Package ‘normfluodbf’

November 28, 2023

Title       Cleans and Normalizes FLUOstar DBF and DAT Files
Version     1.5.2
Description  Cleans and Normalizes FLUOstar DBF and DAT Files obtained from liposome flux assays. Users should verify extended usage of the package on files from other assay types.
License     MIT + file LICENSE
Encoding    UTF-8
RoxygenNote 7.2.3
Suggests    knitr, learnr, rmarkdown, testthat (&gt;= 3.0.0)
Config/testthat/edition 3
Imports      data.table, foreign, tidyr, tibble, dplyr, emojifont, rio, stats, ggplot2, ggthemes, badger, stringr
Depends     R (&gt;= 2.10)
LazyData    true
URL         https://github.com/AlphaPrime7/normfluodbf,
            https://alphaprime7.github.io/normfluodbf/
BugReports  https://github.com/AlphaPrime7/normfluodbf/issues
VignetteBuilder knitr
NeedsCompilation no
Author       Tingwei Adeck [aut, cre].
             normfluodbf authors [cph] (<https://orcid.org/0009-0009-7450-8863>)
Maintainer   Tingwei Adeck <awesome.tingwei@outlook.com>
Repository   CRAN
Date/Publication 2023-11-28 22:10:03 UTC

R topics documented:

  actual_cols_used ........................................... 3
  check_dat .................................................. 3
  check_dbf .................................................. 4
R topics documented:
clean_odd_dat_optimus .......................... 5
clean_odd_cc ...................................... 6
comma_cleaner ..................................... 6
dat_1 ................................................. 7
dat_2 ................................................ 8
dat_3 ................................................ 8
dat_4 ................................................ 8
dat_5 ................................................ 9
dat_6 ................................................ 9
dat_7 ................................................ 9
dat_col_names_horizontal ....................... 10
dat_col_names_optimus ......................... 11
dat_col_names_prime .............................. 12
dat_col_names_rigid ............................... 13
decimal_scaling ..................................... 15
fluor_threshold_check ............................ 16
fluor_threshold_check_na ....................... 17
fluor_threshold_check_raw ..................... 18
generic_identifier ............................... 19
ggplot_tnp ......................................... 19
liposomes_214 ..................................... 20
liposomes_215 ..................................... 21
liposomes_216 ..................................... 21
liposomes_218 ..................................... 21
liposomes_221 ..................................... 22
liposomes_227 ..................................... 22
log_transformation ............................... 22
min_max_norm ...................................... 23
min_max_norm_percent ............................ 24
normfluodat ....................................... 25
normfluodatfull ................................... 26
normfluodatlite ................................... 28
normfluordat ...................................... 29
normfluordbf ...................................... 31
norm_applier ....................................... 32
norm_tidy_dbf ..................................... 33
norm_z .............................................. 34
resample_dat ....................................... 35
resample_dat_alt .................................. 36
resample_dat_scale ............................... 37
resample_dat_scale_alt ........................... 38
resample_dat_scale_alt_bfv ..................... 39
resample_dat_scale_alt_bf_na ................... 40
resample_dat_scale_alt_na ..................... 41
resample_dat_scale_naretainer .................. 42
resample_dat_scale_optimus .................... 43
resample_dat_scale_optimus_backend .......... 44
resample_dat_scale_optimus_na ................ 45
actual_cols_used

Title: A function to get the actual columns used in the assay.

Description

A function that facilitates a users’ workflow by helping extract the actual columns used in the assay.

Usage

actual_cols_used(dat)

Arguments

dat A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dat" file.

Value

Returns a numeric vector denoting the columns used in the assay.

Author(s)

Tingwei Adeck

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
acutest <- actual_cols_used(fpath)

check_dat

Title: A function to check for DATs in a directory.

Description

A function that facilitates a users’ workflow by helping to check for DATs in a directory.

Usage

check_dat(pathstring)
check_dbf

Arguments
pathstring  A string for a path to a directory containing files.

Value
Returns a list of DAT files or a warning.

Author(s)
Tingwei Adeck

Examples
## Not run:
```
fpath <- system.file("extdata", package = "normfluodbf", mustWork = TRUE)
setwd(fpath)
check_dat(getwd())
```

## End(Not run)
```
## Not run:
fpath <- system.file("extdata", package = "normfluodbf", mustWork = TRUE)
setwd(fpath)
check_dbf(getwd())

## End(Not run)
```

---

clean_odddat_optimus

**Title:** DAT file data frame cleaner.

**Description**

The function takes the dirty data frame obtained from reading the FLUOstar DAT file, applies an original algorithm that inserts NAs in place of the special characters, and then applies a function called comma_cleaner() to the dirty data frame for the removal of commas, and finally, rows with NAs only are removed.

**Usage**

```
clean_odddat_optimus(df)
```

**Arguments**

- **df**: A dirty data frame obtained from the FLUOstar DAT file.

**Value**

A clean data frame with clean NA values retained.

**Author(s)**

Tingwei Adeck

**See Also**

- comma_cleaner()
- clean_odd_cc()

**Examples**

```
opath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
opath <- read.table(file=opath)
partial_cleaned_dat <- clean_odddat_optimus(dat_df)
```
clean_odd_cc

Title: DAT file data frame cleaner.

Description

The function takes the dirty data frame obtained from reading the FLUOstar DAT file and applies a function called comma_cleaner() to the dirty data frame, which automatically inserts NAs in place of the special characters, and rows with NAs only are removed.

Usage

```
clean_odd_cc(df)
```

Arguments

- **df**: A dirty data frame obtained from the FLUOstar DAT file.

Value

A clean data frame with clean NA values retained.

Author(s)

Tingwei Adeck

See Also

- comma_cleaner()
- clean_odddat_optimus()

Examples

```r
fpath <- system.file("extdata", "dat_3.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
cleaned_dat <- clean_odd_cc(dat_df)
```

comma_cleaner

Title: Comma Cleaner function.

Description

This modular function, in the context of this package, is responsible for removing commas from attribute(s) values. Removal of commas facilitates the conversion of attributes into the numeric class.

Usage

```
comma_cleaner(comma_df)
```
**Arguments**

`comma_df`  
A dirty data frame obtained from the FLUOstar DAT file.

**Value**

A clean data frame with numeric no-comma values for attribute(s).

**Author(s)**

Tingwei Adeck

**See Also**

`clean_odd_cc()`, `clean_odd_dat_optimus()`

**Examples**

```r
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- comma_cleaner(dat_df)
```

---

**Description**

FLUOstar .dat files used for creation of the update and unusable for immediate data analysis.

**Usage**

`dat_1`

**Format**

An object of class `data.frame` with 320 rows and 12 columns.
**dat_2**

**Description**
FLUOstar .dat files used for creation of the update and unusable for immediate data analysis.

**Usage**
dat_2

**Format**
An object of class `data.frame` with 320 rows and 12 columns.

---

**dat_3**

**Description**
FLUOstar .dat files used for creation of the update and unusable for immediate data analysis. This file is unique because it validates a major bug fix to ensure that users get the right output.

**Usage**
dat_3

**Format**
An object of class `data.frame` with 320 rows and 12 columns.

---

**dat_4**

**Description**
FLUOstar .dat files used for creation of the update and unusable for immediate data analysis. This file is unique because it validates a major bug fix to ensure that users get the right output.

**Usage**
dat_4

**Format**
An object of class `data.frame` with 320 rows and 1 columns.
**Description**

FLUOstar .dat files used for creation of the update and unusable for immediate data analysis. This file is unique because it validates a major bug fix to ensure that users get the right output.

**Usage**

dat_5

dat_5

**Format**

An object of class data.frame with 105 rows and 1 columns.

dat_6

dat_6

**Description**

FLUOstar .dat files used for creation of the update and unusable for immediate data analysis. This file is unique because it validates a major bug fix to ensure that users get the right output.

**Usage**

dat_6

dat_6

**Format**

An object of class data.frame with 105 rows and 2 columns.

dat_7

dat_7

**Description**

FLUOstar .dat files used for creation of the update and unusable for immediate data analysis. This file is unique because it validates a major bug fix to ensure that users get the right output.

**Usage**

dat_7

dat_7

**Format**

An object of class data.frame with 105 rows and 3 columns.
Title: Attribute(s) naming function.

Description
This function is used to name attribute(s). Attribute(s) names, in this case, are equivalent to the well labels found on the microplate reader. An attribute for a sample loaded into row A - column 1 will be named A1. In short, the function takes a clean data frame and returns attribute names that match the FLUOstar plate layout often presented as an Excel file.

Usage

dat_col_names_horizontal(dat = NULL, df, rows_used = NULL, cols_used = NULL)

Arguments

dat A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dat" file.
df A data frame that requires attribute labels.
rows_used A character vector indicating the rows or tuples used on the microplate (usually a 96-well microplate). Initialized as NULL.
cols_used A numeric vector indicating the plate columns or attributes used. Initialized as NULL.

Value
Returns a character or numeric vector of attribute(s) names for the normalized data frame.

Note
This function was designed to avoid the use of stringr. This function is designed to name attributes when the read direction is specified as horizontal.

Author(s)
Tingwei Adeck

Examples

```
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale(nocomma_dat, tnp=3, cycles=40)
n = c('A','B','C')
sample_col_names <- dat_col_names_horizontal(dat=fpath, resampled_scaled, n)
```
**dat_col_names_optimus**

*Title: Attribute(s) naming function.*

**Description**

This function is used to name attribute(s). Attribute(s) names, in this case, are equivalent to the well labels found on the microplate reader. An attribute for a sample loaded into row A - column 1 will be named A1. In short, the function takes a clean data frame and returns attribute names that match the FLUOstar plate layout often presented as an Excel file.

**Usage**

```r
dat_col_names_optimus(
  dat = NULL,
  df,
  rows_used = NULL,
  cols_used = NULL,
  user_specific_labels = NULL,
  read_direction = NULL
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>dat</code></td>
<td>A string (&quot;dat_1.dat&quot;) if the file is found within the present working directory (pwd) OR a path pointing directly to a &quot;.dat&quot; file.</td>
</tr>
<tr>
<td><code>df</code></td>
<td>A data frame that requires attribute labels.</td>
</tr>
<tr>
<td><code>rows_used</code></td>
<td>A character vector indicating the rows or tuples used on the microplate (usually a 96-well microplate). Initialized as NULL.</td>
</tr>
<tr>
<td><code>cols_used</code></td>
<td>A numeric vector indicating the plate columns or attributes used. Initialized as NULL.</td>
</tr>
<tr>
<td><code>user_specific_labels</code></td>
<td>A character vector where the user manually enters the used microplate wells based on the FLUOstar plate layout.</td>
</tr>
<tr>
<td><code>read_direction</code></td>
<td>A string input with two choices, “vertical” or “horizontal.” The user indicates “vertical” if the user intends to have a final data frame with samples arranged as sample type triplets (A1, B1, C1, A1, B1, C1) OR “horizontal” if the user intends to have a final data frame with samples</td>
</tr>
</tbody>
</table>

**Value**

Returns a character or numeric vector of attribute(s) names for the normalized data frame.
Note

Users are advised to input rows used but won’t be penalized for not doing so. If the user provides the rows used, then attribute names are generated for the user. The user must check to ensure that the names match the microplate layout.

The user can leave the columns used as NULL if the user loaded samples from column 1 and did so in sequence. If the user fails to load in sequence from the first position, then the user must provide a numeric vector of columns used.

For instance, where the user skips columns, the user will be prompted to interact with the program in order to ensure the final data frame has the correct attribute names.

The user can bypass the rows used and columns used parameters if the user supplies a manually created character vector of the wells used in an experiment.

The read direction parameter is used to determine the presentation of the samples in the final data frame.

Author(s)

Tingwei Adeck

See Also

normfluodat(), dat_col_names_rigid()

Examples

```r
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odd_dat_optimus(dat_df)
resampled_scaled <- resample_dat_scale(nocomma_dat, tnp=3, cycles=40)
n = c('A','B','C')
sample_col_names <- dat_col_names_optimus(dat = fpath, resampled_scaled, n)
```

---

dat_col_names_prime  Title: Attribute(s) naming function.

Description

This function is used to name attribute(s). Attribute(s) names, in this case, are equivalent to the well labels found on the microplate reader. An attribute for a sample loaded into row A - column 1 will be named A1. In short, the function takes a clean data frame and returns attribute names that match the FLUOstar plate layout often presented as an Excel file.
Usage
dat_col_names_prime(
  dat = NULL,
  df,
  rows_used = NULL,
  cols_used = NULL,
  user_specific_labels = NULL
)

Arguments
dat | A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dat" file.
df | A data frame that requires attribute labels.
rows_used | A character vector indicating the rows or tuples used on the microplate (usually a 96-well microplate). Initialized as NULL.
cols_used | A numeric vector indicating the plate columns or attributes used. Initialized as NULL.
user_specific_labels | A character vector where the user manually enters the used microplate wells based on the FLUOstar plate layout.

Value
Returns a character vector of attribute(s) names for the normalized data frame.

Author(s)
Tingwei Adeck

Examples
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale(nocomma_dat, tnp=3, cycles=40)
n = c('A', 'B', 'C')
sample_col_names <- dat_col_names_prime(dat = fpath, resampled_scaled, n)

---

dat_col_names_rigid | Title: Attribute(s) naming function.

Description
This function is used to name attribute(s). Attribute(s) names, in this case, are equivalent to the well labels found on the microplate reader. An attribute for a sample loaded into row A - column 1 will be named A1. In short, the function takes a clean data frame and returns attribute names that match the FLUOstar plate layout often presented as an Excel file.
**Usage**

```r
dat_col_names_rigid(
  dat = NULL,
  df,
  rows_used = NULL,
  cols_used = NULL,
  user_specific_labels = NULL,
  read_direction = NULL
)
```

**Arguments**

- **dat**: A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dat" file.
- **df**: A data frame that requires attribute labels.
- **rows_used**: A character vector indicating the rows or tuples used on the microplate (usually a 96-well microplate). Initialized as NULL.
- **cols_used**: A numeric vector indicating the plate columns or attributes used. Initialized as NULL.
- **user_specific_labels**: A character vector where the user manually enters the used microplate wells based on the FLUOstar plate layout.
- **read_direction**: A string input with two choices, "vertical" or "horizontal." The user indicates "vertical" if the user intends to have a final data frame with samples arranged as sample type triplets (A1, B1, C1, A1, B1, C1) OR "horizontal" if the user intends to have a final data frame with samples arranged as clusters per sample type (A1, A2, A3, B1, B2, B3).

**Value**

Returns a character vector of attribute(s) names for the normalized data frame.

**Note**

Users are advised to input rows used but won’t be penalized for not doing so. If the user provides the rows used, then attribute names are generated for the user. The user must check to ensure that the names match the microplate layout.

The user can leave the columns used as NULL if the user loaded samples from column 1 and did so in sequence. If the user fails to load in sequence from the first position, then the user must provide a numeric vector of columns used.

For instance, where the user skips columns, the user will be prompted to interact with the program in order to ensure the final data frame has the correct attribute names.

The user can bypass the rows used and columns used parameters if the user supplies a manually created character vector of the wells used in an experiment.

The read direction parameter is used to determine the presentation of the samples in the final data frame.

This naming function only returns a character vector hence the rigid suffix.
Title: A decimal scaling function (a machine learning tool).

Usage

decimal_scaling(x)

Arguments

x  Attribute value(s).

Value

A decimal scaled value when applied to a single value or a decimal scaled attribute(s).

Note

The lapply function is required to apply this function across several attributes. This is NOT a normalization function, so data obtained from the decimal scaling function exists on a sliding scale and SHOULD NOT be used for meaningful analysis.

Author(s)

Tingwei Adeck

References

https://www.statology.org/how-to-normalize-data-in-r/
Examples

```r
test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
test_df_norm <- lapply(test_df[1:ncol(test_df)], decimal_scaling)
```

---

**Title:** A fluorescence quantification Quality Control (QC) function.

**Description**

A function designed to check that fluorescence values do not exceed the upper limit (2^15 or 32768) OR fall below the lower limit (2^11 or 2048). Fluorescence values that exceed these thresholds are considered noisy and lead to incorrect interpretation of analysis results.

**Usage**

```r
fluor_threshold_check(clean_df, fun = NA)
```

**Arguments**

- `clean_df`: A cleaned data frame.
- `fun`: A parameter used for Boolean expressions.

**Value**

A polite warning message to the data analyst or researcher.

**Note**

Experimental issues should be investigated at very high or very low fluorescence values. The most common experimental issues arise when ACMA concentrations are out of the tolerated range. Based on my experience, ACMA concentrations between 2 and 5 Micromolar will suffice to get fluorescence values within the tolerance threshold. ACMA concentrations as low as 0.2 Micromolar or as high as 20 Micromolar have proven problematic based on my research experience.

A second issue linked to the FLUOstar instrument revolves around setting the right “gain” to ensure the right level of sensitivity in machine readings. A very high “gain” setting results in increased machine sensitivity even at the right ACMA concentrations and vice versa. In short, we want the machine to be primed to read exactly what we feed it, no more, no less.

This function provides the attribute(s) and tuple(s) for the values that need investigation.

These deductions were obtained from my experimental hiccups and my characterization of the liposome flux assay system.

**Author(s)**

Tingwei Adeck
fluor_threshold_check_na

See Also

fluor_threshold_check_na(), fluor_threshold_check_raw()

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale(nocomma_dat, tnp=3, cycles=40)
resampled_scaled <- resampled_scaled[,c(1:4)]
fluor_threshold_check(resampled_scaled)

---

fluor_threshold_check_na

Title: A missing value (NA) Quality Control (QC) function.

Description

A function designed to check for missing values in a data frame.

Usage

fluor_threshold_check_na(clean_df, fun = NA)

Arguments

clean_df A cleaned data frame.
fun A parameter used for Boolean expressions.

Value

A polite warning message to the data analyst or researcher.

Author(s)

Tingwei Adeck

See Also

fluor_threshold_check(), fluor_threshold_check_raw()

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
fluor_threshold_check_na(nocomma_dat)
Title: A fluorescence quantification Quality Control (QC) function.

Description
A function designed to check that fluorescence values do not exceed the upper limit (2^15 or 32768) OR fall below the lower limit (2^11 or 2048). Fluorescence values that exceed these thresholds are considered noisy and lead to incorrect interpretation of analysis results.

Usage
fluor_threshold_check_raw(clean_df, fun = NA)

Arguments
- clean_df: A cleaned data frame.
- fun: A parameter used for Boolean expressions.

Value
A polite warning message to the data analyst or researcher.

Note
This function works on a different type of data frame but in a similar manner to @seealso {fluor_threshold_check()}. 

Author(s)
Tingwei Adeck

See Also
- {fluor_threshold_check()}, {fluor_threshold_check_na()}

Examples
```r
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odd.dat_optimus(dat_df)
fluor_threshold_check_raw(nocomma_dat)
```
**generic_identifier**

Title: A function to append a generic identifier attribute to any data frame, but users supply a name for said attribute.

**Description**
A function that creates an attribute of seq(numrows) with a step size of 1, where the user provides the attribute name.

**Usage**
generic_identifier(numrows, col_name)

**Arguments**
- numrows: The number of rows the user intends to have in the created data frame.
- col_name: The desired attribute name.

**Value**
A user-named single attribute data frame with nrow = numrows.

**Author(s)**
Tingwei Adeck

**Examples**
generic_identifier(40, col_name="Cycle_No")

---

**ggplot_tnp**

Title: A Visualization function.

**Description**
A visualization function using ggplot2.

**Usage**
ggplot_tnp(df, x, y_list, xlim, ylim, xlab = NULL, ylab = NULL, title = NULL)
Arguments

df  A clean data frame with attributes or tuples containing a mixture of samples.
x  The X-variable often the cycle number OR time.
y_list  A character vector of samples that need to be plotted. Often of the format TNP (Test, Negative, Positive).
xlim  The X-variable scale.
ylim  The Y-variable scale.
xlab  The X axis label. Takes a string.
ylab  The Y-axis label. Takes a string.
title  Graph title. Takes a string.

Value

A nice visual of the clean and normalized data frame.

Author(s)

Tingwei Adeck

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- normfluodat(fpath,3,40, rows_used = c("A","B","C"), norm_scale = 'one')
yvars <- c("A1","B1","C1")
xvar <- c("Cycle_Number", "Time")
xl <- c(0,40)
yl <- c(0,1)
ggplot_tnp(dat_df,xvar,yvars,xl,yl,xlab='Cycle_Number',ylab='Normalized Fluorescence',title='LFA')

Description

FLUOstar .dbf file in wide format and unable to use for data analysis.

Usage

liposomes_214

Format

An object of class data.frame with 11 rows and 52 columns.
Description

FLUOstar .dbf file in wide format and unable to use for data analysis.

Usage

liposomes_215

Format

An object of class data.frame with 11 rows and 52 columns.

Description

FLUOstar .dbf file in wide format and unable to use for data analysis.

Usage

liposomes_216

Format

An object of class data.frame with 8 rows and 52 columns.

Description

FLUOstar .dbf file in wide format and unable to use for data analysis.

Usage

liposomes_218

Format

An object of class data.frame with 11 rows and 52 columns.
### liposomes_221

**Description**

FLUOstar .dbf file in wide format and unable to use for data analysis.

**Usage**

```r
liposomes_221
```

**Format**

An object of class `data.frame` with 38 rows and 52 columns.

### liposomes_227

**Description**

FLUOstar .dbf file in wide format and unable to use for data analysis.

**Usage**

```r
liposomes_227
```

**Format**

An object of class `data.frame` with 29 rows and 52 columns.

### log_transformation

**Title:** A log transformation function.

**Description**

Title: A log transformation function.

**Usage**

```r
log_transformation(x)
```

**Arguments**

- `x`: Attribute value(s).
Value

A log-transformed value when applied to a single value or an attribute with log-transformed values.

Note

The lapply function is required to apply this function across several attributes.

Author(s)

Tingwei Adeck

References

https://www.statology.org/how-to-normalize-data-in-r/

Examples

test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
test_df_norm <- lapply(test_df[1:ncol(test_df)], log_transformation)

dfnorm <- function(x)
  return((x - min(x)) / (max(x) - min(x)))

df <- data.frame(x = c(1, 2, 3, 4, 5))
df$y <- dfnorm(df$x)

Description

Title: Min-Max normalization on a 0-1 scale.

Usage

min_max_norm(x)

Arguments

x

Attribute value(s).

Value

A normalized value (between 0 and 1) when applied to a single value or a normalized attribute with values between 0 and 1.

Note

The lapply function is required to apply this function across several attributes.

Author(s)

Tingwei Adeck
min_max_norm_percent

References

https://www.statology.org/how-to-normalize-data-in-r/

Examples

test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
test_df_norm <- lapply(test_df[1:ncol(test_df)], min_max_norm)

min_max_norm_percent Title: Min-Max normalization on a 0-100 scale.

Description
Title: Min-Max normalization on a 0-100 scale.

Usage

min_max_norm_percent(x)

Arguments

x Attribute value(s).

Value
A normalized value (between 0 and 100) when applied to a single value or a normalized attribute with values between 0 and 100.

Note
The lapply function is required to apply this function across several attributes.

Author(s)
Tingwei Adeck

References

https://www.statology.org/how-to-normalize-data-in-r/

Examples

test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
test_df_norm <- lapply(test_df[1:ncol(test_df)], min_max_norm_percent)
Title: Cleans and normalizes DAT files obtained from experiments using the FLUOstar Omega microplate reader (from BMG LABTECH).

Description

The simplest case scenario entails inputting the name or directory of a DAT file as a string, the number of rows denoted by the tnp (test, negative, positive) parameter, and the number of cycles (selected by the user when running the FLUOstar instrument). The program takes these three baseline parameters, performs cleaning and normalization of the DAT file, and then appends an attribute called “Cycle_Number” to the normalized data frame.

Usage

```r
normfluodat(
  dat,
  tnp,
  cycles,
  rows_used = NULL,
  cols_used = NULL,
  user_specific_labels = NULL,
  read_direction = NULL,
  norm_scale = NULL,
  interval = NULL,
  first_end = NULL,
  pause_duration = NULL,
  end_time = NULL
)
```

Arguments

dat A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dat" file.

tnp A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.

cycles A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

rows_used A character vector of the rows used; ru = c('A','B','C').

cols_used A numeric vector of the columns used; cu = c(1,2,3).

user_specific_labels A character vector manually prepared by the user to denote the wells used on the microplate reader; usl = c('A1','B1','C1').

read_direction A string input with two choices, “vertical” or “horizontal.” The user indicates “vertical” if the user intends to have a final data frame with samples arranged as sample type triplets (A1, B1, C1, A1, B1, C1) OR “horizontal” if the user
normfluodatfull

Title: Cleans and normalizes DAT files obtained from experiments using the FLUOstar Omega microplate reader (from BMG LABTECH).

Description

The simplest case scenario entails inputting the name or directory of a DAT file as a string, the number of rows denoted by the tnp (test, negative, positive) parameter, and the number of cycles (selected by the user when running the FLUOstar instrument). The program takes these three baseline parameters, performs cleaning and normalization of the DAT file, and then appends an attribute called “Cycle_Number” to the normalized data frame.

normscale

This parameter takes sub-parameters: 'raw', 'hundred', 'one', 'z-score', or 'decimal', which denotes the normalization type or scale; Initialized as NULL.

interval

The time interval chosen for the assay often in seconds.

first_end

The end time of the initial run, often the pause for the introduction of a new substance. This can be the cycle number chosen for the initial stop.

pause_duration

The time between the first end (pause) and resumption of the assay.

der_time

The final end time of the assay.

Value

A normalized data frame with an appended "Cycle_Number" attribute. The “Cycle_Number” attribute is the X-variable.

Note

This function is a single-step function leveraging several subordinate functions. It is assumed that the user has the 3 baseline parameters to get this function working. Users must double-check attribute names to ensure they end up with accurate results.

Author(s)

Tingwei Adeck

See Also

normfluodatlite()

Examples

fpath <- system.file("extdata", "dat_4.dat", package = "normfluodbf", mustWork = TRUE)
normalized_fluo_dat <- normfluodat(dat=fpath, tnp = 3, cycles = 40)
Usage

```r
normfluodatfull(
  dat,
  tnp,
  cycles,
  rows_used = NULL,
  cols_used = NULL,
  user_specific_labels = NULL,
  read_direction = NULL,
  norm_scale = NULL,
  na_omit = NULL
)
```

Arguments

dat  A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dat" file.

tnp  A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.

cycles  A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

rows_used  A character vector of the rows used; ru = c('A','B','C').

cols_used  A numeric vector of the columns used; cu = c(1,2,3).

user_specific_labels  A character vector manually prepared by the user to denote the wells used on the microplate reader; usl = c('A1','B1','C1').

read_direction  A string input with two choices, “vertical” or “horizontal.” The user indicates “vertical” if the user intends to have a final data frame with samples arranged as sample type triplets (A1, B1, C1, A1, B1, C1) OR “horizontal” if the user intends to have a final data frame with samples arranged as clusters per sample type (A1, A2, A3, B1, B2, B3).

norm_scale  This parameter takes sub-parameters: 'raw', 'hundred', 'one', 'z-score', or 'decimal', which denotes the normalization type or scale; Initialized as NULL.

na_omit  Takes a string "yes" OR "no".

Value

A normalized data frame with an appended "Cycle_Number" attribute. The “Cycle_Number” attribute is the X-variable.

Note

This function is a single-step function leveraging several subordinate functions. It is assumed that the user has the 3 baseline parameters to get this function working. Users must double-check attribute names to ensure they end up with accurate results.
normfluodatlite

Author(s)
Tingwei Adeck

See Also
normfluodat()

Examples

```r
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
normalized_fluo_dat <- normfluodatfull(dat = fpath, tnp = 3, cycles = 40)
```

description
The simplest case scenario entails inputting the name or directory of a DAT file as a string, the number of rows denoted by the tnp (test, negative, positive) parameter, and the number of cycles (selected by the user when running the FLUOstar instrument). The program takes these three baseline parameters, performs cleaning and normalization of the DAT file, and then appends an attribute called "Cycle_Number" to the normalized data frame.

Usage

```r
normfluodatlite(
  dat,
  tnp,
  cycles,
  rows_used = NULL,
  cols_used = NULL,
  user_specific_labels = NULL,
  read_direction = NULL,
  norm_scale = NULL
)
```

Arguments

dat A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a "dat" file.
tnp A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
cycles A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.
rows_used A character vector of the rows used; ru = c('A','B','C').
cols_used A numeric vector of the columns used; cu = c(1,2,3).

user_specific_labels A character vector manually prepared by the user to denote the wells used on the microplate reader; usl = c('A1','B1','C1').

read_direction A string input with two choices, “vertical” or “horizontal.” The user indicates “vertical” if the user intends to have a final data frame with samples arranged as sample type triplets (A1, B1, C1, A1, B1, C1) OR “horizontal” if the user intends to have a final data frame with samples arranged as clusters per sample type (A1, A2, A3, B1, B2, B3).

norm_scale This parameter takes sub-parameters: 'raw', 'hundred', 'one', 'z-score', or 'decimal', which denotes the normalization type or scale; Initialized as NULL.

Value

A normalized data frame with an appended "Cycle_Number" attribute. The “Cycle_Number” attribute is the X-variable.

Note

This function is a single-step function leveraging several subordinate functions. It is assumed that the user has the 3 baseline parameters to get this function working. Users must double-check attribute names to ensure they end up with accurate results.

Author(s)

Tingwei Adeck

See Also

normfluodat()

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
normalized_fluo_dat <- normfluodatlite(dat=fpath, tnp = 3, cycles = 40)

normfluordat Title: Cleans and normalizes DAT files obtained from experiments using the FLUOstar Omega microplate reader (from BMG LABTECH).

Description

The simplest case scenario entails inputting the name or directory of a DAT file as a string, the number of rows denoted by the tnp (test, negative, positive) parameter, and the number of cycles (selected by the user when running the FLUOstar instrument). The program takes these three baseline parameters, performs cleaning and normalization of the DAT file, and then appends an attribute called “Cycle_Number” to the normalized data frame.
Usage

```r
normfluordat(
  dat,
  tnp,
  cycles,
  rows_used = NULL,
  cols_used = NULL,
  user_specific_labels = NULL,
  read_direction = NULL,
  na_omit = NULL
)
```

Arguments

dat A string ("dat_1.dat") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dat" file.

tnp A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.

cycles A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

rows_used A character vector of the rows used; ru = c('A', 'B', 'C').

cols_used A numeric vector of the columns used; cu = c(1, 2, 3).

user_specific_labels A character vector manually prepared by the user to denote the wells used on the microplate reader; usl = c('A1', 'B1', 'C1').

read_direction A string input with two choices, “vertical” or “horizontal.” The user indicates “vertical” if the user intends to have a final data frame with samples arranged as sample type triplets (A1, B1, C1, A1, B1, C1) OR “horizontal” if the user intends to have a final data frame with samples.

na_omit Takes a string "yes" OR "no".

Value

A normalized data frame with an appended "Cycle_Number" attribute. The “Cycle_Number” attribute is the X-variable.

Note

This function has less optimized space and time complexities than @seealso normfluodat(). In real-time the difference in optimization is not noticeable. This function also takes less parameters than the more optimized version of the function. Use @seealso normfluodat() for better approximation of attribute names.

Author(s)

Tingwei Adeck
See Also

normfluodat()

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
normalized_fluo_dat <- normfluodat(dat=fpath, tnp = 3, cycles = 40)

Title: Cleans and Normalizes DBF files obtained from experiments using the FLUOstar microplate reader.

Description

Input the path to a "dbf" file obtained from the FLUOstar microplate (usually a 96-well microplate) reader; this function will create a data frame, clean the data frame, normalize the data frame, append a "Cycle_Number" column and return a data frame that is ready for analysis. Most importantly, this function is a single_step function. Also, the function can be extended to other "dbf" files if they follow the format for which this function was designed; this is totally at the users’ discretion.

Usage

normfluordbf(file = NULL, norm_scale = NULL, transformed = NULL, fun = NA, ...)

Arguments

file A string ("liposomes_xxx.dbf") if the file is found within the present working directory (pwd) OR a path pointing directly to a "dbf" file, from FLUOstar experiments.
norm_scale This parameter can taken in 'hundred', 'one', or 'z-score' which denotes the normalization type; Initialized as NULL.
transformed This parameter can take in 'log' which denotes a logarithmic box-cox transformation; Initialized as NULL.
fun A variable defined as NA, used for boolean expressions or manipulation.
... A container object that can be used to capture extra variables if needed.

Value

A normalized data frame with an appended "Cycle_Number" attribute.

Note

Re-nomenclature of norm_tidy_dbf to a more appropriate name that facilitates function utilization. Users can continue with the old name ("norm_tidy_dbf") but this is a better name in my opinion.
Author(s)

Tingwei Adeck

Examples

```r
fpath <- system.file("extdata", "liposomes_214.dbf", package = "normfluodb", mustWork = TRUE)
normalized_dbf <- normfluodb(file=fpath, norm_scale = 'raw')
```

---

**norm_applier**

Title: A normalization applier built on lapply.

Description

Applies a function over a list of attributes.

Usage

```r
norm_applier(df, norm_scale = c("one", "hundred", "z-score", "raw", "decimal"))
```

Arguments

- `df`: A data frame.
- `norm_scale`: This parameter takes sub-parameters: 'raw', 'hundred', 'one', 'z-score', or 'decimal', which denotes the normalization type or scale.

Value

A data frame with attribute values obtained from the applied function using `lapply`.

Examples

```r
test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
test_df_norm <- norm_applier(test_df, norm_scale = 'one')
```
Title: Cleans and Normalizes DBF files obtained from experiments using the FLUOstar Omega microplate reader (from BMG LABTECH).

Description
The simplest function utilization scenario entails an input of the path to a DBF file obtained from the FLUOstar microplate (usually a 96-well microplate) reader; In a single step, this function will create a data frame, clean the data frame, normalize the data frame, append a "Cycle_Number" attribute, perform an adjustment to the "time" attribute and return a data frame that is ready for analysis. Since the initial publication of this package, several changes have been made to improve the user experience and to give the user more options to fine-tune the output from the package to meet the users’ aesthetic needs. Users who decide to move past the simplest utility scenario have been given more options to customize the output based on the users’ needs. Notably, several normalization sub-parameters have been provided in the package which yields different outputs based on what the user is used to seeing. Just as the FLUOstar instrument is built to handle an array of assays, this function is designed to be multi-dimensional (meaning it can handle data with the same DBF extension from other assay types), on the condition that the data from assay types other than liposome flux assays follow the same data format this package was designed to handle. Of course, users of this package are advised to pre-analyze DBF files from other assay types to ensure they are compliant with this package (compliance in this scenario is simple meaning DBF files from other assays should be like DBF files from liposome flux assays).

Usage
norm_tidy_dbf(
  file = NULL,
  norm_scale = NULL,
  transformed = NULL,
  fun = NA,
  ...
)

Arguments

file A string ("liposomes_xxx.dbf") if the file is found within the present working directory (pwd) OR a path pointing directly to a ".dbf" file.

norm_scale This parameter takes sub-parameters: 'raw', 'hundred', 'one', 'z-score', or 'decimal', which denotes the normalization type or scale; The parameter is initialized as NULL.

transformed This parameter takes input 'log', which denotes a logarithmic box-cox transformation; Initialized as NULL.

fun A parameter defined as NA is used for Boolean expressions or manipulation.

... An abstract placeholder or container parameter that can be used to capture extra variables if needed.
norm_z

Value

A normalized data frame with an appended "Cycle_Number" attribute.

Note

The default normalization sub-parameter outputs values in the 0-1 range. Unless a "norm_scale" level is specified by the user, the default output is in the 0-1 range. The "norm_scale" sub-parameter “decimal” is a machine-learning tool and should be avoided; it also provides no advantage for basic research analysis as its output operates on a sliding scale just like the raw data. Logarithmic transformation provides a minuscule advantage in data analysis and could/should be avoided. Backward compatibility is maintained in all updates, so there should be no issues with using the package the way the user was used to. The favorite "norm_scale" level is "z-score" since it divides the axis into negative and positive, thus facilitating interpretation.

Author(s)

Tingwei Adeck

See Also

normfluordbf(), normfluodat()

Examples

fpath <- system.file("extdata", "liposomes_214.dbf", package = "normfluodbf", mustWork = TRUE)
normalized_dbf <- norm_tidy_dbf(file=fpath, norm_scale = 'raw')

norm_z

Title: Z-score standardization or normalization function.

Description

Title: Z-score standardization or normalization function.

Usage

norm_z(x)

Arguments

x         Attribute value(s).

Value

A standardized value (Z = N (0,1)) when applied to a single value or a standardized attribute with values (Z = N (0,1)).
Note

The `lapply` function is required to apply this function across several attributes.

Author(s)

Tingwei Adeck

References

https://www.statology.org/how-to-normalize-data-in-r/

Examples

```r
test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
test_df_norm <- lapply(test_df[1:ncol(test_df)], norm_z)
```

Description

Designed as a prototype function to take a single attribute or column consisting of several samples and perform a putative resampling to yield another data frame with a separate attribute for each sample.

Usage

`resample_dat(df, tnp, cycles)`

Arguments

- `df` A clean data frame with attributes or tuples containing a mixture of samples.
- `tnp` A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
- `cycles` A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Author(s)

Tingwei Adeck
resample_dat_alt

**See Also**

resample_dat_scale(), resample_dat_scale_optimus()

**Examples**

```r
fpath <- system.file("extdata", "dat_5.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
samples_delineated <- resample_dat(nocomma_dat, tnp=3, cycles=40)
```

---

**Title:** A function to create an attribute or column for each sample loaded into the microplate wells.

**Description**

Designed as a prototype function to take a single tuple or row consisting of several samples and perform a putative resampling to yield another data frame with a separate attribute for each sample.

**Usage**

```r
resample_dat_alt(df, tnp, cycles)
```

**Arguments**

- `df` A clean data frame with attributes or tuples containing a mixture of samples.
- `tnp` A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
- `cycles` A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

**Value**

A new data frame where separated samples are assigned a separate attribute or column.

**Author(s)**

Tingwei Adeck

**See Also**

resample_dat_scale_alt()

**Examples**

```r
fpath <- system.file("extdata", "dat_5.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
samples_delineated <- resample_dat_alt(nocomma_dat, tnp=3, cycles=40)
```
Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description

Creates a data frame where each sample loaded into the microplate wells has a separate attribute.

Usage

resample_dat_scale(df, tnp, cycles)

Arguments

df          A clean data frame with attributes or tuples containing a mixture of samples.
tnp         A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
cycles      A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Note

This function builds on or scales-up @seealso resample_dat(), hence the suffix scale. This function is less optimized than @seealso resample_dat_scale_optimus().

Author(s)

Tingwei Adeck

See Also

resample_dat()

Examples

fpath <- system.file("extdata", "dat_4.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale(nocomma_dat, tnp=3, cycles=40)
Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description
A function that takes tuples or rows consisting of several samples and perform a putative resampling to yield another data frame with a separate attribute for each sample.

Usage
resample_dat_scale_alt(df, tnp, cycles, na_omit = NULL)

Arguments
- df: A clean data frame with attributes or tuples containing a mixture of samples.
- tnp: A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
- cycles: A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.
- na_omit: Takes a string "yes" OR "no".

Value
A new data frame where separated samples are assigned a separate attribute or column.

Author(s)
Tingwei Adeck

See Also
resample_dat_alt()

Examples
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
nocomma_dat <- resample_dat_scale_alt(nocomma_dat, tnp=3, cycles=40)
Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description

A function that takes tuples or rows consisting of several samples and perform a putative resampling to yield another data frame with a separate attribute for each sample.

Usage

resample_dat_scale_alt_bfv(df, tnp, cycles)

Arguments

df A clean data frame with attributes or tuples containing a mixture of samples.
tnp A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
cycles A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Author(s)

Tingwei Adeck

See Also

resample_dat_alt(), resample_dat_scale_alt()

Examples

fpath <- system.file("extdata", "dat_4.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odd_dat_optimus(dat_df)
resampled_scaled <- resample_dat_scale_alt_bfv(nocomma_dat, tnp=3, cycles=40)
Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description

A function that takes tuples or rows consisting of several samples and perform a putative resampling to yield another data frame with a separate attribute for each sample.

Usage

resample_dat_scale_alt_bf_na(df, tnp, cycles)

Arguments

df
A clean data frame with attributes or tuples containing a mixture of samples.

tnp
A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.

cycles
A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Author(s)

Tingwei Adeck

See Also

resample_dat_alt(), resample_dat_scale_alt()

Examples

fpath <- system.file("extdata", "dat_4.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale_alt_bf_na(nocomma_dat, tnp=3, cycles=40)
Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description

A function that takes tuples or rows consisting of several samples and perform a putative resampling to yield another data frame with a separate attribute for each sample. NA values are retained.

Usage

resample_dat_scale_alt_na(df, tnp, cycles)

Arguments

df A clean data frame with attributes or tuples containing a mixture of samples.
tnp A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
cycles A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Author(s)

Tingwei Adeck

See Also

resample_dat_alt()

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale_alt_na(nocomma_dat, tnp=3, cycles=40)
A function to create an attribute or column for each sample loaded into the microplate wells.

Description

Creates a data frame where each sample loaded into the microplate wells has a separate attribute. NA values are retained for more control.

Usage

resample_dat_scale_naretainer(df, tnp, cycles)

Arguments

- df: A clean data frame with attributes or tuples containing a mixture of samples.
- tnp: A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
- cycles: A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Note

This function builds on or scales-up @seealso `resample_dat()`, hence the suffix scale. This function is less optimized than @seealso `resample_dat_scale_optimus()`.

Author(s)

Tingwei Adeck

See Also

resample_dat()

Examples

```r
fpath <- system.file("extdata", "dat_4.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odd_dat_optimus(dat_df)
nresampled_scaled <- resample_dat_scale_naretainer(nocomma_dat, tnp=3, cycles=40)
```
Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description

Creates a data frame where each sample loaded into the microplate wells has a separate attribute.

Usage

```r
resample_dat_scale_optimus(df, tnp, cycles)
```

Arguments

- `df`: A clean data frame with attributes or tuples containing a mixture of samples.
- `tnp`: A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
- `cycles`: A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Note

This function builds on or scales-up @seealso `resample_dat()`, hence the suffix scale. This function is more optimized than @seealso `resample_dat_scale()`, hence the suffix scale_optimus.

Author(s)

Tingwei Adeck

See Also

- `resample_dat()`

Examples

```r
fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale_optimus(nocomma_dat, tnp=3, cycles=40)
```
resample_dat_scale_optimus_backend

Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description

Creates a data frame where each sample loaded into the microplate wells has a separate attribute.

Usage

resample_dat_scale_optimus_backend(df, tnp, cycles, na_omit = NULL)

Arguments

df  A clean data frame with attributes or tuples containing a mixture of samples.
tnp  A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
cycles  A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.
na_omit  Takes a string "yes" OR "no".

Value

A new data frame where separated samples are assigned a separate attribute or column.

Note

This function builds on or scales-up @seealso resample_dat(), hence the suffix scale. This function is more optimized than @seealso resample_dat_scale(), hence the suffix scale_optimus.

Author(s)

Tingwei Adeck

See Also

resample_dat()

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale_optimus_backend(nocomma_dat, tnp=3, cycles=40)
Title: A function to create an attribute or column for each sample loaded into the microplate wells.

Description

Creates a data frame where each sample loaded into the microplate wells has a separate attribute. NA values are retained.

Usage

resample_dat_scale_optimus_na(df, tnp, cycles)

Arguments

df A clean data frame with attributes or tuples containing a mixture of samples.
tnp A numeric value indicating the number of rows used. TNP is used as an acronym for Test, Negative, Positive.
cycles A numeric value indicating the number of cycles selected by the user when running the FLUOstar instrument.

Value

A new data frame where separated samples are assigned a separate attribute or column.

Note

This function builds on or scales-up @seealso resample_dat(), hence the suffix scale. This function is more optimized than @seealso resample_dat_scale(), hence the suffix scale_optimus.

Author(s)

Tingwei Adeck

See Also

resample_dat()

Examples

fpath <- system.file("extdata", "dat_1.dat", package = "normfluodbf", mustWork = TRUE)
dat_df <- read.table(file=fpath)
nocomma_dat <- clean_odddat_optimus(dat_df)
resampled_scaled <- resample_dat_scale_optimus_na(nocomma_dat, tnp=3, cycles=40)
roundfluor  

Title: A value rounding function.

Description
Round attribute values to three decimal places.

Usage
roundfluor(x)

Arguments
x  Attribute value(s).

Value
A rounded value with three decimal places when applied to a single value or an attribute with log-transformed values.

Examples
```r
test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
test_df_norm <- lapply(test_df[1:ncol(test_df)], roundfluor)
```

time_attribute  

Title: A time attribute generating function

Description
A function to help the researcher reproduce the time attribute.

Usage
time_attribute(
  interval = NULL,
  first_end = NULL,
  pause_duration = NULL,
  end_time = NULL,
  cycles = NULL
)
```
**Arguments**

- **interval**: The time interval chosen for the assay often in seconds.
- **first_end**: The end time of the initial run, often the pause for the introduction of a new substance. This can be the cycle number chosen for the initial stop.
- **pause_duration**: The time between the first end (pause) and resumption of the assay.
- **end_time**: The final end time of the assay.
- **cycles**: The number of cycles in the assay as selected by the user or researcher.

**Value**

The time attribute.

**Note**

The original function had an option for minutes which was for less time conscious people but the final version for this package has no such option. Users MUST provide numbers in seconds.

**Examples**

```r
time_test = time_attribute(30, 8, 136, 1276, 40)
time_test = time_attribute(60, 8, 136, 2460, 40)
```

---

**unique_identifier**

**Title**: A function to append a unique identifier attribute to any data frame within the normfluodbf package.

**Description**

The function in the context of normfluodbf creates an attribute called Cycle_Number and appends this attribute to the cleaned or wrangled data frame derived from the dirty DBF file.

**Usage**

```r
unique_identifier(df)
```

**Arguments**

- **df**: A data frame with 1:n number of rows.

**Value**

A data frame with the Cycle_Number attribute appended to the end of the data frame.

**Note**

The function operates in a closed system, meaning it is primarily designed to work with this package ONLY. Other use cases are simply a coincidence.
Author(s)
Tingwei Adeck

See Also

normfluodat(), norm_tidy_dbf(), normfluordbf(), generic_identifier()

Examples

test_df <- as.data.frame(c(seq(40)))
colnames(test_df) <- "test"
unique_identifier(test_df)
Index

* datasets
  dat_1, 7
  dat_2, 8
  dat_3, 8
  dat_4, 8
  dat_5, 9
  dat_6, 9
  dat_7, 9
  liposomes_214, 20
  liposomes_215, 21
  liposomes_216, 21
  liposomes_218, 21
  liposomes_221, 22
  liposomes_227, 22

actual_cols_used, 3

check_dat, 3
check_dbf, 4
clean_odd_cc, 6
clean_odd_cc(), 6, 7
clean_odd_dat_optimus, 6
clean_odd_dat_optimus(), 6, 7
comma_cleaner, 6
comma_cleaner(), 5, 6

dat_1, 7
dat_2, 8
dat_3, 8
dat_4, 8
dat_5, 9
dat_6, 9
dat_7, 9
dat_col_names_horizontal, 10
dat_col_names_optimus, 11
dat_col_names_optimus(), 15
dat_col_names_prime, 12
dat_col_names_rigid, 13
dat_col_names_rigid(), 12
decimal_scaling, 15

fluor_threshold_check, 16
fluor_threshold_check(), 17, 18
fluor_threshold_check_na, 17
fluor_threshold_check_na(), 17, 18
fluor_threshold_check_raw, 18
fluor_threshold_check_raw(), 17
generic_identifier, 19
generic_identifier(), 48
ggplot_tnp, 19
liposomes_214, 20
liposomes_215, 21
liposomes_216, 21
liposomes_218, 21
liposomes_221, 22
liposomes_227, 22
log_transformation, 22

min_max_norm, 23
min_max_norm_percent, 24
norm_applier, 32
norm_tidy_dbf, 33
norm_tidy_dbf(), 48
norm_z, 34
normfluodat, 25
normfluodat(), 12, 28–31, 34, 48
normfluodatfull, 26
normfluodatlite, 28
normfluodatlite(), 26
normfluordat, 29
normfluordbf, 31
normfluordbf(), 34, 48

resample_dat, 35
resample_dat(), 37, 42–45
resample_dat_alt, 36
resample_dat_alt(), 38–41
resample_dat_scale, 37
resample_dat_scale(), 36, 43–45
resample_dat_scale_alt, 38
resample_dat_scale_alt(), 36, 39, 40
resample_dat_scale_alt_bf_na, 40
resample_dat_scale_alt_bfv, 39
resample_dat_scale_alt_na, 41
resample_dat_scale_naretainer, 42
resample_dat_scale_optimus, 43
resample_dat_scale_optimus(), 36, 37, 42
resample_dat_scale_optimus_backend, 44
resample_dat_scale_optimus_na, 45
roundfluor, 46

time_attribute, 46

unique_identifier, 47