

Package ‘raptr’

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Type Package

Title Representative and Adequate Prioritization Toolkit in R

Version 0.1.3

Description Biodiversity is in crisis. The overarching aim of conservation is to preserve biodiversity patterns and processes. To this end, protected areas are established to buffer species and preserve biodiversity processes. But resources are limited and so protected areas must be cost-effective. This package contains tools to generate plans for protected areas (prioritizations), using spatially explicit targets for biodiversity patterns and processes. To obtain solutions in a feasible amount of time, this package uses the commercial 'Gurobi' software package (obtained from <http://www.gurobi.com/>). For more information on using this package, see Hanson et al. (2017) <doi:10.1111/2041-210X.12862>.

Imports utils, methods, assertthat, Matrix, boot, grDevices, PBSmapping, graphics, stats, scales, shape, adehabitatHR, RgoogleMaps, RandomFields, RColorBrewer, plyr, parallel, doParallel, rgeos, rgdal, hypervolume(>= 2.0.7), ks, gdalUtils, mvtnorm, ggplot2

Depends R(>= 3.1.0), sp, raster

LinkingTo Rcpp, RcppEigen, BH

LazyData true

License GPL-3

URL <https://jeffrey-hanson.com/raptr>,
<https://github.com/jeffreyhanson/raptr>

BugReports <https://github.com/jeffreyhanson/raptr/issues>

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Suggests knitr, roxygen2, dplyr, vegan, gurobi, gridExtra, rgl, testthat

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 'generics.R' 'DemandPoints.R' 'misc.R' 'PlanningUnitPoints.R'
 'AttributeSpace.R' 'AttributeSpaces.R' 'GurobiOpts.R'
 'ManualOpts.R' 'calcSpeciesAverageInPus.R' 'calcBoundaryData.R'
 'RapData.R' 'RapReliableOpts.R' 'RapResults.R'
 'RapUnreliableOpts.R' 'RapUnsolved.R' 'RapSolved.R'
 'SpatialPolygons2PolySet.R' 'data.R' 'rap.R' 'raptr.R'
 'rrap.proportion.held.R' 'sim.pus.R' 'sim.space.R'
 'sim.species.R' 'urap.proportion.held.R' 'zzz.R'

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R topics documented:

amount.held	4
amount.target	5
as.list	6
AttributeSpace	7
AttributeSpace-class	7
AttributeSpaces	8
AttributeSpaces-class	9
blank.raster	9
calcBoundaryData	10
calcSpeciesAverageInPus	11
casestudy_data	12
DemandPoints	13
DemandPoints-class	14
dp.subset	14
GurobiOpts	15
GurobiOpts-class	16
is.gdalInstalled	17
is.GurobiInstalled	18
logging.file	18
make.DemandPoints	19
make.RapData	21
ManualOpts	22
ManualOpts-class	23
maximum.targets	23
names	24

PlanningUnitPoints	25
PlanningUnitPoints-class	26
plot	26
PolySet-class	28
print	28
prob.subset	29
pu.subset	30
randomPoints	31
rap	32
RapData	33
RapData-class	34
RapOpts-class	35
RapReliableOpts	35
RapReliableOpts-class	36
RapResults	36
RapResults-class	38
RapSolved	39
RapSolved-class	39
raptr	40
RapUnreliableOpts	40
RapUnreliableOpts-class	41
RapUnsolved	41
RapUnsolved-class	42
rasterizeGDAL	43
rrap.proportion.held	44
score	45
selections	46
show	47
sim.pus	48
sim.space	49
sim.species	50
simulated_data	52
solve	53
SolverOpts-class	54
space.held	55
space.plot	56
space.target	57
SpatialPolygons2PolySet	58
spp.plot	59
spp.subset	61
summary	62
update	63
urap.proportion.held	65

amount.held	<i>Extract amount held for a solution</i>
-------------	---

Description

This function returns the amount held for each species in a solution.

Usage

```
amount.held(x, y, species)

## S3 method for class 'RapSolved'
amount.held(x, y = 0, species = NULL)
```

Arguments

x	RapResults or RapSolved object.
y	Available inputs include: NULL to return all values, integer number specifying the solution for which the value should be returned, and 0 to return the value for the best solution.
species	NULL for all species or integer indicating species.

Value

[matrix](#) or numeric vector depending on arguments.

See Also

[RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# amount held (\%) in best solution for each species
amount.held(sim_rs, 0)

# amount held (\%) in best solution for species 1
amount.held(sim_rs, 0, 1)

# amount held (\%) in second solution for each species
amount.held(sim_rs, 2)

# amount held (\%) in each solution for each species
amount.held(sim_rs, NULL)
```

amount.target	<i>Amount targets</i>
---------------	-----------------------

Description

This function sets or returns the target amounts for each species.

Usage

```
amount.target(x, species)

amount.target(x, species) <- value

## S3 method for class 'RapData'
amount.target(x, species = NULL)

## S3 replacement method for class 'RapData'
amount.target(x, species = NULL) <- value

## S3 method for class 'RapUnsol0rSol1'
amount.target(x, species = NULL)

## S3 replacement method for class 'RapUnsol0rSol1'
amount.target(x, species = NULL) <- value
```

Arguments

x	RapData , RapUnsolved , or RapSolved object.
species	NULL for all species or integer indicating species.
value	numeric new target.

Value

codenumeric vector.

See Also

[RapData](#), [RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# extract amount targets for all species
amount.target(sim_rs)
```

```
# set amount targets for all species
amount.target(sim_rs) <- 0.1

# extract amount targets for first species
amount.target(sim_rs, 1)

# set amount targets for for first species
amount.target(sim_rs, 1) <- 0.5
```

as.list

Convert object to list

Description

Convert [GurobiOpts](#) object to list.

Usage

```
## S3 method for class 'GurobiOpts'
as.list(x, ...)
```

Arguments

x [GurobiOpts](#) object.
... not used.

Value

list

Note

This function will not include the `NumberSolutions` slot, the `MultipleSolutionsMethod` slot, or the `TimeLimit` slot if it is not finite.

See Also

[GurobiOpts](#).

Examples

```
# make GuboriOpts object
x <- GurobiOpts()

# convert to list
as.list(x)
```

AttributeSpace	Create new AttributeSpace object
----------------	----------------------------------

Description

This function creates a new AttributeSpace object.

Usage

```
AttributeSpace(planning.unit.points, demand.points, species)
```

Arguments

`planning.unit.points` [PlanningUnitPoints](#) for planning unit in the space.
`demand.points` [DemandPoints](#) object for the space.
`species` integer species id to indicate which species the space is associated with.

See Also

[DemandPoints-class](#), [PlanningUnitPoints-class](#).

Examples

```
space <- AttributeSpace(  
  PlanningUnitPoints(  
    matrix(rnorm(100), ncol = 2),  
    seq_len(50)),  
  DemandPoints(  
    matrix(rnorm(100), ncol = 2),  
    runif(50)),  
  species = 1L)
```

AttributeSpace-class	AttributeSpace: An S4 class to represent an attribute space.
----------------------	--

Description

This class is used to store planning unit points and demand points for a single species in an attribute space.

Slots

`planning.unit.points` [PlanningUnitPoints](#) for planning unit in the space.
`demand.points` [DemandPoints](#) object for the space.
`species` integer species id to indicate which species the space is associated with.

See Also

[DemandPoints-class](#), [PlanningUnitPoints-class](#).

AttributeSpaces

Create new AttributeSpaces object

Description

This function creates a new AttributeSpaces object.

Usage

```
AttributeSpaces(spaces, name)
```

Arguments

spaces	list of AttributeSpace objects for different species.
name	character name to identify the attribute space.

See Also

[AttributeSpace-class](#).

Examples

```
space1 <- AttributeSpace(  
  PlanningUnitPoints(  
    matrix(rnorm(100), ncol = 2),  
    seq_len(50)),  
  DemandPoints(  
    matrix(rnorm(100), ncol = 2),  
    runif(50)),  
  species = 1L)  
  
space2 <- AttributeSpace(  
  PlanningUnitPoints(  
    matrix(rnorm(100), ncol = 2),  
    seq_len(50)),  
  DemandPoints(  
    matrix(rnorm(100), ncol = 2),  
    runif(50)),  
  species = 2L)  
  
spaces <- AttributeSpaces(list(space1, space2), "spaces")
```

AttributeSpaces-class *AttributeSpaces*: An S4 class to represent a collection of attribute spaces for different species.

Description

This class is used to store a collection of attribute spaces for different species.

Slots

spaces list of [AttributeSpace](#) objects for different species.

name character name to identify the attribute space.

See Also

[AttributeSpace-class](#).

blank.raster	<i>Blank raster</i>
--------------	---------------------

Description

This functions creates a blank raster based on the spatial extent of a Spatial object.

Usage

```
blank.raster(x, res)
```

Arguments

x [Spatial-class](#) object.

res numeric vector specifying resolution of the output raster in the x and y dimensions. If vector is of length one, then the pixels are assumed to be square.

Examples

```
# make SpatialPolygons
polys <- sim.pus(225L)

# make RasterLayer from SpatialPolygons
blank.raster(polys, 1)
```

calcBoundaryData	<i>Calculate boundary data for planning units</i>
------------------	---

Description

This function calculates boundary length data for [PolySet](#), [SpatialPolygons](#), and [SpatialPolygonsDataFrame](#) objects. Be aware that this function is designed with performance in mind, and as a consequence, if this function is used improperly then it may crash R. Furthermore, multipart polygons with touching edges will likely result in inaccuracies. If argument set to [SpatialPolygons](#) or [SpatialPolygonsDataFrame](#), this will be converted to [PolySet](#) before processing.

Usage

```
calcBoundaryData(x, tol, length.factor, edge.factor)
```

```
## S3 method for class 'PolySet'
```

```
calcBoundaryData(x, tol = 0.001, length.factor = 1,  
  edge.factor = 1)
```

```
## S3 method for class 'SpatialPolygons'
```

```
calcBoundaryData(x, tol = 0.001,  
  length.factor = 1, edge.factor = 1)
```

Arguments

x	PolySet , SpatialPolygons or SpatialPolygonsDataFrame object.
tol	numeric to specify precision of calculations. In other words, how far apart vertices have to be to be considered different?
length.factor	numeric to scale boundary lengths.
edge.factor	numeric to scale boundary lengths for edges that do not have any neighbors, such as those that occur along the margins.
...	not used.

Value

data.frame with 'id1' (integer), 'id2' (integer), and 'amount' (numeric) columns.

See Also

This function is based on the algorithm in QMARXAN <https://github.com/tsw-afropos/qmarxan> for calculating boundary length.

Examples

```
# simulate planning units
sim_pus <- sim.pus(225L)

# calculate boundary data
bound.dat <- calcBoundaryData(sim_pus)

# print summary of boundary data
summary(bound.dat)
```

```
calcSpeciesAverageInPus
```

Calculate average value for species data in planning units

Description

This function calculates the average of species values in each planning unit. Be aware that using polygons with overlaps will result in inaccuracies. By default all polygons will be treated as having separate ids.

Usage

```
calcSpeciesAverageInPus(x, ...)

## S3 method for class 'SpatialPolygons'
calcSpeciesAverageInPus(x, y,
  ids = seq_len(nlayers(y)), ncores = 1, gdal = FALSE, ...)

## S3 method for class 'SpatialPolygonsDataFrame'
calcSpeciesAverageInPus(x, y,
  ids = seq_len(nlayers(y)), ncores = 1, gdal = FALSE,
  field = NULL, ...)
```

Arguments

x	SpatialPolygons or SpatialPolygonsDataFrame object.
...	not used.
y	RasterLayer-class , RasterStack-class , or RasterBrick-class object.
ids	integer vector of ids. Defaults to indices of layers in argument to y.
ncores	integer number of cores to use for processing. Defaults to 1.
gdal	logical Should raster processing be performed using GDAL libraries? Defaults to FALSE.
field	integer index or character name of column with planning unit ids. Valid only when x is a SpatialPolygonsDataFrame object. Default behavior is to treat each polygon as a different planning unit.

Value

`data.frame` with sum of raster values in each polygon.

See Also

`is.gdalInstalled`, <http://www.gdal.org/>, <http://trac.osgeo.org/gdal/wiki/DownloadingGdalBinaries>.

Examples

```
# simulate data
sim_pus <- sim.pus(225L)
sim_spp <- lapply(c("uniform", "normal", "bimodal"), sim.species, n = 1,
                 res = 1, x = sim_pus)

# calculate average for 1 species
puvspr1.dat <- calcSpeciesAverageInPus(sim_pus, sim_spp[[1]])

# calculate average for multiple species
puvspr2.dat <- calcSpeciesAverageInPus(sim_pus, stack(sim_spp))
```

casestudy_data

Case-study dataset for a conservation planning exercise

Description

This dataset contains data to generate example prioritizations for the pale-headed Rosella (*Platycercus adscitus*) in Queensland, Australia.

Usage

`cs_pus`

`cs_space`

`cs_spp`

Format

`cs_pus`: `SpatialPolygonsDataFrame`, `cs_spp`: `RasterLayer-class`, `cs_space`: `RasterStack-class`.

Details

The objects in the dataset are listed below.

cs_pus `SpatialPolygonsDataFrame` planning units. The units were generated as $30km^2$ squares across the species' range, and then clipped to the Queensland, Australia (using data obtained from the <http://www.abs.gov.au/ausstats/abs@.nsf/mf/1259.0.30.001?OpenDocument>). They were then overlaid with Australia's protected area network (obtained from the World Database on Protected Areas (WDPA) at <http://www.protectedplanet.net/>). This attribute table has 3 fields. The area field denotes the amount of land encompassed by each unit, the cost field is set to 1 for all units, and the status field indicates if 50% or more of the units' extent is covered by protected areas.

cs_spp `RasterLayer-class` probability distribution map for the *P. adscitus* clipped to Queensland, Australia. This map was derived from records obtained from The Atlas of Living Australia (<http://ala.org.au/>).

cs_space `stack` describing broad-scale climate variation across Queensland (obtained from <http://www.worldclim.org/>, and resampled to $10km^2$ resolution).

Examples

```
# load data
data(cs_pus, cs_spp, cs_space)

# plot data

plot(cs_pus)
plot(cs_spp)
plot(cs_space)
```

DemandPoints

Create new DemandPoints object

Description

This function creates a new DemandPoints object

Usage

```
DemandPoints(coords, weights)
```

Arguments

`coords` `matrix` of coordinates for each demand point.
`weights` numeric weights for each demand point.

See Also

[DemandPoints-class](#).

Examples

```
# make demand points
dps <- DemandPoints(
  matrix(rnorm(100), ncol=2),
  runif(50))

# print object
print(dps)
```

DemandPoints-class *DemandPoints: An S4 class to represent demand points*

Description

This class is used to store demand point information.

Slots

coords [matrix](#) of coordinates for each demand point.
weights numeric weights for each demand point.

See Also

[DemandPoints](#).

dp.subset *Subset demand points*

Description

Subset demand points from a [RapData](#), [RapUnsolved](#), or [RapSolved](#) object.

Usage

```
dp.subset(x, space, species, points)

## S3 method for class 'RapData'
dp.subset(x, space, species, points)

## S3 method for class 'RapUnsolvedOrSolved'
dp.subset(x, space, species, points)
```

Arguments

x	RapData , RapUnsolved , or RapSolved object.
space	integer vector to specify the index of the space to subset demand points from.
species	integer vector to specify the index of the species to subset demand points from.
points	integer vector to specify the index of demand points to subset.

Value

[RapData](#) or [RapUnsolved](#) object depending on input object.

See Also

[RapData](#), [RapUnsolved](#), [RapSolved](#).

Examples

```
# load data
data(sim_ru)

# generate new object with first 10 planning units
sim_ru2 <- dp.subset(sim_ru, 1, 1, seq_len(10))
```

GurobiOpts

Create GurobiOpts object

Description

This function creates a new GurobiOpts object.

Usage

```
GurobiOpts(Threads = 1L, MIPGap = 0.1, Method = 0L, Presolve = 2L,
  TimeLimit = NA_integer_, NumberSolutions = 1L,
  MultipleSolutionsMethod = c("benders.cuts", "solution.pool.0",
  "solution.pool.1", "solution.pool.2")[1])
```

Arguments

Threads	integer number of cores to use for processing. Defaults to 1L.
MIPGap	numeric MIP gap specifying minimum solution quality. Defaults to 0.1.
Method	integer Algorithm to use for solving model. Defaults to 0L.
Presolve	integer code for level of computation in presolve (lp_solve parameter). Defaults to 2.
TimeLimit	integer number of seconds to allow for solving. Defaults to NA_integer_, and so a time limit is not imposed.

NumberSolutions

integer number of solutions to generate. Defaults to 1L.

MultipleSolutionsMethod

integer name of method to obtain multiple solutions (used when NumberSolutions is greater than one). Available options are "benders.cuts", "solution.pool.0", "solution.pool.1", and "solution.pool.2". The "benders.cuts" method produces a set of distinct solutions that are all within the optimality gap. The "solution.pool.0" method returns all solutions identified whilst trying to find a solution that is within the specified optimality gap. The "solution.pool.1" method finds one solution within the optimality gap and a number of additional solutions that are of any level of quality (such that the total number of solutions is equal to number_solutions). The "solution.pool.2" finds a specified number of solutions that are nearest to optimality. The search pool methods correspond to the parameters used by the Gurobi software suite (see <http://www.gurobi.com/documentation/8.0/refman/poolsearchmode.html#parameter:PoolSearchMode>). Defaults to "benders.cuts".

Value

GurobiOpts object

See Also

[GurobiOpts-class](#).

Examples

```
# create GurobiOpts object using default parameters
GurobiOpts(Threads = 1L, MIPGap = 0.1, Method = 0L, Presolve=2L,
           TimeLimit = NA_integer_, NumberSolutions = 1L)
```

GurobiOpts-class

GurobiOpts: An S4 class to represent Gurobi parameters

Description

This class is used to store Gurobi input parameters.

Slots

Threads integer number of cores to use for processing. Defaults to 1L.

MIPGap numeric MIP gap specifying minimum solution quality. Defaults to 0.1.

Method integer Algorithm to use for solving model. Defaults to 0L.

Presolve integer code for level of computation in presolve. Defaults to 2.

TimeLimit integer number of seconds to allow for solving. Defaults to NA_integer_, and so a time limit is not imposed.

NumberSolutions integer number of solutions to generate. Defaults to 1L.

MultipleSolutionsMethod integer name of method to obtain multiple solutions (used when NumberSolutions is greater than one). Available options are "benders.cuts", "solution.pool.0", "solution.pool.1", and "solution.pool.2". The "benders.cuts" method produces a set of distinct solutions that are all within the optimality gap. The "solution.pool.0" method returns all solutions identified whilst trying to find a solution that is within the specified optimality gap. The "solution.pool.1" method finds one solution within the optimality gap and a number of additional solutions that are of any level of quality (such that the total number of solutions is equal to number_solutions). The "solution.pool.2" finds a specified number of solutions that are nearest to optimality. The search pool methods correspond to the parameters used by the Gurobi software suite (see <http://www.gurobi.com/documentation/8.0/refman/poolsearchmode.html#parameter:PoolSearchMode>). Defaults to "benders.cuts".

See Also

[GurobiOpts](#).

is.gdalInstalled	<i>Test if GDAL is installed on computer</i>
------------------	--

Description

This function tests if GDAL is installed on the computer. If not, download it here: <http://download.osgeo.org/gdal>.

Usage

```
is.gdalInstalled()
```

Value

logical is GDAL installed?

See Also

[gdal_setInstallation](#).

Examples

```
# check if gdal is installed on system  
  
is.gdalInstalled()
```

is.GurobiInstalled *Test if Gurobi is installed*

Description

This function determines if the Gurobi R package is installed on the computer and that it can be used [options](#).

Usage

```
is.GurobiInstalled(verbose = TRUE)
```

Arguments

verbose logical should messages be printed?

Value

logical Is it installed and ready to use?

See Also

[options](#).

Examples

```
# check if Gurobi is installed
is.GurobiInstalled()

# print cached status of installation
options()$GurobiInstalled
```

logging.file *Log file*

Description

This function returns the Gurobi log file (*.log) associated with solving an optimization problem.

Usage

```
logging.file(x, y)

## S3 method for class 'RapResults'
logging.file(x, y = 0)

## S3 method for class 'RapSolved'
logging.file(x, y = 0)
```

Arguments

x	RapResults or RapSolved object.
y	Available inputs include: NULL to return all values, integer number specifying the solution for which the log file should be returned, and 0 to return log file for the best solution.

Note

The term logging file was used due to collisions with the log function.

See Also

[RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# log file for the best solution
cat(logging.file(sim_rs, 0))

# log file for the second solution
cat(logging.file(sim_rs, 2))

# log files for all solutions
cat(logging.file(sim_rs, NULL))
```

make.DemandPoints	<i>Generate demand points for RAP</i>
-------------------	---------------------------------------

Description

This function generates demand points to characterize a distribution of points.

Usage

```
make.DemandPoints(points, n = 100L, quantile = 0.5,
  kernel.method = c("ks", "hypervolume")[1], ...)
```

Arguments

points	matrix object containing points.
n	integer number of demand points to use for each attribute space for each species. Defaults to 100L.
quantile	numeric quantile to generate demand points within. If 0 then demand points are generated across the full range of values the points intersect. Defaults to 0.5.
kernel.method	character name of kernel method to use to generate demand points. Defaults to 'ks'.
...	arguments passed to kernel density estimating functions

Details

Broadly speaking, demand points are generated by fitting a kernel to the input points. A shape is then fit to the extent of the kernel, and then points are randomly generated inside the shape. The demand points are generated as random points inside the shape. The weights for each demand point are calculated the estimated density of input points at the demand point. By supplying 'ks' as an argument to method in kernel.method, the shape is defined using a minimum convex polygon [mcp](#) and [kde](#) is used to fit the kernel. Note this can only be used when the data is low-dimensional ($d < 3$). By supplying "hypervolume" as an argument to method, the [hypervolume](#) function is used to create the demand points. This method can be used for hyper-dimensional data ($d \ll 3$).

Value

[DemandPoints](#) object.

See Also

[hypervolume](#), [kde](#), [mcp](#).

Examples

```
# set random number generator seed
set.seed(500)

# load data
data(cs_spp, cs_space)

# generate species points
species.points <- randomPoints(cs_spp[[1]], n = 100, prob = TRUE)
env.points <- raster::extract(cs_space, species.points)

# generate demand points for a 1d space using ks
dps1 <- make.DemandPoints(points = env.points[, 1], kernel.method = "ks")
```

```

# print object
print(dps1)

# generate demand points for a 2d space using hypervolume
dps2 <- make.DemandPoints(points = env.points,
                          kernel.method = "hypervolume",
                          samples.per.point = 50,
                          verbose = FALSE)

# print object
print(dps2)

```

make.RapData

Make data for RAP using minimal inputs

Description

This function prepares spatially explicit planning unit, species data, and landscape data layers for RAP processing.

Usage

```

make.RapData(pus, species, spaces = NULL, amount.target = 0.2,
             space.target = 0.2, n.demand.points = 100L, kernel.method = c("ks",
             "hypervolume")[1], quantile = 0.5, species.points = NULL,
             n.species.points = ceiling(0.2 * raster::cellStats(species, "sum")),
             include.geographic.space = TRUE, scale = TRUE, verbose = FALSE,
             ...)

```

Arguments

pus	SpatialPolygons with planning unit data.
species	raster with species probability distribution data.
spaces	list of/or raster representing projects of attribute space over geographic space. Use a list to denote separate attribute spaces.
amount.target	numeric vector for area targets (%) for each species. Defaults to 0.2 for each attribute space for each species.
space.target	numeric vector for attribute space targets (%) for each species. Defaults to 0.2 for each attribute space for each species and each space.
n.demand.points	integer number of demand points to use for each attribute space for each species. Defaults to 100L.
kernel.method	character name of kernel method to use to generate demand points. Use either "ks" or "hypervolume".

quantile	numeric quantile to generate demand points within. If species.points intersect. Defaults to 0.5.
species.points	list of/or SpatialPointsDataFrame or SpatialPoints with species presence records. Use a list of objects to represent different species. Must have the same number of elements as species. If not supplied then use n.species.points to sample points from the species distributions.
n.species.points	numeric vector specifying the number points to sample the species distributions to use to generate demand points. Defaults to 20% of the distribution.
include.geographic.space	logical should the geographic space be considered an attribute space?
scale	logical scale the attribute spaces to unit mean and standard deviation? This prevents overflow. Defaults to TRUE.
verbose	logical print statements during processing?
...	additional arguments to calcBoundaryData and calcSpeciesAverageInPus .

See Also

[RapData-class](#), [RapData](#).

Examples

```
# load data
data(cs_pus, cs_spp, cs_space)

# make RapData object using the first 10 planning units in the dat
x <- make.RapData(cs_pus[1:10,], cs_spp, cs_space,
                 include.geographic.space = TRUE)

# print object
print(x)
```

ManualOpts

Create ManualOpts object

Description

This function creates a new ManualOpts object.

Usage

```
ManualOpts(NumberSolutions = 1L)
```

Arguments

NumberSolutions
integer number of solutions to generate. Defaults to 1L.

Value

[ManualOpts](#) object

See Also

[ManualOpts-class](#).

Examples

```
# create ManualOpts object
ManualOpts(NumberSolutions = 1L)
```

ManualOpts-class	<i>ManualOpts: An S4 class to represent parameters for manually specified solutions</i>
------------------	---

Description

This class is used to store parameters.

Slots

NumberSolutions integer number of solutions.

See Also

[ManualOpts](#).

maximum.targets	<i>Maximum targets</i>
-----------------	------------------------

Description

This function accepts a [RapUnsolved](#) object and returns a `data.frame` containing the amount-based and space-based targets for each species and attribute space. These are calculated using a prioritization that contains all the available planning units. Note that the maximum amount-based targets are always 1.

Usage

```
maximum.targets(x, verbose)

## S3 method for class 'RapUnsolvedOrSolved'
maximum.targets(x, verbose = FALSE)
```

Arguments

x [RapUnsolved](#) or [RapSolved](#) object.
 verbose logical should messages be printed during calculations? Defaults to FALSE.

Value

data.frame object.

Examples

```
# load RapSolved objects
data(sim_ru)

# calculate maximum metrics
maximum.targets(sim_ru)
```

names	<i>Names</i>
-------	--------------

Description

This function sets or returns the species names in an object.

Usage

```
## S3 replacement method for class 'RapData'
names(x) <- value

## S3 method for class 'RapData'
names(x)

## S3 replacement method for class 'RapUnsolvedOrSolved'
names(x) <- value

## S3 method for class 'RapUnsolvedOrSolved'
names(x)
```

Arguments

x [RapData](#), [RapUnsolved](#), or [RapSolved](#) object.
 value new species names.

See Also

[RapData](#), [RapUnsolved](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# show names
names(sim_rs)

# change names
names(sim_rs) <- c('spp1', 'spp2', 'spp3')

# show new names
names(sim_rs)
```

PlanningUnitPoints *Create new PlanningUnitPoints object*

Description

This function creates a new PlanningUnitPoints object.

Usage

```
PlanningUnitPoints(coords, ids)
```

Arguments

coords [matrix](#) coordinates for each point.
ids integer planning unit ids.

See Also

[AttributeSpace-class](#).

Examples

```
# create PlanningUnitPoints object
x <- PlanningUnitPoints(matrix(rnorm(150), ncol = 1), seq_len(150))

# print object
print(x)
```

PlanningUnitPoints-class

PlanningUnitPoints: An S4 class to represent planning units in an attribute space

Description

This class is used to planning units in an attribute space.

Slots

coords [matrix](#) coordinates for each point.

ids integer planning unit ids.

See Also

[AttributeSpace](#).

plot

Plot object

Description

This function plots the solutions contained in [RapSolved](#) objects. It can be used to show a single solution, or the the selection frequencies of planning units contained in a single [RapSolved](#) object. Additionally, two [RapSolved](#) objects can be supplied to plot the differences between them.

Usage

```
## S4 method for signature 'RapSolved,numeric'
plot(x, y, basemap = "none",
     pu.color.palette = c("#e5f5f9", "#00441b", "#FFFF00", "#FF0000"), alpha =
     ifelse(basemap == "none", 1, 0.7), grayscale = FALSE, main = NULL,
     force.reset = FALSE)
```

```
## S4 method for signature 'RapSolved,missing'
plot(x, y, basemap = "none",
     pu.color.palette = c("PuBu", "#FFFF00", "#FF0000"),
     alpha = ifelse(basemap == "none", 1, 0.7),
     grayscale = FALSE, main = NULL,
     force.reset = FALSE)
```

```
## S4 method for signature 'RapSolved,RapSolved'
plot(x, y, i = NULL, j = i,
     basemap = "none",
```

```
pu.color.palette = ifelse(is.null(i), c("RdYlBu", "#FFFF00",
"#FF0000"), "Accent"),
alpha = ifelse(basemap == "none", 1, 0.7),
grayscale = FALSE, main = NULL, force.reset = FALSE)
```

Arguments

x	RapSolved object.
y	Available inputs are: NULL to plot selection frequencies, numeric number to plot a specific solution, 0 to plot the best solution, and a RapSolved object to plot differences in solutions between objects. Defaults to NULL.
i	Available inputs are: NULL to plot selection frequencies. numeric to plot a specific solution, 0 to plot the best solution. This argument is only used when y is a RapSolved object. Defaults to NULL.
j	Available inputs are: NULL to plot selection frequencies. numeric to plot a specific solution, 0 to plot the best solution. This argument is only used when y is a RapSolved object. Defaults to argument j.
basemap	character object indicating the type of basemap to use (see basemap). Valid options include "none", "roadmap", "mobile", "satellite", "terrain", "hybrid", "mapmaker-roadmap", "mapmaker-hybrid". Defaults to "none".
pu.color.palette	character name of colors or color palette (brewer.pal) to indicate planning unit statuses. Defaults to c("grey30", "green", "yellow", "black", "gray80", "red", "orange")
alpha	numeric value to indicating the transparency level for coloring the planning units.
grayscale	logical should the basemap be gray-scaled?
main	character title for the plot. Defaults to NULL and a default title is used.
force.reset	logical if basemap data has been cached, should it be re-downloaded?

See Also

[RapSolved](#).

Examples

```
# load example data set with solutions
data(sim_rs)

# plot selection frequencies
plot(sim_rs)

# plot best solution
plot(sim_rs, 0)

# plot second solution
plot(sim_rs, 2)

# plot different between best and second solutions
plot(sim_rs, sim_rs, 0 ,2)
```

PolySet-class	<i>PolySet</i>
---------------	----------------

Description

Object contains PolySet data.

See Also

[PolySet](#).

print	<i>Print objects</i>
-------	----------------------

Description

Prints objects.

Usage

```
## S3 method for class 'AttributeSpace'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'AttributeSpaces'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'GurobiOpts'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'ManualOpts'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'RapData'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'RapReliableOpts'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'RapResults'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'RapUnreliableOpts'  
print(x, ..., header = TRUE)  
  
## S3 method for class 'RapUnsolved'
```

```
print(x, ...)

## S3 method for class 'RapSolved'
print(x, ...)
```

Arguments

x	GurobiOpts , RapUnreliableOpts , RapReliableOpts , RapData , RapUnsolved , RapResults , or RapSolved object.
...	not used.
header	logical should object header be included?

See Also

[GurobiOpts](#), [RapUnreliableOpts](#), [RapReliableOpts](#), [RapData](#), [RapUnsolved](#), [RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_ru, sim_rs)

# print GurobiOpts object
print(GurobiOpts())

# print RapReliableOpts object
print(RapReliableOpts())

# print RapUnreliableOpts object
print(RapUnreliableOpts())

# print RapData object
print(sim_ru@data)

# print RapUnsolved object
print(sim_ru)

# print RapResults object
print(sim_rs@results)

# print RapSolved object
print(sim_rs)
```

prob.subset

Subset probabilities above a threshold

Description

This function subsets out probabilities assigned to planning units above a threshold. It effectively sets the probability that species inhabit planning units to zero if they are below the threshold.

Usage

```

prob.subset(x, species, threshold)

## S3 method for class 'RapData'
prob.subset(x, species, threshold)

## S3 method for class 'RapUnsolOrSol'
prob.subset(x, species, threshold)

```

Arguments

x	RapData , RapUnsolved , or RapSolved object.
species	integer vector specifying the index of the species to which the threshold should be applied.
threshold	numeric probability to use a threshold.

Value

[RapData](#) or [RapUnsolved](#) object depending on input object.

See Also

[RapData](#), [RapUnsolved](#), [RapSolved](#).

Examples

```

# load data
data(sim_ru)

# generate new object with first 10 planning units
sim_ru2 <- prob.subset(sim_ru, seq_len(3), c(0.1, 0.2, 0.3))

```

pu.subset

Subset planning units

Description

Subset planning units from a [RapData](#), [RapUnsolved](#), or [RapSolved](#) object.

Usage

```

pu.subset(x, pu)

## S3 method for class 'RapData'
pu.subset(x, pu)

## S3 method for class 'RapUnsolOrSol'
pu.subset(x, pu)

```

Arguments

x [RapData](#), [RapUnsolved](#), or [RapSolved](#) object.
pu integer vector to specify the index of planning units to subset.

Value

[RapData](#) or [RapUnsolved](#) object depending on input object.

See Also

[RapData](#), [RapUnsolved](#), [RapSolved](#).

Examples

```
# load data
data(sim_ru)

# generate new object with first 10 planning units
sim_ru2 <- pu.subset(sim_ru, seq_len(10))
```

randomPoints	<i>Sample random points from a RasterLayer</i>
--------------	--

Description

This function generates random points in a [raster](#) object.

Usage

```
randomPoints(mask, n, prob = FALSE)
```

Arguments

mask [raster](#) object
n integer number of points to sample
prob logical should the raster values be used as weights? Defaults to FALSE.

Value

[matrix](#) with x-coordinates, y-coordinates, and cell values.

See Also

This function is similar to `dismo::randomPoints`.

Examples

```
# simulate data
sim_pus <- sim.pus(225L)
sim_spp <- sim.species(sim_pus, model = "normal", n = 1, res = 0.25)

# generate points
pts1 <- randomPoints(sim_spp, n = 5)
pts2 <- randomPoints(sim_spp, n = 5, prob = TRUE)

# plot points
plot(sim_spp)
points(pts1, col = "red")
points(pts2, col = "black")
```

 rap

Generate prioritizations using RAP

Description

This is a general function to create Rap objects from scratch and solve them to generate solutions.

Usage

```
rap(pus, species, spaces = NULL, formulation = c("unreliable",
  "reliable")[1], solve = TRUE, ...)
```

Arguments

pus	SpatialPolygons object representing planning units.
species	raster object with species distribution data.
spaces	list of raster objects. Each elements denotes the spatial distribution for each space. Defaults to NULL.
formulation	character to indicate if the "unreliable" or "reliable" formulation should be used to generate prioritizations. Defaults to "unreliable".
solve	logical should solutions be generated?
...	arguments are passed to GurobiOpts , make.RapData , and RapReliableOpts or RapUnreliableOpts functions.

Value

[RapSolved](#) object if solve is TRUE, otherwise an [RapUnsolved](#) is returned.

Note

Type `vignette("raptr")` to see the package vignette for a tutorial.

See Also

[GurobiOpts](#), [RapReliableOpts](#), [RapUnreliableOpts](#), [RapData](#), [RapResults](#), [RapUnsolved](#), [RapSolved](#).

 RapData

Create new RapData object

Description

This function creates a "RapData" object using pre-processed data.

Usage

```
RapData(pu, species, targets, pu.species.proBABILITIES, attribute.spaces,
        boundary, polygons = NA, skipchecks = FALSE, .cache = new.env())
```

Arguments

pu	data.frame planning unit data. Columns must be "cost" (numeric), "area" (numeric), and "status" (integer).
species	data.frame with species data. Columns must be "name" (character).
targets	data.frame with species data. Columns must be "species" (integer), "target" (integer), "proportion" (numeric).
pu.species.proBABILITIES	data.frame with data on the probability of species in each planning unit. Columns must be "species", (integer), "pu" (integer), and "value" (numeric).
attribute.spaces	list of AttributeSpaces objects with the demand points and planning unit coordinates.
boundary	data.frame with data on the shared boundary length of planning units. Columns must be "id1" (integer), "id2" (integer), and "boundary" (integer).
polygons	PolySet planning unit spatial data or NULL if data not available.
skipchecks	logical Skip data integrity checks? May improve speed for big data sets.
.cache	environment used to cache calculations.

Value

RapData object

Note

Generally, users are not encouraged to change arguments to `.cache`.

See Also

[PolySet](#), [SpatialPoints](#), [SpatialPointsDataFrame](#), [make.RapData](#), [RapData-class](#).

Examples

```

# load data
data(cs_pus, cs_spp, cs_space)

# create data for RapData object
attribute.spaces <- list(
  AttributeSpaces(name = "geographic", list(
    AttributeSpace(
      planning.unit.points = PlanningUnitPoints(
        rgeos::gCentroid(cs_pus[1:10,], byid = TRUE)@coords, seq_len(10)),
      demand.points = make.DemandPoints(
        randomPoints(cs_spp[[1]], n = 10, prob = TRUE)),
      species = 1L))),
  AttributeSpaces(name = "environmental", list(
    AttributeSpace(
      planning.unit.points = PlanningUnitPoints(
        raster::extract(cs_space[[1]], cs_pus[1:10,], fun = mean),
        seq_len(10)),
      demand.points = make.DemandPoints(
        cs_space[[1]][raster::Which(!is.na(cs_space[[1]]))]),
      species = 1L))))
pu.species.proBABILITIES <- calcSpeciesAverageInPus(cs_pus[1:10,],
                                                    cs_spp[[1]])

polygons <- SpatialPolygons2PolySet(cs_pus[1:10,])
boundary <- calcBoundaryData(cs_pus[1:10,])

x <- RapData(pu = cs_pus@data[1:10,], species = data.frame(name = "test"),
             target = data.frame(species = 1L, target = 0:2,
                                 proportion = 0.2),
             pu.species.proBABILITIES = pu.species.proBABILITIES,
             attribute.spaces = attribute.spaces,
             polygons = polygons,
             boundary = boundary)

# print object
print(x)

```

RapData-class

RapData: An S4 class to represent RAP input data

Description

This class is used to store RAP input data.

Slots

polygons [PolySet](#) planning unit spatial data or NULL if data not available.

pu [data.frame](#) planning unit data. Columns must be "cost" (numeric), "area" (numeric), and "status" (integer).

species [data.frame](#) with species data. Columns must be "name" (character).

targets [data.frame](#) with species data. Columns must be "species" (integer), "target" (integer), "proportion" (numeric).

pu.species.probabilities [data.frame](#) with data on the probability of species in each planning unit. Columns must be "species" (integer), "pu" (integer), and "value" (numeric).

attribute.spaces list of AttributeSpaces objects with the demand points and planning unit coordinates.

boundary [data.frame](#) with data on the shared boundary length of planning units. Columns must be "id1" (integer), "id2" (integer), and "boundary" (numeric).

skipchecks logical Skip data integrity checks? May improve speed for big data sets.

.cache [environment](#) used to cache calculations.

See Also

[PolySet](#).

RapOpts-class

RapOpts class

Description

Object is either [RapReliableOpts](#) or [RapUnreliableOpts](#).

RapReliableOpts

Create RapReliableOpts object

Description

This function creates a new [RapReliableOpts](#) object.

Usage

```
RapReliableOpts(BLM = 0, failure.multiplier = 1.1, max.r.level = 5L)
```

Arguments

BLM numeric boundary length modifier. Defaults to 0.

failure.multiplier numeric multiplier for failure planning unit. Defaults to 1.1.

max.r.level numeric maximum R failure level for approximation. Defaults to 5L.

Value

[RapReliableOpts](#) object

See Also

[RapReliableOpts-class](#).

Examples

```
# create RapReliableOpts using defaults
RapReliableOpts(BLM = 0, failure.multiplier = 1.1, max.r.level = 5L)
```

RapReliableOpts-class *RapReliableOpts: An S4 class to represent input parameters for the reliable formulation of RAP.*

Description

This class is used to store input parameters for the reliable formulation of RAP.

Slots

BLM numeric boundary length modifier. Defaults to 0.

failure.multiplier numeric multiplier for failure planning unit. Defaults to 1.1.

max.r.level numeric maximum R failure level for approximation. Defaults to 5L.

See Also

[RapReliableOpts](#).

RapResults	<i>Create RapResults object</i>
------------	---------------------------------

Description

This function creates a new [RapResults](#) object.

Usage

```
RapResults(summary, selections, amount.held, space.held, logging.file,
  .cache = new.env())
```

Arguments

summary	<code>data.frame</code> with summary information on solutions. See details below for more information.
selections	<code>matrix</code> with binary selections. The cell x_{ij} denotes if planning unit j is selected in the i 'th solution.
amount.held	<code>matrix</code> with the amount held for each species in each solution.
space.held	<code>matrix</code> with the proportion of attribute space sampled for each species in each solution.
logging.file	character Gurobi log files.
.cache	<code>environment</code> used to cache calculations.

Details

The summary table follows Marxan conventions (summary.dat in http://marxan.net/downloads/uq_marxan_web_2/module5.html). The columns are:

Run_Number The index of each solution in the object.

Status The status of the solution. The values in this column correspond to outputs from the Gurobi software package (http://www.gurobi.com/documentation/6.5/refman/optimization_status_codes.html).

Score The objective function for the solution.

Cost Total cost associated with a solution.

Planning_Units Number of planning units selected in a solution.

Connectivity_Total The total amount of shared boundary length between all planning units. All solutions in the same object should have equal values for this column.

Connectivity_In The amount of shared boundary length among planning units selected in the solution.

Connectivity_Edge The amount of exposed boundary length in the solution.

Connectivity_Out The number of shared boundary length among planning units not selected in the solution.

Connectivity_Fraction The ratio of shared boundary length in the solution (`Connectivity_In`) to the total amount of boundary length (`Connectivity_Edge`). This ratio is an indicator of solution quality. Solutions with a lower ratio will have less planning units and will be more efficient.

Value

RapResults object

Note

slot best is automatically determined based on data in summary.

See Also

[RapResults-class read.RapResults.](#)

RapResults-class *RapResults: An S4 class to represent RAP results*

Description

This class is used to store RAP results.

Details

The summary table follows Marxan conventions ("summary.dat" in http://marxan.net/downloads/uq_marxan_web_2/module5.html). The columns are:

Run_Number The index of each solution in the object.

Status The status of the solution. The values in this column correspond to outputs from the Gurobi software package (http://www.gurobi.com/documentation/6.5/refman/optimization_status_codes.html).

Score The objective function for the solution.

Cost Total cost associated with a solution.

Planning_Units Number of planning units selected in a solution.

Connectivity_Total The total amount of shared boundary length between all planning units. All solutions in the same object should have equal values for this column.

Connectivity_In The amount of shared boundary length among planning units selected in the solution.

Connectivity_Edge The amount of exposed boundary length in the solution.

Connectivity_Out The number of shared boundary length among planning units not selected in the solution.

Connectivity_Fraction The ratio of shared boundary length in the solution (Connectivity_In) to the total amount of boundary length (Connectivity_Edge). This ratio is an indicator of solution quality. Solutions with a lower ratio will have less planning units and will be more efficient.

Slots

summary `data.frame` with summary information on solutions.

selections `matrix` with binary selections. The cell x_{ij} denotes if planning unit j is selected in the i 'th solution.

amount.held `matrix` with the amount held for each species in each solution.

space.held `matrix` with the proportion of attribute space sampled for each species in each solution.

best integer with index of best solution.

logging.file character Gurobi log files.

.cache `environment` used to store extra data.

See Also

[RapResults](#), [read.RapResults](#).

RapSolved	<i>Create new RapSolved object</i>
-----------	------------------------------------

Description

This function creates a [RapSolved](#) object.

Usage

```
RapSolved(unsolved, solver, results)
```

Arguments

unsolved	RapUnsolved object.
solver	GurobiOpts or ManualOpts object.
results	RapResults object.

Value

[RapSolved](#) object.

See Also

[RapSolved-class](#), [RapResults-class](#), [link{solve}](#).

RapSolved-class	<i>RapSolved: An S4 class to represent RAP inputs and outputs</i>
-----------------	---

Description

This class is used to store RAP input and output data in addition to input parameters.

Slots

opts	RapReliableOpts or RapUnreliableOpts object used to store input parameters.
solver	GurobiOpts or ManualOpts object used to store solver information/parameters.
data	RapData object used to store input data.
results	RapResults object used to store results.

See Also

[RapReliableOpts-class](#), [RapUnreliableOpts-class](#), [RapData-class](#), [RapResults-class](#).

raptr

*raptr: Representative and Adequate Prioritization Toolkit in R***Description**

Biodiversity is in crisis. The overarching aim of conservation is to preserve biodiversity patterns and processes. To this end, protected areas are established to buffer species and preserve biodiversity processes. But resources are limited and so protected areas must be cost-effective. This package contains tools to generate plans for protected areas (prioritizations). Conservation planning data are used to construct an optimization problem, which is then solved to yield prioritizations. To solve the optimization problems in a feasible amount of time, this package uses the commercial 'Gurobi' software package (obtained from <http://www.gurobi.com/>). For more information on using this package, see Hanson et al. (2017) <doi:10.1111/2041-210X.12862>.

Details

The main classes used in this package are used to store input data and prioritizations:

[GurobiOpts-class](#) parameters for solving optimization problems using Gurobi.

[RapReliableOpts-class](#) parameters for the reliable formulation of RAP.

[RapUnreliableOpts-class](#) parameters for the unreliable formulation of RAP.

[RapData-class](#) planning unit, species data, and demand points for RAP.

[RapUnsolved-class](#) contains all the data and input parameters required to generate prioritizations using RAP. This class contains a [GurobiOpts-class](#) object, a [RapReliableOpts-class](#) or [RapUnreliableOpts-class](#) object, and a [RapData-class](#) object.

[RapResults-class](#) prioritizations and summary statistics on their performance.

[RapSolved-class](#) contains all the input data, parameters and output data. This class contains all the objects in a [RapUnsolved](#) object and also a [RapResults-class](#) object.

Type vignette("raptr") for a tutorial on how to use this package.

RapUnreliableOpts

*Create RapUnreliableOpts object***Description**

This function creates a new RapUnreliableOpts object.

Usage

```
RapUnreliableOpts(BLM = 0)
```

Arguments

BLM numeric boundary length modifier. Defaults to 0.

Value

[RapUnreliableOpts](#) object

See Also

[RapUnreliableOpts-class](#).

Examples

```
# create RapUnreliableOpts using defaults
RapUnreliableOpts(BLM = 0)
```

RapUnreliableOpts-class

RapUnreliableOpts: An S4 class to represent parameters for the unreliable RAP problem

Description

This class is used to store input parameters for the unreliable RAP problem formulation.

Slots

BLM numeric boundary length modifier. Defaults to 0.

RapUnsolved

Create a new RapUnsolved object

Description

This function creates a [RapUnsolved](#) object using a [GurobiOpts](#), a [RapReliableOpts](#) or [RapUnreliableOpts](#) object, and a [RapData](#) object.

Usage

```
RapUnsolved(opts, data)
```

Arguments

opts [RapReliableOpts](#) or [RapUnreliableOpts](#) object.
 data [RapData](#) object.

Value

[RapUnsolved](#) object.

See Also

[RapReliableOpts-class](#), [RapUnreliableOpts-class](#), [RapData-class](#).

Examples

```
# set random number generator seed
set.seed(500)

# load data
data(cs_pus, cs_spp)

# create inputs for RapUnsolved
ro <- RapUnreliableOpts()
rd <- make.RapData(cs_pus[seq_len(10), ], cs_spp, NULL,
                  include.geographic.space = TRUE, n.demand.points = 5L)

# create RapUnsolved object
ru <- RapUnsolved(ro, rd)

# print object
print(ru)
```

RapUnsolved-class

RapUnsolved: An S4 class to represent RAP inputs

Description

This class is used to store RAP input data and input parameters.

Slots

opts [RapReliableOpts](#) or [RapUnreliableOpts](#) object used to store input parameters.

data [RapData](#) object used to store input data.

See Also

[RapReliableOpts-class](#), [RapUnreliableOpts-class](#), [RapData-class](#).

`rasterizeGDAL`*Rasterize polygon data using GDAL*

Description

This function converts a `SpatialPolygonsDataFrame` to a `RasterLayer` using GDAL. It is expected to be faster than `rasterize` for large datasets. However, it will be significantly slower for small datasets because the data will need to be written and read from disk.

Usage

```
rasterizeGDAL(x, y, field = NULL)
```

Arguments

<code>x</code>	<code>SpatialPolygonsDataFrame</code> object.
<code>y</code>	<code>raster</code> with dimensions, extent, and resolution to be used as a template for new raster.
<code>field</code>	character column name with values to burn into the output raster. If not supplied, default behaviour is to burn polygon indices into the <code>raster</code> .

Value

`RasterLayer` object.

See Also

[rasterize](#), [is.gdalInstalled](#).

Examples

```
# load dat
data(cs_pus, cs_spp)

# rasterize spatial polygon data
x <- rasterizeGDAL(cs_pus[1:5,], cs_spp[[1]])

# plot data
par(mfrow = c(1,2))
plot(cs_pus[1:5,], main = "original data")
plot(x, main = "rasterized data")
```

rrap.proportion.held *Proportion held using reliable RAP formulation.*

Description

This is a convenience function to quickly calculate the proportion of variation that one set of points captures in a another set of points using the reliable formulation.

Usage

```
rrap.proportion.held(pu.coordinates, pu.probabilities, dp.coordinates,  
  dp.weights, failure.distance,  
  maximum.r.level = as.integer(length(pu.probabilities)))
```

Arguments

pu.coordinates *matrix* of planning unit coordinates.

pu.probabilities
numeric vector of planning unit probabilities.

dp.coordinates *matrix* of demand point coordinates.

dp.weights numeric vector of demand point weights.

failure.distance
numeric indicating the cost of the failure planning unit.

maximum.r.level
integer maximum failure (R) level to use for calculations.

Value

numeric value indicating the proportion of variation that the demand points explain in the planning units

Examples

```
rrap.proportion.held(as.matrix(iris[1:2,-5]), runif(1:2),  
  as.matrix(iris[1:5,-5]), runif(1:5), 10)
```

score	<i>Solution score</i>
-------	-----------------------

Description

Extract solution score from [RapResults](#) or [RapSolved](#) object.

Usage

```
score(x, y)

## S3 method for class 'RapResults'
score(x, y = 0)

## S3 method for class 'RapSolved'
score(x, y = 0)
```

Arguments

x	RapResults or RapSolved object.
y	Available inputs include: NULL to return all scores, integer number specifying the solution for which the score should be returned, and 0 to return score for the best solution.

Value

matrix or numeric vector with solution score(s) depending on arguments.

See Also

[RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# score for the best solution
score(sim_rs, 0)

# score for the second solution
score(sim_rs, 2)

# score for all solutions
score(sim_rs, NULL)
```

`selections`*Extract solution selections*

Description

Extract selections for a given solution from a [RapResults](#) or [RapSolved](#) object.

Usage

```
selections(x, y)

## S3 method for class 'RapResults'
selections(x, y = 0)

## S3 method for class 'RapSolved'
selections(x, y = 0)
```

Arguments

<code>x</code>	RapResults or RapSolved object.
<code>y</code>	NULL to return all values, integer 0 to return values for the best solution, integer value greater than 0 for y'th solution value.
<code>...</code>	not used.

Value

[matrix](#) or numeric vector depending on arguments.

See Also

[RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# selections for the best solution
selections(sim_rs, 0)

# selections for the second solution
selections(sim_rs, 2)

# selections for each solution
selections(sim_rs)
```

show	<i>Show objects</i>
------	---------------------

Description

Shows objects.

Usage

```
## S4 method for signature 'GurobiOpts'  
show(object)  
  
## S4 method for signature 'ManualOpts'  
show(object)  
  
## S4 method for signature 'RapData'  
show(object)  
  
## S4 method for signature 'RapReliableOpts'  
show(object)  
  
## S4 method for signature 'RapResults'  
show(object)  
  
## S4 method for signature 'RapUnreliableOpts'  
show(object)  
  
## S4 method for signature 'RapUnsolved'  
show(object)  
  
## S4 method for signature 'RapSolved'  
show(object)
```

Arguments

object [GurobiOpts](#), [RapUnreliableOpts](#), [RapReliableOpts](#), [RapData](#), [RapUnsolved](#), [RapResults](#), or [RapSolved](#) object.

See Also

[GurobiOpts](#), [RapUnreliableOpts](#), [RapReliableOpts](#), [RapData](#), [RapUnsolved](#), [RapResults](#), [RapSolved](#).

Examples

```
# load data  
data(sim_ru, sim_rs)  
  
# show GurobiOpts object
```

```

GurobiOpts()

# show RapReliableOpts object
RapReliableOpts()

# show RapUnreliableOpts object
RapUnreliableOpts()

# show RapData object
sim_ru@data

# show RapUnsolved object
sim_ru

# show RapResults object
sim_rs@results

# show RapSolved object
sim_rs

```

sim.pus

Simulate planning units

Description

This function simulates planning units for RAP.

Usage

```

sim.pus(n, xmn = -sqrt(n)/2, xmx = sqrt(n)/2, ymn = -sqrt(n)/2,
        ymx = sqrt(n)/2)

```

Arguments

n	integer number of planning units. \sqrt{n} must yield a valid number.
xmn	numeric value for minimum x-coordinate.
xmx	numeric value for maximum x-coordinate.
ymn	numeric value for minimum y-coordinate.
ymx	numeric value for maximum y-coordinate.

Details

Square planning units are generated in the shape of a square. Default coordinate arguments are such that the planning units will be centered at origin. The data slot contains an "id" (integer), "cost" (numeric), "status" (integer), and "area" (numeric).

Value

[SpatialPolygons](#) with planning units.

Examples

```
# generate 225 square planning units arranged in a square
# with 1 unit height / width
x <- sim.pus(225)

# generate 225 rectangular pus arranged in a square
y <- sim.pus(225, xmn = -5, xmx = 10, ymn = -5, ymx = 5)

par(mfrow = c(1, 2))
plot(x, main = "x")
plot(y, main = "y")
par(mfrow = c(1, 1))
```

sim.space

Simulate attribute space data for RAP

Description

This function simulates attribute space data for RAP.

Usage

```
sim.space(x, ...)

## S3 method for class 'RasterLayer'
sim.space(x, d = 2,
  model = RandomFields::RMgauss(), ...)

## S3 method for class 'SpatialPolygons'
sim.space(x, res, d = 2,
  model = RandomFields::RMgauss(), ...)
```

Arguments

x	RasterLayer or SpatialPolygons object delineate the spatial extent to delineate study area.
...	parameters passed to RandomFields .
d	integer number of dimensions. Defaults to 2.
model	RMmodel model to simulate species distributions with. Defaults RPgauss .
res	numeric resolution to simulate distributions. Only needed when SpatialPolygons supplied.

Details

Distributions are simulated by passing model to [RFsimulate](#).

Value

RasterStack with layers for each dimension of the space.

See Also

[RFsimulate](#).

Examples

```
# simulate plannign units
sim_pus <- sim.pus(225L)

# simulate 1d space using RasterLayer
s1 <- sim.space(blank.raster(sim_pus, 1), d = 1)

# simulate 1d space using SpatialPolygons
s2 <- sim.space(sim_pus, res = 1, d = 1)

# simulate 2d space using SpatialPolygons
s3 <- sim.space(sim_pus, res = 1, d = 2)

# plot simulated spaces
par(mfrow = c(2,2))
plot(s1, main = "s1")
plot(s2, main = "s2")
plot(s3[[1]], main = "s3: first dimension")
plot(s3[[2]], main = "s3: second dimension")
```

sim.species

Simulate species distribution data for RAP

Description

This function simulates species distributions for RAP.

Usage

```
sim.species(x, ...)
```

```
## S3 method for class 'RasterLayer'
sim.species(x, n = 1, model = list("uniform",
  "normal", "bimodal", RandomFields::RPgauss()[[1]]), ...)
```

```
## S3 method for class 'SpatialPolygons'
sim.species(x, res, n = 1,
  model = list("normal", "uniform", "bimodal",
  RandomFields::RPgauss()[[1]]), ...)
```

Arguments

x	RasterLayer-class or SpatialPolygons object delineate the spatial extent to delineate study area.
...	parameters passed to RandomFields .
n	integer number of species. Defaults to 1.
model	RMmodel model to simulate species distributions with. Defaults RPgauss .
res	numeric resolution to simulate distributions. Only needed when SpatialPolygons supplied.

Details

Distributions are simulated by passing model to [RFsimulate](#) and converting to logistic values using [inv.logit](#).

Value

RasterStack with layers for each species.

See Also

[RFsimulate](#).

Examples

```
# make polygons
sim_pus <- sim.pus(225L)

# simulate 1 uniform species distribution using RasterLayer
s1 <- sim.species(blank.raster(sim_pus, 1), n = 1, model = "uniform")

# simulate 1 uniform species distribution based on SpatialPolygons
s2 <- sim.species(sim_pus, res = 1, n = 1, model = "uniform")

# simulate 1 normal species distributions
s3 <- sim.species(sim_pus, res = 1, n = 1, model = "normal")

# simulate 1 bimodal species distribution
s4 <- sim.species(sim_pus, res = 1, n = 1, model = "bimodal")

# simulate 1 species distribution using a RModel object from RandomFields
s5 <- sim.species(sim_pus, res = 1, n = 1, model = RandomFields::RPgauss())

# simulate 5 species distribution using a RModel object from RandomFields
s6 <- sim.species(sim_pus, res = 1, n = 5, model = RandomFields::RPgauss())

# plot simulations
par(mfrow = c(2,2))
plot(s2, main = "constant")
plot(s3, main = "normal")
plot(s4, main = "bimodal")
```

```
plot(s5, main = "RPgauss()")
```

simulated_data

Simulated dataset for a conservation planning exercise

Description

This dataset contains all the data needed to generate prioritizations for three simulated species. This dataset contains planning units, species distribution maps, and demand points for each species. For the purposes of exploring the behaviour of the problem, demand points were generated using the centroids of planning units and the probability that they are occupied by the species. Note that methodology is not encouraged for real-world conservation planning.

Usage

```
sim_ru
```

```
sim_rs
```

Format

[SpatialPolygonsDataFrame](#), [RasterStack-class](#), list of [DemandPoints](#) objects.

Details

The species were simulated to represent various simplified species distributions.

uniform This species has an equal probability (0.5) of occurring in all planning units.

normal This species has a single range-core where it is most likely to be found. It is less likely to be found in areas further away from the center of its range.

bimodal This species has two distinct ecotypes. Each ecotype has its own core and marginal area.

The objects contained in this dataset are listed below.

sim_ru A [RapUnsolved](#) object with all the simulated data.

sim_rs A [RapSolved](#) object with 5 near-optimal solutions.

Examples

```
# load data
data(sim_ru, sim_rs)
```

```
# plot species distributions
spp.plot(sim_ru, 1)
spp.plot(sim_ru, 2)
spp.plot(sim_ru, 3)
```

```
# plot selection frequencies
plot(sim_rs)

# plot best solution
plot(sim_rs, 0)
```

solve	<i>Solve RAP object</i>
-------	-------------------------

Description

This function uses Gurobi to find prioritizations using the input parameter and data stored in a [RapUnsolved](#) object, and returns a [RapSolved](#) object with outputs in it.

Usage

```
## S4 method for signature 'RapUnsolved,missing'
solve(a, b, ..., verbose = FALSE)

## S4 method for signature 'RapUnsolved,GurobiOpts'
solve(a, b, verbose = FALSE)

## S4 method for signature 'RapUnsolved,matrix'
solve(a, b, verbose = FALSE)

## S4 method for signature 'RapUnsolved,numeric'
solve(a, b, verbose = FALSE)

## S4 method for signature 'RapUnsolved,logical'
solve(a, b, verbose = FALSE)
```

Arguments

a	RapUnsolved or RapSolved object.
b	missing to generate solutions using Gurobi. Prioritizations can be specified using <code>logical</code> , <code>numeric</code> , or <code>matrix</code> objects. This may be useful for evaluating the performance of solutions obtained using other software.
verbose	<code>logical</code> should messages be printed during creation of the initial model matrix?.
...	not used.

Value

[RapSolved](#) object

Note

This function is used to solve a [RapUnsolved](#) object that has all of its inputs generated. The rap function (without lower case 'r') provides a more general interface for generating inputs and outputs.

See Also

[RapUnsolved](#), [RapSolved](#).

Examples

```
# load RapUnsolved object
data(sim_ru)

# solve it using Gurobi
sim_rs <- solve(sim_ru)

# evaluate manually specified solution using planning unit indices
sim_rs2 <- solve(sim_ru, seq_len(10))

# evaluate manually specified solution using binary selections
sim_rs3 <- solve(sim_ru, c(rep(TRUE, 10), rep(FALSE, 90)))

# evaluate multiple manually specified solutions
sim_rs4 <- solve(sim_ru, matrix(sample(c(0, 1), size = 500, replace = TRUE),
                                ncol = 100, nrow = 5))
```

SolverOpts-class

SolverOpts class

Description

Object stores parameters used to solve problems.

See Also

[GurobiOpts](#).

space.held	<i>Extract attribute space held for a solution</i>
------------	--

Description

This function returns the attribute space held for each species in a solution.

Usage

```
space.held(x, y, species, space)

## S3 method for class 'RapSolved'
space.held(x, y = 0, species = NULL,
           space = NULL)
```

Arguments

x	RapResults or RapSolved object.
y	Available inputs include: NULL to return all values, integer number specifying the solution for which the value should be returned, and 0 to return the value for the best solution.
species	NULL for all species or integer indicating species.
space	NULL for all spaces or integer indicating a specific space.

Value

codematrix object.

See Also

[RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# space held (\%) for each species in best solution
space.held(sim_rs, 0)

# space held (\%) for each species in second solution
space.held(sim_rs, 2)

# space held (\%) for each species in each solution
space.held(sim_rs)
```

space.plot

*Plot space***Description**

This function plots the distribution of planning units and the distribution of demand points for a particular species in an attribute space. Note that this function only works for attribute spaces with one, two, or three dimensions.

Usage

```
space.plot(x, species, space, ...)

## S3 method for class 'RapData'
space.plot(x, species, space = 1,
  pu.color.palette = c("#4D4D4D4D", "#00FF0080", "#FFF0080",
    "#FF0004D"), main = NULL, ...)

## S3 method for class 'RapUnsolved'
space.plot(x, species, space = 1,
  pu.color.palette = c("#4D4D4D4D", "#00FF0080", "#FFF0080",
    "#FF0004D"), main = NULL, ...)

## S3 method for class 'RapSolved'
space.plot(x, species, space = 1, y = 0,
  pu.color.palette = c("#4D4D4D4D", "#00FF0080", "#FFF0080",
    "#FF0004D"), main = NULL, ...)
```

Arguments

x	RapData , RapUnsolved , or RapSolved object.
species	character name of species, or integer index for species.
space	integer index of attribute space.
...	not used.
pu.color.palette	character name of colors or color palette (brewer.pal) to indicate planning unit statuses. Defaults to c("grey30", "green", "black", "red") which indicate non selected, selected, locked in, and locked out (respectively).
main	character title for the plot. Defaults to NULL and a default title is used.
y	integer number specifying the solution to be plotted. The value 0 can be used to plot the best solution.

Examples

```
# load RapSolved objects
data(sim_ru, sim_rs)

# plot first species in first attribute space
space.plot(sim_ru, 1, 1)

# plot distribution of solutions for first species in first attribute space
space.plot(sim_rs, 1, 1)
```

space.target	<i>Attribute space targets</i>
--------------	--------------------------------

Description

This function sets or returns the attribute space targets for each species.

Usage

```
space.target(x, species, space)

space.target(x, species, space) <- value

## S3 method for class 'RapData'
space.target(x, species = NULL, space = NULL)

## S3 replacement method for class 'RapData'
space.target(x, species = NULL,
             space = NULL) <- value

## S3 method for class 'RapUnsolOrSol'
space.target(x, species = NULL, space = NULL)

## S3 replacement method for class 'RapUnsolOrSol'
space.target(x, species = NULL,
             space = NULL) <- value
```

Arguments

x	RapData , RapUnsolved , or RapSolved object.
species	NULL for all species or integer indicating species.
space	NULL for all spaces or integer indicating a specific space.
value	numeric new target.

Value

numeric matrix.

See Also

[RapData](#), [RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# extract space targets for all species
space.target(sim_rs)

# set space targets for all species
space.target(sim_rs) <- 0.1

# extract target for first species for first space
space.target(sim_rs, 1, 1)

# set space targets for first species for first space
space.target(sim_rs, 1, 1) <- 0.5
```

SpatialPolygons2PolySet

Convert SpatialPolygons to PolySet data

Description

This function converts spatial [SpatialPolygons](#) and [SpatialPolygonsDataFrame](#) objects to [PolySet](#) objects.

Usage

```
SpatialPolygons2PolySet(x, n_preallocate)

## S3 method for class 'SpatialPolygonsDataFrame'
SpatialPolygons2PolySet(x,
  n_preallocate = 10000L)

## S3 method for class 'SpatialPolygons'
SpatialPolygons2PolySet(x,
  n_preallocate = 10000L)
```

Arguments

`x` [SpatialPolygons](#) or [SpatialPolygonsDataFrame](#) object.

`n_preallocate` integer How much memory should be preallocated for processing? Ideally, this number should equal the number of vertices in the [SpatialPolygons](#) object. If data processing is taking too long consider increasing this value.

Value

[PolySet](#) object.

Note

Be aware that this function is designed to be as fast as possible, but as a result it depends on C++ code and if used inappropriately this function will crash R.

See Also

For a slower, more stable equivalent see `maptools::SpatialPolygons2PolySet`.

Examples

```
# generate SpatialPolygons object
sim_pus <- sim.pus(225L)

# convert to PolySet
x <- SpatialPolygons2PolySet(sim_pus)
```

spp.plot

Plot species

Description

This function plots the distribution of species across the study area.

Usage

```
spp.plot(x, species, ...)
```

```
## S3 method for class 'RapData'
spp.plot(x, species, prob.color.palette = "YlGnBu",
  pu.color.palette = c("#4D4D4D", "#00FF00", "#FFFF00", "#FF0000"),
  basemap = "none", alpha = ifelse(basemap == "none", 1, 0.7),
  grayscale = FALSE, main = NULL, force.reset = FALSE, ...)
```

```
## S3 method for class 'RapUnsolved'
spp.plot(x, species, prob.color.palette = "YlGnBu",
```

```

pu.color.palette = c("#4D4D4D", "#00FF00", "#FFFF00", "#FF0000"),
basemap = "none", alpha = ifelse(basemap == "none", 1, 0.7),
grayscale = FALSE, main = NULL, force.reset = FALSE, ...)

## S3 method for class 'RapSolved'
spp.plot(x, species, y = 0,
  prob.color.palette = "YlGnBu", pu.color.palette = c("#4D4D4D",
  "#00FF00", "#FFFF00", "#FF0000"), basemap = "none",
  alpha = ifelse(basemap == "none", 1, 0.7), grayscale = FALSE,
  main = NULL, force.reset = FALSE, ...)

```

Arguments

x	RapData , RapUnsolved , or RapSolved object.
species	character name of species, or integer index for species.
...	not used.
prob.color.palette	character name of color palette to denote probability of occupancy of the species in planning units (see brewer.pal). Defaults to "YlGnBu".
pu.color.palette	character name of colors or color palette (brewer.pal) to indicate planning unit statuses. Defaults to c("grey30", "green", "black", "red") which indicate non selected, selected, locked in, and locked out (respectively).
basemap	character object indicating the type of basemap to use (see basemap). Valid options include "none", "roadmap", "mobile", "satellite", "terrain", "hybrid", "mapmaker-roadmap", "mapmaker-hybrid". Defaults to "none".
alpha	numeric value to indicating the transparency level for plotting the planning units.
grayscale	logical should the basemap be gray-scaled?
main	character title for the plot. Defaults to NULL and a default title is used.
force.reset	logical if basemap data has been cached, should it be re-downloaded?
y	NULL integer 0 to return values for the best solution, integer value greater than 0 for y'th solution value.

Examples

```

# load RapSolved objects
data(sim_ru, sim_rs)

# plot first species in sim_ru
spp.plot(sim_ru, species = 1)

# plot "bimodal" species in sim_rs
spp.plot(sim_rs, species = "bimodal")

```

spp.subset	<i>Subset species</i>
------------	-----------------------

Description

Subset species from a [RapData](#), [RapUnsolved](#), or [RapSolved](#) object.

Usage

```
spp.subset(x, species)

## S3 method for class 'RapData'
spp.subset(x, species)

## S3 method for class 'RapUnsolvedOrSolved'
spp.subset(x, species)
```

Arguments

x [RapData](#), [RapUnsolved](#), or [RapSolved](#) object.

species integer, or character vectors to specify the index or species names to subset.

Value

[RapData](#) or [RapUnsolved](#) object depending on input object.

See Also

[RapData](#), [RapUnsolved](#), [RapSolved](#).

Examples

```
# load data
data(sim_ru)

# generate new object with only species 1
sim_ru2 <- spp.subset(sim_ru, 1)
```

summary

*Summary of solutions***Description**

Extracts summary of solutions in a [RapResults](#) or [RapSolved](#) object.

Arguments

object	RapResults , or RapSolved object.
...	not used.

Details

This table follows Marxan conventions ("summary.dat" in http://marxan.net/downloads/uq_marxan_web_2/module5.html). The columns are:

Run_Number The index of each solution in the object.

Status The status of the solution. The values in this column correspond to outputs from the Gurobi software package (http://www.gurobi.com/documentation/6.5/refman/optimization_status_codes.html).

Score The objective function for the solution.

Cost Total cost associated with a solution.

Planning_Units Number of planning units selected in a solution.

Connectivity_Total The total amount of shared boundary length between all planning units. All solutions in the same object should have equal values for this column.

Connectivity_In The amount of shared boundary length among planning units selected in the solution.

Connectivity_Edge The amount of exposed boundary length in the solution.

Connectivity_Out The number of shared boundary length among planning units not selected in the solution.

Connectivity_Fraction The ratio of shared boundary length in the solution ([Connectivity_In](#)) to the total amount of boundary length ([Connectivity_Edge](#)). This ratio is an indicator of solution quality. Solutions with a lower ratio will have less planning units and will be more efficient.

Value

data.frame

See Also

[RapResults](#), [RapSolved](#).

Examples

```
# load data
data(sim_rs)

# show summary
summary(sim_rs)
```

update	<i>Update object</i>
--------	----------------------

Description

This function updates parameters or data stored in an existing [GurobiOpts](#), [RapUnreliableOpts](#), [RapReliableOpts](#), [RapData](#), [RapUnsolved](#), or [RapSolved](#) object.

Usage

```
## S3 method for class 'GurobiOpts'
update(object, Threads = NULL, MIPGap = NULL,
       Method = NULL, Presolve = NULL, TimeLimit = NULL,
       NumberSolutions = NULL, MultipleSolutionsMethod = NULL, ...)

## S3 method for class 'ManualOpts'
update(object, NumberSolutions = NULL, ...)

## S3 method for class 'RapData'
update(object, species = NULL, space = NULL,
       name = NULL, amount.target = NULL, space.target = NULL,
       pu = NULL, cost = NULL, status = NULL, ...)

## S3 method for class 'RapReliableOpts'
update(object, BLM = NULL,
       failure.multiplier = NULL, max.r.level = NULL, ...)

## S3 method for class 'RapUnreliableOpts'
update(object, BLM = NULL, ...)

## S3 method for class 'RapUnsolOrSol'
update(object, ..., formulation = NULL,
       solve = TRUE)
```

Arguments

object	GurobiOpts , RapUnreliableOpts , RapReliableOpts , RapData , RapUnsolved , or RapSolved object.
Threads	integer number of cores to use for processing.

MIPGap	numeric MIP gap specifying minimum solution quality.
Method	integer Algorithm to use for solving model.
Presolve	integer code for level of computation in presolve.
TimeLimit	integer number of seconds to allow for solving.
NumberSolutions	integer number of solutions to generate.
MultipleSolutionsMethod	integer name of method to obtain multiple solutions (used when NumberSolutions is greater than one). Available options are "benders.cuts", "solution.pool.0", "solution.pool.1", and "solution.pool.2". The "benders.cuts" method produces a set of distinct solutions that are all within the optimality gap. The "solution.pool.0" method returns all solutions identified whilst trying to find a solution that is within the specified optimality gap. The "solution.pool.1" method finds one solution within the optimality gap and a number of additional solutions that are of any level of quality (such that the total number of solutions is equal to number_solutions). The "solution.pool.2" finds a specified number of solutions that are nearest to optimality. The search pool methods correspond to the parameters used by the Gurobi software suite (see http://www.gurobi.com/documentation/8.0/refman/poolsearchmode.html#parameter:PoolSearchMode). Defaults to "benders.cuts".
...	parameters passed to update.RapReliableOpts , update.RapUnreliableOpts , or update.RapData .
species	integer or character denoting species for which targets or name should be updated.
space	integer denoting space for which targets should be updated.
name	character to rename species.
amount.target	numeric vector for new area targets (%) for the specified species.
space.target	numeric vector for new attribute space targets (%) for the specified species and attribute spaces.
pu	integer planning unit indices that need to be updated.
cost	numeric new costs for specified planning units.
status	integer new statuses for specified planning units.
BLM	numeric boundary length modifier.
failure.multiplier	numeric multiplier for failure planning unit.
max.r.level	numeric maximum R failure level for approximation.
formulation	character indicating new problem formulation to use. This can be either "unreliable" or "reliable". The default is NULL so that formulation in object is used.
solve	logical should the problem be solved? This argument is only valid for RapUnsolved and RapSolved objects. Defaults to TRUE.

Value

[GurobiOpts-class](#), [RapUnreliableOpts-class](#), [RapReliableOpts-class](#), [RapData-class](#), [RapUnsolved-class](#), or [RapSolved-class](#) object depending on argument to x.

See Also

[GurobiOpts-class](#), [RapUnreliableOpts-class](#), [RapReliableOpts-class](#), [RapData-class](#), [RapUnsolved-class](#), [RapSolved-class](#).

Examples

```
# load data
data(sim_ru, sim_rs)

# GurobiOpts
x <- GurobiOpts(MIPGap = 0.7)
y <- update(x, MIPGap = 0.1)
print(x)
print(y)

# RapUnreliableOpts
x <- RapUnreliableOpts(BLM = 10)
y <- update(x, BLM = 2)
print(x)
print(y)

# RapReliableOpts
x <- RapReliableOpts(failure.multiplier = 2)
y <- update(x, failure.multiplier = 4)
print(x)
print(y)

# RapData
x <- sim_ru@data
y <- update(x, space.target = c(0.4, 0.7, 0.1))
print(space.target(x))
print(space.target(y))

## RapUnsolved
x <- sim_ru
y <- update(x, amount.target = c(0.1, 0.2, 0.3), BLM = 3, solve = FALSE)
print(x@opts@BLM); print(amount.target(x))
print(y@opts@BLM); print(space.target(y))

## RapSolved
x <- sim_rs
y <- update(x, space.target = c(0.4, 0.6, 0.9), BLM = 100, Presolve = 1L,
           solve = FALSE)
print(x@opts@BLM); print(amount.target(x))
print(y@opts@BLM); print(space.target(y))
```

Description

This is a convenience function to quickly calculate the proportion of variation that one set of points captures in a another set of points using the unreliable formulation.

Usage

```
urap.proportion.held(x, y, y.weights = rep(1, nrow(y)))
```

Arguments

x	matrix of points
y	matrix of points
y.weights	numeric vector of weights for each point in y. Defaults to equal weights for all points in y.

Value

numeric value indicating the proportion of variation that x explains in y

Examples

```
urap.proportion.held(as.matrix(iris[1:2,-5]), as.matrix(iris[1:5,-5]))
```

Index

*Topic **datasets**

- casestudy_data, [12](#)
- simulated_data, [52](#)

- amount.held, [4](#)
- amount.target, [5](#)
- amount.target<- (amount.target), [5](#)
- as.list, [6](#)
- AttributeSpace, [7](#), [8](#), [9](#), [26](#)
- AttributeSpace-class, [7](#)
- AttributeSpaces, [8](#), [33](#)
- AttributeSpaces-class, [9](#)

- basemap, [27](#), [60](#)
- blank.raster, [9](#)
- brewer.pal, [27](#), [56](#), [60](#)

- calcBoundaryData, [10](#), [22](#)
- calcSpeciesAverageInPus, [11](#), [22](#)
- casestudy_data, [12](#)
- cs_pus (casestudy_data), [12](#)
- cs_space (casestudy_data), [12](#)
- cs_spp (casestudy_data), [12](#)

- data.frame, [12](#), [33–35](#), [37](#), [38](#)
- DemandPoints, [7](#), [13](#), [14](#), [20](#), [52](#)
- DemandPoints-class, [14](#)
- dp.subset, [14](#)

- environment, [33](#), [35](#), [37](#), [38](#)

- gdal_setInstallation, [17](#)
- GurobiOpts, [6](#), [15](#), [17](#), [29](#), [32](#), [33](#), [39](#), [41](#), [47](#), [54](#), [63](#)
- GurobiOpts-class, [16](#), [40](#)

- hypervolume, [20](#)

- inv.logit, [51](#)
- is.gdalInstalled, [12](#), [17](#), [43](#)
- is.GurobiInstalled, [18](#)

- kde, [20](#)

- logging.file, [18](#)

- make.DemandPoints, [19](#)
- make.RapData, [21](#), [32](#), [33](#)
- ManualOpts, [22](#), [23](#), [39](#)
- ManualOpts-class, [23](#)
- matrix, [4](#), [13](#), [14](#), [20](#), [25](#), [26](#), [31](#), [37](#), [38](#), [44](#), [46](#), [53](#), [66](#)
- maximum.targets, [23](#)
- mcp, [20](#)

- names, [24](#)
- names<- .RapData (names), [24](#)
- names<- .RapUnsolOrSol (names), [24](#)

- options, [18](#)

- PlanningUnitPoints, [7](#), [25](#)
- PlanningUnitPoints-class, [26](#)
- plot, [26](#)
- plot,RapSolved,missing-method (plot), [26](#)
- plot,RapSolved,numeric-method (plot), [26](#)
- plot,RapSolved,RapSolved-method (plot), [26](#)
- PolySet, [10](#), [28](#), [33–35](#), [58](#), [59](#)
- PolySet (PolySet-class), [28](#)
- PolySet-class, [28](#)
- print, [28](#)
- prob.subset, [29](#)
- pu.subset, [30](#)

- RandomFields, [49](#), [51](#)
- randomPoints, [31](#)
- rap, [32](#)
- RapData, [5](#), [14](#), [15](#), [22](#), [24](#), [29–31](#), [33](#), [33](#), [39](#), [41](#), [42](#), [47](#), [56–58](#), [60](#), [61](#), [63](#)
- RapData-class, [34](#), [40](#)
- RapOpts (RapOpts-class), [35](#)
- RapOpts-class, [35](#)

- RapReliableOpts, [29](#), [32](#), [33](#), [35](#), [35](#), [36](#), [39](#), [41](#), [42](#), [47](#), [63](#)
- RapReliableOpts-class, [36](#), [40](#)
- RapResults, [4](#), [5](#), [19](#), [29](#), [33](#), [36](#), [36](#), [39](#), [45–47](#), [55](#), [58](#), [62](#)
- RapResults-class, [38](#), [40](#)
- RapSolved, [4](#), [5](#), [14](#), [15](#), [19](#), [24](#), [26](#), [27](#), [29–33](#), [39](#), [39](#), [45–47](#), [52–58](#), [60–64](#)
- RapSolved-class, [39](#), [40](#)
- raptr, [40](#)
- raptr-package (raptr), [40](#)
- RapUnreliableOpts, [29](#), [32](#), [33](#), [35](#), [39](#), [40](#), [41](#), [42](#), [47](#), [63](#)
- RapUnreliableOpts-class, [40](#), [41](#)
- RapUnsolved, [5](#), [14](#), [15](#), [23](#), [24](#), [29–33](#), [39–41](#), [41](#), [47](#), [52–54](#), [56](#), [57](#), [60](#), [61](#), [63](#), [64](#)
- RapUnsolved-class, [40](#), [42](#)
- raster, [21](#), [31](#), [32](#), [43](#)
- rasterize, [43](#)
- rasterizeGDAL, [43](#)
- read.RapResults, [37](#), [39](#)
- RFsimulate, [49–51](#)
- RMmodel, [49](#), [51](#)
- RPgauss, [49](#), [51](#)
- rrap.proportion.held, [44](#)

- score, [45](#)
- selections, [46](#)
- show, [47](#)
- show, GurobiOpts-method (show), [47](#)
- show, ManualOpts-method (show), [47](#)
- show, RapData-method (show), [47](#)
- show, RapReliableOpts-method (show), [47](#)
- show, RapResults-method (show), [47](#)
- show, RapSolved-method (show), [47](#)
- show, RapUnreliableOpts-method (show), [47](#)
- show, RapUnsolved-method (show), [47](#)
- sim.pus, [48](#)
- sim.space, [49](#)
- sim.species, [50](#)
- sim_rs (simulated_data), [52](#)
- sim_ru (simulated_data), [52](#)
- simulated_data, [52](#)
- solve, [53](#)
- solve, RapUnsolOrSol, GurobiOpts-method (solve), [53](#)
- solve, RapUnsolOrSol, logical-method (solve), [53](#)
- solve, RapUnsolOrSol, matrix-method (solve), [53](#)
- solve, RapUnsolOrSol, missing-method (solve), [53](#)
- solve, RapUnsolOrSol, numeric-method (solve), [53](#)
- SolverOpts (SolverOpts-class), [54](#)
- SolverOpts-class, [54](#)
- space.held, [55](#)
- space.plot, [56](#)
- space.target, [57](#)
- space.target<- (space.target), [57](#)
- SpatialPoints, [22](#), [33](#)
- SpatialPointsDataFrame, [22](#), [33](#)
- SpatialPolygons, [10](#), [11](#), [21](#), [32](#), [48](#), [49](#), [51](#), [58](#), [59](#)
- SpatialPolygons2PolySet, [58](#)
- SpatialPolygonsDataFrame, [10–13](#), [43](#), [52](#), [58](#), [59](#)
- spp.plot, [59](#)
- spp.subset, [61](#)
- stack, [13](#)
- summary, [62](#)

- update, [63](#)
- update.RapData, [64](#)
- update.RapReliableOpts, [64](#)
- update.RapUnreliableOpts, [64](#)
- urap.proportion.held, [65](#)