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

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Type Package

Title What the Package Does (Title Case)

Version 0.8.13

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BugReports `https://github.com/LEEF-UZH/LEEF.measurement.flowcytometer/issues`

URL `https://github.com/LEEF-UZH/LEEF.measurement.flowcytometer`

Description More about what it does (maybe more than one line) Use four spaces when indenting paragraphs within the Description.

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Depends R (>= 3.5.0)

Imports R.utils, flowCore (>= 2.0), tiff, yaml, plyr, tidyr, loggit, magrittr

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Suggests testthat, openssl

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

RemoteUrl https://github.com/LEEF-UZH/LEEF.measurement.flowcytometer

RemoteRef master

RemoteSha bfa9bb3121db3e16150c657dfc91a311f6963b41

Contents

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

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 `flowcytometer` is located which contains the new files.
`output`	A folder, which contains a subfolder called `flowcytometer`, i.e. the usually the raw data folder, into which the fioles will be moved to.

Value

a `list` which contains the individual reseults for each file. `TRUE` if moved, `FALSE` if an error occured. Details of the eror re in the error files in the `input/flowcytometer` directory.

`extractor_flowcytometer` *Extractor flowcytometer data*

Description

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

Usage

```
extractor_flowcytometer(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_flowcytometer_gating`

Extractor flowcytometer data

Description

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

Usage

```
extractor_flowcytometer_gating(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_flowcytometer_preparation`

Extractor flowcytometer preparation data

Description

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

Usage

```
extractor_flowcytometer_preparation(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

`load_parameter` *Load parameter from* `file`

Description

Load parameter from `file`

Usage

```
load_parameter(file = "parameter.yaml")
```

Arguments

`file`	name of parameter file

Value

invisibly TRUE

`par_template` *Template function to assign value to parameter in the package wide cache*

Description

assign the function to a new cvariable and the name of the function woll be used for the parameter name. e.g:

- fps <- par_template

Usage

```
par_template(value)
```

Arguments

`value`	if missing, the value of the parameter will be returned, `NULL` if the parameter does not exist; if specified, the parameter will be set to the value

Value

the (new) value of the argument

`pre_processor_flowcytometer` *Preprocessor flowcytometer data*

Description

Just copy all files

Usage

```
pre_processor_flowcytometer(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

`pre_processor_flowcytometer_c6` *Preprocessor flowcytometer data FOR c6 FILES!!!*

Description

Convert all `.c6` files in `flowcytometrie` folder to `.fcs` files in output folder

Usage

```
pre_processor_flowcytometer_c6(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

`print_parameter` *Print the flowcytometer parameter*

Description

Print the flowcytometer parameter

Usage

```
print_parameter(print_as_yaml = TRUE, echo = TRUE)
```

Arguments

`print_as_yaml`	Print in yaml formated text; ~ stands for NULL
`echo`	if `TRUE` print the parameter, if `FALSE` just return them as list

Value

invisible returns list of parameter for further processing

`raw_data_ok` *Check if data in raw data folder is OK*

Description

Check if data in raw data folder is OK

Usage

```
raw_data_ok(input)
```

Arguments

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

Value

`TRUE` if ok, `FALSE` or `list` of problems if not

Examples

```
## Not run:
raw_data_ok()

## End(Not run)
```

`register` *Register the processing of flowcytometer data in the LEEF package*

Description

Register the processing of flowcytometer data in the LEEF package

Usage

```
register()
```

Value

invisibly `TRUE` when completed successful

`save_parameter` *Save parameter into `.yaml` file*

Description

Save parameter into `.yaml` file

Usage

```
save_parameter(file = "parameter.yaml")
```

Arguments

`file`	name of parameter file

Value

invisibly `TRUE`

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