

Package: LEEF.measurement.bemovi (via r-universe)

October 25, 2024

Type Package

Title Prepares Movies for Analysis with Bemovi and Extracts Data

Description Module for the LEEF pipeline to process bemovi data.

Version 0.8.40

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BugReports <https://github.com/LEEF-UZH/LEEF.measurement.bemovi/issues/>

URL <https://leef-uzh.github.io/LEEF.measurement.bemovi/>,

<https://github.com/LEEF-UZH/LEEF.measurement.bemovi/>

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Depends R (>= 3.5.0)

Imports bemovi.LEEF (>= 1.0.1), R.utils, utils, parallel, data.table, dplyr, purrr, tidyselect, magrittr, yaml, rlang, e1071, loggit

Additional_repositories <https://leef-uzh.github.io/drat/>

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Suggests testthat, openssl

Repository <https://leef-uzh.r-universe.dev>

RemoteUrl <https://github.com/LEEF-UZH/LEEF.measurement.bemovi>

RemoteRef master

RemoteSha 1a2748d6150043a2000991927fd087c253ed441e

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add_new_data	<i>Check if data in input folder is OK and move to raw data folder</i>
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Description

Check if data in input folder is OK and move to raw data folder

Usage

```
add_new_data(input, output)
```

Arguments

input	The folder, where a folder bemovi is located which contains the new files.
output	A folder, which contains a subfolder called bemovi, i.e. the usually the raw data folder, into which the files will be moved to.

Value

a list which contains the individual results for each file. TRUE if moved, FALSE if an error occurred. Details of the error re in the error files in the input/bemovi directory.

check_tools_path	<i>Checks tools_path() if all tools are there or downloads them</i>
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Description

Checks tools_path() if all tools are there or downloads them

Usage

```
check_tools_path(path = tools_path(), download = FALSE)
```

Arguments

path	path for the tools. defaults to tools_path()
download	if TRUE, the tools are downloaded. If FALSE, the default, the tools path is only checked.

Value

TRUE if all tools are installed. a named list of tools which are not installed.

Examples

```
check_tools_path()
```

classify	<i>Classify morph_mvt nad calculates densities</i>
----------	--

Description

Classify morph_mvt nad calculates densities

Usage

```
classify(  
  bemovi_extract,  
  morph_mvt,  
  trajectory_data,  
  classifiers_constant,  
  classifiers_increasing,  
  video_description_file,  
  composition  
)
```

Arguments

morph_mvt merged track data - one row per particle
classifiers_constant
 constant tempersture classifier
classifiers_increasing
 increasing temperature classifier

Value

morph_mvt with the classified species and probabilities

extractor_bemovi *Extractor bemovi data*

Description

Analyse all .avi files in bemovi folder and save as .rds file.

Usage

```
extractor_bemovi(input, output)
```

Arguments

input directory from which to read the data
output directory to which to write the data

Details

This function is executing extractor_bemovi_particle(), extractor_bemovi_trajectory() and finally extractor_bemovi_merge() for all parameter files in the format bemovi_extract*.yaml

Value

invisibly TRUE when completed successful

`extractor_bemovi_classify`*Extractor bemovi to id species and calculate density*

Description

This function id's the species and calculates the densities.

Usage

```
extractor_bemovi_classify(input, output)
```

Arguments

input	directory from which to read the data
output	directory to which to write the data

Value

invisibly TRUE when completed successful

`extractor_bemovi_filter`*Extractor bemovi to filter traced particles*

Description

This function applies a filter.

Usage

```
extractor_bemovi_filter(input, output)
```

Arguments

input	directory from which to read the data
output	directory to which to write the data

Value

invisibly TRUE when completed successful

extractor_bemovi_merge

Extractor bemovi data

Description

Analyse all .avi files in bemovi folder and save as .rds file.

Usage

```
extractor_bemovi_merge(input, output)
```

Arguments

input	only for compatibility - not used
output	directory to which to write the data

Details

This function is extracting data to be added to the database (and therefore make accessible for further analysis and forecasting) from .avi files.

Value

invisibly TRUE when completed successful

extractor_bemovi_overlay

Extractor bemovi data trajectories

Description

This function is calculating the trajectories

Usage

```
extractor_bemovi_overlay(input, output)
```

Arguments

input	only for compatibility - not used
output	directory to which to write the data

Value

invisibly TRUE when completed successful

extractor_bemovi_particle
Extractor bemovi data particles

Description

This function **requires** the following files and directories:

Usage

```
extractor_bemovi_particle(input, output)
```

Arguments

input	directory from which to read the data
output	directory to which to write the data

Details

- one input directory which contains
 - a folder named bemovi with
 - * the .avi files
 - * a file bemovi_extract.yml containing all the parameter for the analysis. This parameter file will be loaded for the analysis.
 - a folder named 00.general.parameter at the same level as input

This function **creates** the following folder if it does not exist:

- output\bemovi in which will contain
 - diverse output as created by bemovi.LEEF::locate_and_measure_particles()
 - all metadata et al files in the input/bemovi folder which are **not** .avi and .metadata files

Value

invisibly TRUE when completed successful

`extractor_bemovi_trajectory`*Extractor bemovi data trajectories*

Description

This function is calculating the trajectories

Usage

```
extractor_bemovi_trajectory(input, output)
```

Arguments

input	only for compatibility - not used
output	directory to which to write the data

Value

invisibly TRUE when completed successful

`pre_processor_bemovi` *Preprocessor bemovi data*

Description

Convert all .xcd files in the input/bemovi folder to non-proprietary avi format.

Usage

```
pre_processor_bemovi(input, output)
```

Arguments

input	directory from which to read the data
output	directory to which to write the data

Details

This function **requires** the following files and directories:

- one input directory which contains
 - a folder named `bemovi` with
 - * the `.cxd` files
 - * a file `bemovi_extract.yml` containing all the parameter for the analysis. This parameter file will be loaded for the analysis.
 - a folder named `00.general.parameter` at the same level as input

This function **creates** the following folder if it does not exist:

- `output\bemovi` in which will contain
 - the `.avi` files (converted `.cxd` files)
 - the `.metadata` text files containing the extracted metadata from the `.cxd` files
 - the files recursively copied from the `00.general.parameter` folder

Value

invisibly TRUE when completed successful

<code>raw_data_ok</code>	<i>Check if data in raw data folder is OK</i>
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Description

Check if data in raw data folder is OK

Usage

```
raw_data_ok(input)
```

Arguments

`input` raw data folder containing bemovi data, i.e usually is `some/path/bemovi`

Value

TRUE if ok, FALSE or list of problems if not

Examples

```
## Not run:
raw_data_ok()

## End(Not run)
```

register	<i>Register the processing of bemovi data in the LEEF package</i>
----------	---

Description

Register the processing of bemovi data in the LEEF package

Usage

```
register()
```

Value

invisibly TRUE when completed successful

tools_path	<i>Read and write tools_path</i>
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Description

Read or write the tools path where the tools are located in. If no parameter is given, the path will be returned as a list.

Usage

```
tools_path(tools_path)
```

Arguments

tools_path	character vector of length one containing the directory where the tools are located
------------	---

Value

tools directory. If values have set, the value before the change.

Examples

```
tools_path()
```

```
tools_path("./temp")
```

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