secrdesign - sampling design for spatially explicit capture–recapture

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The R package **secrdesign** is a set of tools to assist the design of studies using spatially explicit capture–recapture (SECR). It provides convenient wrappers for simulation and model fitting functions in package **secr** to emulate many features of the 'Simulator' module of Density 5.0 (Efford 2012). Other tools may be added in future.

This document is a technical guide to using the package. It assumes an understanding of estimator properties such as bias, precision, and confidence interval coverage, and the use of Monte Carlo simulation to predict the frequentist performance of different sampling designs. Using **secrdesign** can be daunting because it allows for many different combinations of data generation, model fitting and summary statistics. Several examples are given to indicate the range of possibilities.

Contents

1 Introduction

When designing a study we assume you have in mind –

(i) a population parameter you want to measure (probably density or population size),

(ii) one or more design variables over which you have some control (number and spacing of detectors, number of sampling occasions etc.),

(iii) some pilot data, or parameter estimates from published studies, and

(iv) a criterion by which to evaluate different designs. This is most likely the precision of the estimates, as this in turn determines your ability (power) to recognise changes. Cost or effort may be an explicit criterion, or the designs may be constructed to allocate constant effort in different ways.

Once you have sorted these out, you can proceed to use Monte Carlo simulation in **secrdesign** to evaluate how alternative sampling scenarios perform with respect to your chosen criterion.

1.1 Overview

Fig. 1 shows the sequence of steps taken in **secrdesign** to conduct simulations and summarise the results. Each step is described in detail in a later section. Simulations are specified by 'scenarios' stored in a dataframe. The scenario dataframe will usually be constructed with `make.scenarios()`. You may construct it manually, but there is a rigid list of required columns (Section 3).

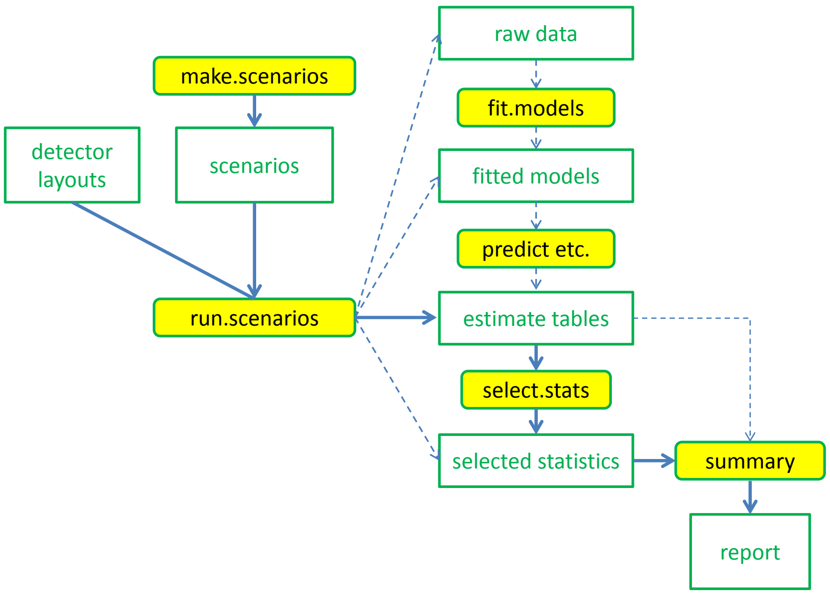


Figure 1: Core functions in **secrdesign** (yellow) and their main inputs and outputs. Output from the simulation function `run.scenarios()` may be saved as whole fitted models, predicted values (parameter estimates), or selected statistics. Each form of output requires different subsequent handling. The default path is shown by solid blue arrows.

Typically, you will (i) construct detector array(s), (ii) construct a dataframe of scenarios, (iii) use `run.scenarios()` to generate data and fit SECR models,

(iv) select some statistics with `select.stats()`, and (v) summarise and plot the results.

1.2 A simple example

As an introductory example, we construct a simple set of scenarios and perform some simulations. The trap layout is a default 6 x 6 grid of multi-catch traps at 20-m spacing. Density takes one of two levels (5/ha or 10/ha) and detection parameters sigma and g0 are fixed.

```
> library(secrdesign)
> scen1 <- make.scenarios(D = c(5, 10), sigma = 25, g0 = 0.2)
> traps1 <- make.grid()
> sims1 <- run.scenarios(nrepl = 50, trapset = traps1,
     scenarios = scen1, seed = 345, fit = TRUE)
```

The output is an object of class `c( "estimatetables", "secrdesign", "list")`. We use the summary method for estimatetables to view results, and here display only the summary output (omitting a header that describes the simulations).

```
> summary(sims1)$OUTPUT

$`D = 5`
             n     mean      se
estimate    50  5.23767 0.24994
SE.estimate 50  1.84409 0.05958
lcl         50  2.70152 0.16476
ucl         50 10.28534 0.37589
RB          50  0.04753 0.04999
RSE         50  0.36890 0.00962
COV         50  0.92000 0.03876

$`D = 10`
             n     mean      se
estimate    50  9.58795 0.36972
SE.estimate 50  2.45915 0.05721
lcl         50  5.86410 0.27453
ucl         50 15.75842 0.47775
RB          50 -0.04121 0.03697
RSE         50  0.26727 0.00668
COV         50  0.92000 0.03876
```

Later sections show how to customize the summary and plot results.

1.3 Terminology

We use 'relative standard error' (RSE) for the relative precision of an estimate. This is sometimes called the coefficient of variation (CV) of the estimate, but RSE is more appropriate. We use 'accuracy' in the sense of Williams et al. (2002 p.45) and other authors from the United States. Accuracy combines both systematic error (bias) and precision: one measure is the square root of the mean squared difference between the true value and the estimate (RMSE).

2 Detector layouts

Detector layouts are specified as **secr** 'traps' objects. These may be input from text files using `read.traps` or constructed according to a particular geometry and spacing with functions such as `make.grid`, `make.circle`, `make.systematic` or `trap.builder`. See the help files for these **secr** functions for further details. The detector type (multi-catch trap, proximity detector etc.) is stored as an attribute of each 'traps' object, which may also include detector-level covariates.

Multiple layouts are combined in a single list object; component names will be used to annotate later output.

```
> library(secrdesign)
> mydetectors <- list(grid6x6 = make.grid(6, 6), grid8x9 = make.grid(8,
     9), grid12x12 = make.grid(12, 12))
```

This creates square grids with the default detector type 'multi' and default spacing 20 m. See ?secr::make.grid for other options.

3 The scenarios dataframe

The function `make.scenarios()` constructs a dataframe in which each row defines a simulation scenario. Its arguments are:

```
make.scenarios (trapsindex = 1, noccasions = 3, nrepeats = 1, D, g0,
    sigma, lambda0, detectfn = 0, recapfactor = 1, popindex = 1,
    detindex = 1, fitindex = 1, crosstraps = TRUE)
```

Each argument except for 'crosstraps' may be used to specify a range of values for a parameter. Four ('trapsindex', 'popindex', 'detindex', 'fitindex') are actually surrogate numerical indices; the index is used to select one component from a list of possibilities later provided as input to `run.scenarios()`.

By default, a scenario is formed from each unique combination of the input values (trapsindex, noccasions, nrepeats, D, g0, sigma, lambda0, detectfn, recapfactor, popindex, and fitindex) using `expand.grid`. For example,

```
> make.scenarios(trapsindex = 1:3, noccasions = 4, D = 5,
     g0 = 0.2, sigma = c(20, 30))

  scenario trapsindex noccasions nrepeats D  g0 sigma detectfn
1        1          1          4        1 5 0.2    20        0
2        2          2          4        1 5 0.2    20        0
3        3          3          4        1 5 0.2    20        0
4        4          1          4        1 5 0.2    30        0
5        5          2          4        1 5 0.2    30        0
6        6          3          4        1 5 0.2    30        0
  recapfactor popindex detindex fitindex
1           1        1        1        1
2           1        1        1        1
3           1        1        1        1
4           1        1        1        1
5           1        1        1        1
6           1        1        1        1
```

In this case three different grids (possibly differing in number of traps) are trapped for the same number of occasions. A more interesting possibility is to vary the number of occasions inversely with the number of traps. However, if we naively set e.g., noccasions = c(8, 4, 2), this would generate all combinations of grid and number of occasions (18 different scenarios).

The alternative is to set `crosstraps = FALSE`. Then the vectors 'trapsindex', 'noccasions', and 'nrepeats' are locked together (if fewer values are provided in one of the vectors then it is re-used as required), and only the combination is crossed with the remaining parameter scenarios:

```
> make.scenarios(trapsindex = 1:3, noccasions = c(8, 4,
     2), D = 5, g0 = 0.2, sigma = c(20, 30), crosstraps = FALSE)

  scenario trapsindex noccasions nrepeats D  g0 sigma detectfn
1        1          1          8        1 5 0.2    20        0
2        2          2          4        1 5 0.2    20        0
3        3          3          2        1 5 0.2    20        0
4        4          1          8        1 5 0.2    30        0
5        5          2          4        1 5 0.2    30        0
6        6          3          2        1 5 0.2    30        0
```

```
  recapfactor popindex detindex fitindex
1           1        1        1        1
2           1        1        1        1
3           1        1        1        1
4           1        1        1        1
5           1        1        1        1
6           1        1        1        1
```

All arguments except 'fitindex' control the generation of data. Note that 'g0' and 'lambda0' are alternatives: use the one appropriate to the detection function specified with 'detectfn' (see ?detectfn for codes). 'D' is omitted if an inhomogeneous Poisson distribution is specified using a mask covariate (see 6.3). D is in animals / hectare (1 ha = 0.01km^2) and sigma is in metres, as in **secr**.

The `nrepeats` column refers to the number of notional independent replicates of the particular detector layout. Notional replicates are simulated by (invisibly) multiplying density (D) by this factor, and ultimately dividing it into the estimate. Think of 5 grids of automatic cameras so widely separated that no animal moves between the grids. As detections of different animals are ordinarily modelled as independent, the entire design is equivalent to 5 times the density of animals interacting with one grid. This breaks down, of course, if animals compete for traps (as with single-catch traps), and should not be used in that case except as a rough approximation.

Just as `trapsindex` serves as a placeholder for entire detector arrays, `popindex`, `detindex` and `fitindex` tell `run.scenarios()` which set of arguments to select from `pop.args` and `fit.args` for `sim.popn`, `sim.capthist` and `secr.fit` respectively. These are for more advanced use: you may not need them.

4 Running simulations

The function `run.scenarios()` generates multiple datasets and, if requested, fits an SECR model to each one. In this section we describe its main arguments, with additional detail on habitat masks and customizing the output.

4.1 Arguments of `run.scenarios()`

```
run.scenarios (nrepl, scenarios, trapset, maskset, xsigma = 4,
    nx = 32, pop.args, det.args, fit = FALSE, fit.args, extractfn =
    NULL, ncores = 1, seed = 123)
```

`nrepl` determines the number of replicate simulations. Make this large enough that the summary statistics have enough precision to answer your question. This is usually a matter for experimentation, remembering that precision (SE) is proportional to the square root of `nrepl`.

`scenarios` is the dataframe constructed with `make.scenarios()` as described in the last section.

`trapset` is a single 'traps' object or a list of traps objects. as described in 'Detector layouts' above.

`maskset` is an optional set of habitat masks, usually one per detector layout. If not specified, then masks will be constructed 'on the fly' using `secr::make.mask` with a 'buffer' of width xsigma $\times$ σ and 'nx' cells in the x dimension.

`pop.args` provides additional control over `sim.popn` (see ?sim.popn for more). You may wish, for example, to set `pop.args = list(Ndist = "fixed")` to override the default of Poisson variation in the total number of simulated animals.

`det.args` provides additional control over `sim.capthist` (see ?sim.capthist for more). One use is to retain the simulated population as an attribute of the capthist object by setting `det.args = list(savepopn = TRUE)`; another is to set the `binomN` argument for count detectors. The `sim.capthist` arguments `traps, popn, detectpar, detectfn` and `noccasions` are defined in the scenario or `pop.args` and cannot be overridden by setting `det.args`.

Use `fit = FALSE` to generate and summarise detection data without fitting SECR models. This lets you check that your scenarios result in reasonable numbers of detected individuals (n), detections (ndet), and movements (nmov), before launching a full-blown simulation.

`fit.args` lets you specify how SECR models will be fitted to the simulated data. Most default arguments of `secr.fit` may be overridden by including them in `fit.args`. For example, to specify a negative exponential detection function use `fit.args = list(detectfn = "EX")`. If you wish to compare nspec different model specifications then `fit.args` should be a list of lists, one per specification, with `fitindex` taking values in the range 1:nspec.

4.2 Customising run.scenarios()

The output from run.scenarios() is controlled by its argument `extractfn`. This is a short function that is applied either (i) to each simulated raw dataset (capthist object) (`fit = FALSE`), or (ii) to each fitted model (`fit = TRUE`).

The default (builtin) `extractfn` behaves appropriately for either data type:

```
extractfn <- function(x) {
    if (inherits(x, "capthist")) {
        ## assume single-session CH
        nmoves <- sum(unlist(sapply(moves(x), function(y) y>0)))
        ## detectors per animal
        dpa <- if (length(dim(x)) == 2)
            mean(apply(abs(x), 1, function(y) length(unique(y[y>0]))))
        else
            mean(apply(apply(abs(x), c(1,3), sum)>0, 1, sum))
        c(n=nrow(x), ndet=sum(abs(x)>0), nmov = nmoves, dpa = dpa)
    }
    else if (inherits(x, "secr"))
        predict(x)
    else
        data.frame()   ## 0 rows, 0 columns
}
```

When `fit = FALSE`, the default output from each replicate is a vector of 4 summary statistics:

- n - number of different individuals
- ndet - total number of detections (‘captures’ and ‘recaptures’)
- nmov - total number of detections at a detector other than the one where an animal was last detected
- dpa - detectors per animal (average number of detectors at which each animal was recorded)

When `fit = TRUE`, the default output from each replicate is the result of applying ‘predict’ to the fitted model, i.e. a dataframe of ‘real’ parameter estimates and their standard errors etc. (an empty dataframe is returned if model fitting fails). Nearly the same is achieved by setting `extractfn = predict`; for the ‘beta’ coefficients set `extractfn = coef`. For a conditional likelihood fit it may be appropriate to set `extractfn = derived`. To focus on population size in the masked region, set `extractfn = region.N`.

The user may also choose to save the entire dataset (`fit = FALSE`) or the entire fitted model (secr object; `fit = TRUE`) for each replicate by setting `extractfn = identity`. For a large analysis there is a risk of exceeding memory limits in R, and saving everything is generally not a good idea. For most purposes it is sufficient to save a trimmed version of the fitted model `extractfn = trim` (note **secr** defines the function ‘trim’). However, the full model is needed for `derived.SL` or `regionN.SL`.

`run.scenarios()` sets the class[1] of its output to distinguish among fitted models ("fittedmodels"), estimate tables from predict, coef etc. ("estimatetables"), and numeric values ready for summarisation ("selectdstatistics") class. Simulated data saved with `fit = FALSE, extractfn = identity` have class c("rawdata", "secrdesign", "list"). An attribute 'outputtype' is used to make finer distinctions among these types of output ('secrfit', 'predicted', coef', 'capthist', or 'numeric'). Output from `extractfn = derived` is treated as 'predicted'.

When `fit = TRUE`, analyses are performed with `secr.fit`. Other analyses may be specified by setting `fit = FALSE` and providing the analysis function as the value for `extractfn`. The function should accept a 'capthist' object as input. For example, conventional closed-population estimates may be obtained with

```
> run.scenarios(nrepl = 1000, scenarios = scen1, trapset = traps1,
      extractfn = closedN, estimator = c("null", "h2",
          "jackknife"))
```

This applies various *nonspatial* estimators to simulated *spatial* samples. Named arguments of `extractfn` may be included (here, 'estimator'); these are used for all scenarios, unlike `fit.args` which may vary among scenarios. Summarisation of alternative analyses will usually require careful selection of 'parameter' and 'statistics' in `select.stats()` (5.2).

4.3 More on masks

A habitat mask in **secr** is a raster representation of the region near the detectors in which the centres of detected animals may lie. This excludes both nearby non-habitat, and habitat that is so distant that it is implausible any animal centred there would reach a detector. It is often convenient to define a mask to include all cells whose centre is within a certain distance of a detector - the buffer radius.

Within **secrdesign**, a mask is used both when generating populations of animals with `sim.popn` and when fitting SECR models with `secr.fit`. The extent of the mask used to generate populations is important if you are concerned with population size (for example, if you set `extractfn = region.N`). Then the size of the region determines the 'true' value of the parameter of interest (N), and influences its sampling variance. The extent of the mask is less critical when density is the parameter of interest.

The default behaviour of `run.scenarios()` is to use a concave buffer of width `xsigma` $\times$ sigma around the particular detector layout. The 'coarseness'

[1]the full class is actually c(x, "secrdesign", "list") where x is as described

of the mask is determined by `nx`; note that the default for `run.scenarios()` (32) is coarser than the default for `secr::make.mask` (64). This makes for speed, and is fairly safe when the buffer width is well matched to the scale of movement (of course we know sigma, so the default buffer width *is* well-matched). The same mask is used both for generating populations and fitting models.

Users may specify their own masks in the 'maskset' list argument. If the number of masks in 'maskset' is one or a number equal to the number of detector layouts, then a column 'maskindex' is added automatically to the 'scenarios' dataframe (all 1, or equal to trapsindex, in the two cases). Otherwise, the user must have manually added a maskindex column to 'scenarios' to clarify which mask should be used with which scenario.

5 Summarising simulation output

`run.scenarios()` usually takes a long time to run, but having saved its output you can quickly extract and summarise the results in many different ways.

We saw in the previous section and Fig. 1 that the output from `run.scenarios()` for each replicate may be a fitted model, a table of parameter estimates, or a numeric vector. Summarisation across replicates (the `summary` method) requires output in 'selected statistics' form, so each of the other forms must be processed first[2].

Look again at Fig. 1: you will see that the primary input to the `summary` function is in the form of selected statistics. A secondary route is to automatically extract statistics from estimates tables, as shown by the dashed line in Fig. 1 – we used this in the simple example of 1.2. We now address how other forms of output from `run.scenarios()` can be processed into 'selected statistics' form.

5.1 Extracting estimate tables from fitted models

The methods `predict` and `coef` for the 'fittedmodels' class and the function `derived.SL` are provided to extract estimates of 'real' parameters from each fitted model. These are direct analogues of `predict`, `coef` and `derived` in **secr**. Here, they apply across all replicates of all scenarios and return an object of class 'estimatetables'. `regionN.SL` is another possibility.

In each case, the result is a dataframe or list of dataframes for each replicate. Rows correspond to estimated parameters (or 'R.N' and 'E.N' for `regionN.SL`) and columns to the respective estimates, standard errors, and confidence limits

[2]Processing happens silently using default settings of `select.stats()` when `summary` is applied directly to 'estimate tables' output

(with some variations).

The ... argument lets you pass arguments such as ‘alpha’ to the **secr** functions `predict.secr` and `derived`.

We can skip this step for the output from our simple example as it is already in ‘estimatetables’ form.

5.2 Choosing the statistics to summarise

Given tabular output from `predict()` or `derived.SL()`, we must select replicate-specific numerical quantities for further summarisation.[3] This is the role of `select.stats()`, which has arguments –

```
select.stats(object, parameter = "D", statistics)
```

The parameter of interest defaults to density (“D”); others such as “g0” or “sigma” may be substituted,so long as they appear in the input object. To check which parameters are available use

```
find.param(object)
```

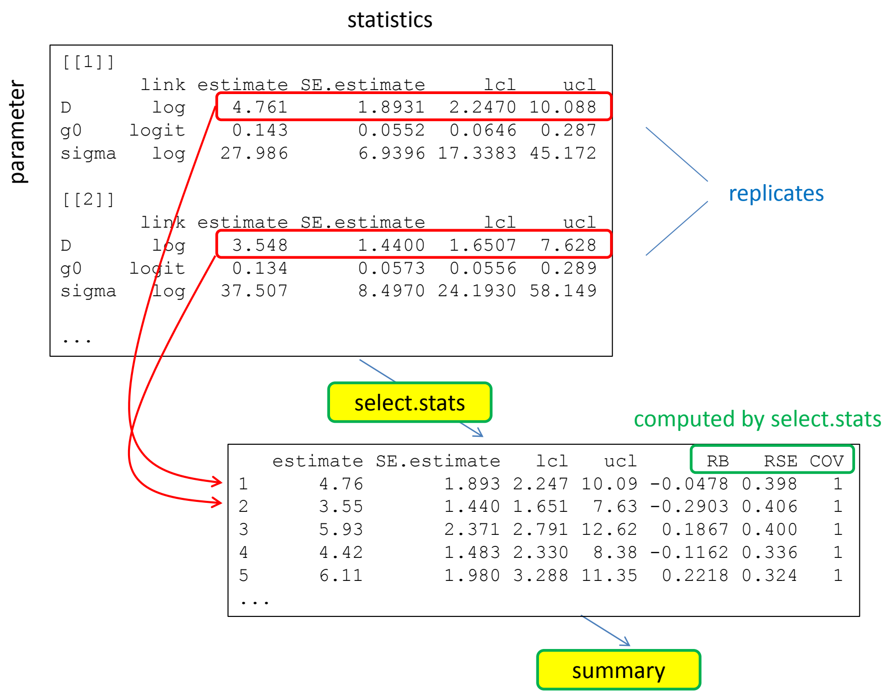
The task of `select.stats()` is to reduce each replicate to a vector of numeric values - we can think of the result as a replicate $\times$ value matrix for each scenario (Fig. 2) . A later step (`summary`) computes statistics (‘fields’) such as mean and SE for each column in the matrix, as described in the next section.

Here we describe the replicate-specific statistics that form the numeric vector. These may be simply ‘estimate’, ‘SE.estimate’, ‘lcl’ and ‘ucl’ as output from `predict.secr`.

Additionally, when `fit = TRUE`, we can include statistics derived from the estimates of a parameter (Table 1). To describe these we use ‘true’ to stand for the known value of a real parameter, and ‘estimate’ for the estimate from a particular replicate.

We use (‘lcl’, ‘ucl’) to represent a confidence interval for ‘estimate’. Usually these are 95% intervals, but the level may be varied by setting the argument ‘alpha’ in `predict` (e.g., alpha = 0.1 for a 90% interval). Intervals from

[3]If `run.scenarios()` has been used with `fit = FALSE`, then the output from each replicate is probably already in the form of selected statistics (the default raw data summaries ‘n’, ‘ndet’,‘nmov’ and ‘dpa’) and `select.stats()` is not relevant. The same may also apply with a user-provided `extractfn` when `fit = TRUE`.



```
[[1]]
        link estimate SE.estimate     lcl    ucl
D        log    4.761      1.8931  2.2470 10.088
g0     logit    0.143      0.0552  0.0646  0.287
sigma    log   27.986      6.9396 17.3383 45.172

[[2]]
        link estimate SE.estimate     lcl    ucl
D        log    3.548      1.4400  1.6507  7.628
g0     logit    0.134      0.0573  0.0556  0.289
sigma    log   37.507      8.4970 24.1930 58.149

...
```

```
  estimate SE.estimate   lcl   ucl      RB   RSE COV
1     4.76       1.893 2.247 10.09 -0.0478 0.398   1
2     3.55       1.440 1.651  7.63 -0.2903 0.406   1
3     5.93       2.371 2.791 12.62  0.1867 0.400   1
4     4.42       1.483 2.330  8.38 -0.1162 0.336   1
5     6.11       1.980 3.288 11.35  0.2218 0.324   1
...
```

Figure 2: Operation of `select.stats()`

`predict.secr` are symmetrical on the link scale, and hence asymmetrical on the natural scale. Note also the argument `loginterval` in `derived`; the default `loginterval = TRUE` gives an asymmetrical interval on the natural scale.

The coverage indicator COV is a binary value; this becomes interesting later when averaged over a large number of replicates to give a coverage proportion. The absolute deviation also comes into its own later as the basis for RMSE. In a sense the same is true of replicate-specific RB: RB should be reported only as an average over a large number of replicates.

Returning to our simple example, we apply `select.stats()` to focus on the density parameter "D".

```
> stats1 <- select.stats(sims1, parameter = "D", statistics = c("estimate",
     "lcl", "ucl", "RB", "RSE", "COV"))
> lapply(stats1$output, head, 4)

$`1`
  estimate      lcl      ucl          RB       RSE COV
1 4.563484 2.320220 8.975609 -0.08730323 0.3556572   1
2 3.625584 1.766920 7.439423 -0.27488310 0.3794131   1
```

Table 1: Computed statistics available in `select.stats()`

Statistic	Short name	Value
Relative bias[1]	RB	(estimate – true) / true
Relative SE[2]	RSE	SE.estimate / estimate
Absolute deviation	ERR	abs(estimate – true)
Coverage indicator	COV	(estimate > lcl) & (estimate < ucl)

1. Also called 'normalised bias'
2. Also called 'coefficient of variation'

```
3 3.860603 1.838079 8.108603 -0.22787945 0.3926149   1
4 4.455237 2.395654 8.285477 -0.10895269 0.3246465   1

$`2`
   estimate       lcl      ucl          RB       RSE COV
1 16.329709 11.210633 23.78629  0.63297089 0.1936836   0
2  9.600765  5.694946 16.18535 -0.03992348 0.2712667   1
3 10.305960  6.417433 16.55067  0.03059603 0.2452631   1
4 12.628829  8.370561 19.05336  0.26288289 0.2121620   1
```

The two scenarios yield two replicates × statistic matrices, from which we display the first 4 rows.

5.3 Disposing of rogue values

Simulation output may contain rogue values due to idiosyncracies of model fitting. For example, nonidentifiability due to inadequate data can result in spurious extreme 'estimates' of the sampling variance. The median (chosen as a 'field' value in `summary`) is recommended as a robust alternative to the mean when there are some extreme estimates.

```
validate (x, test, validrange = c(0, Inf), targets = test)
```

Another way to deal with the problem is to set statistics to NA when a simulation fails. The function `validate` sets selected 'target' statistics to NA for replicates in which another 'test' statistic is out-of-range or NA. The permissable bounds are usually arbitrary, and the method should be used with care. The keyword "all" may be used for `targets` to indicate all columns.

`validate` accepts a 'selectedstatistics' object (x) as input and returns a modified 'selectedstatistics' object. See 8.2 for an application.

5.4 Summary method

The `summary` method for 'selectedstatistics' objects reports both header information on the simulation scenarios and user-selected summaries of the pre-selected statistics.

```
summary (object, dec = 5, fields = c("n", "mean", "se"), alpha = 0.05,
    type = c("list", "dataframe", "array"), ...)
```

Here the summary statistics are called 'fields' to distinguish them from the 'statistics' in each column of the numeric replicate $\times$ value matrix for each scenario (see 5.2). The task of the summary method is to compute the 'field' value for each 'statistic', summarising across replicates to give a 'statistic' $\times$ 'field' matrix for each scenario. The choice of 'fields' is shown in Table 2.

Table 2: Statistic 'fields' available in the `summary` method for 'selectedstatistics' objects

Field	Description
n	number of non-missing values
mean	mean
se	standard error
sd	sample standard deviation
min	minimum
max	maximum
lcl	lower $100(1-\alpha)$ % confidence limit
ucl	upper $100(1-\alpha)$ % confidence limit
rms	root mean square
median	median
qxxx	xxx/1000 quantile
qyyy	yyy/1000 quantile

The summary fields 'lcl' and 'ucl' are for a simple Wald interval $(\bar{x}+z_{\alpha/2}\mathrm{SE}(x), \bar{x}+z_{1-\alpha/2}\mathrm{SE}(x))$ where z_α is the 100α-percentile of a standard normal distribution (e.g., $z_{0.975} = 1.96$). [Do not confuse these with the confidence limit statistics of the same name that are symmetrical only on the link scale].

Quantiles are specified as 'qxxx' and 'qyyy' where xxx and yyy are integers between 1 and 999 corresponding to quantiles 0.001 to 0.999. For example, 'q025' refers to the 2.5% quantile.

Applying the 'rms' field to the absolute deviation of an estimate ('ERR') provides the root-mean-square-error 'RMSE'.

To recap – a summary value is reported for each combination of a selected statistic, computed for each replicate, and a ‘field’ that summarises the statistic across replicates, potentially resulting in a table with this structure:

	Fields											
Statistics	n	mean	se	sd	min	max	lcl	ucl	rms	median	q025	q975
estimate	●	●	●	●	●	●	●	●		●	●	●
SE.estimate	●	●	●	●	●	●	●	●		●	●	●
lcl	●	●	●	●	●	●				●	●	●
ucl	●	●	●	●	●	●				●	●	●
RB	●	●	●	●	●	●				●	●	●
RSE	●	●	●	●	●	●	●	●		●	●	●
ERR	●	●	●	●	●	●	●	●	●	●	●	●
COV	●	●	●	●	●	●						

Cells are left blank for combinations that are unlikely to be meaningful. ‘rms’ is useful with ‘ERR’ (i.e. RMSE), but not when applied to other statistics. ‘n’, ‘mean’ and ‘se’ summarise the ‘COV’ indicator, but other potential summaries are (almost) meaningless.

Apply this to the selected statistics from our simple example:

```
> summary(stats1)

run.scenarios(nrepl = 50, scenarios = scen1, trapset = traps1,
    fit = TRUE, seed = 345)

Replicates     50
Started        11:07:01 02 May 2014
Run time       1.693  minutes
Output class   selectedstatistics

$constant
             value
trapsindex       1
noccasions       3
nrepeats         1
g0             0.2
sigma           25
detectfn         0
recapfactor      1
popindex         1
detindex         1
```

```
fitindex        1
maskindex       1

$varying
 scenario  D
        1  5
        2 10

$detectors
 trapsindex trapsname
          1    traps1

OUTPUT
$`D = 5`
          n     mean      se
estimate 50  5.23767 0.24994
lcl      50  2.70152 0.16476
ucl      50 10.28534 0.37589
RB       50  0.04753 0.04999
RSE      50  0.36890 0.00962
COV      50  0.92000 0.03876

$`D = 10`
          n     mean      se
estimate 50  9.58795 0.36972
lcl      50  5.86410 0.27453
ucl      50 15.75842 0.47775
RB       50 -0.04121 0.03697
RSE      50  0.26727 0.00668
COV      50  0.92000 0.03876
```

5.5 Plot method

Use the `plot` method to visualise the distributions of 'selectedstatistics' that you have simulated. You may plot either (i) histograms of the selected statistics (type = 'hist') or (ii) the estimate and confidence interval for each replicate (type = 'CI'). One histogram is plotted for each combination of scenario and statistic – you may want to select a subset of scenarios and statistics, and use the graphics options mfcol or mfrow to control the layout. For type = 'CI' the statistics must include 'estimate', 'lcl' and 'ucl' (or 'beta', 'lcl' and 'ucl' if outputtype = 'coef').

```
> par(mfrow = c(2, 2))
> plot(stats1, type = "hist", statistic = "estimate")
> plot(stats1, type = "CI")
```

See Fig. 3 for the result.

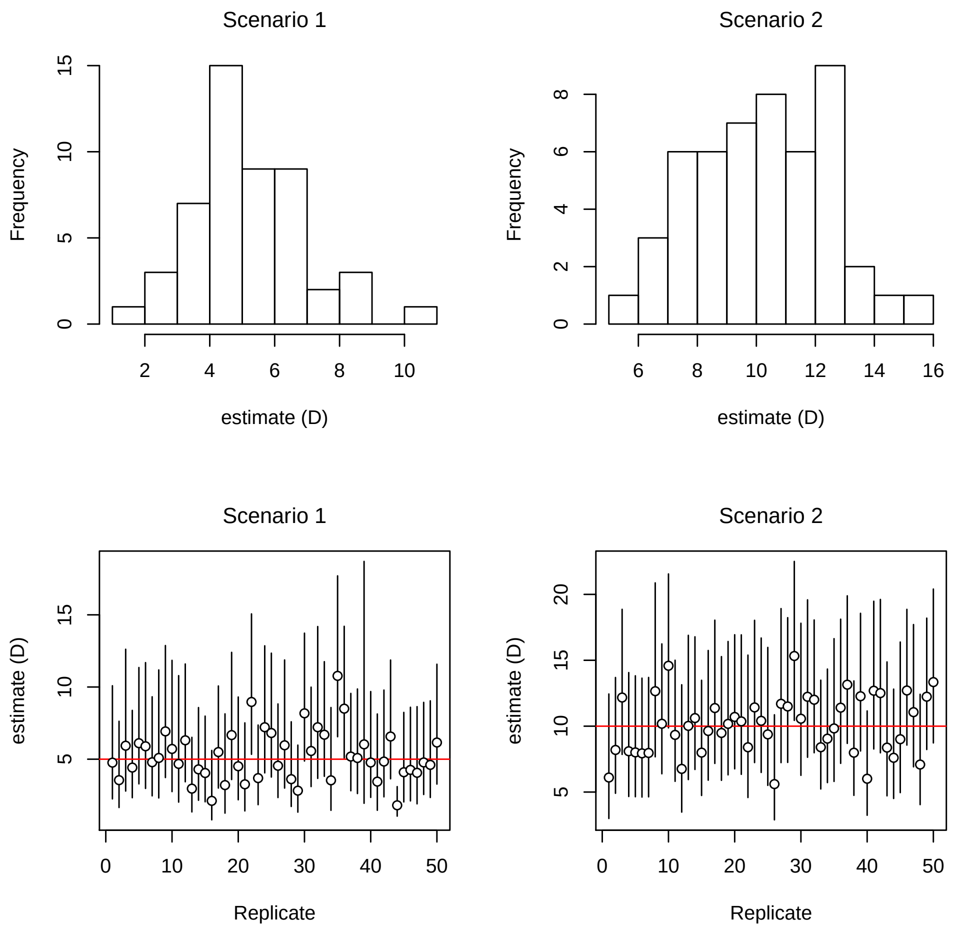


Figure 3: Plot method applied to a 2-scenario 'selectedstatistics' object with type = 'hist' (top) and type = 'CI' (bottom)

6 Additional topics

6.1 Parallel processing

Setting `ncores > 1` causes `run.scenarios()` to run separate scenarios on separate cores. This uses the R package **parallel**. Technically, it relies on Rscript, and communication between the master and worker processes is via sockets. As stated in the R **parallel** documentation "Users of Windows and Mac OS X may expect pop-up dialog boxes from the firewall asking if an R process should accept incoming connections". It appears to be safe to accept these.

Use `parallel::detectCores()` to get an idea of how many cores are available on your machine; this may (in Windows) include virtual cores over and above the number of physical cores. If you use the maximum available cores for `run.scenarios()` then expect any other processes on the machine to slow down!

Running one scenario per core is suboptimal if scenarios differ widely in how long they take to run: the system waits for the slowest. There is no way around this limitation in **secrdesign**.

Random number generation for multiple cores uses the "L'Ecuyer-CMRG" random number generator as described in `?RNG`.

6.2 Shortcut evaluation of precision

The asymptotic variance (and hence RSE) of a maximum likelihood estimate is typically obtained from the curvature of the likelihood computed numerically at the fitted value of the parameter(s) (i.e., at the MLE). Fitting SECR models is slow. An alternative estimate of the RSE that is sufficient for most purposes may be got from the curvature of the likelihood computed at the known 'true' value(s) of the parameter(s). This is much faster as it does not require the model to be fitted.

`secr.fit` may be 'tricked' into providing this variance estimate by setting `method = "none"` and providing the true values as the `start` vector. `run.scenarios()` makes this easy by assuming that if you specify `method = "none"` you wish to use `start = "true"`. However, this works only when there is a 1:1 relationship between 'beta' and 'real' parameters; it does not work when 'recapfactor' is specified.

```
> sims2 <- run.scenarios(nrepl = 50, trapset = traps1,
     scenarios = scen1, fit = TRUE, fit.args = list(method = "none"))
```

```
Completed scenario  1
Completed scenario  2
Completed in 0.403 minutes
```

```
> summary(sims2)
```

```
run.scenarios(nrepl = 50, scenarios = scen1, trapset = traps1,
    fit = TRUE, fit.args = list(method = "none"))
```

```
Replicates    50
Started       00:12:45 05 Jun 2014
Run time      0.403  minutes
Output class  selectedstatistics

$constant
            value
trapsindex      1
noccasions      3
nrepeats        1
g0            0.2
sigma          25
detectfn        0
recapfactor     1
popindex        1
detindex        1
fitindex        1
maskindex       1

$varying
 scenario  D
        1  5
        2 10

$detectors
 trapsindex trapsname
          1    traps1

$fit.args
 fitindex method
        1   none

OUTPUT
$`D = 5`
             n     mean      se
estimate    50  5.00000 0.00000
SE.estimate 49  1.88876 0.04280
lcl         49  2.46033 0.03457
ucl         49 10.27008 0.16263
RB           0       NA      NA
```

```
RSE          49  0.37775 0.00856
COV           0       NA      NA

$`D = 10`
              n     mean      se
estimate     50 10.00000 0.00000
SE.estimate  50  2.66698 0.05948
lcl          50  6.00324 0.06291
ucl          50 16.75599 0.19230
RB            0       NA      NA
RSE          50  0.26670 0.00595
COV           0       NA      NA
```

Each estimate of RSE is essentially the same as before, but the run time is reduced by nearly 80%. Note the true value of density appears as a constant "estimate" in the summary. Care is need with this method as its performance in extreme cases has not been investigated fully.

6.3 Non-uniform populations

The simulated population by default has a uniform (homogeneous) Poisson distribution. To generate and sample from a spatially inhomogeneous population we use the 'IHP' option for argument 'model2D' in `secr::sim.popn`. This involves three steps:

1. Create a habitat mask object with the desired extent.
2. Add to the mask a covariates dataframe with one or more columns defining pixel-specific densities.
3. In `run.scenarios()` specify a list of pop.args including `model2D = "IHP"` and `D = "XX"` where XX is the name of the particular mask covariate you wish to use for density, and name your mask in the 'maskset' argument.

A full demonstration is given in the Appendix (8.3).

To visualise simulated populations you should set `savepopn = TRUE` in det.args and later extract the popn attribute from the capthist object (for example, with a custom extractfn).

To compare several inhomogeneous distributions, specify several pop.args lists and use the popindex argument in `make.scenarios()`. The distribution may be varied simply by using the `sim.popn()` argument 'D' to select different covariates of one mask.

The columns 'nrepeats' and 'D' in the scenarios object as input are ignored when `model2D = "IHP"`. 'D' is replaced by the average density over the mask, which is used as the 'true' value of density in computing RB, RSE etc. in summaries. For stratified analyses you will have to define your own extractfn.

6.4 Splitting data generation and model fitting

Each new detector layout or new model specification (in a `fit.args` list) defines a new scenario. The default procedure is to generate new data (both animal locations and simulated detection histories) for each scenario. To compare different models applied to the same dataset, save raw data from an initial call to `run.scenarios()` with `fit = FALSE, extractfn = identity`, and separately fit a list of models with `fit.models`. You can also peek at the raw data with the `summary` method.

```
> scen3 <- make.scenarios(D = c(5, 10), sigma = 25, g0 = 0.2)
> traps3 <- make.grid()
> raw3 <- run.scenarios(nrepl = 20, trapset = traps3, scenarios = scen3,
     fit = FALSE, extractfn = identity)
> summary(raw3)
> sims3 <- fit.models(raw3, fit.args = list(list(model = g0 ~
     1), list(model = g0 ~ T)), fit = TRUE, ncores = 4)
> summary(sims3)
```

Here, `scen3` describes two scenarios, and in the call to `fit.models` each of these is split into two new scenarios, one for each component of `fit.args`.

It is not possible within **secrdesign** precisely to evaluate the application to the same animal distribution (population) of differing detector layouts or specifications for the fitted model (cf Fewster and Buckland 2004). Comparisons inevitably include variance from the varying number and placement of animals, and the sampling process; this variance may be reduced by fixing the number of individuals (`pop.args = list(Ndist = "fixed")`).

6.5 Limitations, tips and troubleshooting

`secrdesign` has some limitations (Surprise!).

1. A progress message is output only on the completion of each scenario, which can be annoying, and when using multiple cores even this message is lost. It is strongly recommended that you start by generating summaries of raw data only (`run.scenarios()` with `fit = FALSE`), and confirm that

your scenarios are realistic by reviewing the simulated number of detected individuals, total number of detections, etc. If these are inadequate or unrealistically large then there's no point going on. Then, try fitting with just a few replicates to be sure you have specified the model you intended and to assess the likely run time. Only then submit a run with a large number of replicates.

2. Only 2-parameter detection functions are allowed for data generation. This excludes the hazard-rate function, the cumulative gamma, and some others.

3. The default `extractfn` does does not handle models that produce more than one estimates table per replicate (e.g., finite mixture models). A custom `extractfn` is needed; it should either produce a numeric vector of 'selected statistics' or mimic single-dataframe output from `predict()`.

4. The function `secr::sim.capthist` that generates detection histories for **secrdesign** has limited capacity for simulating temporal, behavioural or other heterogeneity in detection probability. The capacity of `run.scenarios()` is even more limited: only a general learned response is allowed (`recapfactor`).

5. As noted before, the same mask is used for generating populations and fitting models. It would be possible to replace the maskset component of a 'rawdata' object before running `fit.models`, but this is not recommended.

6. It is easy to forget the random number seed. Consider replacing the default value.

7. The method for fitting a fixed-N model (`distribution = binomial`) is somewhat fragile: it can fail when given a start value for D that is less than the minimum density observed (i.e., the number of distinct individuals divided by the mask area). This can easily happen when a population is simulated with `pop.args = list(Ndist = "poisson")` (the default) and sampled with high detection probability, but `secr.fit` is called with (`distribution = "binomial"`). The solution is to use `pop.args = list(Ndist = "fixed")`.

8. If your summaries do not include enough significant digits, increase the 'dec' argument!

7 References

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

Cooch, E. and White, G. (eds) (2014) *Program MARK: A Gentle Introduction*. 13th edition. Available online at http://www.phidot.org/software/mark/docs/book/.

Efford, M. G. (2012) *DENSITY 5.0: software for spatially explicit capture–recapture*. Department of Mathematics and Statistics, University of Otago, Dunedin, New Zealand http://www.otago.ac.nz/density.

Efford, M. G. and Fewster, R. M. (2013) Estimating population size by spatially explicit capture–recapture. *Oikos* **122**, 918–928.

Efford, M. G., Borchers D. L. and Byrom, A. E. (2009) Density estimation by spatially explicit capture–recapture: likelihood-based methods. In: D. L. Thomson, E. G. Cooch, M. J. Conroy (eds) *Modeling Demographic Processes in Marked Populations*. Springer. Pp 255–269.

Efford, M. G., Dawson, D. K. and Borchers, D. L. (2009) Population density estimated from locations of individuals on a passive detector array. *Ecology* **90**, 2676–2682.

Fewster, R. M. and Buckland, S. T. (2004) Assessment of distance sampling estimators. In: S. T. Buckland, D. R. Anderson, K. P. Burnham, J. L. Laake, D. L. Borchers and L. Thomas (eds) *Advanced distance sampling*. Oxford University Press, Oxford, U. K. Pp. 281–306.

Williams, B. K., Nichols, J. D. and Conroy, M. J. (2002) *Analysis and management of animal populations*. Academic Press, San Diego

8 Appendix. Examples

Here we give some annotated examples of simulation code and selected output. Running this code with reduced `nrepl`, and viewing the output, will give you an idea of how `secrdesign` works.

8.1 Multiple grids, varying number of occasions

This is the other example from the main text, slightly extended

```
traps4 <- list(grid6x6 = make.grid(6,6),
               grid8x9 = make.grid(8,9),
               grid12x12 = make.grid(12,12))
```

```
scen4 <- make.scenarios (trapsindex = 1:3, noccasions = c(8,4,2), D = 5,
    g0 = 0.2, sigma = c(20,30), crosstraps = FALSE)

sims4 <- run.scenarios(nrepl = 500, trapset = traps4, scenarios =
     scen4, fit = FALSE, ncores = 3)
class(sims4)        ## just peeking
find.stats(sims4)   ## just peeking
summary(sims4)
par(mfrow=c(2,3))
plot(sims4, statistic = "n", breaks = seq(0,80,5))  ## number of animals
plot(sims4, statistic = "nmov", breaks = seq(0,140,10))
```

8.2 Learned trap response

Here we assess the bias in $\hat{D}$ caused by ignoring a learned trap response .

```
## set up and run simulations
traps5 <- list(grid6x6 = make.grid(6,6),
               grid10x10 = make.grid(10,10))
scen5 <- make.scenarios (trapsindex = 1:2, noccasions = 5, D = 5,
    g0 = 0.2, sigma = 25, recapfactor = c(0.5, 1, 2), fitindex = 1:2)
sims5 <- run.scenarios(nrepl = 500, trapset = traps5, scenarios =
    scen5, fit = TRUE, fit.args = list(list(model = g0 ~ 1),
    list(model = g0 ~ b)), ncores = 6)

## select statistics and throw out any replicates with SE > 100
## (there is one -- see reduced n in output for scenario 11)
stats5 <- select.stats(sims5)
stats5 <- validate(stats5, "SE.estimate", c(0,100), "all")

## plot
sum5 <- summary(stats5, fields = c("n","mean","se","lcl","ucl", "median"))
plot(c(0.5,6.5), c(-0.2,0.4), type="n", xlab = "Scenario", ylab = "RB(D-hat)")
for (i in 1:12) {
    xv <- if (i<=6) i else (i-6)+0.05
    segments (xv, sum5$OUTPUT[[i]]["RB","lcl"], xv, sum5$OUTPUT[[i]]["RB","ucl"])
    ptcol <- if (i<=6) "white" else "black"
    points(xv, sum5$OUTPUT[[i]]["RB","mean"], pch = 21, bg = ptcol)
}
abline(h = 0, col="red")
text(c(1.5,3.5,5.5), rep(0.38,3), paste("recapfactor", c(0.5,1,2), sep = " = "))
```

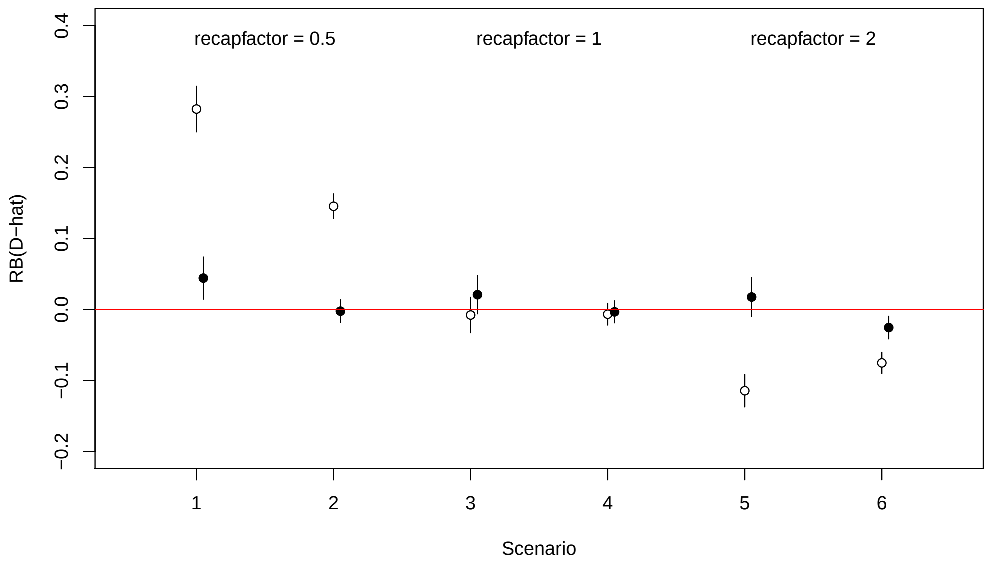


Figure 4: Relative bias of SECR density estimate from null model (filled circles) and `g0` $\sim$ `b` model (open circles) when data were generated with negative, zero, or positive learned response.

```
## look at extended output
sum5

run.scenarios(nrepl = 500, scenarios = scen5, trapset = traps5,
    fit = TRUE, fit.args = list(list(model = g0 ~ 1), list(model = g0 ~
        b)), ncores = 6)

Replicates    500
Started       12:05:03 02 May 2014
Run time      99.6  minutes
Output class  selectedstatistics

$constant
           value
noccasions     5
nrepeats       1
D              5
g0           0.2
sigma         25
```

```
detectfn        0
popindex        1
detindex        1

$varying
 scenario trapsindex recapfactor fitindex maskindex
        1          1         0.5        1         1
        2          2         0.5        1         2
        3          1         1.0        1         1
        4          2         1.0        1         2
        5          1         2.0        1         1
        6          2         2.0        1         2
        7          1         0.5        2         1
        8          2         0.5        2         2
        9          1         1.0        2         1
       10          2         1.0        2         2
       11          1         2.0        2         1
       12          2         2.0        2         2

$detectors
 trapsindex trapsname
          1   grid6x6
          2 grid10x10

$fit.args
 fitindex  model
        1 g0 ~ 1
        2 g0 ~ b

OUTPUT
$`trapsindex = 1, recapfactor = 0.5, fitindex = 1, maskindex = 1`
              n     mean      se      lcl      ucl   median
estimate    500  6.41255 0.08204  6.25175  6.57334  6.25433
SE.estimate 500  1.99650 0.02054  1.95623  2.03676  1.93299
lcl         500  3.55072 0.05517  3.44258  3.65885  3.36304
ucl         500 11.67837 0.12692 11.42960 11.92714 11.32535
RB          500  0.28251 0.01641  0.25035  0.31467  0.25087
RSE         500  0.32141 0.00251  0.31649  0.32633  0.31316
COV         500  0.86000 0.01553  0.82956  0.89044  1.00000

$`trapsindex = 2, recapfactor = 0.5, fitindex = 1, maskindex = 2`
```

```
              n    mean      se     lcl     ucl  median
estimate    500 5.72766 0.04459 5.64026 5.81506 5.66648
SE.estimate 500 1.02213 0.00456 1.01319 1.03107 1.01752
lcl         500 4.05010 0.03642 3.97872 4.12148 4.00269
ucl         500 8.10669 0.05348 8.00187 8.21152 8.03134
RB          500 0.14553 0.00892 0.12805 0.16301 0.13330
RSE         500 0.18094 0.00069 0.17958 0.18229 0.17943
COV         500 0.88000 0.01455 0.85149 0.90851 1.00000

$`trapsindex = 1, recapfactor = 1, fitindex = 1, maskindex = 1`
              n     mean      se      lcl     ucl   median
estimate    500  4.96161 0.06381  4.83654 5.08669  4.98843
SE.estimate 500  1.47525 0.01175  1.45223 1.49828  1.47518
lcl         500  2.81512 0.04459  2.72772 2.90251  2.78540
ucl         500  8.79952 0.08750  8.62803 8.97102  8.84495
RB          500 -0.00768 0.01276 -0.03269 0.01734 -0.00231
RSE         500  0.30992 0.00240  0.30521 0.31463  0.29930
COV         500  0.95000 0.00976  0.93088 0.96912  1.00000

$`trapsindex = 2, recapfactor = 1, fitindex = 1, maskindex = 2`
              n     mean      se      lcl     ucl   median
estimate    500  4.96749 0.03917  4.89071 5.04426  4.92346
SE.estimate 500  0.88098 0.00375  0.87364 0.88832  0.88014
lcl         500  3.52016 0.03224  3.45698 3.58334  3.47659
ucl         500  7.01611 0.04641  6.92515 7.10708  6.97002
RB          500 -0.00650 0.00783 -0.02186 0.00885 -0.01531
RSE         500  0.18008 0.00073  0.17866 0.18151  0.17812
COV         500  0.96000 0.00877  0.94281 0.97719  1.00000

$`trapsindex = 1, recapfactor = 2, fitindex = 1, maskindex = 1`
              n     mean      se      lcl      ucl   median
estimate    500  4.42837 0.05842  4.31386  4.54287  4.41579
SE.estimate 500  1.29956 0.00981  1.28034  1.31878  1.30119
lcl         500  2.53232 0.04180  2.45039  2.61425  2.49668
ucl         500  7.80193 0.07721  7.65061  7.95325  7.80782
RB          500 -0.11433 0.01168 -0.13723 -0.09143 -0.11684
RSE         500  0.30702 0.00243  0.30225  0.31178  0.29720
COV         500  0.94400 0.01029  0.92383  0.96417  1.00000

$`trapsindex = 2, recapfactor = 2, fitindex = 1, maskindex = 2`
              n     mean      se      lcl      ucl   median
```

```
estimate    500  4.62434 0.03824  4.54939  4.69929  4.59226
SE.estimate 500  0.81600 0.00362  0.80891  0.82309  0.81839
lcl         500  3.28267 0.03149  3.22094  3.34440  3.23926
ucl         500  6.52046 0.04528  6.43172  6.60920  6.49095
RB          500 -0.07513 0.00765 -0.09012 -0.06014 -0.08155
RSE         500  0.17943 0.00076  0.17795  0.18092  0.17822
COV         500  0.93200 0.01127  0.90991  0.95409  1.00000

$`trapsindex = 1, recapfactor = 0.5, fitindex = 2, maskindex = 1`
              n    mean      se     lcl      ucl  median
estimate    500 5.22167 0.07578 5.07315  5.37019 5.18323
SE.estimate 500 1.74583 0.02123 1.70423  1.78744 1.71095
lcl         500 2.78488 0.05062 2.68566  2.88410 2.70792
ucl         500 9.94459 0.12380 9.70195 10.18723 9.75850
RB          500 0.04433 0.01516 0.01463  0.07404 0.03665
RSE         500 0.34976 0.00350 0.34290  0.35661 0.33759
COV         500 0.94200 0.01046 0.92149  0.96251 1.00000

$`trapsindex = 2, recapfactor = 0.5, fitindex = 2, maskindex = 2`
              n     mean      se      lcl     ucl   median
estimate    500  4.98864 0.04090  4.90848 5.06880  4.97724
SE.estimate 500  0.92341 0.00434  0.91490 0.93192  0.92743
lcl         500  3.48357 0.03322  3.41845 3.54868  3.47396
ucl         500  7.15203 0.04916  7.05567 7.24838  7.15163
RB          500 -0.00227 0.00818 -0.01830 0.01376 -0.00455
RSE         500  0.18824 0.00084  0.18659 0.18989  0.18550
COV         500  0.94600 0.01012  0.92617 0.96583  1.00000

$`trapsindex = 1, recapfactor = 1, fitindex = 2, maskindex = 1`
              n     mean      se      lcl      ucl   median
estimate    500  5.10488 0.06876  4.97011  5.23966  4.95098
SE.estimate 500  1.72420 0.08918  1.54942  1.89899  1.58177
lcl         500  2.78061 0.04719  2.68812  2.87311  2.67837
ucl         500 10.08840 0.61405  8.88488 11.29193  9.19703
RB          500  0.02098 0.01375 -0.00598  0.04793 -0.00980
RSE         500  0.34471 0.01301  0.31922  0.37021  0.32122
COV         500  0.95800 0.00898  0.94040  0.97560  1.00000

$`trapsindex = 2, recapfactor = 1, fitindex = 2, maskindex = 2`
              n     mean      se      lcl     ucl   median
estimate    500  4.98399 0.03952  4.90652 5.06145  4.95613
```

```
SE.estimate 500  0.90665 0.00427  0.89827 0.91502  0.90778
lcl         500  3.50121 0.03202  3.43845 3.56397  3.48533
ucl         500  7.10126 0.04781  7.00755 7.19497  7.08731
RB          500 -0.00320 0.00790 -0.01870 0.01229 -0.00877
RSE         500  0.18461 0.00076  0.18313 0.18609  0.18262
COV         500  0.95000 0.00976  0.93088 0.96912  1.00000

$`trapsindex = 1, recapfactor = 2, fitindex = 2, maskindex = 1`
              n    mean      se       lcl     ucl  median
estimate    499 5.08846 0.06975  4.95175 5.22517 5.08003
SE.estimate 499 1.58825 0.01682  1.55528 1.62122 1.57657
lcl         499 2.81611 0.04749  2.72302 2.90920 2.80196
ucl         499 9.28585 0.10583  9.07842 9.49327 9.22943
RB          499 0.01769 0.01395 -0.00965 0.04503 0.01601
RSE         499 0.32504 0.00269  0.31976 0.33031 0.31165
COV         499 0.93587 0.01098  0.91436 0.95739 1.00000

$`trapsindex = 2, recapfactor = 2, fitindex = 2, maskindex = 2`
              n     mean      se       lcl      ucl   median
estimate    500  4.87325 0.04075  4.79337  4.95313  4.82339
SE.estimate 500  0.89038 0.00427  0.88201  0.89876  0.88879
lcl         500  3.41845 0.03312  3.35353  3.48337  3.39162
ucl         500  6.95444 0.04902  6.85836  7.05052  6.91494
RB          500 -0.02535 0.00815 -0.04133 -0.00937 -0.03532
RSE         500  0.18580 0.00080  0.18422  0.18737  0.18290
COV         500  0.94800 0.00994  0.92852  0.96748  1.00000
```

8.3 Non-uniform possums

Code to illustrate the use of homogeneous and inhomogeneous density models.

```
## add covariates to builtin secr object possummask
## D1 is homogeneous density
## D2 is artificial SW - NE gradient in density

xy <- apply(possummask,1,sum) / 500
covariates(possummask)[, "D1"] <- 2
covariates(possummask)[, "D2"] <- xy - mean(xy) + 2.5

## Note that this object already had a covariates dataframe
## -- if it didn't we would use
## covariates(possummask) <- data.frame ( D1 = ..., D2 = ...)

## specify scenarios
## anticipate two different sets of arguments for sim.popn
## with popindex = 1:2

scen5 <- make.scenarios (g0 = 0.2, sigma = 45, noccasions = 5,
    popindex = 1:2)

## specify alternate models for distribution of animals

poplist <- list(list(model2D = "IHP", D = "D1"),
                list(model2D = "IHP", D = "D2"))

## run scenarios and summarise
## we use the trap layout from the builtin secr object possumCH

sims5 <- run.scenarios (50, scen5, traps(possumCH), possummask,
    pop.args = poplist)
summary(sims5)

## output follows

run.scenarios(nrepl = 50, scenarios = scen5, trapset = traps(possumCH),
    maskset = possummask, pop.args = poplist)

Replicates    50
Started       09:53:30 29 Apr 2014
Run time      0.092  minutes
Output class  selectedstatistics

$constant
            value
trapsindex      1
noccasions      5
nrepeats        1
g0            0.2
sigma          45
detectfn        0
recapfactor     1
detindex        1
```

```
fitindex        1
maskindex       1

$varying
 scenario   D popindex
        1 2.0        1
        2 2.5        2

$detectors
 trapsindex trapsname
          1    traps1

$pop.args
 popindex model2D  D
        1     IHP D1
        2     IHP D2

OUTPUT
$`D = 2, popindex = 1`
      n      mean      se
n    50 110.20000 1.38210
ndet 50 272.18000 3.51773
nmov 50 144.38000 2.15006
dpa  50   2.21054 0.01278

$`D = 2.5, popindex = 2`
      n      mean      se
n    50 136.46000 1.50026
ndet 50 328.76000 3.92497
nmov 50 170.46000 2.39101
dpa  50   2.16096 0.01142
```

To visualise individual realisations of the distribution of animals, use `fit = FALSE` (the default), `det.args = list(savepopn = TRUE)`, and save the entire capthist object (`extractfn = identity`). Here we create a single replicate.

```
tmp <- run.scenarios (1, scen5, traps(possumCH), possummask,
    pop.args = poplist, det.args = list(savepopn = TRUE),
    extractfn = identity)

## tmp$output is now a list (one component per scenario) of lists
## (one component per replicate) of simulated capthist objects, each
## with its 'popn' object embedded as an attribute

par(mfrow = c(1,2))
plot(possummask, covariate = "D1")
plot(traps(possumCH), detpar=list(col='green', pch=15), add=T)
plot(attr(tmp$output[[1]][[1]], "popn"), frame = FALSE, add = TRUE,
    col = "blue", pch = 16, cex = 0.6)
plot(possummask, covariate = 'D2')
plot(traps(possumCH), detpar=list(col='green', pch=15), add=T)
plot(attr(tmp$output[[2]][[1]], "popn"), frame = FALSE, add = TRUE,
    col = "blue", pch = 16, cex = 0.6)

## click on map to display height; Esc to exit
spotHeight(possummask, prefix = "D2")
```

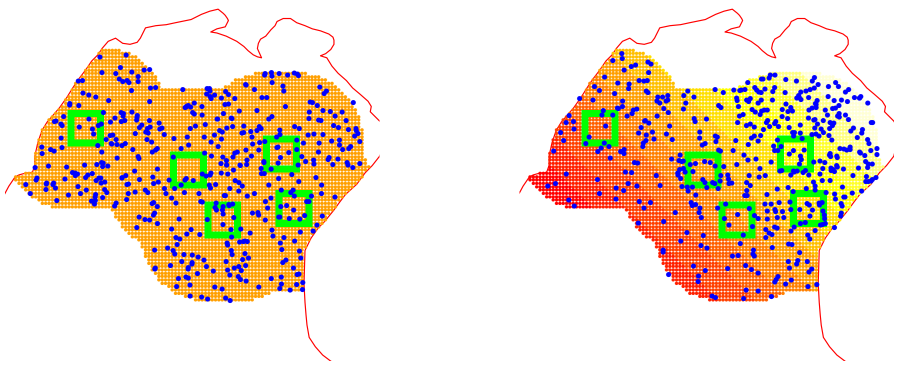


Figure 5: Simulated homogeneous (left) and inhomogeneous (right) distributions of brushtail possums at Waitarere, New Zealand. Traps in green (each hollow grid 180 m square).