

Package ‘rtimicropem’

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Type Package

Title Supports the Analysis of RTI MicroPEM Output Files

Version 1.4.0

Description Supports the input and reproducible analysis of RTI MicroPEM output files.

License GPL (>= 2)

URL <https://github.com/ropensci/rtimicropem>,
<https://docs.ropensci.org/rtimicropem/>

BugReports <https://github.com/ropensci/rtimicropem/issues>

Depends R (>= 3.3.0)

Imports changepoint, dplyr (>= 0.4.3), fs, ggplot2, knitr, lazyeval,
lubridate, methods, R6, rbokeh, readr, stringr, tibble, tidyr

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R topics documented:

rtimicropem-package	2
batch_convert	3
CHAI	4
chai_alarm	4
clean_measures	5
Columbia	6
Columbia2	6
convert_output	7
identify_lags	7
micropem	8
micropemC1	9
micropemC2	10
micropemChai	10
run_shiny_app	11
Index	12

rtimicropem-package *Supports the analyses of RTI MicroPEM output files.*

Description

micropem allows you to read and analyse data from MicroPEM output files in a reproducible way.

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See Also

Useful links:

- <https://github.com/ropensci/rtimicropem>
- <https://docs.ropensci.org/rtimicropem/>
- Report bugs at <https://github.com/ropensci/rtimicropem/issues>

batch_convert	<i>Reading several MicroPEM files and saving the settings and measurement tables to csv.</i>
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Description

Reading several MicroPEM files and saving the settings and measurement tables to csv.

Usage

```
batch_convert(path_input, path_output = path_input)
```

Arguments

path_input	path to the directory with files (character)
path_output	path where the files should be created, by default equal to path_input (character). The function saves results in the input directory as csv files with a "," as separator. One file is settings.csv with all settings, the other one is measures.csv It saves them directly for not loading all of them at the same time in the session.

Examples

```
## Not run:  
batch_convert(path_input = c(system.file('extdata', 'dummyCHAI.csv', package = 'micropem'),  
system.file('extdata', 'dummyCHAI.csv', package = 'micropem')),  
path_output = getwd())  
## End(Not run)
```

CHAI	<i>A micropem output file.</i>
------	--------------------------------

Description

A csv micropem output file of version CHAI of the output file.

Format

A csv micropem output file of version CHAI of the output file.

Examples

```
## Not run:  
micropemExample <- convert_output(system.file('extdata', 'CHAI.csv', package = 'rtimicropem'))  
micropemExample$plot()  
  
## End(Not run)
```

chai_alarm	<i>Generates alarm indicators for a micropem object.</i>
------------	--

Description

Generates alarm indicators for a micropem object.

Usage

```
chai_alarm(micropem_object)
```

Arguments

```
micropem_object  
the MicroPEM object
```

Value

A data table with a column for the name of the indicator and a column with booleans. If no alarm was flagged, the data table only has one line indicating that all is good.

Examples

```
data(micropemChai)  
chai_alarm(micropemChai)
```

clean_measures	<i>Outputs clean rh_corrected_nephelometer measures for analysis.</i>
----------------	---

Description

Outputs clean rh_corrected_nephelometer measures for analysis.

Usage

```
clean_measures(micropem_object, hepa_start = FALSE, hepa_end = FALSE)
```

Arguments

micropem_object	the MicroPEM object
hepa_start	Boolean indicating whether there were measurements with HEPA filters at the beginning.
hepa_end	Boolean indicating whether there were measurements with HEPA filters at the end.

Details

rh_corrected_nephelometer values are set to NA if they are negative or if the RH at the same time is higher than 90%. rh_corrected_nephelometer values are also corrected for the HEPA zeroings (start and end, if there were done): if a stable period longer than 3 minutes can be identified for the HEPA period, using the changepoint `cpt.mean` function, there is a zero value. There can be no zero values, only one (beginning or end) or two. If there is only one zero value, it is subtracted from all rh_corrected_nephelometer values. If there are two, a linear interpolation is done between the two values and the resulting vector is subtracted from the rh_corrected_nephelometer values.

Value

A MicroPEM object.

Examples

```
data(micropemChai)
cleanMP <- clean_measures(micropemChai)
cleanMP$summary()
```

Columbia

A micropem output file.

Description

A csv micropem output file of version Columbia of the output file.

Format

A csv micropem output file of version Columbia of the output file.

Examples

```
## Not run:  
micropemExample <- convert_output(system.file('extdata', 'Columbia.csv', package = 'rtimicropem'))  
micropemExample$plot()  
  
## End(Not run)
```

Columbia2

A micropem output file.

Description

A csv micropem output file of version Columbia2 of the output file.

Format

A csv micropem output file of version Columbia2 of the output file.

Examples

```
## Not run:  
micropemExample <- convert_output(system.file('extdata', 'Columbia2.csv', package = 'rtimicropem'))  
micropemExample$plot()  
  
## End(Not run)
```

convert_output	<i>Uses output file from MicroPEM to create a micropem object.</i>
----------------	--

Description

Uses output file from MicroPEM to create a micropem object.

Usage

```
convert_output(path)
```

Arguments

path the path to the file (character)

Value

A micropem object.

Examples

```
micropem_example <- convert_output(system.file('extdata', 'CHAI.csv', package = 'rtimicropem'))
micropem_example$plot()
micropem_example$plot(title = "wow")
```

identify_lags	<i>Identify time gaps in the data collection period</i>
---------------	---

Description

Identify time gaps in the data collection period

Usage

```
identify_lags(micropem, column = "rh_corrected_nephelometer")
```

Arguments

micropem a R6 micropem object
column by default "rh_corrected_nephelometer", but could be "nephelometer", the column in which to look for gaps (character).

Value

A data.frame with all the rows of measures where the nephelometer measures is missing with a time to previous missing values smaller than the nephelometer log.

Examples

```
micropem_na <- convert_output(system.file("extdata", "file_with_na.csv",
                                         package = "rtimicropem"))
micropem_na$plot()
identify_lags(micropem_na)
```

 micropem

An R6 class to represent MicroPEM output information.

Description

An R6 class to represent MicroPEM output information.

Usage

```
micropem
```

Format

[R6Class](#) object.

Value

Object of [R6Class](#).

Fields

settings `Data.frame (dplyr "tbl_df")` with settings of the micropem device and other information such as download time.

calibration List of calibration information.

filename Filename from which the object was built.

measures `Data.frame (dplyr "tbl_df")` with all time-varying measures, possibly:

datetime Time and date of each measurement, as a POSIXt object. Depending on the different logs of the time-varying variables there is not a measure for all variables associated to each timepoint.

rh_corrected_nephelometer Measures of nephelometer in microgram/meter cube (numeric).

temp Measures of temperature in centigrade (numeric).

rh Measures of relative humidity that are a proportion and as such do not have an unit (numeric).

battery Measures of battery in Volt (numeric).

orifice_press Measures of orifice pressure in inches of water (numeric).

inlet_press Measures of inlet pressure in inches of water (numeric).

flow Measures of flow in liters per minute (numeric).

x_axis x-axis accelerometer in m/s² (numeric).

y_axis y-axis accelerometer in m/s² (numeric).
z_axis z-axis accelerometer in m/s² (numeric).
vector_sum_composite vector sum m/s² (numeric).
message Shutdown reason (factor).

original Boolean. Is this an original micropem object (TRUE) or was it e.g. filtered or cleaned (FALSE).

Methods

plot Method for getting a quick plot of all time-varying measurements. Either type = "plain" or type = "interactive", see examples. The method returns a plot of the ggplot-class. One can add a title via the title argument.

summary Method for getting a summary table (dplyr "tbl_df") of all time-varying numeric measurements.

print Method for printing both the summary table of all time-varying numeric measurements and all settings from the settings field.

Examples

```
data("micropemChai")
# Plot method, type = "plain" by default.
micropemChai$plot()
# Example with type = "interactive", for RStudio viewer,
# RMarkdown html documents and Shiny apps.
## Not run:
library("rbokeh")
p <- micropemChai$plot(type = "interactive")
p
# Summary method
micropemChai$summary()
# Print method
micropemChai$print()

## End(Not run)
```

micropemC1

A micropem object.

Description

A micropem object.

Format

A micropem object.

Examples

```
data("micropemC1")
micropemC1$plot()
```

micropemC2

A micropem object.

Description

A micropem object.

Format

A micropem object.

Examples

```
data("micropemC2")
micropemC2$plot()
```

micropemChai

A micropem object.

Description

A micropem object.

Format

A micropem object.

Examples

```
data("micropemChai")
micropemChai$plot()
```

run_shiny_app	<i>Run a built-in Shiny App.</i>
---------------	----------------------------------

Description

Run a built-in Shiny App.

Usage

```
run_shiny_app()
```

Details

This app allows you to upload a single MicroPEM file and to explore it via several tabs, one with the summary of measures, one with settings, one with a plot and with alarms (see [chai_alarm](#)). The app can e.g. be used after one day of field work to quickly check files.

Examples

```
## Not run:  
run_shiny_app()  
  
## End(Not run)
```

Index

*Topic **data**

- CHAI, [4](#)
- Columbia, [6](#)
- Columbia2, [6](#)
- micropem, [8](#)
- micropemC1, [9](#)
- micropemC2, [10](#)
- micropemChai, [10](#)

[batch_convert](#), [3](#)

[CHAI](#), [4](#)
[chai_alarm](#), [4](#), [11](#)
[clean_measures](#), [5](#)
[Columbia](#), [6](#)
[Columbia2](#), [6](#)
[convert_output](#), [7](#)
[cpt.mean](#), [5](#)

[identify_lags](#), [7](#)

[micropem](#), [8](#)
[micropemC1](#), [9](#)
[micropemC2](#), [10](#)
[micropemChai](#), [10](#)

[R6Class](#), [8](#)
[rtimicropem](#) ([rtimicropem-package](#)), [2](#)
[rtimicropem-package](#), [2](#)
[run_shiny_app](#), [11](#)