

# Package ‘rifiComparative’

September 15, 2025

**Title** 'rifiComparative' compares the output of rifi from two different conditions.

**Version** 1.8.0

**Description** 'rifiComparative' is a continuation of rifi package. It compares two conditions output of rifi using half-life and mRNA at time 0 segments. As an input for the segmentation, the difference between half-life of both conditions and log2FC of the mRNA at time 0 are used. The package provides segmentation, statistics, summary table, fragments visualization and some additional useful plots for further analysis.

**Depends** R (>= 4.2)

**Imports** cowplot, doMC, parallel, dplyr, egg, foreach, ggplot2, ggrepel, graphics, grDevices, grid, methods, nnet, rlang, S4Vectors, scales, stats, stringr, tibble, rtracklayer, utils, writexl, DTA, LSD, reshape2, devtools, SummarizedExperiment

**Suggests** DescTools, knitr, rmarkdown, BiocStyle

**VignetteBuilder** knitr

**biocViews** RNASeq, DifferentialExpression, GeneRegulation, Transcriptomics, Microarray, Software

**BugReports** <https://github.com/CyanolabFreiburg/rifiComparative>

**License** GPL-3 + file LICENSE

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## Contents

|                                         |    |
|-----------------------------------------|----|
| adjusting_HLToInt . . . . .             | 2  |
| annot_g . . . . .                       | 4  |
| data_combined_minimal . . . . .         | 5  |
| df_comb_minimal . . . . .               | 7  |
| df_mean_minimal . . . . .               | 8  |
| differential_expression . . . . .       | 9  |
| figures_fun . . . . .                   | 9  |
| fragmentation . . . . .                 | 11 |
| fragment_int . . . . .                  | 12 |
| gff3_preprocess . . . . .               | 13 |
| inp_f . . . . .                         | 14 |
| inp_s . . . . .                         | 16 |
| joining_data_column . . . . .           | 18 |
| joining_data_row . . . . .              | 18 |
| loading_fun . . . . .                   | 19 |
| make_pen . . . . .                      | 20 |
| penalties . . . . .                     | 22 |
| penalties_df . . . . .                  | 23 |
| pen_HL . . . . .                        | 24 |
| pen_int . . . . .                       | 24 |
| rifiComparative . . . . .               | 25 |
| rifi_visualization_comparison . . . . . | 26 |
| statistics . . . . .                    | 28 |
| stats_df_comb_minimal . . . . .         | 29 |
| stats_se_cdt1 . . . . .                 | 30 |
| stats_se_cdt2 . . . . .                 | 32 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>35</b> |
|--------------|-----------|

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|                   |                                                                                                      |
|-------------------|------------------------------------------------------------------------------------------------------|
| adjusting_HLToInt | <i>adjusting_HLToInt Creates one table merging HL and intensity fragments with genome annotation</i> |
|-------------------|------------------------------------------------------------------------------------------------------|

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## Description

'adjusting\_HLToInt' merges HL and intensity segments adapting the positions to each other and combining to the genome annotation. To make HL and intensity segments comparable, log2FC(HL) is used to generate the data frame instead of distance. The fragments should have a significant p\_value from t-test at least from one segmentation, either HL or intensity.

**Usage**

```
adjusting_HLToInt(data, Strand = c("+", "-"), annotation)
```

**Arguments**

|            |                                                  |
|------------|--------------------------------------------------|
| data       | data frame: data frame combined data by column   |
| Strand     | string: either "+" or "-"                        |
| annotation | data frame: data frame from processed gff3 file. |

**Details**

The functions used are:

1. `p_value_function` extracts and return the `p_values` of HL and intensity segments respectively.
2. `eliminate_outlier_hl` eliminates outliers from HL fragments.
3. `eliminate_outlier_int` eliminates outliers from intensity fragments.
4. `mean_length_int` calculates the mean of the `log2FC(intensity)` fragments adapted to `HL_fragments` and their lengths
5. `mean_length_hl` calculates the mean of `log2FC(HL)` fragments adapted to the intensity fragments and their lengths.
6. `calculating_rate` calculates decay rate and `log2FC(intensity)`. Both are used to calculate synthesis rate.

**Value**

The data frame with the corresponding columns:

**position:** Integer, position of the first fragment  
**region:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** Boolean. The bin/probe specific strand (+/-)  
**fragment\_HL:** String, HL fragments  
**fragment\_int:** String, intensity fragments  
**position\_frg\_int:** Integer, position of the first fragment and the last position of the last fragment  
**mean\_HL\_fragment:** Integer, mean of the HL of the fragments involved  
**mean\_int\_fragment:** Integer, mean of the intensity of the fragments involved  
**log2FC(decay\_rate):** Integer,  $\log_2FC(\text{decay}(\text{condition1})/\text{decay}(\text{condition2}))$   
**log2FC(synthesis\_rate):** Integer, sum of  $\log_2FC(\text{decay\_rate})$  and  $\log_2FC(\text{intensity})$   
**intensity\_FC:** Integer,  $\log_2FC(\text{mean}(\text{intensity}(\text{condition1}))/\text{mean}(\text{intensity}(\text{condition2})))$   
**Log2FC(HL)+Log2FC(int):** Integer, sum of  $\log_2FC(\text{decay\_rate})$  and  $\log_2FC(\text{intensity})$   
**p\_value:** String, indicated by "\*" means at least one fragment either HL fragment or intensity fragment has a significant `p_value`

## Examples

```
data(stats_df_comb_minimal)
data(annot_g)
df_mean_minimal <- adjusting_HLToInt(data = stats_df_comb_minimal,
  annotation = annot_g[[1]])
```

---

|         |                                                                                                                                                           |
|---------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|
| annot_g | <i>The result of gff3_preprocessing of gff3 file A list containing all necessary information from a gff file for adjusting_HLToInt and visualization.</i> |
|---------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

The result of gff3\_preprocessing of gff3 file A list containing all necessary information from a gff file for adjusting\_HLToInt and visualization.

## Usage

```
data(annot_g)
```

## Format

A list with 2 items:

**data annotation:** a data frame with 5853 rows and 6 variables

**region:** the region from the gff file

**start:** the start of the annotation

**end:** the end of the annotation

**strand:** the strand of the annotation

**gene:** the annotated gene name

**locus\_tag:** the annotated locus tag

**genome length:** a numeric vector containing the length of the genome

## Source

<https://github.com/CyanolabFreiburg/rifiComparative>

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data\_combined\_minimal *The result of joining\_by\_row for inp\_s and inp\_f example data A data frame containing the output of joining\_by\_row as a data frame*

---

## Description

The result of joining\_by\_row for inp\_s and inp\_f example data A data frame containing the output of joining\_by\_row as a data frame

## Usage

```
data(data_combined_minimal)
```

## Format

A data frame with 600 rows and 49 variables:

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**FLT:** The bin/probe flag for background level

**intensity:** The relative intensity at time point 0

**probe\_TI:** An internal value to determine which fitting model is applied

**flag:** Information on which fitting model is applied

**position\_segment:** The position based segment

**delay:** The delay value of the bin/probe

**half\_life:** The half-life of the bin/probe

**TI\_termination\_factor:** The termination factor of the bin/probe

**delay\_fragment:** The delay fragment the bin belongs to

**velocity\_fragment:** The velocity value of the respective delay fragment

**intercept:** The vintercept of fit through the respective delay fragment

**slope:** The slope of the fit through the respective delay fragment

**HL\_fragment:** The half-life fragment the bin belongs to

**HL\_mean\_fragment:** The mean half-life value of the respective half-life fragment

**intensity\_fragment:** The intensity fragment the bin belongs to

**intensity\_mean\_fragment:** The mean intensity value of the respective intensity fragment

**TU:** The overarching transcription unit

**TI\_termination\_fragment:** The TI fragment the bin belongs to

**TI\_mean\_termination\_factor:** The mean termination factor of the respective TI fragment

**seg\_ID:** The combined ID of the fragment

**pausing\_site:** presence of pausing site indicated by +/-

**iTSS\_I:** presence of iTSS\_I indicated by +/-

**ps\_ts\_fragment:** The fragments involved in pausing site or iTSS\_I

**event\_ps\_itss\_p\_value\_Ttest:** p\_value of pausing site or iTSS\_I

**p\_value\_slope:** p\_value of the slope

**delay\_frg\_slope:** the slope value of the respective delay fragment

**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments

**event\_duration:** Integer, the duration between two delay fragments

**event\_position:** Integer, the position middle between 2 fragments with an event

**FC\_fragment\_HL:** Integer, the fold change value of 2 intensity fragments

**FC\_HL:** Integer, the fold change value of 2 HL fragments#'

**p\_value\_HL:** p\_value of the fold change of HL fragments

**FC\_intensity:** Integer, the fold change value of 2 intensity fragments

**FC\_fragment\_intensity:** String, fragments involved in fold change between 2 intensity fragments

**p\_value\_intensity:** p\_value of the fold change of intensity fragments

**FC\_HL\_intensity:** ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_intensity\_fragment:** fragments involved on ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_adapted:** Integer, the fold change of half-life/ fold change of intensity, position of the half-life fragment is adapted to intensity fragment

**synthesis\_ratio:** Integer, the value corresponding to synthesis rate

**synthesis\_ratio\_event:** String, the event assigned by synthesis rate either Termination or iTSS

**p\_value\_Manova:** p\_value of the variance between two fold-changes, HL and intensity

**p\_value\_TI:** p\_value of TI fragment

**TI\_fragments\_p\_value:** p\_value of 2 TI fragments

**cdt:** The condition assigned to the experiment here cdt2

**logFC\_int:** The bin/probe log2 fold change of intensity at time 0

**P.Value:** The bin/probe p\_value adjusted

## Source

<https://github.com/CyanolabFreiburg/rifi>

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|                 |                                                                                                                                                    |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------|
| df_comb_minimal | <i>The result of joining_by_column for data_combined_minimal example data A data frame containing the output of joining_by_row as a data frame</i> |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

The result of joining\_by\_column for data\_combined\_minimal example data A data frame containing the output of joining\_by\_row as a data frame

## Usage

```
data(df_comb_minimal)
```

## Format

A data frame with 300 rows and 18 variables:

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**intensity.cdt1:** The relative intensity at time point 0 for condition 1

**position\_segment:** The position based segment

**half\_life.cdt1:** The half-life of the bin/probe condition 1

**TI\_termination\_factor.cdt1:** The termination factor of the bin/probe condition 1

**HL\_fragment.cdt1:** The half-life fragment the bin belongs to condition 1

**intensity\_fragment.cdt1:** The intensity fragment the bin belongs to condition 1

**TI\_termination\_fragment.cdt1:** The TI fragment the bin belongs to condition 1

**logFC\_int:** The bin/probe log2 fold change of intensity at time 0

**P.Value:** The bin/probe p\_value adjusted

**intensity.cdt2:** The relative intensity at time point 0 condition 2

**half\_life.cdt2:** The half-life of the bin/probe condition 2

**TI\_termination\_factor.cdt2:** The termination factor of the bin/probe condition 2

**HL\_fragment.cdt2:** The half-life fragment the bin belongs to condition 2

**intensity\_fragment.cdt2:** The intensity fragment the bin belongs to condition 2

**TI\_termination\_fragment.cdt2:** The TI fragment the bin belongs to condition 2

## Source

<https://github.com/CyanolabFreiburg/rifiComparative>

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|                 |                                                                                                                                                                      |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| df_mean_minimal | <i>The result of adjusting_HLToInt for stats_df_comb_minimal and annotation example data A data frame containing the output of adjusting_HLToInt as a data frame</i> |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

The result of adjusting\_HLToInt for stats\_df\_comb\_minimal and annotation example data A data frame containing the output of adjusting\_HLToInt as a data frame

## Usage

```
data(df_mean_minimal)
```

## Format

A data frame with 52 rows and 15 variables:

**position:** The bin/probe specific position

**region:** the region from the gff file

**gene:** the annotated gene name

**locus\_tag:** the annotated locus tag

**strand:** The strand specific

**fragment\_HL:** The half-life fragment the bin belongs

**fragment\_int:** The intensity fragment the bin belongs

**position\_frg\_int:** The position of the first fragment and the last position of the last fragment

**mean\_HL\_fragment:** The mean half-life value of the respective half-life fragments

**mean\_int\_fragment:** The mean intensity value of the respective intensity fragments

**log2FC(decay\_rate):**  $\log_2\text{FC}(\text{decay}(\text{condition1})/\text{decay}(\text{condition2}))$

**Log2FC(HL)-Log2FC(int):**  $\log_2\text{FC}(\text{decay\_rate}/\text{intensity})$

**log2FC(synthesis\_rate):**  $\log_2\text{FC}(\text{decay\_rate}) + \log_2\text{FC}(\text{intensity})$

**intensity\_FC:**  $\log_2\text{FC}(\text{mean}(\text{intensity}(\text{condition1}))/\text{mean}(\text{intensity}(\text{condition2})))$

**p\_value:** indicated by "\*" means at least one fragment either HL fragment or intensity fragment has a significant p\_value

## Source

<https://github.com/CyanolabFreiburg/rifiComparative>

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differential\_expression

*An example data frame from Synechosystis PCC 6803 differential probes expression obtained from limma package and only interesting variables were selected. The data frame was used entirely.*

---

### Description

An example data frame from Synechosystis PCC 6803 differential probes expression obtained from limma package and only interesting variables were selected. The data frame was used entirely.

### Usage

```
data(differential_expression)
```

### Format

A data frame of differential\_expression with 55508 rows and 4 variables:

**position:** The bin/probe specific position

**strand:** The strand specific

**logFC\_int:** The bin/probe differential expression

**P.Value:** The bin/probe p\_value adjusted

### Source

<https://github.com/CyanolabFreiburg/rifiComparative>

---

figures\_fun

*'figures\_fun': generates several plots*

---

### Description

'figures\_fun' plots at one the density of HL, the HL category as histogram, log2FC of decay and synthesis rate and their heatscatter. Scatter plot of HL and volcano plot. The function uses the four output generated previously.

**Usage**

```
figures_fun(
  data.1,
  data.2,
  input.1,
  input.2,
  cdt1,
  cdt2,
  y = 30,
  x = 30,
  limits = c(0, 20)
)
```

**Arguments**

|         |                                                           |
|---------|-----------------------------------------------------------|
| data.1  | data frame output of statistic                            |
| data.2  | data frame joining two outputs from rfi_stats by row      |
| input.1 | data frame joining two outputs from rfi_stats by column   |
| input.2 | data frame of differential gene expression at time 0      |
| cdt1    | string for the first condition                            |
| cdt2    | string for the second condition                           |
| y       | integer to break the scaling in scatter plot for y_axis   |
| x       | integer to break the scaling in scatter plot for x_axis   |
| limits  | vector to limit the scaling in scatter plot for both axis |

**Details**

The functions used are:

plot\_decay\_synt: plots the changes in RNA decay rates versus the changes in RNA synthesis rates

plot\_heatscatter: plots the changes in RNA decay rates versus the changes in RNA synthesis rates with density.

plot\_volcano: plots statistical significance versus magnitude of change .

plot\_histogram: plot a histogram of probe/bin half-life categories from 2 to 20 minutes in both conditions.

plot\_density: plots the probe/bin half-life density in both conditions.

plot\_scatter: plots of the bin/probe half-life in one condition1 vs. condition2.

extract the object of rfi\_statistics from both conditions. The differential gene expression at time 0 needs to be run separately. The columns log2FC, p\_value adjusted, position and strand are extracted and saved to a data frame. loading\_fun\_fig joins the differential gene expression table and the output from rfi statistics into one data frame.

**Value**

several plots

**Examples**

```
data(data_combined_minimal)
data(df_comb_minimal)
data(differential_expression)
data(df_mean_minimal)
figures_fun(data.1 = df_mean_minimal, data.2 = data_combined_minimal,
input.1 = df_comb_minimal, input.2 = differential_expression, cdt1 = "sc",
cdt2 = "fe")
```

---

fragmentation

*fragmentation: Conveniently wraps all fragmentation steps*


---

**Description**

fragmentation fragments the half-life and intensity into segments using the penalties output.

**Usage**

```
fragmentation(data, pen_HL, pen_int, cores = 2)
```

**Arguments**

|         |                                                                                                   |
|---------|---------------------------------------------------------------------------------------------------|
| data    | data frame: data frame combined data by column                                                    |
| pen_HL  | list: list of the penalties set optimal for the fragmentation for half-life                       |
| pen_int | list: list of the penalties set optimal for the fragmentation for intensity                       |
| cores   | integer: the number of assigned cores for the task. It needs to be increased in case of big data. |

**Value**

Two data frames with half-life and intensity fragments and the mean of the coefficient fragment based.

**Examples**

```
data(penalties_df)
data(pen_HL)
data(pen_int)
df_comb_minimal <- fragmentation(data = penalties_df, pen_HL,
pen_int)
```

---

|              |                                                                                                                                         |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| fragment_int | <i>The result of fragmentation for df_comb_minimal example data A data frame containing the output of fragmentation as a data frame</i> |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

The result of fragmentation for df\_comb\_minimal example data A data frame containing the output of fragmentation as a data frame

## Usage

```
data(fragment_int)
```

## Format

A data frame with 500 rows and 24 variables:

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**intensity.cdt1:** The relative intensity at time point 0 for condition 1

**position\_segment:** The position based segment

**half\_life.cdt1:** The half-life of the bin/probe condition 1

**TI\_termination\_factor.cdt1:** The termination factor of the bin/probe condition 1

**HL\_fragment.cdt1:** The half-life fragment the bin belongs to condition 1

**intensity\_fragment.cdt1:** The intensity fragment the bin belongs to condition 1

**TI\_termination\_fragment.cdt1:** The TI fragment the bin belongs to condition 1

**logFC\_int:** The bin/probe log2 fold change of intensity at time 0

**P.Value:** The bin/probe p\_value adjusted

**intensity.cdt2:** The relative intensity at time point 0 condition 2

**half\_life.cdt2:** The half-life of the bin/probe condition 2

**TI\_termination\_factor.cdt2:** The termination factor of the bin/probe condition 2

**HL\_fragment.cdt2:** The half-life fragment the bin belongs to condition 2

**intensity\_fragment.cdt2:** The intensity fragment the bin belongs to condition 2

**TI\_termination\_fragment.cdt2:** The TI fragment the bin belongs to condition 2

**distance\_HL:** The bin/probe difference of half-life from both conditions

**distance\_int:** The bin/probe log2 fold change of intensity at time 0

**HL\_comb\_fragment:** The half-life fragment the bin belongs to both conditions

**HL\_mean\_comb\_fragment:** The half-life mean of the fragment the bin belongs to both conditions

**intensity\_comb\_fragment:** The intensity fragment the bin belongs to both conditions

**intensity\_mean\_comb\_fragment:** The intensity mean of the fragment the bin belongs to both conditions

**Source**

<https://github.com/CyanolabFreiburg/rifiComparative>

---

|                 |                                                          |
|-----------------|----------------------------------------------------------|
| gff3_preprocess | <i>gff3_preprocess processes gff3 file from database</i> |
|-----------------|----------------------------------------------------------|

---

**Description**

gff3\_preprocess processes the gff3 file extracting gene names and locus\_tag from all coding regions (CDS). UTRs/ncRNA/asRNA if available, are also extracted. The resulting dataframe contains region, positions, strand, gene and locus\_tag.

**Usage**

```
gff3_preprocess(path)
```

**Arguments**

path                      path: path to the directory containing the gff3 file.

**Value**

A list with 2 items:

**data annotation: region:** String, the region from the gff file  
**start:** Integer, the start of the annotation  
**end:** Integer, the end of the annotation  
**strand:** Boolean, the strand of the annotation  
**gene:** String, the annotated gene name  
**locus\_tag:** String, the annotated locus tag  
**genome length:** a numeric vector containing the length of the genome

**Examples**

```
gff3_preprocess(
  path = gzfile(system.file("extdata", "gff_synechocystis_6803.gff.gz",
    package = "rifiComparative"))
)
```

---

|       |                                                                                                                                                  |
|-------|--------------------------------------------------------------------------------------------------------------------------------------------------|
| inp_f | <i>The result of loading_fun for stats_se_cdt2 example data Two data frame containing the output of loading_fun as second element of a list.</i> |
|-------|--------------------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

The result of loading\_fun for stats\_se\_cdt2 example data Two data frame containing the output of loading\_fun as second element of a list.

## Usage

```
data(inp_f)
```

## Format

A data frame with 500 rows and 49 variables:

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**FLT:** The bin/probe flag for background level

**intensity:** The relative intensity at time point 0

**probe\_TI:** An internal value to determine which fitting model is applied

**flag:** Information on which fitting model is applied

**position\_segment:** The position based segment

**delay:** The delay value of the bin/probe

**half\_life:** The half-life of the bin/probe

**TI\_termination\_factor:** The termination factor of the bin/probe

**delay\_fragment:** The delay fragment the bin belongs to

**velocity\_fragment:** The velocity value of the respective delay fragment

**intercept:** The vintercept of fit through the respective delay fragment

**slope:** The slope of the fit through the respective delay fragment

**HL\_fragment:** The half-life fragment the bin belongs to

**HL\_mean\_fragment:** The mean half-life value of the respective half-life fragment

**intensity\_fragment:** The intensity fragment the bin belongs to

**intensity\_mean\_fragment:** The mean intensity value of the respective intensity fragment

**TU:** The overarching transcription unit

**TI\_termination\_fragment:** The TI fragment the bin belongs to

**TI\_mean\_termination\_factor:** The mean termination factor of the respective TI fragment

**seg\_ID:** The combined ID of the fragment

**pausing\_site:** presence of pausing site indicated by +/-

**iTSS\_I:** presence of iTSS\_I indicated by +/-

**ps\_ts\_fragment:** The fragments involved in pausing site or iTSS\_I

**event\_ps\_itss\_p\_value\_Ttest:** p\_value of pausing site or iTSS\_I

**p\_value\_slope:** p\_value of the slope

**delay\_frg\_slope:** the slope value of the respective delay fragment

**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments

**event\_duration:** Integer, the duration between two delay fragments

**event\_position:** Integer, the position middle between 2 fragments with an event

**FC\_HL:** Integer, the fold change value of 2 HL fragments

**FC\_fragment\_HL:** Integer, the fold change value of 2 intensity fragments

**p\_value\_HL:** p\_value of the fold change of HL fragments

**FC\_intensity:** Integer, the fold change value of 2 intensity fragments

**FC\_fragment\_intensity:** String, fragments involved in fold change between 2 intensity fragments

**p\_value\_intensity:** p\_value of the fold change of intensity fragments

**FC\_HL\_intensity:** ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_intensity\_fragment:** fragments involved on ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_adapted:** Integer, the fold change of half-life/ fold change of intensity, position of the half-life fragment is adapted to intensity fragment

**synthesis\_ratio:** Integer, the value corresponding to synthesis rate

**synthesis\_ratio\_event:** String, the event assigned by synthesis rate either Termination or iTSS

**p\_value\_Manova:** p\_value of the variance between two fold-changes, HL and intensity

**p\_value\_TI:** p\_value of TI fragment

**TI\_fragments\_p\_value:** p\_value of 2 TI fragments

**cdt:** The condition assigned to the experiment here cdt2

**logFC\_int:** The bin/probe log2 fold change of intensity at time 0

**P.Value:** The bin/probe p\_value adjusted

## Source

<https://github.com/CyanolabFreiburg/rifiComparative>

---

|       |                                                                                                                                                 |
|-------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| inp_s | <i>The result of loading_fun for stats_se_cdt1 example data Two data frame containing the output of loading_fun as first element of a list.</i> |
|-------|-------------------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

The result of loading\_fun for stats\_se\_cdt1 example data Two data frame containing the output of loading\_fun as first element of a list.

## Usage

```
data(inp_s)
```

## Format

A data frame with 500 rows and 49 variables:

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**FLT:** The bin/probe flag for background level

**intensity:** The relative intensity at time point 0

**probe\_TI:** An internal value to determine which fitting model is applied

**flag:** Information on which fitting model is applied

**position\_segment:** The position based segment

**delay:** The delay value of the bin/probe

**half\_life:** The half-life of the bin/probe

**TI\_termination\_factor:** The termination factor of the bin/probe

**delay\_fragment:** The delay fragment the bin belongs to

**velocity\_fragment:** The velocity value of the respective delay fragment

**intercept:** The vintercept of fit through the respective delay fragment

**slope:** The slope of the fit through the respective delay fragment

**HL\_fragment:** The half-life fragment the bin belongs to

**HL\_mean\_fragment:** The mean half-life value of the respective half-life fragment

**intensity\_fragment:** The intensity fragment the bin belongs to

**intensity\_mean\_fragment:** The mean intensity value of the respective intensity fragment

**TU:** The overarching transcription unit

**TI\_termination\_fragment:** The TI fragment the bin belongs to

**TI\_mean\_termination\_factor:** The mean termination factor of the respective TI fragment

**seg\_ID:** The combined ID of the fragment

**pausing\_site:** presence of pausing site indicated by +/-

**iTSS\_I:** presence of iTSS\_I indicated by +/-

**ps\_ts\_fragment:** The fragments involved in pausing site or iTSS\_I

**event\_ps\_itss\_p\_value\_Ttest:** p\_value of pausing site or iTSS\_I

**p\_value\_slope:** p\_value of the slope

**delay\_frg\_slope:** the slope value of the respective delay fragment

**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments

**event\_duration:** Integer, the duration between two delay fragments

**event\_position:** Integer, the position middle between 2 fragments with an event

**FC\_HL:** Integer, the fold change value of 2 HL fragments

**FC\_fragment\_HL:** Integer, the fold change value of 2 intensity fragments

**p\_value\_HL:** p\_value of the fold change of HL fragments

**FC\_intensity:** Integer, the fold change value of 2 intensity fragments

**FC\_fragment\_intensity:** String, fragments involved in fold change between 2 intensity fragments

**p\_value\_intensity:** p\_value of the fold change of intensity fragments

**FC\_HL\_intensity:** ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_intensity\_fragment:** fragments involved on ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_adapted:** Integer, the fold change of half-life/ fold change of intensity, position of the half-life fragment is adapted to intensity fragment

**synthesis\_ratio:** Integer, the value corresponding to synthesis rate

**synthesis\_ratio\_event:** String, the event assigned by synthesis rate either Termination or iTSS

**p\_value\_Manova:** p\_value of the variance between two fold-changes, HL and intensity

**p\_value\_TI:** p\_value of TI fragment

**TI\_fragments\_p\_value:** p\_value of 2 TI fragments

**cdt:** The condition assigned to the experiment here cdt1

**logFC\_int:** The bin/probe log2 fold change of intensity at time 0

**P.Value:** The bin/probe p\_value adjusted

## Source

<https://github.com/CyanolabFreiburg/rifiComparative>

---

|                     |                                                            |
|---------------------|------------------------------------------------------------|
| joining_data_column | <i>joining_data_column joins two data frames by column</i> |
|---------------------|------------------------------------------------------------|

---

**Description**

'joining\_data\_column': joins two data frames from different conditions by column.

**Usage**

```
joining_data_column(data)
```

**Arguments**

|      |                                                     |
|------|-----------------------------------------------------|
| data | data frame with joined columns from both conditions |
|------|-----------------------------------------------------|

**Value**

The data frame with joined columns from both conditions with the corresponding columns: strand, position, ID, intensity.cdt1, position\_segment, half\_life.cdt1, TI\_termination\_factor.cdt1", HL\_fragment.cdt1, intensity\_fragment.cdt1, TI\_termination\_fragment.cdt1, logFC\_int, P.Value, intensity.cdt2, half\_life.cdt2, TI\_termination\_factor.cdt2, HL\_fragment.cdt2, intensity\_fragment.cdt2, TI\_termination\_fragment.cdt2.

cdt1: first condition, cdt2: second condition.

**Examples**

```
data(data_combined_minimal)
df_comb_minimal <- joining_data_column(data = data_combined_minimal)
```

---

|                  |                                                      |
|------------------|------------------------------------------------------|
| joining_data_row | <i>joining_data_row joins two data frames by row</i> |
|------------------|------------------------------------------------------|

---

**Description**

joining\_data\_row joins two data frames from different conditions by row.

**Usage**

```
joining_data_row(input1, input2)
```

**Arguments**

|        |                                                                                                    |
|--------|----------------------------------------------------------------------------------------------------|
| input1 | data frame from SummarizedExperiment output of rfi_stats from rfi package of the first condition.  |
| input2 | data frame from SummarizedExperiment output of rfi_stats from rfi package of the second condition. |

**Value**

The data frame with joined rows from both conditions with the corresponding columns: ID with position, strand, intensity, probe\_TI, flag, position\_segment, delay, half\_life, TI\_termination\_factor, delay\_fragment, velocity\_fragment, intercept, slope, HL\_fragment, HL\_mean\_fragment, intensity\_fragment, intensity\_mean\_fragment, TU, TI\_termination\_fragment, TI\_mean\_termination\_factor, seg\_ID, pausing\_site, iTSS\_I, ps\_ts\_fragment, event\_ps\_itss\_p\_value\_Ttest, p\_value\_slope, delay\_frg\_slope, velocity\_ratio, event\_duration, event\_position, FC\_HL, FC\_fragment\_HL, p\_value\_HL, FC\_intensity, FC\_fragment\_intensity, p\_value\_intensity, FC\_HL\_intensity, FC\_HL\_intensity\_fragment, FC\_HL\_adapted, synthesis\_ratio, synthesis\_ratio\_event, p\_value\_Manova, p\_value\_TI, cdt (condition), logFC\_int (log2FC(intensity)), P.Value of log2FC(intensity)

**Examples**

```
data(inp_s)
data(inp_f)
data_combined_minimal <-
  joining_data_row(input1 = inp_s, input2 = inp_f)
```

loading\_fun

*loading\_fun loads the data of all conditions***Description**

loading\_fun extract outputs from rifi\_stats of all conditions and join each data to the differential expression table. The differential gene expression at time 0 needs to be run separately. The columns log2FC, p\_value adjusted, position and strand are extracted and saved to a data frame. loading\_fun joins the differential gene expression table and the output from rifi statistics into one data frame.

**Usage**

```
loading_fun(data1, data2, data3)
```

**Arguments**

|       |                                                        |
|-------|--------------------------------------------------------|
| data1 | data frame from rifi_stats of one condition            |
| data2 | data frame from rifi_stats of other condition          |
| data3 | data frame from differential gene expression at time 0 |

**Value**

A list of two data frames with joined columns from differential expression and output of rifi\_stats with the corresponding columns: ID with position, strand, intensity, probe\_TI, flag, position\_segment, delay, half\_life, TI\_termination\_factor, delay\_fragment, velocity\_fragment, intercept, slope, HL\_fragment, HL\_mean\_fragment, intensity\_fragment, intensity\_mean\_fragment, TU, TI\_termination\_fragment, TI\_mean\_termination\_factor, seg\_ID, pausing\_site, iTSS\_I, ps\_ts\_fragment, event\_ps\_itss\_p\_value\_Ttest, p\_value\_slope, delay\_frg\_slope, velocity\_ratio, event\_duration, event\_position, FC\_HL, FC\_fragment\_HL, p\_value\_HL, FC\_intensity, FC\_fragment\_intensity, p\_value\_intensity, FC\_HL\_intensity, FC\_HL\_intensity\_fragment,

FC\_HL\_adapted, synthesis\_ratio, synthesis\_ratio\_event, p\_value\_Manova, p\_value\_TI, cdt (condition), logFC\_int (log2FC(intensity)), P.Value of log2FC(intensity).

### Examples

```
data(stats_se_cdt1)
data(stats_se_cdt2)
data(differential_expression)
inp_s <-
loading_fun(stats_se_cdt1, stats_se_cdt2, differential_expression)[[1]]
inp_f <-
loading_fun(stats_se_cdt1, stats_se_cdt2, differential_expression)[[2]]
```

---

make\_pen

*make\_pen assigns automatically penalties*

---

### Description

make\_pen calls one of four available penalty functions to automatically assign penalties for the dynamic programming. The two functions to be called are:

1. fragment\_HL\_pen
2. fragment\_inty\_pen

### Usage

```
make_pen(
  probe,
  FUN,
  cores = 1,
  logs,
  dpt = 1,
  smpl_min = 10,
  smpl_max = 100,
  sta_pen = 0.5,
  end_pen = 4.5,
  rez_pen = 9,
  sta_pen_out = 0.5,
  end_pen_out = 3.5,
  rez_pen_out = 7
)
```

### Arguments

|       |                                                                |
|-------|----------------------------------------------------------------|
| probe | data frame: data frame combined data by column                 |
| FUN   | function: one of the four bottom level functions (see details) |
| cores | integer: the number of assigned cores for the task             |

|             |                                                                                                                       |
|-------------|-----------------------------------------------------------------------------------------------------------------------|
| logs        | numeric vector: the logbook vector.                                                                                   |
| dpt         | integer: the number of times a full iteration cycle is repeated with a more narrow range based on the previous cycle. |
| smpl_min    | integer: the smaller end of the sampling size.                                                                        |
| smpl_max    | integer: the larger end of the sampling size.                                                                         |
| sta_pen     | numeric: the lower starting penalty.                                                                                  |
| end_pen     | numeric: the higher starting penalty.                                                                                 |
| rez_pen     | numeric: the number of penalties iterated within the penalty range.                                                   |
| sta_pen_out | numeric: the lower starting outlier penalty.                                                                          |
| end_pen_out | numeric: the higher starting outlier penalty.                                                                         |
| rez_pen_out | numeric: the number of outlier penalties iterated within the outlier penalty range.                                   |

### Details

The two functions called return the amount of statistically correct and statistically wrong splits at a specific pair of penalties. 'make\_pen' iterates over many penalty pairs and picks the most suitable pair based on the difference between wrong and correct splits. The sample size, penalty range and resolution as well as the number of cycles can be customized. The primary start parameters create a matrix with  $n = \text{rez\_pen}$  rows and  $n = \text{rez\_pen\_out}$  columns with values between  $\text{sta\_pen}/\text{sta\_pen\_out}$  and  $\text{end\_pen}/\text{end\_pen\_out}$ . The best penalty pair is picked. If  $\text{dpt}$  is bigger than 1 the same process is repeated with a new matrix of the same size based on the result of the previous cycle. Only position segments with length within the sample size range are considered for the penalties to increase run time.

### Value

A list with 4 items:

**logbook:** The logbook vector containing all penalty information

**penalties:** a vector with the respective penalty and outlier penalty

**correct:** a matrix of the correct splits

**wrong:** a matrix of the incorrect splits

### Examples

```
data(df_comb_minimal)

df_comb_minimal$distance_HL <- df_comb_minimal$half_life.cdt1 -
df_comb_minimal$half_life.cdt2

df_comb_minimal$distance_int <- df_comb_minimal$logFC_int

pen_HL <- make_pen(
  probe = df_comb_minimal, FUN = rfiComparative:::fragment_HL_pen,
  cores = 2, logs = as.numeric(rep(NA, 8)), dpt = 1, smpl_min = 10,
  smpl_max = 50, sta_pen = 0.5, end_pen = 4.5, rez_pen = 9, sta_pen_out = 0.5,
```

```

    end_pen_out = 3.5, rez_pen_out = 7
  )

  pen_int <- make_pen(
    probe = df_comb_minimal, FUN = rfiComparative::fragment_inty_pen,
    cores = 2, logs = as.numeric(rep(NA, 8)), dpt = 1, smpl_min = 10,
    smpl_max = 50, sta_pen = 0.5, end_pen = 4.5, rez_pen = 9, sta_pen_out = 0.5,
    end_pen_out = 3.5, rez_pen_out = 7
  )

```

---

penalties

*penalties wraps conveniently all penalty steps*


---

### Description

penalties finds the best set of penalties for half-life and intensity fragmentation using dynamic programming. The segmentation of the HL uses the difference between 2 conditions and the segmentation of the intensity uses the log2FC.

### Usage

```
penalties(data, cores = 2)
```

### Arguments

|       |                                                                                                   |
|-------|---------------------------------------------------------------------------------------------------|
| data  | data frame with the joined columns from differential expression and output of rfi_stats.          |
| cores | integer: the number of assigned cores for the task. It needs to be increased in case of big data. |

### Details

The function uses 4 functions:

score\_fun\_ave.r

make\_pen.r

fragment\_HL\_pen.r

fragment\_inty\_pen.r

### Value

A list of data frame and penalties, The first element is data frame with 2 more variables, second and third are HL and intensity penalties respectively.

**Examples**

```
data(df_comb_minimal)
penalties_df <- penalties(df_comb_minimal)[[1]]
pen_HL <- penalties(df_comb_minimal)[[2]]
pen_int <- penalties(df_comb_minimal)[[3]]
```

---

|              |                                                                                                                                 |
|--------------|---------------------------------------------------------------------------------------------------------------------------------|
| penalties_df | <i>The result of penalties for df_comb_minimal example data A data frame containing the output of penalties as a data frame</i> |
|--------------|---------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

The result of penalties for df\_comb\_minimal example data A data frame containing the output of penalties as a data frame

**Usage**

```
data(penalties_df)
```

**Format**

A data frame with 300 rows and 20 variables:

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**intensity.cdt1:** The relative intensity at time point 0 for condition 1

**position\_segment:** The position based segment

**half\_life.cdt1:** The half-life of the bin/probe condition 1

**TI\_termination\_factor.cdt1:** The termination factor of the bin/probe condition 1

**HL\_fragment.cdt1:** The half-life fragment the bin belongs to condition 1

**intensity\_fragment.cdt1:** The intensity fragment the bin belongs to condition 1

**TI\_termination\_fragment.cdt1:** The TI fragment the bin belongs to condition 1

**logFC\_int:** The bin/probe log2 fold change of intensity at time 0

**P.Value:** The bin/probe p\_value adjusted

**intensity.cdt2:** The relative intensity at time point 0 condition 2

**half\_life.cdt2:** The half-life of the bin/probe condition 2

**TI\_termination\_factor.cdt2:** The termination factor of the bin/probe condition 2

**HL\_fragment.cdt2:** The half-life fragment the bin belongs to condition 2

**intensity\_fragment.cdt2:** The intensity fragment the bin belongs to condition 2

**TI\_termination\_fragment.cdt2:** The TI fragment the bin belongs to condition 2

**distance\_HL:** The bin/probe difference of half-life from both conditions

**distance\_int:** The bin/probe log2 fold change of intensity at time 0

**Source**

<https://github.com/CyanolabFreiburg/rifiComparative>

---

|        |                                                                                                                                                             |
|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| pen_HL | <i>The result of penalties for df_comb_minimal example data. A list containing the output from penalties including the logbook and two penalty objects.</i> |
|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

The result of penalties for df\_comb\_minimal example data. A list containing the output from penalties including the logbook and two penalty objects.

**Usage**

```
data(pen_HL)
```

**Format**

A list with 5 items:

**pen\_obj\_HL:** A list with 4 items:

**logbook:** The logbook vector containing half-life penalty information

**HL\_penalties:** a vector with the half-life penalty and half-life outlier penalty

**correct:** a matrix of the correct splits

**wrong:** a matrix of the incorrect splits

**Source**

<https://github.com/CyanolabFreiburg/rifi>

---

|         |                                                                                                                                                             |
|---------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| pen_int | <i>The result of penalties for df_comb_minimal example data. A list containing the output from penalties including the logbook and two penalty objects.</i> |
|---------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

The result of penalties for df\_comb\_minimal example data. A list containing the output from penalties including the logbook and two penalty objects.

**Usage**

```
data(pen_int)
```

**Format**

A list with 5 items:

**pen\_int:** A list with 4 items:

**logbook:** The logbook vector containing intensity penalty information

**int\_penalties:** a vector with the intensity penalty and intensity outlier penalty

**correct:** a matrix of the correct splits

**wrong:** a matrix of the incorrect splits

**Source**

<https://github.com/CyanolabFreiburg/rifi>

---

rifiComparative      %

=====

**rifiComparative**

*rifiComparative a successor package of rifi. It compares 2 rifi outputs from 2 different conditions of the same organism.*

---

**Description**

rifiComparative was developed to compare 2 rifi outputs from 2 conditions. The rifi output may differ significantly from 2 conditions. The complexity of the segments number, position, length and the events make the comparison between 2 conditions nearly impossible. rifiComparative uses a simple strategy to generate single segments for both conditions, extract the features and make them comparable.

**Details**

Five major steps are described in rifiComparative:

1. Joining data
2. penalties
3. fragmentation
4. statistics
5. visualization

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---

```
rifi_visualization_comparison
```

```
rifi_visualization_comparison plots the segments and genome annotation
```

---

## Description

rifi\_visualization\_comparison plots the genome annotation, half-life difference (HL), log2FC(intensity) fragments. It uses several functions to plot TUs and genes including small-RNAs. Additionally it plots the statistical t-test between the neighboring fragment, significant p-values from t-test are assigned with '\*\*'.

## Usage

```
rifi_visualization_comparison(
  data,
  data_c,
  genomeLength = annot_g[[2]],
  annot = annot_g[[1]],
  condition = c("cdt1", "cdt2"),
  Strand = c("+", "-"),
  region = c("CDS", "asRNA", "5'UTR", "ncRNA", "3'UTR", "tRNA"),
  color_region = c("grey0", "red", "blue", "orange", "yellow", "green", "white",
    "darkseagreen1", "grey50", "black"),
  color_TU = c("cyan", "yellow", "orange"),
  scaling_TU = c(0, 3.4, 6.6),
  color_text.1 = "grey0",
  color_text.2 = "black",
  Alpha = 0.5,
  size_tu = 1.6,
  size_locusTag = 1.6,
  size_gene = 1.6,
  Limit = 10,
  shape = 22,
  face = "bold",
  tick_length = 0.3,
  arrow.color = "darkseagreen1",
  col_above20 = "#00FFFF",
  fontface = "plain",
  shape_above20 = 14,
  axis_text_y_size = 3,
  axis_title_y_size = 6,
  iTSS_threshold = 1.2,
  p_value_manova = 0.05,
  termination_threshold = 0.8
)
```

**Arguments**

|                                    |                                                                                                                          |
|------------------------------------|--------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>                  | dataframe: the probe based dataframe with joined columns.                                                                |
| <code>data_c</code>                | dataframe: the probe based dataframe with joined rows.                                                                   |
| <code>genomeLength</code>          | integer: genome length output of <code>gff3_preprocess</code> function.                                                  |
| <code>annot</code>                 | dataframe: the annotation file.                                                                                          |
| <code>condition</code>             | string: assigned as <code>cdt1</code> (condition 1) and <code>cdt2</code> (condition2), it could be adapted to any name. |
| <code>Strand</code>                | string: either "+" or "-".                                                                                               |
| <code>region</code>                | dataframe: gff3 features of the genome.                                                                                  |
| <code>color_region</code>          | string vector: vector of colors.                                                                                         |
| <code>color_TU</code>              | string. TU color                                                                                                         |
| <code>scaling_TU</code>            | vector: values to adjusted termination and iTSSs to TUs.                                                                 |
| <code>color_text.1</code>          | string: TU color text                                                                                                    |
| <code>color_text.2</code>          | string: genes color text                                                                                                 |
| <code>Alpha</code>                 | integer: color transparency degree.                                                                                      |
| <code>size_tu</code>               | integer: TU size                                                                                                         |
| <code>size_locusTag</code>         | integer: locus_tag size                                                                                                  |
| <code>size_gene</code>             | integer: font size for gene annotation.                                                                                  |
| <code>Limit</code>                 | integer: value for y-axis limit.                                                                                         |
| <code>shape</code>                 | integer: value for shape.                                                                                                |
| <code>face</code>                  | string: label font.                                                                                                      |
| <code>tick_length</code>           | integer: value for ticks.                                                                                                |
| <code>arrow.color</code>           | string: arrows color.                                                                                                    |
| <code>col_above20</code>           | string: color for probes/bin above value 20.                                                                             |
| <code>fontface</code>              | integer: font type                                                                                                       |
| <code>shape_above20</code>         | integer: shape for probes/bins above value 20.                                                                           |
| <code>axis_text_y_size</code>      | integer: text size for y-axis.                                                                                           |
| <code>axis_title_y_size</code>     | integer: title size for y-axis.                                                                                          |
| <code>iTSS_threshold</code>        | integer: threshold for iTSS_II selected to plot, default 1.2.                                                            |
| <code>p_value_manova</code>        | integer: p_value of manova test fragments to plot, default 0.05.                                                         |
| <code>termination_threshold</code> | integer: threshold for termination to plot, default .8.                                                                  |

Details

The functions used are:

strand\_selection: plots HL, intensity fragments from both strands.

splitGenome\_function: splits the genome into fragments.

annotation\_plot\_comp: plots the corresponding annotation.

indice\_function: assign a new column to the data to distinguish between fragments, outliers from delay or HL or intensity.

empty\_data\_positive: plots empty boxes in case no data is available for positive strand

empty\_data\_negative: plots empty boxes in case no data is available for negative strand

TU\_annotation: designs the segments border for the genes and TUs annotation.

gene\_annot\_function: it requires gff3 file, returns a dataframe adjusting each fragment according to its annotation. It allows as well the plot of genes and TUs shared into two pages.

secondaryAxis: adjusts the half-life or delay to 20 in case of the dataframe row numbers is equal to 1 and the half-life or delay exceed the limit, they are plotted with different shape and color.

my\_arrow: creates an arrow for the annotation.

arrange\_byGroup: selects the last row for each segment and add 40 nucleotides in case of negative strand for a nice plot.

my\_segment\_T: plots terminals and pausing sites labels.

Value

The plot.

Examples

```
data(data_combined_minimal)
data(stats_df_comb_minimal)
data(annot_g)
rifi_visualization_comparison(
  data = data_combined_minimal,
  data_c = stats_df_comb_minimal,
  genomeLength = annot_g[[2]],
  annot = annot_g[[1]]
)
```

---

|            |                                                                      |
|------------|----------------------------------------------------------------------|
| statistics | <i>statistics check segments significance using statistical test</i> |
|------------|----------------------------------------------------------------------|

---

Description

statistics uses t-test to check HL and intensity segments significance. The function returns the data frame with p\_value and p\_value adjusted. The function used is t\_test\_function.

**Usage**

```
statistics(data)
```

**Arguments**

**data** data frame: data frame output of fragmentation

**Value**

A list of two data frames, the first one contains all segments with p\_value and p\_value adjusted. The second one removes the duplicated segments from intensity and could be saved as an excel file.

**Examples**

```
data(fragment_int)
stats_df_comb_minimal <- statistics(data= fragment_int)[[1]]
df_comb_uniq_minimal <- statistics(data= fragment_int)[[2]]
```

---

**stats\_df\_comb\_minimal** *The result of statistics for fragment\_int example data A data frame containing the output of statistics as a data frame*

---

**Description**

The result of statistics for fragment\_int example data A data frame containing the output of statistics as a data frame

**Usage**

```
data(stats_df_comb_minimal)
```

**Format**

A data frame with 500 rows and 26 variables:

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**intensity.cdt1:** The relative intensity at time point 0 for condition 1

**position\_segment:** The position based segment

**half\_life.cdt1:** The half-life of the bin/probe condition 1

**TI\_termination\_factor.cdt1:** The termination factor of the bin/probe condition 1

**HL\_fragment.cdt1:** The half-life fragment the bin belongs to condition 1

**intensity\_fragment.cdt1:** The intensity fragment the bin belongs to condition 1

**TI\_termination\_fragment.cdt1:** The TI fragment the bin belongs to condition 1

**logFC\_int:** The bin/probe log2 fold change of intensity at time 0

**P.Value:** The bin/probe p\_value adjusted

**intensity.cdt2:** The relative intensity at time point 0 condition 2

**half\_life.cdt2:** The half-life of the bin/probe condition 2

**TI\_termination\_factor.cdt2:** The termination factor of the bin/probe condition 2

**HL\_fragment.cdt2:** The half-life fragment the bin belongs to condition 2

**intensity\_fragment.cdt2:** The intensity fragment the bin belongs to condition 2

**TI\_termination\_fragment.cdt2:** The TI fragment the bin belongs to condition 2

**distance\_HL:** The bin/probe difference of half-life from both conditions

**distance\_int:** The bin/probe log2 fold change of intensity at time 0

**HL\_comb\_fragment:** The half-life fragment the bin belongs to both conditions

**HL\_mean\_comb\_fragment:** The half-life mean of the fragment the bin belongs to both conditions

**intensity\_comb\_fragment:** The intensity fragment the bin belongs to both conditions

**intensity\_mean\_comb\_fragment:** The intensity mean of the fragment the bin belongs to both conditions

**p\_value\_distance\_HL:** The p\_value adjusted of the half-life fragment the bin belongs to both conditions

**p\_value\_distance\_intensity:** The p\_value adjusted of the intensity fragment the bin belongs to both conditions

## Source

<https://github.com/CyanolabFreiburg/rifiComparative>

---

|               |                                                                                                                                                        |
|---------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|
| stats_se_cdt1 | <i>An example SummarizedExperiment from Synechosystis PCC 6803 first condition obtained from rifi_statistics and used as input for rifiComparative</i> |
|---------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

An example SummarizedExperiment from Synechosystis PCC 6803 first condition obtained from rifi\_statistics and used as input for rifiComparative

## Usage

```
data(stats_se_cdt1)
```

**Format**

A rowRanges of SummarizedExperiment with 500 rows and 50 variables:

**seqnames:** The sequence name chromosome  
**start:** The bin/probe start position  
**end:** The bin/probe end position  
**width:** The bin/probe length  
**strand:** The strand specific  
**position:** The bin/probe specific position  
**ID:** The bin/probe specific ID  
**FLT:** The bin/probe flag for background level  
**intensity:** The relative intensity at time point 0  
**probe\_TI:** An internal value to determine which fitting model is applied  
**flag:** Information on which fitting model is applied  
**position\_segment:** The position based segment  
**delay:** The delay value of the bin/probe  
**half\_life:** The half-life of the bin/probe  
**TI\_termination\_factor:** The termination factor of the bin/probe  
**delay\_fragment:** The delay fragment the bin belongs to  
**velocity\_fragment:** The velocity value of the respective delay fragment  
**intercept:** The vintercept of fit through the respective delay fragment  
**slope:** The slope of the fit through the respective delay fragment  
**HL\_fragment:** The half-life fragment the bin belongs to  
**HL\_mean\_fragment:** The mean half-life value of the respective half-life fragment  
**intensity\_fragment:** The intensity fragment the bin belongs to  
**intensity\_mean\_fragment:** The mean intensity value of the respective intensity fragment  
**TU:** The overarching transcription unit  
**TI\_termination\_fragment:** The TI fragment the bin belongs to  
**TI\_mean\_termination\_factor:** The mean termination factor of the respective TI fragment  
**seg\_ID:** The combined ID of the fragment  
**pausing\_site:** presence of pausing site indicated by +/-  
**iTSS\_I:** presence of iTSS\_I indicated by +/-  
**ps\_ts\_fragment:** The fragments involved in pausing site or iTSS\_I  
**event\_ps\_itss\_p\_value\_Ttest:** p\_value of pausing site or iTSS\_I#'  
**delay\_frg\_slope:** the slope value of the respective delay fragment  
**p\_value\_slope:** p\_value of the slope  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments  
**event\_duration:** Integer, the duration between two delay fragments

**event\_position:** Integer, the position middle between 2 fragments with an event

**FC\_HL:** Integer, the fold change value of 2 HL fragments

**FC\_fragment\_HL:** Integer, the fold change value of 2 intensity fragments

**p\_value\_HL:** p\_value of the fold change of HL fragments

**FC\_intensity:** Integer, the fold change value of 2 intensity fragments

**FC\_fragment\_intensity:** String, fragments involved in fold change between 2 intensity fragments

**p\_value\_intensity:** p\_value of the fold change of intensity fragments

**FC\_HL\_intensity:** ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_intensity\_fragment:** fragments involved on ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_adapted:** Integer, the fold change of half-life/ fold change of intensity, position of the half-life fragment is adapted to intensity fragment

**synthesis\_ratio:** Integer, the value corresponding to synthesis rate

**synthesis\_ratio\_event:** String, the event assigned by synthesis rate either Termination or iTSS

**p\_value\_Manova:** p\_value of the variance between two fold-changes, HL and intensity

**p\_value\_TI:** p\_value of TI fragment

**TI\_fragments\_p\_value:** p\_value of 2 TI fragments

## Source

<https://github.com/CyanolabFreiburg/rifiComparative>

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|               |                                                                                                                                                         |
|---------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| stats_se_cdt2 | <i>An example SummarizedExperiment from Synechosystis PCC 6803 second condition obtained from rifi_statistics and used as input for rifiComparative</i> |
|---------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|

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## Description

An example SummarizedExperiment from Synechosystis PCC 6803 second condition obtained from rifi\_statistics and used as input for rifiComparative

## Usage

```
data(stats_se_cdt2)
```

**Format**

A rowRanges of SummarizedExperiment with 500 rows and 50 variables:

**seqnames:** The sequence name chromosome

**start:** The bin/probe start position

**end:** The bin/probe end position

**width:** The bin/probe length

**strand:** The strand specific

**position:** The bin/probe specific position

**ID:** The bin/probe specific ID

**FLT:** The bin/probe flag for background level

**intensity:** The relative intensity at time point 0

**probe\_TI:** An internal value to determine which fitting model is applied

**flag:** Information on which fitting model is applied

**position\_segment:** The position based segment

**delay:** The delay value of the bin/probe

**half\_life:** The half-life of the bin/probe

**TI\_termination\_factor:** The termination factor of the bin/probe

**delay\_fragment:** The delay fragment the bin belongs to

**velocity\_fragment:** The velocity value of the respective delay fragment

**intercept:** The vintercept of fit through the respective delay fragment

**slope:** The slope of the fit through the respective delay fragment

**HL\_fragment:** The half-life fragment the bin belongs to

**HL\_mean\_fragment:** The mean half-life value of the respective half-life fragment

**intensity\_fragment:** The intensity fragment the bin belongs to

**intensity\_mean\_fragment:** The mean intensity value of the respective intensity fragment

**TU:** The overarching transcription unit

**TI\_termination\_fragment:** The TI fragment the bin belongs to

**TI\_mean\_termination\_factor:** The mean termination factor of the respective TI fragment

**seg\_ID:** The combined ID of the fragment

**pausing\_site:** presence of pausing site indicated by +/-

**iTSS\_I:** presence of iTSS\_I indicated by +/-

**ps\_ts\_fragment:** The fragments involved in pausing site or iTSS\_I

**event\_ps\_itss\_p\_value\_Ttest:** p\_value of pausing site or iTSS\_I

**p\_value\_slope:** p\_value of the slope

**delay\_frg\_slope:** the slope value of the respective delay fragment

**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments

**event\_duration:** Integer, the duration between two delay fragments

**event\_position:** Integer, the position middle between 2 fragments with an event

**FC\_HL:** Integer, the fold change value of 2 HL fragments

**FC\_fragment\_HL:** Integer, the fold change value of 2 intensity fragments

**p\_value\_HL:** p\_value of the fold change of HL fragments

**FC\_intensity:** Integer, the fold change value of 2 intensity fragments

**FC\_fragment\_intensity:** String, fragments involved in fold change between 2 intensity fragments

**p\_value\_intensity:** p\_value of the fold change of intensity fragments

**FC\_HL\_intensity:** ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_intensity\_fragment:** fragments involved on ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_adapted:** Integer, the fold change of half-life/ fold change of intensity, position of the half-life fragment is adapted to intensity fragment

**synthesis\_ratio:** Integer, the value corresponding to synthesis rate

**synthesis\_ratio\_event:** String, the event assigned by synthesis rate either Termination or iTSS

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#### Source

<https://github.com/CyanolabFreiburg/rifiComparative>

# Index

## \* datasets

- annot\_g, [4](#)
- data\_combined\_minimal, [5](#)
- df\_comb\_minimal, [7](#)
- df\_mean\_minimal, [8](#)
- differential\_expression, [9](#)
- fragment\_int, [12](#)
- inp\_f, [14](#)
- inp\_s, [16](#)
- pen\_HL, [24](#)
- pen\_int, [24](#)
- penalties\_df, [23](#)
- stats\_df\_comb\_minimal, [29](#)
- stats\_se\_cdt1, [30](#)
- stats\_se\_cdt2, [32](#)

- adjusting\_HLToInt, [2](#)
- annot\_g, [4](#)

- data\_combined\_minimal, [5](#)
- df\_comb\_minimal, [7](#)
- df\_mean\_minimal, [8](#)
- differential\_expression, [9](#)

- figures\_fun, [9](#)
- fragment\_int, [12](#)
- fragmentation, [11](#)

- gff3\_preprocess, [13](#)

- inp\_f, [14](#)
- inp\_s, [16](#)

- joining\_data\_column, [18](#)
- joining\_data\_row, [18](#)

- loading\_fun, [19](#)

- make\_pen, [20](#)

- pen\_HL, [24](#)

- pen\_int, [24](#)

- penalties, [22](#)
- penalties\_df, [23](#)

- rifi\_visualization\_comparison, [26](#)
- rifiComparative, [25](#)

- statistics, [28](#)
- stats\_df\_comb\_minimal, [29](#)
- stats\_se\_cdt1, [30](#)
- stats\_se\_cdt2, [32](#)