

Package ‘osmose’

April 28, 2020

Type Package

Title Object Oriented Simulator of Marine Ecosystems

Version 3.3.4

Date 2020-04-03

Description The multispecies and individual-based model (IBM) 'OSMOSE' (Shin and Curry (2001) <doi:10.1016/S0990-7440(01)01106-8> and Shin and Curry (2004) <doi:10.1139/f03-154>) focuses on fish species. This model assumes opportunistic predation based on spatial co-occurrence and size adequacy between a predator and its prey (size-based opportunistic predation). It represents fish individuals grouped into schools, which are characterized by their size, weight, age, taxonomy and geographical location (2D model), and which undergo major processes of fish life cycle (growth, explicit predation, natural and starvation mortalities, reproduction and migration) and fishing exploitation. The model needs basic biological parameters that are often available for a wide range of species, and which can be found in 'FishBase' for instance (see <<http://www.fishbase.org/search.php>>), and fish spatial distribution data. This package provides tools to build and run simulations using the 'OSMOSE' model.

License CeCILL

Encoding UTF-8

Depends R (>= 3.5.0)

Imports graphics, grDevices, rlist, stats, knitr, rmarkdown, stringr, utils, ncdf4, mgcv, fields

URL <http://www.osmose-model.org/>

LazyData FALSE

BugReports <https://github.com/osmose-model/osmose/issues>

SystemRequirements Java (>= 8)

VignetteBuilder knitr

RoxygenNote 7.1.0

NeedsCompilation no

Author Yunne-Jai Shin [aut] (<<https://orcid.org/0000-0002-7259-9265>>),
 Travers Morgane [aut] (<<https://orcid.org/0000-0003-1493-662X>>),
 Verley Philippe [aut] (<<https://orcid.org/0000-0002-5686-2764>>),
 Ricardo Oliveros-Ramos [aut] (<<https://orcid.org/0000-0002-8069-2101>>),
 Laure Velez [aut],
 Nicolas Barrier [cre] (<<https://orcid.org/0000-0002-1693-4719>>),
 Criscely Lujan [ctb],
 Michael Hurtado [ctb],
 Wencheng Lau-Medrano [ctb]

Maintainer Nicolas Barrier <nicolas.barrier@ird.fr>

Repository CRAN

Date/Publication 2020-04-28 13:00:03 UTC

R topics documented:

osmose-package	3
.osmose.barplot	4
.osmose.format_data_stacked	4
.plot_osmose_dietMatrix	5
.read_2D	6
.read_osmose_ncdf	6
cacheManager	7
configureCalibration	7
getVar	8
get_var.osmose	8
get_var.osmose.config	9
osmose2R	10
osmose_demo	11
plot.osmose	12
plot.osmose.config	22
print.osmose	24
print.summary.osmose	25
readOsmoseConfiguration	25
readOsmoseFiles	26
report	26
report.osmose	27
runOsmose	27
summary.osmose	29
summary.osmose.dietMatrix	29
summary.osmose.mortalityRate	30
updateCache	30
write.osmose	31

Index 32

Description

OSMOSE is a multispecies and Individual-based model (IBM) which focuses on fish species. This model assumes opportunistic predation based on spatial co-occurrence and size adequacy between a predator and its prey (size-based opportunistic predation). It represents fish individuals grouped into schools, which are characterized by their size, weight, age, taxonomy and geographical location (2D model), and which undergo major processes of fish life cycle (growth, explicit predation, natural and starvation mortalities, reproduction and migration) and a fishing mortality distinct for each species (Shin and Cury 2001, 2004). The model needs basic parameters that are often available for a wide range of species, and which can be found in FishBase for instance. This package provides tools to build a model and run simulations using the OSMOSE model. See the [Official website](#) for more details.

Details

osmose package is well documented by help descriptions, demos and vignettes.

Demo scripts:

```
# Check all the available topics
demo(package = "osmose")
# Select and run one of the topics (e.g. osmose.config_class)
demo(package = "osmose", topic = "osmose.config_class")
```

Vignettes:

```
# Check all the available topics
vignette(package = "osmose")
# Select and run one of the topics (e.g. create_run_read)
vignette(package = "osmose", topic = "create_run_read")
```

Author(s)

Yunne-Jai Shin
Ricardo Oliveros-Ramos
Laure Velez
Criscely Luján
Philippe Verley
Maintainer: Nicolas Barrier <nicolas.barrier@ird.fr>

References

[Official website](#) [Documentation website](#)

`.osmose.barplot` *Plots a barplot, with xlabels rotated with a 45degree angle*

Description

Plots a barplot, with xlabels rotated with a 45degree angle

Usage

```
.osmose.barplot(x, add_text = TRUE, color = NULL, ...)
```

Arguments

<code>x</code>	Data array
<code>add_text</code>	True if text should be added.
<code>color</code>	Color of the barplot
<code>...</code>	Additional arguments to the barplot function (color, etc.)

`.osmose.format_data_stacked`
Reformat the data into the ggplot2 stacked plot format. It returns a dataframe with specie, time and predation rate in the columns.

Description

Reformat the data into the ggplot2 stacked plot format. It returns a dataframe with specie, time and predation rate in the columns.

Usage

```
.osmose.format_data_stacked(data, time = NULL)
```

Arguments

<code>data</code>	Data to plot
<code>time</code>	Time vector

.plot_osmose_dietMatrix

Plots diet matrix

Description

Plots diet matrix

Usage

```
.plot_osmose_dietMatrix(  
  x,  
  time.mean,  
  species,  
  thres,  
  color,  
  add_text,  
  plot_name,  
  legsize = 1,  
  ...  
)
```

Arguments

x	Diet matrix
time.mean	If TRUE, the time mean diet matrix is computed is displayed.
species	Species name
thres	Thresholds (in percentage). Time-average predation rates below this threshold are binned together ("other" column).
color	Color of the barplot.
add_text	TRUE if text should be added.
plot_name	Label for ylab in diet matrix plot.
legsize	Size of the legend (default 1), if time.mean is FALSE.
...	Additional plot arguments passed to barplot.

Value

None

<code>.read_2D</code>	<i>Generic function to read 2D output files (dietMatrix, sizeSpectrum, etc). If no file is found, it returns NULL.</i>
-----------------------	--

Description

Generic function to read 2D output files (dietMatrix, sizeSpectrum, etc). If no file is found, it returns NULL.

Usage

```
.read_2D(files, path, ...)
```

Arguments

<code>files</code>	List of input files
<code>path</code>	Data directory
<code>...</code>	Extra arguments passed to the method.

Value

A 3D array (time, species, replicates) or NULL if no file is found.

<code>.read_osmose_ncdf</code>	<i>Function to read osmose netcdf files</i>
--------------------------------	---

Description

Function to read osmose netcdf files

Usage

```
.read_osmose_ncdf(files, path, ...)
```

Arguments

<code>files</code>	String of name of the file that will be read.
<code>path</code>	String of path of the file that will be read
<code>...</code>	Extra arguments

cacheManager	<i>Manage the cache</i>
--------------	-------------------------

Description

The function creates a folder (only once) and then controls files that need to be downloaded and placed in this folder.

Usage

```
cacheManager(nameFile)
```

Arguments

nameFile	the name of the file or folder
----------	--------------------------------

Value

the path to the file we need

Localisation

The localisation of the folder is defined in the '.Renviron' file, by setting the 'OSMOSE_DIR' environment variable: - On Linux/Mac Os X : 'OSMOSE_DIR=/Users/Nicolas/Desktop/OSMOSE_TEST/R'
- On Windows: 'OSMOSE_DIR=C:\Users\Nicolas\Desktop\OSMOSE_TEST\R'

If this variable is not set, the files will be downloaded into a temporary directory.

Author(s)

Arthur PERE

Nicolas BARRIER

configureCalibration	<i>Reads calibration parameters from an osmose.config list.</i>
----------------------	---

Description

The configuration argument must contain a "calibration" entry to work.

Usage

```
configureCalibration(L1)
```

Arguments

L1	osmose.config object (see readOsmoseConfiguration)
----	---

Value

A list of parameters to calibrate ("guess", "max", "min", "phase")

getVar	<i>Get variable from an osmose-like object.</i>
--------	---

Description

Function to get a variable from an object of osmose class. This function uses the get_var method (see the [get_var.osmose](#)).

Usage

```
getVar(object, what, how, ...)
```

```
get_var(object, what, how, ...)
```

Arguments

object	Object of osmose class (see the read_osmose function).
what	Variable to extract
how	Output format
...	Additional arguments of the function.

Value

An array or a list containing the extracted data.

get_var.osmose	<i>get_var method for osmose outputs objects</i>
----------------	--

Description

Get a variable from an osmose object.

Usage

```
## S3 method for class 'osmose'
get_var(object, what, how = c("matrix", "list"), expected = FALSE, ...)
```

Arguments

object	Object of osmose class (see the read_osmose function).
what	Name of variable to extract. See Details.
how	How to return the object. Current options are "matrix" and "list".
expected	A logical parameter. If TRUE, the average over the last dimensions will be performed (only if the output is an array).
...	Additional arguments of the function.

Details

what can be any available variable contained on object (e.g. biomass, abundance, yield, yieldN, etc).

Value

An matrix or a list containing the data.

get_var.osmose.config *get_var method for osmose configuration objects*

Description

Get the configuration files from

Usage

```
## S3 method for class 'osmose.config'
get_var(object, what, ...)
```

Arguments

object	Object of osmose.config class. See the read_osmose and readOsmoseConfiguration functions for more information about this object.
what	Name of the variable to extract from the configuration file.
...	Extra arguments for plotting method.

Value

An object of list class containing all the relevant information about the variable extracted.

`osmose2R`*Read OSMOSE outputs into an R object*

Description

This function create object of class `osmose` with the outputs from OSMOSE in the `path` folder.

Usage

```
osmose2R(path = NULL, version = "v3r2", species.names = NULL, ...)

read_osmose(
  path = NULL,
  input = NULL,
  version = "3.3.3",
  species.names = NULL,
  absolute = TRUE,
  ...
)
```

Arguments

<code>path</code>	Path to the directory containing OSMOSE outputs.
<code>version</code>	OSMOSE version used to run the model.
<code>species.names</code>	Display names for species, overwrite the species names provided to the OSMOSE model. Used for plots and summaries.
<code>...</code>	Additional arguments.
<code>input</code>	Path to a main OSMOSE configuration file.
<code>absolute</code>	Whether the path is absolute (TRUE) or relative (FALSE). Only used if <code>input</code> is not NULL.

Details

`read_osmose` will return a list of fields with the information of whether an OSMOSE running or the configuration that is going to be used in a running. Output class will depend on the read info: If `path` is specified, output class will be `osmose`; otherwise, if ONLY `input` is given, the class will be `osmose.config`. If both are specified, the `osmose` class output will content inside a field (`config`) of class `osmose.config`.

Individual elements can be extracted using the [get_var](#) function.

Author(s)

Ricardo Oliveros-Ramos, Laure Velez

Examples

```
# Read outputs generated by demo (check osmose_demo function)
outdir = cacheManager("outputs")
read_osmose(path = outdir)
```

osmose_demo	<i>Generates required OSMOSE configuration files to run a demo.</i>
-------------	---

Description

This function

Usage

```
osmose_demo(path = NULL, config = "gog")
```

Arguments

path	Path where to put the Osmose configuration file.
config	Reference configuration to run ("gog").

Value

A list containing the configuration file to use (config_file) for running the code and the output directory to use when reading data.

Note

So far, only one configuration is propose ("gog")

Examples

```
## Not run:
rm(list=ls())

library("osmose")

# Copy configuration files into the proper directory
demo = osmose_demo(path="..", config="gog")

# run the osmose model
run_osmose(demo$config_file, parameters=NULL, output=NULL, version="3.3.3",
           options=NULL, verbose=TRUE, clean=TRUE)

# reads output data
data = read_osmose(demo$output_dir)

# summarize output data
```

```
summary(data)

# plot output data
plot(data)

## End(Not run)
```

plot.osmose

Plot method for osmose objects

Description

This method takes a osmose object and produce useful plots

This function implements a plot method for different osmose classes.

Usage

```
## S3 method for class 'osmose'
plot(x, what = "biomass", ...)

## S3 method for class 'osmose.biomass'
plot(
  x,
  ts = TRUE,
  type = 1,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  initialYear = NULL,
  replicates = TRUE,
  freq = 12,
  horizontal = FALSE,
  conf = 0.95,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  alpha = NULL,
  border = NULL,
  lty = 1,
  lwd = 1,
  axes = TRUE,
  legend = TRUE,
  units = "tonnes",
  ...
)
```

```
## S3 method for class 'osmose.abundance'
plot(
  x,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  initialYear = NULL,
  ts = TRUE,
  type = 1,
  replicates = TRUE,
  freq = 12,
  horizontal = FALSE,
  conf = 0.95,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  alpha = NULL,
  border = NULL,
  lty = 1,
  lwd = 1,
  axes = TRUE,
  legend = TRUE,
  units = "individuals",
  ...
)
```

```
## S3 method for class 'osmose.yield'
plot(
  x,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  initialYear = NULL,
  ts = TRUE,
  type = 1,
  replicates = TRUE,
  freq = 12,
  horizontal = FALSE,
  conf = 0.95,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  alpha = NULL,
```

```
border = NULL,
lty = 1,
lwd = 1,
axes = TRUE,
legend = TRUE,
units = "tonnes",
...
)

## S3 method for class 'osmose.yieldN'
plot(
  x,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  initialYear = NULL,
  ts = TRUE,
  type = 1,
  replicates = TRUE,
  freq = 12,
  horizontal = FALSE,
  conf = 0.95,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  alpha = NULL,
  border = NULL,
  lty = 1,
  lwd = 1,
  axes = TRUE,
  legend = TRUE,
  units = "individuals",
  ...
)

## S3 method for class 'osmose.biomassByTL'
plot(
  x,
  type = 1,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  freq = 12,
  horizontal = FALSE,
  factor = 0.001,
```

```
xlim = NULL,  
ylim = NULL,  
col = NULL,  
border = NULL,  
legend = TRUE,  
lty = 1,  
lwd = 1,  
axes = TRUE,  
units = list(x = "", y = "tonnes"),  
...  
)  
  
## S3 method for class 'osmose.biomassBySize'  
plot(  
  x,  
  type = 1,  
  species = NULL,  
  speciesNames = NULL,  
  start = NULL,  
  end = NULL,  
  freq = 12,  
  horizontal = FALSE,  
  factor = 0.001,  
  xlim = NULL,  
  ylim = NULL,  
  col = NULL,  
  border = NULL,  
  legend = TRUE,  
  lty = 1,  
  lwd = 1,  
  axes = TRUE,  
  units = list(x = "cm", y = "tonnes"),  
  ...  
)  
  
## S3 method for class 'osmose.biomassByAge'  
plot(  
  x,  
  type = 1,  
  species = NULL,  
  speciesNames = NULL,  
  start = NULL,  
  end = NULL,  
  freq = 12,  
  horizontal = FALSE,  
  factor = 0.001,  
  xlim = NULL,  
  ylim = NULL,
```

```
col = NULL,  
border = NULL,  
legend = TRUE,  
lty = 1,  
lwd = 1,  
axes = TRUE,  
units = list(x = "years", y = "tonnes"),  
...  
)  
  
## S3 method for class 'osmose.abundanceByTL'  
plot(  
  x,  
  type = 1,  
  species = NULL,  
  speciesNames = NULL,  
  start = NULL,  
  end = NULL,  
  freq = 12,  
  horizontal = FALSE,  
  factor = 0.001,  
  xlim = NULL,  
  ylim = NULL,  
  col = NULL,  
  border = NULL,  
  legend = TRUE,  
  lty = 1,  
  lwd = 1,  
  axes = TRUE,  
  units = list(x = "", y = "individuals"),  
  ...  
)  
  
## S3 method for class 'osmose.abundanceBySize'  
plot(  
  x,  
  type = 1,  
  species = NULL,  
  speciesNames = NULL,  
  start = NULL,  
  end = NULL,  
  freq = 12,  
  horizontal = FALSE,  
  factor = 0.001,  
  xlim = NULL,  
  ylim = NULL,  
  col = NULL,  
  border = NULL,
```

```
    legend = TRUE,
    lty = 1,
    lwd = 1,
    axes = TRUE,
    units = list(x = "cm", y = "individuals"),
    ...
)

## S3 method for class 'osmose.abundanceByAge'
plot(
  x,
  type = 1,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  freq = 12,
  horizontal = FALSE,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  border = NULL,
  legend = TRUE,
  lty = 1,
  lwd = 1,
  axes = TRUE,
  units = list(x = "years", y = "individuals"),
  ...
)

## S3 method for class 'osmose.yieldNBySize'
plot(
  x,
  type = 1,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  freq = 12,
  horizontal = FALSE,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  border = NULL,
  legend = TRUE,
  lty = 1,
```

```
    lwd = 1,
    axes = TRUE,
    units = list(x = "cm", y = "individuals"),
    ...
)

## S3 method for class 'osmose.yieldNByAge'
plot(
  x,
  type = 1,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  freq = 12,
  horizontal = FALSE,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  border = NULL,
  legend = TRUE,
  lty = 1,
  lwd = 1,
  axes = TRUE,
  units = list(x = "years", y = "individuals"),
  ...
)

## S3 method for class 'osmose.yieldBySize'
plot(
  x,
  type = 1,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  freq = 12,
  horizontal = FALSE,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  border = NULL,
  legend = TRUE,
  lty = 1,
  lwd = 1,
  axes = TRUE,
```

```

    units = list(x = "cm", y = "tonnes"),
    ...
)

## S3 method for class 'osmose.yieldByAge'
plot(
  x,
  type = 1,
  species = NULL,
  speciesNames = NULL,
  start = NULL,
  end = NULL,
  freq = 12,
  horizontal = FALSE,
  factor = 0.001,
  xlim = NULL,
  ylim = NULL,
  col = NULL,
  border = NULL,
  legend = TRUE,
  lty = 1,
  lwd = 1,
  axes = TRUE,
  units = list(x = "years", y = "tonnes"),
  ...
)

```

Arguments

x	osmose object.
what	Variable name to plot. By default is what = "biomass". See Details
...	Extra arguments of the function. See Details.
ts	logical parameter. By default ts = TRUE and the plots are going to be time series where the x-axis is the time. For plots where the x-axis is not the time ts = FALSE.
type	A numeric value, indicating the type of plot to be used (type = 1, by default). See Details.
species	A numeric vector specifying the species that will be showed. If NULL (default), all the available species time series will be plotted. See Details.
speciesNames	A vector with the names for each species. If NULL (default) the names of x will be used.
start	A numeric value indicating the first element of the time indexation of the object x is specified with this parameter. By default start = NULL and the time indexation start with the first element of x.
end	A numeric value. The last element of the time indexation of the object x is specified with this parameter. By default end = NULL and the time indexation finish with the last element of x.

initialYear	A numeric value. It specifies the first element that is going to be used on the x axis for the plots.
replicates	logical. It controls to show whether the values in each simulation (TRUE) or the median of the values along the time (FALSE).
freq	A numeric value to indicate the steps by year used in the time series. Default values, see Details.
horizontal	a logical value. If FALSE, plot types that do not represent time series (boxplots and barplots) will be drawn horizontally.
conf	numeric single value indicating the confidence interval showed in the plot as shadow. By default conf = 0.95.
factor	A number to indicate the scale of the variable on the y-axis. By default factor = 1e-3.
xlim, ylim	numeric vectors of length 2, giving the x and y coordinates ranges.
col	A vector with the color names for the plots. By default col = NULL and the colors will be chosen by the function.
alpha	factor modifying the opacity alpha given to confidence interval (CI) polygons (check adjustcolor). By default (NULL), its value will depend on the plot type. See Details.
border	the color to draw the border of CI polygons, bar plots and box plots. The default value (NULL) will depend on the type, see Details.
lty	The line type (check par).
lwd	The line width (check par).
axes	a logical value indicating whether both axes should be drawn on the plot.
legend	logical do you want to show a legend of species? (valid only for those plot types TS-2)
units	String with units of the variable that defines the label set on top of the plot. If NULL (default), the value will depend on the class, see Details.

Details

what argument can take next values:

- "biomass" to plot the species biomass (see [plot.osmose.biomass](#))
- "abundance" to plot the species abundance (see [plot.osmose.abundance](#))
- "yield" to plot the species yield (see [plot.osmose.yield](#))
- "yieldN" to plot the species yield (in numbers) (see [plot.osmose.yieldN](#))

User can select within different plot types depending on the osmose class. So, for classes biomass, abundance, yield and yieldN (**Group 1**) the user must use ts and type arguments to specify the type of plot to draw.

So, for the **Group 1** and ts = TRUE, user will select within:

- type = 1: Generates a matrix plot of the selected variable plotted independently.

- type = 2: Generates a single plot with overlaped time series. You can include confidence interval shadow around lines.
- type = 3: Generates a single plot with cumulated time series. So, the method will sort and overlap the time series values for the selected variable
- type = 4: ONLY valid for a single species. It generates a bar plot of the time series.

For the Group 1 and ts = FALSE, user will select within:

- type = 1: Generates a bar plot of the selected variable by species, including interval confidence bars.
- type = 2: Generates a boxplot of the selected variable by species.

The **Group 2** refers classes of **Group 1** with **By** specification (e.g. yieldNBySize, abundanceByAge, biomassByTL). There are 2 available plot types:

- type = 1: Generates a bar plot of the selected variable by species. The ... will be passed to the internal [barplot](#) function.
- type = 2: Generates a plot using [image.plot](#) function, placing the species in the left axis, the By-variable (e.g. Size) on the bottom and the main variable (e.g. biomass) in a color scale. The ... will be passed to the internal [image.plot](#) function.

Both alpha and border controls the opacity and the color of border, respectively, for polygons, bar plots and box plots. So depending on the ts-type, they will have different default values:

- alpha = 0.3 & border = NA for TS = TRUE with type = 1 or 2.
- alpha = 1 & border = TRUE for Everything else.

species argument follows the indexation way of java: starting in zero, as osmose-java returns species outputs.

Default value for freq will be calculated from x: $freq = 1/xmodelstart$.

units could be whether a single character vector (currently applied on classes **without By**, e.g. osmose.biomass, osmose.yieldN) or a list of length 2 specifying the units for x and y (currently used with classes **with By**, e.g. plot.osmose.biomassBySize, plot.osmose.yieldNByAge).

Extra arguments can be passed from [plot.default](#) using ...: cex, cex.axis, border (useful for [polygon](#), [boxplots](#) and [barplots](#)), etc. It is important to notice that, depending on where the ellipsis is passed, it allows and refuse the use of certain arguments. For instance, if the selected plot is a bar plot, the ... will be passed to the internal barplot call, so if cex argument is used, it will create a conflict and an error (a typical error of using cex in [barplot](#) function).

Value

A graph of an osmose object.

Author(s)

Criscely Lujan Paredes

plot.osmose.config *Plot method for osmose.config objects*

Description

This method takes a `osmose.config` object and produce useful plots.

This function implements a plot method for different `osmose` classes.

Usage

```
## S3 method for class 'osmose.config'  
plot(x, what = "predation", ...)  
  
## S3 method for class 'osmose.config.reproduction'  
plot(  
  x,  
  type = 1,  
  species = 0,  
  speciesNames = NULL,  
  start = NULL,  
  end = NULL,  
  initialYear = NULL,  
  freq = 12,  
  xlim = NULL,  
  ylim = NULL,  
  col = "black",  
  axes = TRUE,  
  border = NA,  
  legend = TRUE,  
  ...  
)  
  
## S3 method for class 'osmose.config.species'  
plot(  
  x,  
  n = 100,  
  type = 1,  
  species = 0,  
  speciesNames = NULL,  
  addElements = c("segments", "points", "polygon", "text"),  
  axes = TRUE,  
  border = NA,  
  xlim = NULL,  
  ylim = NULL,  
  legend = TRUE,  
  col = "black",
```

```

    ...
  )

## S3 method for class 'osmose.config.predation'
plot(
  x,
  type = 1,
  species = 0,
  speciesNames = NULL,
  addElements = c("segments", "points", "text"),
  axes = TRUE,
  border = NA,
  xlim = NULL,
  ylim = NULL,
  col = "gray70",
  legend = TRUE,
  ...
)

```

Arguments

x	osmose like object.
what	Variable name to plot. By default is what = "predation". See Details.
...	Extra arguments of the function.
type	A numeric value, indicating the type of plot to be used (type = 1, by default). See Details.
species	A numeric vector specifying the species that will be showed. If NULL (default), all the available species time series will be plotted. See Details.
speciesNames	A vector with the names for each species. If NULL (default) the names of x will be used.
start	A numeric value indicating the first element of the time indexation of the object x is specified with this parameter. By default start = NULL and the time indexation start with the first element of x.
end	A numeric value. The last element of the time indexation of the object x is specified with this parameter. By default end = NULL and the time indexation finish with the last element of x.
initialYear	A numeric value. It specifies the first element that is going to be used on the x axis for the plots.
freq	A numeric value to indicate the steps by year used in the time series. Default values, see Details.
xlim, ylim	numeric vectors of length 2, giving the x and y coordinates ranges.
col	A vector with the color names for the plots. By default col = NULL and the colors will be chosen by the function.
axes	a logical value indicating whether both axes should be drawn on the plot.

border	the color to draw the border of CI polygons, bar plots and box plots. By default, border = NA, which means that no border will be drawn.
legend	logical do you want to show a legend of species? (valid only for those plot types TS-2)
n	numeric value indicating the number of steps that are going to be used to plot the growth curve (n = 100 as default). The larger is n, the more resolution the curve will have.
addElement	A character vector indicating extra graphical elements that can be included.

Details

Plot types will depend on the class of *x*, which is defined by *what*. Thereby,

- *what* = predation: Generates a plot of size range as shadows for a selected species .
- *what* = reproduction: Generates a single plots of seasonality of reproduction whether as lines (*type* = 1) or bars (*type* = 2)
- *what* = species: Generates a plot of growth curve following the VB parameters defined on configuration files (*type* = 1).

species argument follows the indexation way of java: starting in zero, as *osmose-java* returns species outputs.

Default value for *freq* will be calculated from *x*: $freq = 1/xmodelstart$.

Extra arguments can be passed using *...* and depending on the type, you can modify arguments like: *cex*, *cex.axis*, *border* (useful for polygon and barplots), etc.

Note

Ellipsis (*...*) must be used carefully, since it will pass the arguments to different generic plot functions. For instance, *type* = 2 of *osmose.config.reproduction* method will use *...* to pass arguments to *barplot*, so some arguments like *cex* may match with many formal arguments (e.g. *cex.axis* and *cex.names*), so it may cause errors.

Author(s)

Criscely Lujan Paredes

print.osmose *Print information for an osmose object*

Description

Print information for an osmose object

Usage

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

Arguments

`x` osmose class object (see the [read_osmose](#) function).
`...` Additional arguments for `print`.

`print.summary.osmose` *Print the summary informations about Osmose outputs*

Description

Print the summary informations about Osmose outputs

Usage

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

Arguments

`x` Osmose outputs (see the [read_osmose](#) function)
`...` Additional arguments for `print`.

`readOsmoseConfiguration`
Reads Osmose configuration files.

Description

Reads Osmose configuration files.

Usage

```
readOsmoseConfiguration(file, config = NULL, absolute = TRUE)
```

Arguments

`file` Main configuration file
`config` Configuration object to which file parameters are appended
`absolute` Whether the path is absolute (TRUE) or relative (FALSE)

Value

A list tree.

readOsmoseFiles	<i>Read Osmose output file</i>
-----------------	--------------------------------

Description

Read Osmose output file

Usage

```
readOsmoseFiles(path, type, bySpecies = FALSE, ext = "csv", ...)
```

Arguments

path	Osmose output path
type	Data type ("biomass", etc)
bySpecies	TRUE if should read one file per species.
ext	The extension of the files shich will be read.
...	Additional arguments

Value

Output data frame

report	<i>Report method</i>
--------	----------------------

Description

This function built a report for each class including on osmose package.

Usage

```
report(x, format, output, ...)
```

Arguments

x	Object of class osmose.
format	The format to export the report.
output	Folder where the report will be saved.
...	Extra arguments passed to report function.

Value

A report on specific format.

report.osmose	<i>Report method for osmose objects</i>
---------------	---

Description

Build and export a report of osmose objects using R markdown.

Usage

```
## S3 method for class 'osmose'
report(
  x,
  format = "pdf_document",
  output = NULL,
  tangle = FALSE,
  open = TRUE,
  ...
)
```

Arguments

x	Object of osmose class.
format	The R Markdown output format to convert to (check render).
output	The output directory for the rendered the output file.
tangle	Boolean; whether to tangle the R code from the input file (check render).
open	Do you want to open the output file at the end? (only useful for MS Windows environment).
...	Extra arguments passed to render .

run0smose	<i>Run an OSMOSE configuration</i>
-----------	------------------------------------

Description

This function create a valid configuration by several input files from user input parameters.

Usage

```
run0smose(
  input,
  parameters = NULL,
  output = "output",
  log = "osmose.log",
  version = "4.1.0",
)
```

```

    osmose = NULL,
    java = "java",
    options = NULL,
    verbose = TRUE,
    clean = TRUE
)

run_osmose(
  input,
  parameters = NULL,
  output = NULL,
  log = "osmose.log",
  version = "3.3.3",
  osmose = NULL,
  java = "java",
  options = NULL,
  verbose = TRUE,
  clean = TRUE
)

```

Arguments

input	Filename of the main configuration file
parameters	Parameters to be passed to osmose (version 4 or higher).
output	Output directory. If NULL, the value set in the configuration file is used.
log	File to save OSMOSE execution messages.
version	OSMOSE version. Integer (2, 3, etc.) or releases ('v3r2') are accepted.
osmose	Path to a OSMOSE .jar executable. By default (NULL), uses the stable jar for the current version.
java	Path to the java executable. The default assumes 'java' is on the search path.
options	Java options (e.g. -Xmx2048m to increase memory limit).
verbose	Show messages? (output in the log file if FALSE).
clean	TRUE if the output directory should be cleaned before running OSMOSE.

Details

Basic configurations may not need the use of `buildConfiguration`, but it is required for configuration using interannual inputs or fishing selectivity.

Author(s)

Ricardo Oliveros-Ramos

Examples

```
{
  ## Not run:
  path = cacheManager("gog")
  filename = file.path(path, "osm_all-parameters.csv")
  run_osmose(filename)

  ## End(Not run)
}
```

summary.osmose	osmose <i>object summaries</i>
----------------	--------------------------------

Description

osmose object summaries

Usage

```
## S3 method for class 'osmose'
summary(object, ..., digits = 1L)
```

Arguments

object	osmose class object (see the read_osmose function).
...	Additional arguments for summary.
digits	integer, used for number formatting (by default, 1L). Check summary.default .

summary.osmose.dietMatrix	<i>Title</i>
---------------------------	--------------

Description

Title

Usage

```
## S3 method for class 'osmose.dietMatrix'
summary(object, species = NULL, thres = 1, ...)
```

Arguments

object	an object of class <code>osmose.mortalityRate</code> for which a summary is desired.
species	Name of the species to get a summary.
thres	Threshold which is used to keep values of species matrix.
...	Extra arguments passed to the method.

```
summary.osmose.mortalityRate
    Title
```

Description

Title

Usage

```
## S3 method for class 'osmose.mortalityRate'
summary(object, species = NULL, ...)
```

Arguments

object	an object of class <code>osmose.mortalityRate</code> for which a summary is desired.
species	Name of the species to get a summary.
...	Extra arguments passed to the method.

```
updateCache    Update the cache for the different function
```

Description

This function update the cache for the environmental variables: - wc2-5 - CWD - E

Usage

```
updateCache(nameFile)
```

Arguments

nameFile	The name of the file you want to update. If it's 'NULL' the function will update all the files.
----------	---

Author(s)

Arthur PERE

Examples

```
## Not run:
updateCache()

## End(Not run)
```

write.osmose	<i>Write data in osmose format</i>
--------------	------------------------------------

Description

Write an array or dataframe in the Osmose format. The separator is ";", there are no quotes and a blank column is added for the row names column.

Usage

```
write.osmose(x, file)

write_osmose(
  x,
  file,
  sep = ";",
  col.names = NA,
  quote = FALSE,
  row.names = TRUE,
  ...
)
```

Arguments

x	Object to be written (table or data frame)
file	Output file
sep	The field separator string. Values within each row of x are separated by this string.
col.names	either a logical value indicating whether the column names of x are to be written along with x, or a character vector of column names to be written. See the section on 'CSV files' for the meaning of col.names = NA.
quote	A logical value (TRUE or FALSE) or a numeric vector.
row.names	either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.
...	Extra arguments passed to write.table function.

Index

- *Topic **Internal**
 - cacheManager, 7
- *Topic **ecosystems**
 - osmose-package, 3
- *Topic **marine**
 - osmose-package, 3
- *Topic **modelling**
 - osmose-package, 3
- .osmose.barplot, 4
- .osmose.format_data_stacked, 4
- .plot_osmose_dietMatrix, 5
- .read_2D, 6
- .read_osmose_ncdf, 6

- adjustcolor, 20

- barplot, 21, 24
- boxplot, 21

- cacheManager, 7
- configureCalibration, 7

- get_var, 10
- get_var (getVar), 8
- get_var.osmose, 8, 8
- get_var.osmose.config, 9
- getVar, 8

- image.plot, 21

- osmose (osmose-package), 3
- osmose-package, 3
- osmose2R, 10
- osmose_demo, 11

- par, 20
- plot.default, 21
- plot.osmose, 12
- plot.osmose.abundance, 20
- plot.osmose.biomass, 20
- plot.osmose.config, 22

- plot.osmose.yield, 20
- plot.osmose.yieldN, 20
- polygon, 21
- print.osmose, 24
- print.summary.osmose, 25

- read_osmose, 8, 9, 25, 29
- read_osmose (osmose2R), 10
- readOsmoseConfiguration, 7, 9, 25
- readOsmoseFiles, 26
- render, 27
- report, 26, 26
- report.osmose, 27
- run_osmose (runOsmose), 27
- runOsmose, 27

- summary.default, 29
- summary.osmose, 29
- summary.osmose.dietMatrix, 29
- summary.osmose.mortalityRate, 30

- updateCache, 30

- write.osmose, 31
- write_osmose (write.osmose), 31