

Package: PEcAn.BIOCRO (via r-universe)

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Type Package

Title PEcAn Package for Integration of the BioCro Model

Version 1.7.3.9000

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Description This module provides functions to link BioCro to PEcAn.

Imports PEcAn.logger, PEcAn.remote, PEcAn.utils, PEcAn.settings,
PEcAn.data.atmosphere, PEcAn.data.land, ncd4 (>= 1.15),
lubridate (>= 1.7.0), data.table, dplyr, XML, rlang

Suggests BioCro, knitr, testthat (>= 2.0.0), mockery (>= 0.3.0),
PEcAn.DB, rmarkdown, RPostgreSQL

Remotes github::ebimodeling/biocro@0.951

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VignetteBuilder knitr, rmarkdown

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

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Contents

cf2biocro	2
convert.samples.BIOCRO	3
get_biocro_defaults	4
met2model.BIOCRO	4
model2netcdf.BIOCRO	5
read.biocro.config	6

remove.config.BIOCRO	6
run.biocro	7
write.config.BIOCRO	8
Index	9

cf2biocro	<i>Converts a CF data frame into a BioCro met input</i>
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Description

Converts a CF data frame into a BioCro met input

Usage

```
cf2biocro(met, longitude = NULL, zulu2solarnoon = FALSE)
```

Arguments

met	data.table object with met for a single site; output from load.cfmet
year	int
month	int
day	int: day of month (1-31)
doym	int: day of year (1-366)
hour	int (0-23)
date	YYYY-MM-DD HH:MM:SS POSIXct
wind_speed	num m/s
northward_wind	
eastward_wind	
ppfd	optional; if missing, requires surface_downwelling_shortwave_flux_in_air
surface_downwelling_shortwave_flux_in_air	
air_pressure (Pa)	optional; if missing, requires relative_humidity
specific_humidity	optional; if missing, requires relative_humidity
relative_humidity	optional; if missing, requires air_pressure and specific_humidity
precipitation_flux	
air_temperature	
longitude	in degrees east, used for calculating solar noon
zulu2solarnoon	logical; if TRUE, convert time from GMT to local solar time.

Value

data.table / data.frame with fields

doy day of year

hr hour

solar solar radiation (PPFD)

temp temperature, degrees celsius

rh relative humidity, as fraction (0-1)

windspeed m/s

precip cm/h

Author(s)

David LeBauer

`convert.samples.BIOCRO`

convert parameters from PEcAn database default units to biocro defaults

Description

Performs model specific unit conversions on a list of trait values, such as those provided to `write.config`

Usage

```
convert.samples.BIOCRO(trait.samples, biocro_version = 1)
```

Arguments

`trait.samples` a matrix or dataframe of samples from the trait distribution

`biocro_version` numeric, but currently only checks whether version is less than 1.0

Value

dataframe with values transformed

Author(s)

David LeBauer

get_biocro_defaults *Look for defaults provided as datasets in the BioCro model package*

Description

When available, default parameters come in sets of three: *_initial_values, *_parameters, *_modules

Usage

```
get_biocro_defaults(genus)
```

Arguments

genus Name of the genus (or really any string BioCro uses as a *_parameters prefix)

Value

a list in the format expected by 'BioCro::Gro()', containing four lists named 'type', 'initial_values', 'parameters', and 'modules', or NULL if genus not found

met2model.BIOCRO *Write BioCro met files*

Description

Converts a met CF file to a model specific met file. The input files are called <in.path>/<in.prefix>.YYYY.cf

Usage

```
met2model.BIOCRO(
  in.path,
  in.prefix,
  outfolder,
  overwrite = FALSE,
  lat,
  lon,
  start_date,
  end_date,
  ...
)
```

Arguments

in.path	path on disk where CF file lives
in.prefix	prefix for each file
outfolder	location where model specific output is written
overwrite	logical: Write over any existing file of the same name? If FALSE, leaves the existing file untouched and skips to the next year.
lat, lon	Site latitude and longitude
start_date, end_date	Date range to convert. Each year will be written to a separate file
...	other arguments passed from PEcAn, currently ignored

Value

a dataframe of information about the written file

Author(s)

Rob Kooper, David LeBauer

model2netcdf.BIOCRO *Convert BioCro output to standard netCDF format*

Description

Modified from on model2netcdf.SIPNET and model2netcdf.ED2 by

Usage

```
model2netcdf.BIOCRO(result, genus = NULL, outdir, lat = -9999, lon = -9999)
```

Arguments

result	a dataframe of model output to be converted
genus	character: What kind of plant was being simulated? Used to correct for some genus-specific differences in model output; Eventually that will be handled inside BioCro and this argument will be removed.
outdir	Location of model output
lat	Latitude of the site
lon	Longitude of the site

Author(s)

David LeBauer, Deepak Jaiswal, Rob Kooper

read.biocro.config *Read BioCro config file*

Description

Read BioCro config file

Usage

```
read.biocro.config(config.file = "config.xml")
```

Arguments

config.file Path to XML file

Value

list of run configuration parameters for PEcAn

Author(s)

David LeBauer

remove.config.BIOCRO *Clear out previous config and parameter files.*

Description

Clear out previous config and parameter files.

Usage

```
remove.config.BIOCRO(main.outdir, settings)
```

Arguments

main.outdir Primary PEcAn output directory (will be depreciated)
settings PEcAn settings file

Value

nothing, removes config files as side effect

Author(s)

Shawn Serbin, David LeBauer

run.biocro *Run BioCro at a point*

Description

Run BioCro at a point

Usage

```
run.biocro(  
  lat,  
  lon,  
  metpath,  
  soil.nc = NULL,  
  config = config,  
  coppice.interval = 1  
)
```

Arguments

lat	latitude in decimal degrees
lon	longitude in decimal degrees
metpath	full path and name prefix of a csv file with hourly data in BioCro format, e.g. <code>'/dir/met'</code> if the files to be used are <code>'/dir/met.2004.csv'</code> and <code>'dir/met.2005.csv'</code>
soil.nc	full path and name of a netCDF file with soil data
config	full path and name of a config.xml file containing parameter values and configuration information for BioCro
coppice.interval	numeric, number of years between cuttings for coppice plant or perennial grass. Only used with BioCro 0.9; ignored when using later versions.

Value

output from one of the `BioCro::*.Gro` functions (determined by `config$genus`), as `data.table` object

Author(s)

David LeBauer

write.config.BIOCRO *Writes a configuration files for the biocro model*

Description

Writes a configuration files for the biocro model

Usage

```
write.config.BIOCRO(defaults = NULL, trait.values, settings, run.id)
```

Arguments

defaults	named list with default model parameter values
trait.values	named list (or dataframe of trait values) can either be a data.frame or named list of traits, e.g. data.frame(vmax = 1, b0 = 2) or list(vmax = 1, b0 = 2)
settings	pecan settings file configured for BioCro
run.id	integer; a unique identifier for the run.

Value

nothing, writes configuration file as side effect

Author(s)

David LeBauer

Index

`cf2biocro`, [2](#)
`convert.samples.BIOCRO`, [3](#)

`get_biocro_defaults`, [4](#)

`load.cfmet`, [2](#)

`met2model.BIOCRO`, [4](#)
`model2netcdf.BIOCRO`, [5](#)

`read.biocro.config`, [6](#)
`remove.config.BIOCRO`, [6](#)
`run.biocro`, [7](#)

`write.config.BIOCRO`, [8](#)