

# Package ‘secrdesign’

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**Type** Package

**Title** Tools for Designing Spatially Explicit Capture--Recapture Studies

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**Imports** parallel, abind

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**Description** Tools for designing spatially explicit capture--  
recapture studies of animal populations (primarily a simulation manager for package secr)

**License** GPL (>=2)

**LazyData** yes

**LazyDataCompression** xz

**URL** <http://www.otago.ac.nz/density>

## R topics documented:

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secrdesign-package      *Spatially Explicit Capture–Recapture Study Design*

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## Description

Tools to assist the design of spatially explicit capture–recapture studies of animal populations.

## Details

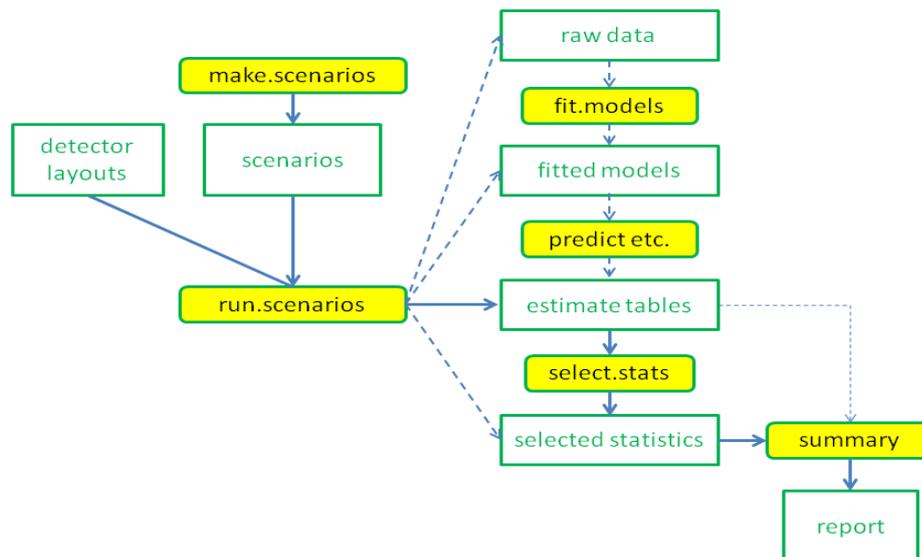
Package:    secr  
Type:        Package  
Version:    2.1.2  
Date:        2014-05-02  
License:    GNU General Public License Version 2 or later

The primary use of **secrdesign** is to predict by Monte Carlo simulation the precision or bias of density estimates from different detector layouts, given pilot values for density and the detection parameters  $g_0$  and  $\sigma$ .

The important functions in **secrdesign** are:

<code>make.scenarios</code>	generate dataframe of parameter values etc.
<code>run.scenarios</code>	perform simulations, with or without model fitting
<code>fit.models</code>	fit SECR model(s) to rawdata output from <code>run.scenarios</code>
<code>predict.fittedmodels</code>	infer ‘real’ parameter estimates from fitted models
<code>select.stats</code>	collect output for a particular parameter
<code>summary.selectedstatistics</code>	numerical summary of results
<code>plot.selectedstatistics</code>	histogram or CI plot for each scenario

Documentation is provided in a vignette [../doc/secrdesign.pdf](#); an Appendix has code for various examples that should help get you started.



`run.scenarios` produces an object of class `c(x, 'secrdesign', 'list')` where `x` depends on the arguments 'fit' and 'extractfn'. The options for `x` (the primary class) are

Class	Output from <code>extractfn()</code> for each replicate –
<code>fittedmodels</code>	complete (or trimmed) fitted model from <code>secr.fit</code>
<code>estimatable</code>	table of estimated parameters
<code>selectedstatistics</code>	vector of numerical values

When output from each replicate is saved from `run.scenarios` as a full or trimmed fitted model, further processing with `predict.fittedmodels` or related functions (`coef.fittedmodels`, `derived.SL`) will be needed before summarization. The default (when `fit = TRUE`) is to bypass this step by saving output from `run.scenarios` in 'estimatable' form.

The help pages are also available as [../doc/secrdesign-manual.pdf](#).

### Author(s)

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### See Also

[make.grid](#), [make.scenarios](#), [run.scenarios](#), [select.stats](#), [predict.fittedmodels](#), [summary.selectedstatist](#), [plot.selectedstatistics](#), [sim.popn](#), [sim.caphist](#) `secr.fit`

---

make.array

*Re-cast Simulated Statistical Output as Array*

---

### Description

This function is used internally by `summary.secrdesign`, and may occasionally be of general use.

**Usage**

```
make.array(object)
```

**Arguments**

`object`            `secrdesign` object containing numerical values for a particular parameter (i.e. output from `select.stats` inheriting from ‘selectedstatistics’)

**Details**

`make.array` converts a particular simulated numerical output into an array with one dimension for each varying input.

**Value**

A numeric array with dimensions corresponding to the varying inputs.

**See Also**

[run.scenarios](#)

**Examples**

```
## collect raw counts
scen1 <- make.scenarios(D = c(5,10), sigma = 25, g0 = 0.2)
traps1 <- make.grid()
tmp1 <- run.scenarios(nrepl = 50, trapset = traps1, scenarios = scen1,
  fit = FALSE)
make.array(tmp1)
```

---

make.scenarios

*Construct Scenario Data Frame*

---

**Description**

This function prepares a dataframe in which each row specifies a simulation scenario. The dataframe is used as input to [run.scenarios](#).

**Usage**

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

**Arguments**

trapsindex	integer vector determining the traps object to use
noccasions	integer vector for the number of sampling occasions
nrepeats	integer vector of multipliers for D (see Details)
D	numeric vector of values for the density parameter (animals / hectare)
g0	numeric vector of values for the g0 parameter
sigma	numeric vector of values for the sigma parameter (m)
lambda0	numeric vector of values for the lambda0 parameter
detectfn	vector of valid detection function codes (numeric or character)
recapfactor	numeric vector of values for recapfactor ( <a href="#">sim.caphist</a> )
popindex	integer vector determining which population model is used
detindex	integer vector determining which detection options are used
fitindex	integer vector determining which model is fitted
crosstraps	logical; if TRUE the output includes all combinations of trapsindex, noccasions and nrepeats

**Details**

The index in trapsindex is used in [run.scenarios](#) to select particular detector arrays from the list of arrays provided as an argument to that function.

The function generates all combinations of the given parameter values using [expand.grid](#). By default, it also generates all combinations of the parameters with trapsindex and the number of sampling occasions. If crosstraps is FALSE then trapsindex, noccasions, and nrepeats are merely used to fill in these columns in the output dataframe.

The argument lambda0 replaces g0 for the hazard detection functions 14–18 ([detectfn](#)).

Designs may use multiple detector arrays with the same internal geometry (e.g., number and spacing of traps). The number of such arrays is varied with the nrepeats argument. For example, you may compare designs with many small arrays or a few large ones. In practice, [run.scenarios](#) simulates a single layout is simulated with density  $D * nrepeats$ . This shortcut is not appropriate when animals compete for traps (detector = 'single').

fitindex allows a choice of different models when the argument fit.args of [run.scenarios](#) is a compound list.

**Value**

Dataframe with one row per scenario and the columns

scenario	a number identifying the scenario
trapsindex	
noccasions	
nrepeats	
D	
g0	or lambda0
sigma	
detectfn	see <a href="#">detectfn</a> ; always numeric

```
recapfactor
popindex
detindex
fitindex
```

### See Also

[run.scenarios](#), [sim.caphist](#)

### Examples

```
make.scenarios(trapsindex = 1, nrepeats = 1, D = c(5,10), sigma = 25,
g0 = 0.2)
```

---

predict.fittedmodels    *Extract Estimates From Fitted Models*

---

### Description

If simulations have been saved from `run.scenarios` as fitted secr models it is necessary to use one of these functions to extract estimates for later summarization.

### Usage

```
## S3 method for class 'fittedmodels'
predict(object, ...)

## S3 method for class 'fittedmodels'
coef(object, ...)

derived.SL(object, ...)

regionN.SL(object, ...)
```

### Arguments

object	fitted model simulation output from <a href="#">run.scenarios</a>
...	other arguments passed to predict, coef, derived or region.N

### Details

These functions are used when output from [run.scenarios](#) has been saved as fitted models. `derived.SL` and `regionN.SL` require a full fit (including the design object) whereas a trimmed model is sufficient for `predict` and `coef`.

`derived.SL` is used to compute the Horvitz-Thompson-like estimate of density when [secur.fit](#) has been used with `CL = TRUE`; it is roughly equivalent to `predict`.

regionN.SL predicts the realised number (R.N) or expected number (E.N) in a masked area. When detector layouts and/or sigma vary, the masked area will also vary (arbitrarily, depending on the buffer argument 'xsigma') unless a mask is provided by the user; this may be done either in run.scenarios or in regionN.SL.

### Value

An object with class ('estimatable', 'secredesign', 'list') with appropriate outputtype ('predicted', 'coef', 'derived', 'regionN'); see also [run.scenarios](#).

### See Also

[run.scenarios](#)

### Examples

```
## using nrepl = 2 just for checking
scen1 <- make.scenarios(D = c(5,10), sigma = 25, g0 = 0.2)
traps1 <- make.grid() ## default 6 x 6 grid of multi-catch traps
tmp1 <- run.scenarios(nrepl = 2, trapset = traps1, scenarios = scen1,
  fit = TRUE, extractfn = trim)
tmp2 <- predict(tmp1)
tmp3 <- select.stats(tmp2, 'D', c('estimate', 'RB', 'RSE'))
summary(tmp3)
```

---

run.scenarios

*Simulate Sampling Designs*

---

### Description

This function performs simulations to predict the precision of abundance estimates from simple 1-session SECR designs. Scenarios are specified via an input dataframe that will usually be constructed with [make.scenarios](#). Each scenario comprises an index to a detector layout, the number of sampling occasions, and specified density (D) and detection parameters (usually  $g_0$  and  $\sigma$ ).

Detector layouts are provided in a separate list trapset. This may comprise an actual field design input with [read.traps](#) or 'traps' objects constructed with [make.grid](#) etc., as in the Examples. Even a single layout must be presented as a component of a list (e.g., `list(make.grid())`).

If ncores > 1 then each scenario will be run in a separate worker process using parLapply from **parallel** (see also [Parallel](#)). Setting ncores greater than the number of scenarios causes an error.

Alternative approaches are offered for predicting precision. Both start by generating a pseudorandom dataset under the design using the parameter values for a particular scenario. The first estimates the parameter values and their standard errors from each dataset by maximizing the full likelihood, as usual in `secre.fit`. The second takes the short cut of computing variances and SE from the Hessian estimated numerically at the known expected values of the parameters, without maximizing the likelihood. Set `method = "none"` for this shortcut.

## Usage

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

fit.models(rawdata, fit = FALSE, fit.args, extractfn = NULL,
  ncores = 1, ...)
```

## Arguments

nrepl	integer number of replicate simulations
scenarios	dataframe of simulation scenarios
trapset	secr traps object or a list of traps objects
maskset	secr mask object or a list of mask objects (optional)
xsigma	numeric buffer width as multiple of sigma (alternative to maskset)
nx	integer number of cells in mask in x direction (alternative to maskset)
pop.args	list of named arguments to <a href="#">sim.popn</a> (optional)
det.args	list of named arguments to <a href="#">sim.caphist</a> (optional)
fit	logical; if TRUE a model is fitted with <code>secr.fit</code> , otherwise data are generated but no model is fitted
fit.args	list of named arguments to <a href="#">secr.fit</a> (optional)
extractfn	function to extract a vector of statistics from secr model
ncores	integer number of cores for parallel processing
seed	integer pseudorandom number seed
...	other arguments passed to <code>extractfn</code>
rawdata	'rawdata' object from previous call to <code>run.scenarios</code>

## Details

Designs are constructed from the trap layouts in `trapset`, the numbers of grids in `ngrid`, and the numbers of sampling occasions (secondary sessions) in `noccasions`. These are *not* crossed: the number of designs is the maximum length of any of these arguments. Any of these arguments whose length is less than the maximum will be replicated to match.

`pop.args` is used to customize the simulated population distribution. It will usually comprise a single list, but may be a list of lists (one per `popindex` value in `scenarios`).

`det.args` may be used to customize some aspects of the detection modelling in `sim.caphist`, but not `traps`, `popn`, `detectpar`, `detectfn`, and `noccasions`, which are controlled directly by the `scenarios`. It will usually comprise a single list, but may be a list of lists (one per `detindex` value in `scenarios`).

`fit.args` is used to customize the fitted model; it will usually comprise a single list. If you are interested in precision alone, use `fit.args=list(method = 'none')` to obtain variance estimates from the hessian evaluated at the parameter estimates. This is much faster than a complete model fit, and usually accurate enough.

If no `extractfn` is supplied then a default is used - see Examples. Replacement functions should follow this pattern i.e. test for whether the single argument is an `secr` object, and if not supply a named vector of NA values of the correct length.

The L'Ecuyer pseudorandom generator is used with a separate random number stream for each core (see [clusterSetRNGStream](#)).

A summary method is provided (see [summary.secrdesign](#)). It is usually necessary to process the simulation results further with [predict.fittedmodels](#) and/or [select.stats](#) before summarization.

### Value

An object of class (x, 'secrdesign', 'list'), where x is one of 'fittedmodels', 'estimatetables', 'selectedstatistics' or 'rawdata', with components

call	function call
version	character string including the software version number
starttime	character string for date and time of run
proctime	processor time for simulations, in seconds
scenarios	dataframe as input
trapset	list of trap layouts as input
maskset	list of habitat masks (input or generated)
xsigma	from input
nx	from input
pop.args	from input
det.args	from input
fit	from input
fit.args	from input
extractfn	function used to extract statistics from each simulation
seed	from input
nrepl	from input
output	list with one component per scenario
outputtype	character code - see vignette

If `fit = FALSE` and `extractfn = identity` the result is of class ('rawdata', 'secrdesign', 'list'). This may be used as input to `fit.models`, which interprets each model specification in `fit.args` as a new 'sub-scenario' of each input scenario (i.e. all models are fitted to every dataset). The output possibilities are the same as for `run.scenarios`.

### Note

100 ha = 1 km<sup>2</sup>

### Note

For `ncores > 1` it pays to keep an eye on the processes from the Performance page of Windows Task Manager (<ctrl><alt><del>), or 'top' in linux OS. If you interrupt `run.scenarios` (<Esc> from Windows) you may occasionally find some processes do not terminate and have to be manually terminated from the Task Manager - they appear as Rscript.exe on the Processes page.

### Author(s)

Murray Efford

**See Also**

[predict.fittedmodels](#), [select.stats](#), [summary.secrdesign](#), [summary.selectedstatistics](#), [sim.popn](#), [sim.caphist](#), [secr.fit](#)

**Examples**

```
## Simple example: generate and summarise trapping data
## at two densities and for two levels of sampling frequency
scen1 <- make.scenarios(D = c(5,10), sigma = 25, g0 = 0.2, noccasions =
  c(5,10))
traps1 <- make.grid() ## default 6 x 6 trap grid
tmp1 <- run.scenarios(nrepl = 20, trapset = traps1, scenarios = scen1,
  fit = FALSE)
summary(tmp1)

## Not run:

#####
## 2-phase example
## first make and save rawdata
scen1 <- make.scenarios(D = c(5,10), sigma = 25, g0 = 0.2)
traps1 <- make.grid() ## default 6 x 6 trap grid
tmp1 <- run.scenarios(nrepl = 20, trapset = traps1, scenarios = scen1,
  fit = FALSE, extractfn = identity)

## review rawdata
summary(tmp1)

## then fit and summarise models
tmp2 <- fit.models(tmp1, fit.args = list(list(model = g0~1),
  list(model = g0~T)), fit = TRUE, ncores = 4)
summary(tmp2)
#####

## Construct a list of detector arrays
## Each is a set of 5 parallel lines with variable between-line spacing;
## the argument that we want to vary (spacey) follows nx, ny and spacex
## in the argument list of make.grid().

spacey <- seq(2000,5000,500)
names(spacey) <- paste('line', spacey, sep = '.')
trapset <- lapply(spacey, make.grid, nx = 101, ny = 5, spacex = 1000,
  detector = 'proximity')

## Make corresponding set of masks with constant spacing (1 km)
maskset <- lapply(trapset, make.mask, buffer = 8000, spacing = 1000,
  type = 'trapbuffer')

## Generate scenarios
scen <- make.scenarios (trapsindex = 1:length(spacey), nrepeats = 8,
  noccasions = 2, D = 0.0002, g0 = c(0.05, 0.1), sigma = 1600, cross = TRUE)

## RSE without fitting model
sim <- run.scenarios (50, scenarios = scen, trapset = trapset, maskset = maskset,
  ncores = 8, fit = TRUE, fit.args = list(method = 'none'), seed = 123)
```

```

## Extract statistics for predicted density
sim <- select.stats(sim, parameter = 'D')

## Plot to compare line spacing
summ <- summary(sim, type='array', fields = c('mean','lcl','ucl'))$summary
plot(0,0,type='n', xlim=c(1.500,5.500), ylim = c(0,0.36), yaxs = 'i',
     xaxs = 'i', xlab = 'Line spacing km', ylab = 'RSE (D)')
xv <- seq(2,5,0.5)
points(xv, summ$mean[,1,'RSE'], type='b', pch=1)
points(xv, summ$mean[,2,'RSE'], type='b', pch=16)
segments(xv, summ$lcl[,1,'RSE'], xv, summ$ucl[,1,'RSE'])
segments(xv, summ$lcl[,2,'RSE'], xv, summ$ucl[,2,'RSE'])
legend(4,0.345, pch=c(1,16), title = 'Baseline detection',
      legend = c('g0 = 0.05', 'g0 = 0.1'))

## End(Not run)

```

---

select.stats

*Select Statistics to Summarize*


---

## Description

When the results of each simulation with `run.scenarios` are saved as a dataframe (e.g. from `predict()`) it is necessary to select estimates of just one parameter for numerical summarization. This does the job. `find.param` is a helper function to quickly display the parameters available for summarisation.

## Usage

```

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

```

## Arguments

<code>object</code>	'estimatetables' object from <code>run.scenarios</code>
<code>parameter</code>	character name of parameter to extract
<code>statistics</code>	character vector of statistic names

## Details

`select.stats` is used to select a particular vector of numeric values for summarization. The 'parameter' argument indexes a row in the dataframe for one replicate (i.e., one 'real' parameter). Each 'statistic' is either a column in that dataframe or a statistic derived from a column.

If `statistics` is not specified, the default is to use all numeric columns in the input (i.e., `c('estimate', 'SE.estimate', 'lcl', 'ucl')` for `predict` and `c('beta', 'SE.beta', 'lcl', 'ucl')` for `coef`).

statistics may include any of 'estimate', 'SE.estimate', 'lcl', 'ucl', 'true', 'RB', 'RSE', 'COV' and 'ERR' (for outputtype 'coef' use 'beta' and 'SE.beta' instead of 'estimate' and 'SE.estimate'). 'true' refers to the known parameter value used to generate the data.

The computed statistics are:

Statistic	Name	Value
RB	Relative bias	(estimate - true) / true
RSE	Relative SE	SE.estimate / estimate
ERR	Absolute deviation	abs(estimate - true)
COV	Coverage	(estimate > lcl) & (estimate < ucl)

'RB', 'COV' and 'ERR' relate an estimate to the known (true) value of the parameter in object\$scenarios. They are computed only when a model has been fitted without method = 'none'.

'COV' remains binary (0/1) in the output from select.stats; the result of interest is the mean of this statistic across replicates (see [summary.secrdesign](#)). Similarly, 'ERR' is used with field 'rms' in [summary.secrdesign](#) to compute the root-mean-squared-error RMSE.

find.param and find.stats may be used to 'peek' at objects of class 'estimatetables' and 'select-edstatistics' respectively to recall the available parameter estimates or 'statistics'.

## Value

For select.stats, an object with class c('selectedstatistics', 'secrdesign', 'list') suitable for numerical summarization with [summary.selectedstatistics](#). The value of 'parameter' is stored as an attribute.

For find.param, a character vector of the names of parameters with estimates in object.

## See Also

[run.scenarios](#), [validate](#)

## Examples

```
## using nrepl = 2 just for checking
scen1 <- make.scenarios(D = c(5,10), sigma = 25, g0 = 0.2)
traps1 <- make.grid()
tmp1 <- run.scenarios(nrepl = 2, trapset = traps1, scenarios = scen1,
  fit = TRUE, extractfn = trim)
tmp2 <- predict(tmp1)
tmp3 <- select.stats(tmp2, 'D', c('estimate', 'RB', 'RSE', 'COV'))
summary(tmp3)
```

---

summary.secrdesign      *Generic Methods for secrdesign Objects*

---

## Description

Methods to summarize simulated datasets.

**Usage**

```
## S3 method for class 'secrdesign'
summary(object, ...)

## S3 method for class 'rawdata'
summary(object, ...)

## S3 method for class 'estimatable'
summary(object, ...)

## S3 method for class 'selectedstatistics'
summary(object, dec = 5, fields = c('n', 'mean',
'se'), alpha = 0.05, type = c('list', 'dataframe', 'array'), ...)

## S3 method for class 'selectedstatistics'
plot(x, scenarios, statistic, type =
c('hist', 'CI'), refline, xlab = NULL, ...)

header(object)
```

**Arguments**

object	object of class simulations from run.scenarios
dec	number of decimal places in output
fields	character vector; names of required summary statistics (see Details)
alpha	alpha level for confidence intervals and quantiles
type	character code for type of output (see Details)
...	other arguments – not currently used by summary but passed to <a href="#">hist</a> by the plot method
x	object of class 'selectedstatistics' from run.scenarios
scenarios	integer indices of scenarios to plot (all plotted if not specified)
statistic	integer or character indices if the statistics in x for which histograms are requested
refline	logical; if TRUE a reference line is plotted at the true value of a parameter
xlab	character; optional label for x-axis

**Details**

If object inherits from 'selectedstatistics' then the numeric

If object inherits from 'selectedstatistics' then the numeric results from replicate simulations are summarized using the chosen 'fields' (by default, the number of non-missing values, mean and standard error), along with header information describing the simulations. Otherwise the header alone is returned.

fields is a vector of any selection from c('n', 'mean', 'sd', 'se', 'min', 'max', 'lcl', 'ucl', 'median', 'q', 'rms'), or the character value 'all'.

Field 'q' provides 1000 alpha/2 and 1000[1 - alpha/2] quantiles qxxx and qyyy.

'lcl' and 'ucl' refer to the upper and lower limits of a  $100(1 - \alpha)\%$  confidence interval for the statistic, across replicates.

'rms' gives the root-mean-square of the statistic - most useful for the statistic 'ERR' (see [select.stats](#)) when it represents the overall accuracy or RMSE.

The plot method plots either (i) histograms of the selected statistics (type = 'hist') or (ii) the estimate and confidence interval for each replicate (type = 'CI'). The default for type = 'hist' is to plot the first statistic - this is usually 'n' (number of detected animals) when `fit = FALSE`, and 'estimate' (parameter estimate) when `fit = TRUE`. If `length(statistic) > 1` then more than one plot will be produced, so a multi-column or multi-row layout should be prepared with `par` arguments 'mfc' or 'mfrow'.

For type = 'CI' the statistics must include 'estimate', 'lcl' and 'ucl' (or 'beta', 'lcl' and 'ucl' if `outputtype = 'coef'`).

### Value

List with components 'header'

<code>call</code>	original function call
<code>starttime</code>	from object
<code>proctime</code>	from object
<code>constants</code>	small dataframe with values of non-varying inputs
<code>varying</code>	small dataframe with values of varying inputs
<code>fit.args</code>	small dataframe with values arguments for <code>secr.fit</code> , if specified

and 'OUTPUT', a list with one component for each field. Each component may be a list or an array.

### See Also

[run.scenarios](#), [make.array](#), [select.stats.validate](#)

### Examples

```
## collect raw counts
scen1 <- make.scenarios(D = c(5,10), sigma = 25, g0 = 0.2)
traps1 <- make.grid()
tmp1 <- run.scenarios(nrepl = 50, trapset = traps1, scenarios = scen1,
  fit = FALSE)

opar <- par(mfrow=c(2,3))
plot(tmp1, statistic = 1:3)
par(opar)

summary(tmp1)

summary(tmp1, field=c('q025', 'median', 'q975'))
```

---

validate *Reject Implausible Statistics*

---

### Description

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. Undue influence of rogue replicates can be reduced by using the median as a summary field rather than the mean. This function is another way to deal with the problem, by setting to NA selected statistics from replicates for which some ‘test’ statistic is out-of-range.

### Usage

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

### Arguments

x	object that inherits from ‘selectedstatistics’
test	character; name of statistic to check
validrange	numeric vector comprising the minimum and maximum permitted values of ‘test’, or a matrix (see details)
targets	character vector with names of one or more statistics to set to missing (NA) when test is out-of-range

### Details

Values of ‘test’ and ‘targets’ should be columns in each component ‘replicate x statistic’ matrix (i.e., scenario) of `x$output`. You can check for these with [find.stats](#).

If `validrange` is a matrix its first and second columns are interpreted as scenario-specific bounds (minima and maxima), and the number of rows must match the number of scenarios.

If all non-missing values of ‘test’ are in the valid range, the effect is to force the target statistics to NA wherever ‘test’ is NA.

The default is to change only the test field itself. If the value of ‘test’ does not appear in ‘targets’ then the test field is unchanged.

If `targets = "all"` then all columns are set to NA when the test fails.

### Value

An object of class `c(‘selectedstatistics’, ‘secrdesign’, ‘list’)` with the same structure and header information as the input, but possibly with some values in the ‘output’ component converted to NA.

### See Also

[select.stats](#), [find.stats](#)

**Examples**

```
## Not run:

## generate some data
scen1 <- make.scenarios(D = c(5,10), sigma = 25, g0 = 0.2)
traps1 <- make.grid()
tmp1 <- run.scenarios(nrepl = 5, trapset = traps1, scenarios = scen1,
  fit = TRUE, extractfn = trim)
tmp2 <- predict(tmp1)
tmp3 <- select.stats(tmp2, 'D', c('estimate','RB','RSE','COV'))

## just for demonstration --
## apply scenario-specific +/- 20% bounds for estimated density
## set RB, RSE and COV to NA when estimate is outside this range
permitted <- outer(tmp3$scenarios$D, c(0.8,1.2))
permitted ## a 2 x 2 matrix
tmp4 <- validate(tmp3, 'estimate', permitted, c('RB', 'RSE','COV'))

## what have we done?!
tmp4$output
summary(tmp4)

## End(Not run)
```

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