Package 'mptools'

August 29, 2016

Type Package

Version 1.0.1

Title RAMAS Metapop Tools

Description 'RAMAS Metapop' <https://www.ramas.com/ramas.htm#metapop> is a
popular software package for performing spatially-explicit population
viability analysis. It is primarily GUI-driven, but can benefit from
integration into an R workflow, wherein model results can be subjected to
further analysis. 'RAMAS Metapop' stores metapopulation model parameter
settings and population dynamics simulation results in plain text files
(.mp files). This package facilitates access, summary and visualisation of
'RAMAS Metapop 5' outputs in order to better integrate 'RAMAS' analyses into
an R workflow.

URL <https://github.com/johnbaums/mptools>

BugReports <https://github.com/johnbaums/mptools/issues>

Depends R (>= 3.2.0)

Imports methods, utils, grDevices, graphics, stats, raster, sp,
animation, lattice, zoo, rasterVis, latticeExtra, viridis

Suggests knitr, rmarkdown, rgdal, devtools

VignetteBuilder knitr

License GPL-3

LazyData true

RoxygenNote 5.0.1

NeedsCompilation no

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Repository CRAN

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R **topics documented:**

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actions   *Extract Metapop management action details*

Description

Extract management action details from RAMAS Metapop .mp files.

Usage

```
actions(mp)
```

Arguments

mp   A character string containing the path to a RAMAS Metapop .mp file.

Value

A data.frame containing one row per management action, with columns:

do.action   Logical. Will the action be performed (TRUE) or ignored (FALSE).

action   Factor. The type of action to be performed.

sourcepop   The identity of the source population.

targetpop   The identity of the target population.

start   The timestep at which the action will commence.

end   The timestep at which the action will end.

freq   The frequency of the action, in timestep units.

after.dispersal
                     Logical. Whether the action will be performed after (TRUE) or before (FALSE) dispersal has taken place.

quantity   Factor. Whether the action affects an absolute number of individuals, or a proportion of the source population.

number	The absolute number of individuals involved in the action.
proportion	The proportion of the source population involved in the action.
fromstage	The lowest stage involved in the action.
tostage	The highest stage involved in the action.
condition	The condition under which the action will be performed.
thr1	If condition is either N<thr1 or N<thr1_and_N>thr2, this is the abundance threshold thr1.
thr2	If condition is either N>thr2 or N<thr1_and_N>thr2, this is the abundance threshold thr2.
unknownfield	Unknown.
linear.to	If condition is linear, this is the upper quantity (absolute number, or proportion, depending on quantity) towards which linear change will move.
linear.lowerN	If condition is linear, this is the abundance at which the quantity affected is equal to number or proportion, depending on the value of quantity.
linear.upperN	If condition is linear, this is the abundance at which the quantity affected is equal to linear.to.
N.comprises.stages	
	Factor. The stages included in the definition of N, when calculating thr1, thr2, linear.lowerN and linear.upperN.
N.comprises.pops	
	Factor. The populations included in the definition of N, when calculating thr1, thr2, linear.lowerN and linear.upperN.

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kch	*Extract Metapop KCH*

Description

Extract KCH time series for each RAMAS Metapop population.

Usage

```
kch(meta, path)
```

Arguments

meta	The R object holding Metapop metadata returned by meta.
path	A character string giving the full path to the directory containing .kch files referred to in object meta.

Value

A matrix containing one column per population, giving the carrying capacity at each time step (i.e. each row).

Examples

```
mp <- system.file('example.mp', package='mptools')
k <- kch(meta=meta(mp), path=dirname(mp))
```

---

knt   *Plot carrying capacity and abundance trajectories*

Description

Plot each population's carrying capacity and abundance over time.

Usage

```
knt(meta, kch, pops, samelims = FALSE, show_N = FALSE, results, ...)
```

Arguments

meta	The R object holding population info returned by meta.
kch	The R object holding kch data returned by kch.
pops	(Optional) A character vector of population names. The metapopulation will be subset to these populations before plotting. If not provided, all populations will be plotted (see Note below).
samelims	(logical) If TRUE, the y-axis limits will be constant across plots.
show_N	(logical) If TRUE, mean population abundance will be plotted (solid lines) in addition to carrying capacity (dashed lines).
results	(required only if show_N is TRUE) The R object holding simulation results returned by results.
...	Additional arguments to lattice::xyplot, e.g., layout.

Value

A lattice object is returned invisibly, and plotted if not assigned.

Note

When plotting many populations, layout should be set appropriately, and it may be useful to plot to, e.g., a pdf device.

Examples

```
mp <- system.file('example.mp', package='mptools')
met <- meta(mp)

# Subset of populations
knt(met, pops=c('Pop 169', 'Pop 170', 'Pop 174', 'Pop 175'),
    kch(met, dirname(mp)), show_N=TRUE, results=results(mp),
    layout=c(2, 2), samelims=TRUE)
```

---

meta   *Extract Metapop population metadata*

Description

Extract population details from RAMAS Metapop .mp files.

Usage

```
meta(mp)
```

Arguments

mp   A character string containing the path to a RAMAS Metapop .mp file contain-
                ing simulation results. Metapop .mp files are plain text files that store settings
                describing RAMAS metapopulation models, and the results of simulating pop-
                ulation dynamics according to those models.

Value

A `data.frame` containing one row per population, with columns:

popName   The name of the population.

xMetapop, yMetapop

                The spatial coordinates of the population centroid, in RAMAS's coordinate sys-
                tem (see [mp2xy](#)).

initN   The initial abundance.

ddType   The density dependence type.

Rmax   The maximum growth rate.

K   The initial carrying capacity.

Ksd   The standard deviation in K, if applicable.

allee   The allee parameter, if applicable.

kch   A constant, or reference to a .kch file describing temporal change in K.

ddDispSourcePopN

                The parameter indicating the effect of source population abundance on its dis-
                persal rate.

cat1LocalMulti The local multiplier for probablity of Catastrophe 1, if applicable.

cat1LocalProb   The local probability of Catastrophe 1, if applicable.

includeInTotal Indicates whether abundance of this population is included in totals reported in
                simulation results.

stageMatrix   The name of the stage matrix in use by the population.

relFec   The mean fecundity of this population, relative to those given in the stage matrix.

relSurv	The mean survival rates of this population, relative to those given in the stage matrix.
localThr	The abundance threshold below which the population might be considered dead (depending on global options specified elsewhere).
cat2LocalMulti	The local multiplier for probability of Catastrophe 2, if applicable.
cat2LocalProb	The local probablity of Catastrophe 2, if applicable.
sdMatrix	The name of the standard deviation matrix in use.
ddDispTargetPopK	
	The target population K below which dispersal out of this population is reduced.
tSinceCat1	The number of time steps since this population last experienced Catastrophe 1.
tSinceCat2	The number of time steps since this population last experienced Catastrophe 2.
relDisp	Dispersal rates of this population relative to those specified by the global dispersal matrix/function.
relVarFec	Variation in fecundity rates of this population, relative to those given in the standard deviation matrix.
relVarSurv	Variation in survival rates of this population, relative to those given in the standard deviation matrix.

Note

mptools has been tested with outputs generated by RAMAS Metapop version 5, and may produce unexpected results for other versions. A warning is issued if the user attempts to access files originating from other versions of RAMAS Metapop.

References

- Akcakaya, H. R., Burgman, M. A., Kindvall, O., Wood, C. C., Sjogren-Gulve, P., Hatfield, J. S., & McCarthy, M. A. (2004). *Species Conservation and Management: Case Studies*. New York: Oxford University Press.

- RAMAS Software

- RAMAS GIS and RAMAS Metapop Frequently Asked Questions

See Also

results

Examples

```
mp <- system.file('example.mp', package='mptools')
res <- meta(mp)
head(res)
```

---

mp2sp   *Create a SpatialPointsDataFrame describing Metapop population centroids*

Description

Create a SpatialPointsDataFrame representing the centroid of each population, with attributes: pop (population name), time (the time step), and N (the mean population size).

Usage

```
mp2sp(mp, coords, start, s_p4s, t_p4s)
```

Arguments

mp	A RAMAS Metapop .mp file containing simulation results.
coords	An object containing population coordinates. This object can be created by using [mp2xy](mp2xy)
start	The value of the first timestep. If timesteps are not in increments of 1, it may be best to use start=1, in which case 'time' in the resulting shapefile's attribute table will refer to the timestep number.
s_p4s	(Optional) The coordinate reference system of the source cordinates given in coords. These can be supplied as a CRS object or as a proj4 string.
t_p4s	(Optional) The target coordinate reference system to which coordinates will be projected, if supplied. These can be supplied as a CRS object or as a proj4 string.

Value

A SpatialPointsDataFrame.

See Also

[mp2xy](mp2xy)

Examples

```
mp <- system.file('example.mp', package='mptools')
r <- system.file('example_001.tif', package='mptools')
coords <- mp2xy(mp, r, 9.975)
spdf <- mp2sp(mp, coords, start=2000)
spdf
```

---

mp2xy   *Back-transform RAMAS Metapop coordinates*

Description

Extracts population coordinates from a RAMAS Metapop .mp file, and converts them back to the coordinate system of the original habitat suitability grids (i.e. the grids supplied to the RA-MAS patch-identification module, patch.exe or, in more recent versions of RAMAS GIS, Spatial-Data.exe).

Usage

```
mp2xy(mp, r, cell.length, plot = TRUE)
```

Arguments

mp	A character string containing the path to a RAMAS Metapop .mp file.
r	Either a character string containing the path to any of the raster files that were used by RAMAS Spatial Data for patch identification, or a Raster* object that was used for that purpose.
cell.length	Numeric. The cell length of the grid, as specified in RAMAS Spatial Data (note: this may be different to the native resolution of the grids).
plot	Logical. Should the points be plotted? If r is a Raster* object with more than one layer, the first layer will be plotted.

Value

A data.frame containing the names of all populations referred to in the .mp file, as well as their coordinates (in both Metapop and original coordinate systems). If plot is TRUE, a plot of the raster layer, r, overlaid with points for all populations in the metapopulation, is also produced.

Note

mptools has been tested with outputs generated by RAMAS Metapop version 5, and may produce unexpected results for other versions. A warning is issued if the user attempts to access files origi-nating from other versions of RAMAS Metapop. It is advised to verify that the returned coordinates are sensible by referring to the plot that is returned by this function.

See Also

[mp2sp](#)

Examples

```
mp <- system.file('example.mp', package='mptools')
r <- system.file('example_001.tif', package='mptools')
coords <- mp2xy(mp, r, 9.975)
```

---

mptools	*mptools: Extract, summarise and visualise RAMAS Metapop model information*

Description

RAMAS Metapop is a popular software package for performing spatially-explicit population viability analysis. It is primarily GUI-driven, and stores metapopulation model parameter settings and simulation results in plain text files (.mp files). This package facilitates access, summary and visualisation of Metapop outputs in order to better integrate RAMAS analyses into an R workflow.

Note

mptools has been tested with outputs generated by RAMAS Metapop version 5, and may produce unexpected results for other versions. When using results, meta, mp2xy, or actions a warning is issued if the user attempts to access files originating from other versions of RAMAS Metapop.

References

- Akcakaya, H. R., Burgman, M. A., Kindvall, O., Wood, C. C., Sjogren-Gulve, P., Hatfield, J. S., & McCarthy, M. A. (2004). *Species Conservation and Management: Case Studies*. New York: Oxford University Press.

- RAMAS Software

- RAMAS GIS and RAMAS Metapop Frequently Asked Questions

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mp_animate	*Animate the output of a RAMAS Metapop simulation.*

Description

Animate temporal habitat and abundance dynamics on a gridded landscape.

Usage

```
mp_animate(dat, habitat, outfile, zlim, axes = FALSE, col.regions = NULL,
  pt.col = NULL, pt.cex = 1, height = 800, width = 800,
  interval = 0.05, label = TRUE, label.pos = c(0.98, 0.05),
  label.just = "right", label.cex = 1.5, label.font = 2,
  overwrite = FALSE)
```

Arguments

dat	A SpatialPointsDataFrame object returned by [mp2xy](#).
habitat	A RasterStack or RasterBrick object. The number of Raster layers should equal the number of simulation time steps. Further, the layers should be ordered temporally, and should correspond to the levels of dat$time. It is assumed that the time step between layers is consistent (i.e., the interval between animation frames is constant).
outfile	A character string giving the desired output path and filename.
zlim	A numeric vector of length 2 giving the lower and upper limits of the color scale indicating habitat quality. If this is not provided, a pretty range will be calculated (though this will impact efficiency).
axes	Logical. Should axes be drawn?
col.regions	A [colorRampPalette](#) function that will be used to generate the colour ramp for grids. If NULL, a default colour ramp based on [terrain.colors](#) is used.
pt.col	A [colorRampPalette](#) function that will be used to generate the colour ramp for points. These colours will be interpolated into 100 colours, which indicate relative mean population size, ranging from 1 (first element of the colour ramp) to the maximum mean population size that exists in the simulation output. If NULL, a default colour ramp ranging from white to black is used.
pt.cex	Point size magnifier, relative to the default.
height	Numeric. The height of the animation, in pixels. Default is 800.
width	Numeric. The width of the animation, in pixels. Default is 800.
interval	The time interval of the animation, in seconds. Default is 0.05, i.e. 20 frames per second.
label	Should a time step counter be plotted?
label.pos	A vector of two numbers giving the normalised parent coordinates at which the time step counter will be plotted. The first number gives the x-coordinate (0 = left edge, 1 = right edge) and the second gives the y-coordinate (0 = bottom edge, 1 = top edge). The default value of c(0.98, 0.05) plots the label at the bottom right corner. Ignored if label is FALSE.
label.just	Justification of the time step counter label, relative to label.pos. See the description of just at [grid.text](#). Ignored if label is FALSE.
label.cex	Size of the time step counter text. Ignored if label is FALSE.
label.font	Font face of the time step counter text. See fontface at [gpar](#) for available options. Ignored if label is FALSE.
overwrite	Should outfile be overwritten if it already exists?

Details

mp_animate requires that either http://www.imagemagick.org or http://www.graphicsmagick.org are installed on the system. See the documentation for animation::[im.convert](#) for further details.

An animated gif is created, with points indicating the location of populations with mean abundance greater than zero, overlaid upon a raster grid indicating habitat suitability. Relative population

size is represented by point colour, with white corresponding to a population with mean abundance between 0 and 1 populations and time steps, and black corresponding to the maximum mean abundance. Colours for intermediate values are scaled linearly. The colour key indicates carrying capacity, and corresponds to the colour of grid cells.

An example of this function's use is provided in the vignette "Introduction to mptools" (`vignette('intro', 'mptools')`).

Value

`NULL`. The animation is saved as an animated .gif file at the specified path (`outfile`).

See Also

[mp2sp](mp2sp)

---

print.mpresults	*Print a metapop results object*

Description

Print summary information about a RAMAS Metapop simulation.

Usage

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

Arguments

x	An mpresults object
...	ignored

Details

The print method for `mpresults` objects shows only summary information. To see the full structure of `mpresults` object `x`, see `str(x)`. Individual elements can be accessed as for a normal `list`.

See Also

results

results	*Extract simulation results from RAMAS Metapop .mp files*

Description

Extract population size simulation results (mean, sd, min and max), including expected minimum abundance (EMA) and its standard deviation, from a RAMAS Metapop .mp file.

Usage

```
results(mp)
```

Arguments

mp	A character string containing the path to a RAMAS Metapop .mp file containing simulation results. Metapop .mp files are plain text files that store settings describing RAMAS metapopulation models, and the results of simulating population dynamics according to those models.

Value

A list containing:

version	The version of RAMAS Metapop from which the file indicated by mp originated (if identifiable).
results	An array containing simulation results extracted from file. The number of rows is equal to the number of time steps in the simulation. The array has four columns, containing mean, sd, min and max of population size across iterations at each time step (i.e. each row), and the number of array slices is equal to the number of populations. The third dimension is named according to population names (numeric component only).
iter_min	A sorted vector of minimum abundance, across time steps, for each iteration.
iter_max	A sorted vector of maximum abundance, across time steps, for each iteration.
iter_terminal	A sorted vector of terminal abundance for each iteration.
qe_thr	The quasi-extinction threshold. When the total abundance is beneath qe_thr, the metapopulation is considered to be quasi-extinct.
qe_prob	The probability and cumulative probability of exceeding the quasi-extinction threshold (qe_thr) at each time step.
EMA	The mean minimum abundance (i.e. the mean, across iterations, of the minimum abundance for each simulation trajectory).
SDMA	The standard deviation of minimum abundance (i.e. the sd, across iterations, of the minimum abundance for each simulation trajectory).
timestamp	A POSIXlt object representing the date and time at which the simulation was completed.

n_pops	The number of populations in the simulation.
duration	The number of time steps in the simulation
n_iters	The number of iterations performed.

Note

mptools has been tested with outputs generated by RAMAS Metapop version 5, and may produce unexpected results for other versions. A warning is issued if the user attempts to access files originating from other versions of RAMAS Metapop.

References

- Akcakaya, H. R., Burgman, M. A., Kindvall, O., Wood, C. C., Sjogren-Gulve, P., Hatfield, J. S., & McCarthy, M. A. (2004). *Species Conservation and Management: Case Studies*. New York: Oxford University Press.
- RAMAS Software
- RAMAS GIS and RAMAS Metapop Frequently Asked Questions

See Also

meta

Examples

```
mp <- system.file('example.mp', package='mptools')
res <- results(mp)
str(res)

# look at the simulation results for the first array slice (NB: this slice is
# all pops combined):
res$results[,, 1]
# equivalently, subset by name:
res$results[,, 'ALL']
res$results[,, 'Pop 190']
res$results[,, '240A24']
dimnames(res$results)[[3]] # population names

# return a matrix of mean population sizes, where columns represent
# populations and rows are time steps:
res$results[, 1, ] # or res$results[, 'mean', ]

# sd across iterations:
res$results[, 2, ] # or res$results[, 'sd', ]

# min pop sizes across iterations:
res$results[, 3, ] # or res$results[, 'min', ]

# max pop sizes across iterations:
res$results[, 4, ] # or res$results[, 'max', ]
```

---

ths *Extract THS from a folder of RAMAS Metapop .ptc files*

Description

Extracts Total Habitat Suitability from RAMAS .ptc file.

Usage

```
ths(ptc)
```

Arguments

ptc   A character string containing the path to a directory containing the .ptc files of interest. This should contain no .ptc other than those to be included in the extraction. Order will be taken from the numeric component of filenames.

Value

A numeric vector with length equal to the number of .ptc files in the directory specified by ptc.

Note

This has been tested for RAMAS version 5, and may produce unexpected results for other versions.

See Also

results

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