

Analysing data with secr

Gather SECR data
 SECR 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 `secur` provides methods for estimating animal abundance from SECR data under many different conditions. First, you need to get your data into the format `secur` wants.

Analyse data
 This sheet shows you how to build SECR models and extract results on animal abundance, detectability, and important covariates.

(1) Read in SECR inputs

To build models in `secur` you need to have already loaded:

- 1 A “caphist” 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 detector locations that observations are extremely unlikely.

```
ch <- read.caphist(captfile = "ch.txt",
  trapfile = "tf.txt", 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 SECR assumption is that detection probability (or frequency) **decreases with distance** to activity centre. Shape is given by the **detection function** (`detectfn` in `secur.fit`), with a small number of parameters to be estimated.

Detection function models

These model the **probability** of detection. The most common option is “half-normal” (HN), with parameters g_0 and σ , see `?detectfn` for others.

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

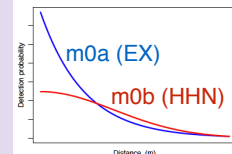
“EX” function, another option

Encounter function models

These model the **expected number** of (equivalently the **hazard**) of detection. They are particularly useful for “count” detectors. The most common option is “hazard half-normal” (HHN), with parameters λ_0 and σ , see `?detectfn` for others.

Plot detection functions
`plot(m0a)`

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



(2) Fit a model

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

Run SECR models with `secur.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, λ_0 control encounter rate, σ controls range of animal movement

density, ~ 1 for constant density

! “ ~ 1 ” means no covariate effects, and a single parameter is estimated for each of D , λ_0 , and σ

Including covariates

Any of D , λ_0 , and σ can depend on covariates in the call to `secur.fit`.

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

Encounter hazard λ_0 depends on whether detector is close to water

Density depends on elevation

Very flexible e.g. can do regression splines with $D \sim s(elev)$

! Covariates on density (D) must be attached to the mask object, covariates on detection parameters (g_0 , λ_0 , σ) 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
λ_0 water	-4.4403272	0.17332682	-4.7800415	-4.1006128
λ_0 WaterYes	0.2277942	0.27803197	-0.3171385	0.7727268
σ	8.8583684	0.08326936	8.6951634	9.0215733

`secur` has a number of automatically generated “canned predictors” that can be referred to directly in formulae without needing to be constructed. These include b (learned animal responses to detectors), k (site learned response) and $session$, t and T (time effects), among others.

(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      -9.518329 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 are underdeveloped but see `secur.test`.

Multi-session models

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

Can run `secur.fit` as in (2). Parameters are shared between sessions by default but any of D , λ_0 , and σ 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))
```