

Package ‘flippant’

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Title Dithionite Scramblase Assay Analysis

Description The lipid scrambling activity of protein extracts and purified scramblases is often determined using a fluorescence-based assay involving many manual steps. flippant offers an integrated solution for the analysis and publication-grade graphical presentation of dithionite scramblase assays, as well as a platform for review, dissemination and extension of the strategies it employs. The package's name derives from a play on the fact that lipid scrambling is also sometimes referred to as 'flipping'.

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Depends R (>= 3.3.2), ggplot2 (>= 2.2.1)

Suggests bookdown, devtools, microbenchmark, multipanelfigure, pander,
roxygen2, tools

Imports assertive.files (>= 0.0-2), assertive.numbers (>= 0.0-2),
assertive.properties (>= 0.0-4), assertive.strings (>= 0.0-3),
assertive.types (>= 0.0-3), data.table (>= 1.10.4), magrittr
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extract_case_study_data

Extract the case study dataset

Description

Extracts the data files used by the case study from the zip archive.

Usage

```
extract_case_study_data(exdir = ".", files = NULL)
```

Arguments

exdir	A string giving the path to the extraction directory. Passed to unzip .
files	A character vector of files to extract, or NULL to extract all files. Passed to unzip .

Value

A character vector of the extracted file paths is invisibly returned.

Author(s)

Richard Cotton

See Also

[unzip](#)

Examples

```
extract_case_study_data(tempfile("flippant"))
```

flippant	<i>flippant</i>
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Description

A package for the analysis of data provided by dithionite scrambling assays.

Author(s)

Johannes Graumann

parse_felix_32_output	<i>parse_felix_32_output</i>
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Description

Parse spectra from files provided by a QuantaMaster fluorimeter (Photon Technology International, Inc., Edison, New Jersey) using Felix32 v1.20

Usage

```
parse_felix_32_output(x = NULL)
```

Arguments

x [character](#) vector resulting from [readLines](#) of the corresponding data file.

Details

A helper function to [parse_fluorimeter_output](#).

Value

See [parse_fluorimeter_output](#).

Author(s)

Johannes Graumann

See Also

[parse_fluorimeter_output](#), [parse_felix_gx_output](#), [parse_manual_output](#)

parse_felix_gx_output *parse_felix_gx_output*

Description

Parse spectra from files provided by a QuantaMaster fluorimeter (Photon Technology International, Inc., Edison, New Jersey) using FelixGX v4.1

Usage

```
parse_felix_gx_output(x = NULL)
```

Arguments

x [character](#) vector resulting from [readLines](#) of the corresponding data file.

Details

A helper function to [parse_fluorimeter_output](#).

Value

See [parse_fluorimeter_output](#).

Author(s)

Johannes Graumann

See Also

[parse_fluorimeter_output](#), [parse_felix_32_output](#), [parse_manual_output](#)

parse_fluorimeter_output

parse_fluorimeter_output

Description

Parse fluorimeter spectra

Usage

```
parse_fluorimeter_output(spec_file = NULL, adjust = TRUE,  
  file_type = c("auto", "FelixGXv4.1.0.3096", "Felix32v1.20", "manual"))
```

Arguments

spec_file	Path to a '*.txt' file as a character object.
adjust	A logical indicating of whether (default) or not acquisition time should be reset to have 0 (zero) coincide with the addition of dithionite (see 'Details' section).
file_type	A string specifying whether or the file was created using Felix GX or Felix 32 or is a "manual" tab delimited file.

Details

A function to read fluorimeter output directly. Intended as a helper function to scramble activity determinations from dithionite assays.

The function is currently capable to deal with input derived from QuantaMaster instruments (Photon Technology International, Inc., Edison, New Jersey) running software versions FelixGX v4.1 (see [parse_felix_gx_output](#)) and Felix32 v1.20 (see [parse_felix_32_output](#)). The format used in a given file is divined from the data structure and appropriate internal parsing functions are called.

If requested the time point of dithionite addition to a sample is determined using **wmts**a-supplied methodology and the acquisition time reset accordingly (0 henceforth corresponds to the time of addition).

Value

A data frame with two columns:

Time.in.sec Numeric. Number of seconds since the start of experiment.

Fluorescence.Intensity Numeric. Intensity of fluorescence (relative scale, no official unit).

For Felix GX, if the file contains the information, the return value will also have an attribute `WaveLengthsInNanometres`, which contains the excitation and emission wavelengths.

Author(s)

Johannes Graumann

See Also

[scramblase_assay_input_validation](#), [parse_felix_gx_output](#), [parse_felix_32_output](#), [parse_manual_output](#)

Examples

```
library(magrittr)
# Extract example data
analysis_dir <- file.path(tempdir(), "flippant-case-study")
fluor_file <- extract_case_study_data(analysis_dir, "wildtypeEx1_0.txt")
# Parse an exemplary file
parse_fluorimeter_output(fluor_file) %>%
  str()
```

parse_manual_output *parse_manual_output*

Description

Parse spectra from files provided in a manually assembled format.

Usage

```
parse_manual_output(x = NULL)
```

Arguments

x [character](#) vector resulting from [readLines](#) of the corresponding data file.

Details

A helper function to [parse_fluorimeter_output](#). The file in question is supposed to contain a tab-delimited table with the columns Time (sec) and Fluorescence Intensity.

Value

See [parse_fluorimeter_output](#).

Author(s)

Johannes Graumann

See Also

[parse_fluorimeter_output](#), [parse_felix_gx_output](#), [parse_felix_32_output](#)

scramblase_assay_input_template
 scramblase_assay_plot

Description

Functions for the presentation and evaluation of dithionite scramblase assays

Usage

```
scramblase_assay_input_template(path = "scramblase_assay_input_template.txt")
```

```
scramblase_assay_plot(x, scale_to = c("model", "data"),
  ppr_scale_factor = 0.65, force_through_origin = TRUE,
  generation_of_algorithm = c(2, 1), split_by_experiment = TRUE,
  r_bar = 88, sigma_r_bar = 28)
```

```
scramblase_assay_stats(x, scale_to = c("model", "data"),
  ppr_scale_factor = 0.65, force_through_origin = TRUE,
  generation_of_algorithm = c(2, 1), split_by_experiment = TRUE,
  r_bar = 88, sigma_r_bar = 28)
```

```
scramblase_assay_traces(x, ppr_scale_factor = 0.65, time_min_sec = NA_real_,
  time_max_sec = NA_real_, adjust = TRUE)
```

Arguments

path **character** object giving the path of an **empty** template for a spreadsheet that can provide **x**.

x **data.frame** or path to a tab delimited file representing it (see "Details").

scale_to Defines the source of **y**max, defaulting to **model**. See "Details".

ppr_scale_factor

numeric object providing a scale factor to adjust internally calculated Protein per Phospholipid (mg/ μ mol) ratios (PPR; see "Details").

force_through_origin

logical indicating whether to force the fitted curve(s) to penetrate the origin (defaulting to **TRUE**). See "Details".

generation_of_algorithm

Either 2 or 1 (**numeric**; defaulting to 2). See "Details".

split_by_experiment

A single **logical**, indicating whether or not calculations and plots will treat experimental series from different experiments separately (**TRUE**, default) or whether data from all experiments included is used for a single calculation/plot per experimental series (**FALSE**). While the former emphasizes reproducibility, the latter likely produces a more reliable fit.

r_bar

A **numeric**, representing the average radius of the liposomes used in the assay. Only used in **generation_of_algorithm** = 2 and defaulting to 88 (see Ploier et al. 2016 for details).

sigma_r_bar

A **numeric**, representing the standard deviation average of the radius distribution of the liposomes used in the assay. Only used in **generation_of_algorithm** = 2 and defaulting to 28 (see Ploier et al. 2016 for details).

time_min_sec

A single **numeric**. If given, **scramblase_assay_traces** produces a time/**x** axis trimmed to this value (in seconds).

time_max_sec

A single **numeric**. If given, **scramblase_assay_traces** produces a time/**x** axis trimmed to this value (in seconds).

`adjust` A single **logical**, indicating whether (default) or not spectral traces to be plotted are algorithmically aligned at the time point of dithionite addition.

Details

The `data.frame` accepted by the majority of the functions as an R object or path to a corresponding file (x) must have the following **mandatory** columns:

Path: Paths to existing and readable ASCII output files of a fluorimeter. See `parse_fluorimeter_output` for details and supported formats.

Protein Reconstituted (mg): Self-explanatory.

Further (**facultative**) columns are:

Fluorescence Assay Vol. w/o DT (ul): Volume of the fluorescence assay prior to addition of dithionite (defaulting to 2000).

Fluorescence Assay Vol. with DT (ul): Volume of the fluorescence assay after the addition dithionite (defaulting to 2040).

Lipid in Reconstitution (mmol): Self-explanatory. For the standard phospholipid experiment defaulting to 0.0045 (1 ml of a 4.5 mM solution).

Timepoint of Measurement (s): The time to determine terminal fluorescence, calculated from the point when dithionite is added, in seconds, defaulting to 400.

Experiment: Identifier for any given experiment. Used for `facet_wrap` during generation of `ggplot` output. All data with one Experiment identifier ends up on one plot/facet.

Experimental Series: Identifier for a given series/graph (e.g. Extract and Depleted Extract). Used by color during generation of `ggplot` output to differentiate lines in the same plot/facet.

Based on Goren et al. (2014) and Ploier et al. (2016) data is processed as follows (the majority of the processing is split off into the internal function `scramblase_assay_calculations`):

- Input is format checked and defaults are injected for facultative parameters/columns as appropriate (see input `data.frame` format above). The internal function `scramblase_assay_input_validation` supplies this functionality.
- Fluorescence spectra are parsed using `parse_fluorimeter_output`. This includes automated determination of when dithionite was added to the sample using `wmts`-supplied methodology and resetting the acquisition time accordingly (0 henceforth corresponds to the time of addition).
- Pre-dithionite-addition Baseline Fluorescence is determined for each spectrum by averaging (`median`) over the 10 values preceding dithionite addition.
- Post-dithionite-addition Minimum Fluorescence is determined for each spectrum by averaging (`median`) over the last ten datapoints ≤ 400 s (or Timepoint of Measurement (s), see above).
- The Minimum Fluorescence is volume-corrected based on Reaction Volume w/o DT (ul) and Reaction Volume with DT (ul) (see above).
- For each spectrum/datapoint a measured Fluorescence Reduction is calculated as

$$1 - \left(\frac{\text{Minimum Fluorescence}}{\text{Baseline Fluorescence}} \right)$$

- A Relative Fluorescence Reduction is calculated in comparison to the liposomes-only/no-protein control).
- A Protein per Phospholipid (mg/mmol) ratio (PPR) is calculated. If ppr_scale_factor is not NULL, the value is scaled (divided) by that value to account for liposomes that remain inaccessible to reconstitution with scramblase molecules.
- Depending on split_by_experiment, data are **split** for parallel treatment using either Experimental Series (split_by_experiment = TRUE) or a combined Experimental Series/Experiment (split_by_experiment = FALSE) identifier (see above).
- A probability for a liposome holding ≥ 1 scramblase molecules is calculated using

$$\frac{y - y_0}{y_{\max} - y_0}$$

where y is the Relative Fluorescence Reduction and y_0 is the Relative Fluorescence Reduction in an experiment without addition of protein extract. Depending on the scale_to parameter, y_{\max} is either the maximal Relative Fluorescence Reduction in the series (scale_to = "data") or derived from a mono-exponential fit to the data (scale_to = "model"). The latter (default) is a precaution for the case where the protein/phospholipid titration did not reach the plateau of the saturation curve.

- A monoexponential curve is fitted using **nlsLM**.
If generation_of_algorithm is 1, the underlying formula is derived from Goren et al. (2014) and data is fitted to either

$$p(\geq 1) = b \cdot (1 - e^{-\frac{\text{PPR}}{a}})$$

(if force_through_origin = TRUE; default) or

$$p(\geq 1) = b - c \cdot e^{-\frac{\text{PPR}}{a}}$$

(if force_through_origin = FALSE). The latter implies more degrees of freedom and occasionally results in better fits to experimental data. Mechanistic implication, however, are unclear.

If generation_of_algorithm is 2 (default), the more elaborate model put forth in Ploier et al. (2016) is employed, using either

$$p(\geq 1) = b \cdot \left(\frac{1}{\sqrt{1 + \sigma^2 \cdot a \cdot x}} \right) \cdot \exp\left(\frac{-\bar{r}^2 \cdot a \cdot x}{1 + \sigma^2 \cdot a \cdot x} \right)$$

(if force_through_origin = TRUE; default) or

$$p(\geq 1) = b - c \cdot \left(\frac{1}{\sqrt{1 + \sigma^2 \cdot a \cdot x}} \right) \cdot \exp\left(\frac{-\bar{r}^2 \cdot a \cdot x}{1 + \sigma^2 \cdot a \cdot x} \right)$$

(if force_through_origin = FALSE).

- Data **split** apart above are recombined and a **ggplot** object is assembled with the following layers:
 - Lines (**geom_line**) representing the monoexponential fit(s). color is used to differentiate Experimental Series.

- If `generation_of_algorithm` is 1, segments (`geom_segment`) representing the PPR at which the fit constant a is equal to PPR. This τ value has the implication that at this PPR all vesicles on average have one scramblase and 63% have one or more (i.e. are active). color is used to differentiate Experimental Series. Where `generation_of_algorithm` is 2, interpretation of a is less obvious and this layer is thus omitted in the plot.
- Points (`geom_point`) representing the corresponding datapoints. color is used to differentiate Experimental Series.
- Plots are finally `facet_wrapped` by Experiment (if `split_by_experiment = TRUE`) and labels adjusted cosmetically.

Value

`scramblase_assay_traces` and `scramblase_assay_plot` return `ggplot` objects representing the raw fluorescence traces and a complete PPR plot, respectively. `scramblaseAssayInputTemplate` generates a tab-delimited ASCII file in the file system and does not provide further output. `scramblaseAssayStats` assembles (and prints) assay statistics as a `data.frame`.

Author(s)

Johannes Graumann

References

- Menon, I., Huber, T., Sanyal, S., Banerjee, S., Barre, P., Canis, S., Warren, J.D., Hwa, J., Sakmar, T.P., and Menon, A.K. (2011) <DOI:10.1016/j.cub.2010.12.031>
- Goren, M.A., Morizumi, T., Menon, I., Joseph, J.S., Dittman, J.S., Cherezov, V., Stevens, R.C., Ernst, O.P., and Menon, A.K. (2014) <DOI:10.1038/ncomms6115>
- Ploier, B., Caro, L.N., Morizumi, T., Pandey, K., Pearing, J.N., Goren, M.A., Finnemann, S.C., Graumann, J., Arshavsky, V.Y., Dittman, J.S., Ernst, O.P., Menon, A.K. (2016). <DOI:10.1038/ncomms12832>

See Also

[parse_fluorimeter_output nlsLM](#)

Examples

```
## Not run:
library(magrittr)
library(ggplot2)
# Extract example data
analysis_dir <- file.path(tempdir(), "flippant-case-study")
extract_case_study_data(analysis_dir)
template_file <- file.path(analysis_dir, "inputTable.txt")
# Plot the spectral traces
scramblase_assay_traces(
  template_file,
  time_max_sec = 350)
# Plot the PPR plot(s) faceting by experiment
scramblase_assay_plot(template_file)
# Generate tabular results
```

```
scramblase_assay_stats(template_file)
# Plot the PPR plot(s) forgoing faceting by experiment
scramblase_assay_plot(template_file, split_by_experiment = FALSE)
# Generate tabular results
scramblase_assay_stats(template_file, split_by_experiment = FALSE)

## End(Not run)
```

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