Package: PEcAn.BIOCRO (via r-universe)

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Type Package

Title PEcAn Package for Integration of the BioCro Model

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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, ncdf4 (>= 1.15), lubridate (>= 1.7.0), data.table, dplyr, XML, rlang

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

Remotes github::ebimodeling/biocro@0.951

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`cf2biocro` *Convert CF-formatted met data to BioCro met*

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) • doy 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 samples for biocro*

Description

convert parameters from PEcAn database default units to biocro defaults

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

Details

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

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

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`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` *Function to convert biocro model output to standard netCDF format*

Description

Convert BioCro output to netCDF

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

Details

Converts BioCro output to netCDF. Modified from on model2netcdf.SIPNET and model2netcdf.ED2 by

Author(s)

David LeBauer, Deepak Jaiswal, Rob Kooper

`read.biocro.config` *Read BioCro Config*

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 biocro 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. ‘/dir/met‘ if the files to be used are ‘/dir/met.2004.csv‘ and ‘dir/met.2005.csv’
`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` *Write 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

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