Package ‘frapplot’

Type Package
Title Automatic Data Processing and Visualization for FRAP
Version 0.1.3
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Depends R (>= 2.10)
Imports grDevices, graphics, stats, utils
BugReports https://github.com/GuanqiaoDing/frapplot/issues
URL https://github.com/GuanqiaoDing/frapplot
License MIT + file LICENSE
Encoding UTF-8
LazyData true
RoxygenNote 6.1.1
NeedsCompilation no
Repository CRAN
Date/Publication 2019-01-08 16:30:10 UTC

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example_dataset    Example dataset

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    Exclude samples from the dataset

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

Plot FRAP data of two selected groups

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 frapprocess().

Examples

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

frapprocess

Process FRAP data

Description

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

Usage

frapprocess(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

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