,
 columns = c("elevation",
 "temp"))
```

Buffers

Choose buffer width large enough that animals beyond the buffer have **negligible chance** of being detected.

Rule of thumb is buffer = 4*sigma. Can get a rough estimate of sigma with `RPSV(ch,CC=TRUE)`.

Spacing

Too few grid points means a poor approximation of continuous surfaces, too many points slows down model fitting.

Rule of thumb is spacing < 1*sigma, and try for 1000-3000 grid points.

(3) Read it all in

Load both your `trapfile` and `capthist` files with `read.capthist`.

```
ch <- read.capthist(captfile = "ch.csv",
  trapfile = "tf.csv", detector = "count",
  fmt = "trapID", trapcovnames = c("tri",
  "temp), binary.usage = FALSE)
```

Important options

captfile, trapfile - the CSV files made in the previous steps.

detector - specifies the type of detector you have. Most camera trap surveys will use "multi", "proximity" or "count".

fmt - if trapID used as detector identifier in `capthist` then `fmt = "trapID"`. If X and Y used then `fmt = "XY"`.

trapcovnames - names of covariates in `trapfile`

binary.usage - indicates continuous effort variable present.

(4) Make the habitat mask

A mask is a **set of square grid cells** representing habitat **in the vicinity of detectors** that is **potentially occupied**.

A **mask object** is a 2-column dataframe, each row gives the **x- and y-coordinates** of the centre of one cell.

Constructing masks from detectors with `make.mask`

```
my_traps <- traps(ch)
my_mask <- make.mask(my_traps, buffer =
 24000, spacing = 1000, type = "trapbuffer")
```

Makes a grid extending 24km N, S, E and W of any detectors

Puts mask points down at 1km intervals within the grid

Just 4 mask points for illustration

Make your own mask and `read.mask`

```
my_mask_df <- data.frame(X = c(0,1,0,1), Y
 = c(0,0,1,1), elevation = c(0,110,80,30))
my_mask <- read.mask(data = my_mask_df,
 spacing = 1)
```

Remember that `my_mask_df` must include the buffer region.

X	Y	elevation
0	0	0
1	0	110
0	1	80
1	1	30

Optional covariates - can be same or different to trap covariates

Learn more about the material shown here with the secr vignettes: secr-overview, secr-datainput, secr-tutorial, secr-habitatmasks (available at https://www.otago.ac.nz/density/SECRinR.html)

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Analyzing data
with secr

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Set up data

The R package `secr` provides methods for estimating animal density from SCR data under many different conditions. First, you need to get your data into the format `secr` wants.

Analyze data

This sheet shows you how to build SCR models and extract results on animal density and abundance, detectability, and important covariates.

(1) Read in SCR inputs

To build models in secr you need to have already loaded:

1 A “capthist” object, which contains the capture histories and the trap locations

2 A “mask” object, a set of grid cells that defines the area that is potentially occupied and not so far from any trap locations that observations are extremely unlikely.

```
ch <- read.capthist(captfile = “ch.csv”,
  trapfile = “tf.csv”, detector = "count",
  fmt = "trapID")
my_traps <- traps(ch)
my_mask <- make.mask(my_traps, buffer =
 24000, spacing = 1000, type =
 "trapbuffer")
```

See the guide on “Setting up data” for more details

Detection models

A core SCR assumption is that detection probability (or frequency) **decreases with distance** to activity centre.

Shape is given by the **detection function** (`detectfn` in `secr.fit`), with a small number of parameters to be estimated.

`g0` detection models

These model the **probability** of detection. The most common option is “half-normal” (HN), with parameters `g0` and `sigma`, see `?detectfn` for others.

```
m0a <- secr.fit(ch, detectfn = "HR",
  mask = my_mask, model = list(D ~ 1,
  g0 ~ 1, sigma ~ 1, z ~ 1))
```

HR function, another option

HR has an extra parameter z

`lambda0` detection models

These model the **hazard** of detection. They are useful for quicker computation (especially for “count” detectors).

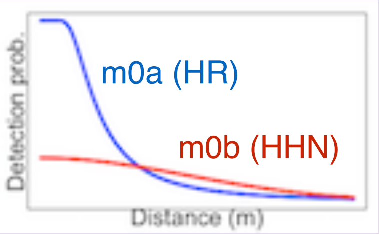
The most common option is “hazard half-normal” (HHN), with parameters `lambda0` and `sigma`, see `?detectfn` for others.

```
m0b <- secr.fit(ch,
  detectfn = "HHN",
  mask = my_mask, model
  = list(D ~ 1, lambda0
  ~ 1, sigma ~ 1))
```

`lambda0` and `g0` are mathematically equivalent and the choice between them is not crucial. Half-normal (HN or HHN) are good default options.

Plot detection functions

`plot(m0a)`



(2) Fit a model

SCR models jointly estimate two spatial models, one for animal density and one for the detection process.

Run SCR models with `secr.fit`, starting with the simplest possible model.

```
m0 <- secr.fit(ch, detectfn = "HHN",
  mask = my_mask, model = list(D ~ 1,
  lambda0 ~ 1, sigma ~ 1))
```

Detection function parameters, `lambda0` control encounter rate, `sigma` controls range of animal movement

density, ~ 1 for constant density

! A “~ 1” means no covariate effects, and a single parameter is estimated for each of `D`, `lambda0`, and `sigma`

Including covariates

Any of `D`, `lambda0`, and `sigma` can depend on covariates and passed to `secr.fit`

```
m1 <- secr.fit(ch, detectfn = "HHN",
  mask = my_mask, model = list(D ~ elev,
  lambda0 ~ water, sigma ~ 1))
```

Encounter hazard `lambda0` depends on whether trap is close to water

Density depends on elevation

Very flexible e.g. can do regression splines with `D ~ s(elev)`

! Covariates on density (`D`) must be attached to the mask object, covariates on detection parameters (`g0`, `lambda0`, `sigma`) must be attached to the trap object.

```
coef(m1)
```

```
Beta parameters (coefficients)
                    beta    SE.beta         lcl        ucl
D             -9.5184241 0.27550956 -10.0584129 -8.9784353
D.elev         0.2443394 0.39160813  -0.5231985  1.0118772
lambda0       -4.4403272 0.17332682  -4.7800415 -4.1006128
lambda0.WaterYes  0.2277942 0.27803197  -0.3171385  0.7727268
sigma          8.8583684 0.08326936   8.6951634  9.0215733
```

`secr` has a number of automatically generated covariates. These can be referred to directly in formulae without needing to be constructed. These include `b` (learned animal responses to detectors), `k` (site learned response), `bk` (animal x site learned response), `session`, `t` (time factor, one per occasion), `T` (time trend, linear over occasions)

(3) Inspect model output

To view model output use `print(m0)`

```
N animals       :  14
N detections    :  99
N occasions     :  1
Count model     :  Poisson
Mask area       :  211725 ha

Model           :  D~1 lambda0~1 sigma~1
Fixed (real)    :  none
Detection fn    :  hazard halfnormal
Distribution    :  poisson
N parameters    :  3
Log likelihood  :  -210.31
AIC             :  426.6199
AICc            :  429.0199

Beta parameters (coefficients)
             beta    SE.beta        lcl       ucl
D       -9.510329 0.26789360 -10.035391 -8.985267
lambda0 -4.387800 0.16494892  -4.711094 -4.064506
sigma    8.852195 0.08157649   8.692308  9.012082

Variance-covariance matrix of beta parameters
                   D       lambda0         sigma
D        0.0717669818 -0.0006783997 -0.0008909627
lambda0 -0.0006783997  0.0272081446 -0.0088657027
sigma   -0.0008909627 -0.0088657027  0.0066547240

Fitted (real) parameters evaluated at base levels of covariates
         link     estimate  SE.estimate          lcl          ucl
D         log 7.408266e-05 2.020773e-05 4.382129e-05 1.252414e-04
lambda0   log 1.242805e-02 2.064016e-03 8.994936e-03 1.717147e-02
sigma     log 6.989717e+03 5.711466e+02 5.956917e+03 8.201582e+03
```

`coef(m0)`

`vcov(m0)`

`predict(m0)`

Main results are in this last table. Density is in animals per hectare.

Model selection

Model selection is by AIC or AICc (small sample size)

```
AIC(m0,m0a,m0b,m1)
```

Goodness-of-fit tests for SCR are not developed yet.

Multi-session models

```
ch <- read.capthist(captfile=“ch.csv”,
  trapfile = c(“sess1.csv”, “sess2.csv”)
my_mask <- make.mask(traps(ch))
```

Can run `secr.fit` as in (2). Parameters are shared between sessions by default but any of `D`, `lambda0`, and `sigma` can be session-specific.

```
m2 <- secr.fit(ch, detectfn = “HHN", mask =
  my_mask, model = list(D ~ 1, lambda0 ~ 1,
  sigma ~ session))
```

Covariate effects can vary by session.

```
m3 <- secr.fit(ch, detectfn = “HHN",
  mask = my_mask, model=list(D ~
  elev*session, lambda0 ~ 1, sigma ~
  session))
```

Learn more about the material shown here with the secr vignettes: secr-overview, secr-densitysurfaces, secr-multisession, secr-varyingeffort (available at https://www.otago.ac.nz/density/SECRinR.html)