

Package: PEcAn.MAESPA (via r-universe)

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Type Package

Title PEcAn Functions Used for Ecological Forecasts and Reanalysis using MAESPA

Version 1.7.3.9000

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Description The Predictive Ecosystem Carbon Analyzer (PEcAn) is a scientific workflow management tool that is designed to simplify the management of model parameterization, execution, and analysis. The goal of PEcAn is to streamline the interaction between data and models, and to improve the efficacy of scientific investigation. This package allows for MAESPA to be run through the PEcAN workflow.

Imports PEcAn.data.atmosphere, PEcAn.logger, PEcAn.remote, PEcAn.utils, lubridate (>= 1.6.0), ncd4 (>= 1.15),

Suggests Maeswrap, coda, testthat (>= 1.0.2)

SystemRequirements MAESPA ecosystem model

OS_type unix

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LazyLoad yes

LazyData FALSE

Encoding UTF-8

RoxygenNote 7.3.2

Repository <https://pecanproject.r-universe.dev>

RemoteUrl <https://github.com/PecanProject/pecan>

RemoteRef HEAD

RemoteSha f22a7c4bbc532e4551f7bc9624cef649da317ac1

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met2model.MAESPA	<i>met2model.MAESPA</i>
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Description

met2model wrapper for MAESPA

Usage

```
met2model.MAESPA(
    in.path,
    in.prefix,
    outfolder,
    start_date,
    end_date,
    overwrite = FALSE,
    verbose = FALSE,
    ...
)
```

Arguments

<code>in.path</code>	location on disk where inputs are stored
<code>in.prefix</code>	prefix of input and output files
<code>outfolder</code>	location on disk where outputs will be stored
<code>start_date</code>	the start date of the data to be downloaded (will only use the year part of the date)
<code>end_date</code>	the end date of the data to be downloaded (will only use the year part of the date)
<code>overwrite</code>	should existing files be overwritten
<code>verbose</code>	should the function be very verbose

Author(s)

Tony Gardella

model2netcdf.MAESPA *Code to convert MAESPA's output into netCDF format*

Description

Convert MAESPA output into the NACP Intercomparison format (ALMA using netCDF)

Usage

```
model2netcdf.MAESPA(  
  outdir,  
  sitelat,  
  sitelon,  
  start_date,  
  end_date,  
  stem_density  
)
```

Arguments

outdir	Location of MAESPA output
sitelat	Latitude of the site
sitelon	Longitude of the site
start_date	Start time of the simulation
end_date	End time of the simulation
stem_density	Number of trees/plotsize. Values in trees.dat

Author(s)

Tony Gardella

write.config.MAESPA *Write MAESPA configuration files*

Description

Writes a config file for Maespa

Usage

```
write.config.MAESPA(defaults, trait.values, settings, run.id)
```

Arguments

<code>defaults</code>	list of defaults to process
<code>settings</code>	list of settings from pecan settings file
<code>run.id</code>	id of run
<code>trait.samples</code>	vector of samples for a given trait

Details

Requires a pft xml object, a list of trait values for a single model run, and the name of the file to create

Value

configuration file for MAESPA for given run

Author(s)

Tony Gardella

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