

# Package: PEcAn.SIBCASA (via r-universe)

September 18, 2024

**Type** Package

**Title** PEcAn Package for Integration of the SiBCASA Model

**Version** 0.0.1.9000

**Description** This module provides functions to link (SiBCASA) to PEcAn.  
It is a work in progress and is not yet fully functional.

**Imports** ncdf4, PEcAn.logger, PEcAn.utils (>= 1.4.8)

**Suggests** testthat (>= 3.0.0), withr

**SystemRequirements** SiBCASA

**OS\_type** unix

**License** BSD\_3\_clause + file LICENSE

**Copyright** Authors

**LazyData** TRUE

**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.SIBCASA      *Write SIBCASA met files*

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### Description

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

### Usage

```
met2model.SIBCASA(in.path, in.prefix, outfolder, overwrite = FALSE)
```

### 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: Replace output if it already exists?

### Value

OK if everything was succesful.

### Author(s)

Tony Gardella

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model2netcdf.SIBCASA      *Convert SIBCASA output into the NACP Intercomparison format (ALMA using netCDF)*

---

### Description

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

### Usage

```
model2netcdf.SIBCASA(outdir, sitelat, sitelon, start_date, end_date)
```

### Arguments

outdir	Location of model 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

**Author(s)**

Tony Gardella

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read\_restart.SIBCASA *Read restart template for SDA*


---

**Description**

Read restart files from model.

**Usage**

read\_restart.SIBCASA(outdir, runid, stop.time, settings, var.names, params)

**Arguments**

outdir	Output directory
runid	Run ID
stop.time	Year that is being read
settings	PEcAn settings object
var.names	Variable names to be extracted
params	Any parameters required for state calculations

**Value**

Forecast numeric matrix

**Author(s)**

Alexey Shiklomanov

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sibcasa\_output\_vars *Output variables for SIBCASA*


---

**Description**

TODO: Provide a complete description here of the dataset, including its origin and purpose. The column descriptions below were written by someone looking at the file with no insight into its usage

**Usage**

sibcasa\_output\_vars

**Format**

data frame with 6 unnamed columns

**1** ? (t 0, t 3, etc)

**2** short name

**3** row number?

**4** description

**5** units

**6** unused

---

write.config.SIBCASA *Writes a SIBCASA config file.*

---

**Description**

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

**Usage**

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

**Arguments**

defaults	list of defaults to process
trait.values	vector of values for a given trait
settings	list of settings from pecan settings file
run.id	id of run

**Value**

configuration file for SIBCASA for given run

**Author(s)**

Anthony Gardella, Rob Kooper

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write\_restart.SIBCASA *Write restart template for SDA*

---

**Description**

Write restart files for model

**Usage**

```
write_restart.SIBCASA(  
  outdir,  
  runid,  
  start.time,  
  stop.time,  
  settings,  
  new.state  
)
```

**Arguments**

outdir	Output directory
runid	Run ID
start.time	Time of current assimilation step
stop.time	Time of next assimilation step
settings	PEcAn settings object
new.state	Analysis state matrix returned by sda.enkf

**Author(s)**

Alexey Shiklomanov

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