

Package ‘frapplot’

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Type Package

Title Automatic Data Processing and Visualization for FRAP

Version 0.1.3

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Description Automatically process Fluorescence Recovery After Photobleaching (FRAP) data and generate consistent, publishable figures. Note: this package does not replace 'ImageJ' (or its equivalence) in raw image quantification. Some references about the methods: Sprague, Brian L. (2004) <[doi:10.1529/biophysj.103.026765](https://doi.org/10.1529/biophysj.103.026765)>; Day, Charles A. (2012) <[doi:10.1002/0471142956.cy0](https://doi.org/10.1002/0471142956.cy0)>

Depends R (>= 2.10)

Imports grDevices, graphics, stats, utils

BugReports <https://github.com/GuanqiaoDing/frapplot/issues>

URL <https://github.com/GuanqiaoDing/frapplot>

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

Repository CRAN

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example_dataset	<i>Example dataset</i>
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Description

Example dataset

Usage

```
example_dataset
```

Format

A list of three matrices: each contains FRAP data for a control or experimental group. For each matrix, nrow = time_points + 1, ncol = sample size.

exclude	<i>Exclude samples from the dataset</i>
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Description

If certain samples are of poor quality, use this function to exclude them from the dataset.

Usage

```
exclude(ds, group, cols)
```

Arguments

ds	Name of the dataset.
group	Name of the group from which to exclude certain samples.
cols	A vector of numbers specifying the column(s) to exclude.

Value

Modified dataset in the same format.

Examples

```
ds <- exclude(example_dataset, group = "mut1", cols = c(1,3))
```

frapplot	<i>Plot FRAP data of two selected groups</i>
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Description

Plot FRAP data of any two groups (e.g. control and mutant) in a consistent and publishable format.

Usage

```
frapplot(path, control, mutant, info)
```

Arguments

path	Path of the output directory
control	Name of the control.
mutant	Name of the mutant.
info	Returned information from fraproccess() .

Examples

```
info <- fraproccess(example_dataset, seq(0, 145, 5))  
frapplot(tempdir(), "control", "mut2", info)
```

fraproccess	<i>Process FRAP data</i>
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Description

Normalize and analyze FRAP data. Perform non-linear regression and calculate ymax, ymin, k, halftime, tau, total_recovery, total_recovery_sd.

Usage

```
fraproccess(ds, time_points)
```

Arguments

ds	A dataset that contains FRAP data for multiple experiment groups
time_points	A vector of time points (in second) that the experiment uses, e.g. 0, 5, 10,

Value

A list of results:

- `$time_points`: a vector of time points
- `$summary`: summary of the regression
- `$sample_means`: a matrix of sample means, `nrow` = num of time points, `ncol` = sample size
- `$sample_sd`: a matrix of standard deviations, `nrow` = num of time points, `ncol` = sample size
- `$model`: a list of models for each group from the non-linear regression
- `$details`: details of the regression for each group

Examples

```
info <- fraprocess(example_dataset, seq(0, 145, 5))
```

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