

# Package ‘rifi’

November 21, 2024

**Title** 'rifi' analyses data from rifampicin time series created by microarray or RNAseq

**Version** 1.10.0

**Description** 'rifi' analyses data from rifampicin time series created by microarray or RNAseq. 'rifi' is a transcriptome data analysis tool for the holistic identification of transcription and decay associated processes. The decay constants and the delay of the onset of decay is fitted for each probe/bin. Subsequently, probes/bins of equal properties are combined into segments by dynamic programming, independent of a existing genome annotation. This allows to detect transcript segments of different stability or transcriptional events within one annotated gene. In addition to the classic decay constant/half-life analysis, 'rifi' detects processing sites, transcription pausing sites, internal transcription start sites in operons, sites of partial transcription termination in operons, identifies areas of likely transcriptional interference by the collision mechanism and gives an estimate of the transcription velocity. All data are integrated to give an estimate of continuous transcriptional units, i.e. operons. Comprehensive output tables and visualizations of the full genome result and the individual fits for all probes/bins are produced.

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**Author** Loubna Youssar [aut, ctb],  
 Walja Wanney [aut, ctb],  
 Jens Georg [aut, cre]  
**Maintainer** Jens Georg <jens.georg@biologie.uni-freiburg.de>

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*apply\_ancova* %

**apply\_ancova**

*apply\_ancova checks the variances between 2 segments showing either pausing site (ps) or internal starting site (ITSS) independently.*

**Description**

*apply\_ancova* is a statistical test to check if fragments showing ps and ITSS events have significant slope using Ancova test. The function uses ancova test. Ancova is applied when the data contains independent variables, dependent variables and covariant variables. In this case, segments are independent variables, position is the dependent variable and the delay is the covariant.

**Usage**

*apply\_ancova*(inp)

**Arguments**

inp SummarizedExperiment: the input data frame with correct format.

**Value**

the SummarizedExperiment with the columns regarding statistics:

ID:	The bin/probe specific ID.
position:	The bin/probe specific position.
strand:	The bin/probe specific strand.
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:	String, the factor of TI fragment.
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_duration:	Integer, the duration between two delay fragments.
event_ps_itss_p_value_Ttest:	p_value of pausing site or iTSS_I.
p_value_slope:	Integer, the p_value added to the inp
delay_frg_slope:	Integer, the slope value of the fit through the respective delay fragment
velocity_ratio:	Integer, the ratio value of velocity from 2 delay fragments

**Examples**

```
data(stats_minimal)
apply_ancova(inp = stats_minimal)
```

---

```
apply_event_position %
```

```
=====
```

**apply\_event\_position**

*apply\_event\_position extracts event time duration for pausing site or iTSS*

---

**Description**

apply\_event\_position is a short version of apply\_Ttest\_delay function to extract event time duration for pausing site or iTSS. Its adds a new column with the duration.

**Usage**

```
apply_event_position(inp)
```

**Arguments**

inp                    SummarizedExperiment: the input data frame with correct format.

**Value**

The SummarizedExperiment with the columns regarding statistics:

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

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

**strand:** The bin/probe specific strand.

**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:** String, the factor of TI fragment.

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

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

**p\_value\_slope:** Integer, the p\_value added to the inp.

**delay\_frg\_slope:** Integer, the slope value of the fit through the respective delay fragment.

**velocity\_ratio:** Integer, the ratio value of velocity from 2 delay fragments.

**event\_position:** Integer, position of the event added to the input.

### Examples

```
data(stats_minimal)
apply_event_position(inp = stats_minimal)
```

---

```
apply_manova %
```

---

#### **apply\_manova**

*apply\_manova checks if the ratio of hl ratio and intensity ratio is statistically significant.*

---

### Description

apply\_manova compares the variance between two fold-changes HL and intensity within the same TU (half-life frgA/half-life frgB/intensity frgA/intensity frgB). HL fragment could cover two intensity fragments therefore this function sets first fragments borders and uses manova\_function. Manova checks the variance between 2 segments (independent variables) and two dependents variables (HL and intensity).

### Usage

```
apply_manova(inp)
```

### Arguments

inp SummarizedExperiment: the input data frame with correct format.

**Value**

The probe data frame with the columns regarding statistics:

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

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

**strand:** The bin/probe specific strand.

**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:** String, the factor of TI fragment.

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

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

**p\_value\_slope:** Integer, the p\_value added to the inp.

**delay\_frg\_slope:** Integer, the slope value of the fit through the respective delay fragment.

**velocity\_ratio:** Integer, the ratio value of velocity from 2 delay fragments.

**event\_position:** Integer, position of the event added to the input.

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

**FC\_fragment\_HL:** String, the fragments corresponding to HL fold change.

**p\_value\_HL:** Integer, the p\_value added to the input of 2 HL fragments.

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

**FC\_fragment\_intensity:** String, the fragments corresponding to intensity fold change.

**p\_value\_intensity:** Integer, the p\_value added to the input of 2 intensity fragments.

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

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

**FC\_HL\_intensity:** Integer, the value corresponding to HL and intensity fold change.

**FC\_HL\_intensity\_fragment:** String, the fragments corresponding to intensity and HL fold change.

**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.

**p\_value\_Manova:** Integer, the p\_value added to the input.

### Examples

```
data(stats_minimal)
apply_manova(inp = stats_minimal)
```

---

```
apply_Ttest_delay      %
```

---

#### **apply\_Ttest\_delay**

*apply\_Ttest\_delay checks the significance of the point between 2 segments showing pausing site (ps) and internal starting site (ITSS) independently*

---

### Description

apply\_Ttest\_delay: is a statistical test to check the significance of the point between 2 segments showing pausing site (ps) and internal starting site (ITSS) independently. The function uses t-test. The last point from the first segment and the first point from the second segment are selected and added to the residuals of each model. The sum is subjected to t-test.

### Usage

```
apply_Ttest_delay(inp)
```

### Arguments

inp                    SummarizedExperiment: the input data frame with correct format.

### Value

the SummarizedExperiment with the columns regarding statistics:

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

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

**strand:** The bin/probe specific strand.

**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:** String, the factor of TI fragment.  
**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\_duration:** Integer, the duration between two delay fragments.  
**event\_ps\_itss\_p\_value\_Ttest:** p\_value of pausing site or iTSS\_I.

## Examples

```
data(stats_minimal)
apply_Ttest_delay(inp = stats_minimal)
```

---

```
apply_t_test          %
```

---

### **apply\_t\_test**

*apply\_t\_test uses the statistical t\_test to check if the fold-change of half -life (HL) fragments and the fold-change intensity fragments respectively are significant.*

---

## Description

apply\_t\_test compares the mean of two neighboring fragments within the same TU to check if the fold-change is significant. Fragments with distance above threshold are not subjected to t-test. Dataframes with less than 3 rows are excluded.

## Usage

```
apply_t_test(inp, threshold = 300)
```

**Arguments**

`inp` SummarizedExperiment: the input data frame with correct format.  
`threshold` integer: threshold.

**Details**

The functions used are:

1. `fragment_function`: checks number of fragments inside TU, less than 2 are excluded otherwise they are gathered for analysis.
2. `t_test_function`: excludes dataframes with less than 3 rows, makes fold-change and apply t-test, assign fragments names and ratio, add columns with the corresponding `p_values`.

**Value**

the SummarizedExperiment with the columns regarding statistics:

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

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

**strand:** The bin/probe specific strand.

**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:** String, the factor of TI fragment.

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

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

- p\_value\_slope:** Integer, the p\_value added to the inp.
- delay\_frg\_slope:** Integer, the slope value of the fit through the respective delay fragment.
- velocity\_ratio:** Integer, the ratio value of velocity from 2 delay fragments.
- event\_position:** Integer, position of the event added to the input.
- FC\_HL:** Integer, the fold change value of 2 HL fragments.
- FC\_fragment\_HL:** String, the fragments corresponding to HL fold change.
- p\_value\_HL:** Integer, the p\_value added to the input of 2 HL fragments.
- FC\_intensity:** Integer, the fold change value of 2 intensity fragments.
- FC\_fragment\_intensity:** String, the fragments corresponding to intensity fold change.
- p\_value\_intensity:** Integer, the p\_value added to the input of 2 intensity fragments.

**Examples**

```
data(stats_minimal)
apply_t_test(inp = stats_minimal, threshold = 300)
```

---

apply\_t\_test\_ti            %

=====

**apply\_t\_test\_ti**

*apply\_t\_test\_ti compares the mean of two neighboring TI fragments within the same TU.*

---

**Description**

apply\_t\_test\_ti uses the statistical t\_test to check if two neighboring TI fragments are significant.

**Usage**

```
apply_t_test_ti(inp)
```

**Arguments**

inp                      SummarizedExperiment: the input data frame with correct format.

**Value**

the SummarizedExperiment with the columns regarding statistics:

- ID:** The bin/probe specific ID.
- position:** The bin/probe specific position.
- strand:** The bin/probe specific strand.
- 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:** String, the factor of TI fragment.

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

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

**p\_value\_slope:** Integer, the p\_value added to the inp.

**delay\_frg\_slope:** Integer, the slope value of the fit through the respective delay fragment.

**velocity\_ratio:** Integer, the ratio value of velocity from 2 delay fragments.

**event\_position:** Integer, position of the event added to the input.

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

**FC\_fragment\_HL:** String, the fragments corresponding to HL fold change.

**p\_value\_HL:** Integer, the p\_value added to the input of 2 HL fragments.

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

**FC\_fragment\_intensity:** String, the fragments corresponding to intensity fold change.

**p\_value\_intensity:** Integer, the p\_value added to the input of 2 intensity fragments.

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

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

**FC\_HL\_intensity:** Integer, the value corresponding to HL and intensity fold change.

**FC\_HL\_intensity\_fragment:** String, the fragments corresponding to intensity and HL fold change.

**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.

**p\_value\_Manova:** Integer, the p\_value added to the input.

**p\_value\_TI:** Integer, the p\_value added to the input.

**TI\_fragments\_p\_value:** String, the fragments subjected to statistical test.

### Examples

```
data(stats_minimal)
apply_t_test_ti(inp = stats_minimal)
```

---

```
check_input          %
```

```
=====
```

### Check\_input

*Check\_input reviews the input given by the user*

---

#### Description

check\_input stops the operation if the input data frame has severe faults. Less severe faults lead to the removal of wrong IDs and a warnings describing the problem. The Summarized Experiment colData must have the columns "timepoint" with the timepoints convertible to numeric and containing the timepoint 0. If replicates are used the column in colData must be called "replicate". The replicate must be convertible to numeric. In the RowRanges, optionally, IDs can be given as character (except ",", "|", "\_"), but need to refer to a unique position/strand combination. Strand information needs to be given. The relative intensity in the assay must be numeric. The relative intensity for the first time point cannot be 0 or NA.

#### Usage

```
check_input(inp, thrsh = 0)
```

#### Arguments

```
inp                SummarizedExperiment: the input data frame with correct format.
thrsh              numeric: the minimal allowed intensity for time point "0".
```

#### Value

the SummarizedExperiment object: checked, and with position, ID and filtration added to the rowRanges.

#### Examples

```
data(example_input_minimal)
check_input(inp = example_input_minimal, thrsh = 0)
```

---

```
dataframe_summary   %
```

```
=====
```

### dataframe\_summary

*dataframe\_summary creates two tables relating gene annotation to fragments*

---

## Description

dataframe\_summary creates two tables summary of segments and their half-lives. The first output is bin/probe features and the second one is intensity fragment based. The dataframe\_summary creates one table with feature\_type, gene, locus\_tag, position, strand, TU, delay\_fragment, HL\_fragment, half\_life, intensity\_fragment, intensity and velocity. The second table is similar to the first one but in compact form. It contains the same columns, the only difference is on position where a start and end position are indicated separately.

## Usage

```
dataframe_summary(data, input)
```

## Arguments

data	SummarizedExperiment: the input data frame with correct format.
input	dataframe: dataframe from event_dataframe function.

## Value

bin_df:	<p>all information regarding bins:</p> <p><b>position:</b> Integer, position of the bin/probe on the genome</p> <p><b>feature_type:</b> String, region annotation covering the fragments</p> <p><b>gene:</b> String, gene annotation covering the fragments</p> <p><b>locus_tag:</b> String, locus_tag annotation covering the fragments</p> <p><b>strand:</b> Boolean. The bin/probe specific strand (+/-)</p> <p><b>segment:</b> String, the bin/probe segment on the genome</p> <p><b>TU:</b> String, The overarching transcription unit</p> <p><b>delay_fragment:</b> The delay fragment the bin belongs to</p> <p><b>delay:</b> Integer, the delay value of the bin/probe</p> <p><b>HL_fragment:</b> The half-life fragment the bin belongs to</p> <p><b>half_life:</b> The half-life of the bin/probe</p> <p><b>intensity_fragment:</b> The intensity fragment the bin belongs to</p> <p><b>intensity:</b> The relative intensity at time point 0</p> <p><b>flag:</b> String, the flag of the bin/probe, contains information or the distribution for the # different fitting models</p> <p><b>TI_termination_factor:</b> String, the TI termination factor determined by TI</p>
frag_df:	<p>all information regarding fragments:</p> <p><b>feature_type:</b> String, region annotation covering the fragments</p> <p><b>gene:</b> String, gene annotation covering the fragments</p> <p><b>locus_tag:</b> String, locus_tag annotation covering the fragments</p> <p><b>first_position_frg:</b> Integer, the bin/probe specific first position</p> <p><b>last_position_frg:</b> Integer, the bin/probe specific last position</p> <p><b>strand:</b> Boolean. The bin/probe specific strand (+/-)</p> <p><b>TU:</b> String, The overarching transcription unit</p> <p><b>segment:</b> String, the bin/probe segment on the genome</p> <p><b>delay_fragment:</b> String, the delay fragment the bin belongs to</p> <p><b>HL_fragment:</b> Integer, the half_life fragment of the bin/probe belongs to</p> <p><b>half_life:</b> Integer, the half-life of the bin/probe</p>

**HL\_SD:** Integer, the half-life standard deviation of the HL fragment, bin/probe based

**HL\_SE:** Integer, the half-life standard error of the HL fragment, bin/probe based

**intensity\_fragment:** Integer, the intensity fragment the bin belongs to

**intensity:** Integer, the relative intensity of bin/probe at time point 0

**intensity\_SD:** Integer, the intensity standard deviation of the intensity fragment, bin/probe based

**intensity\_SE:** Integer, the intensity standard error of the intensity fragment, bin/probe based

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

### Examples

```
data(stats_minimal)
data(res_minimal)
dataframe_summary(data = stats_minimal, input = res_minimal)
```

---

```
dataframe_summary_events
%
```

---

#### dataframe\_summary\_events

*dataframe\_summary\_events creates one table with all events between the segments*

---

### Description

dataframe\_summary\_events creates one table with the following columns: event, features, p\_value, event\_position, event\_duration, position, region, gene, locus\_tag, strand, TU, segment\_1, segment\_2, length, velocity\_ratio, FC\_HL, FC\_intensity, FC\_HL/FC\_intensity.

### Usage

```
dataframe_summary_events(data, data_annotation)
```

### Arguments

**data** SummarizedExperiment: the input data frame with correct format.  
**data\_annotation** dataframe: dataframe from processed gff3 file.

### Value

**event:** String, event type either pausing site, iTSS\_I, iTSS\_II, Termination, HL\_event, Int\_event, HL\_Int\_event and velocity\_change

**p\_value:** Integer, p\_value of the event

**p\_adjusted:** Integer, p\_value adjusted

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

**FC\_intensity:** Integer, the fold change value of 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:** Fold change of half-life/ fold change of intensity

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

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

**feature\_type:** 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 (+/-)

**TU:** String, The overarching transcription unit

**segment\_1:** String, the first segment of the event, includes the segment, TU, delay fragment in case of ps or iTSS\_I. The rest of the events include HL fragment and intensity fragment

**segment\_2:** String, same description as segment\_1 but is the second fragment of the event

**event\_duration:** Integer, the difference (min) between 2 delay fragment when ps or iTSS\_I happen

**gap\_fragments:** Integer, length in position (nt), calculated by the difference between the last position of the first fragment and the first position of the second fragment.

**features:** Integer, number of fragments involved on the event

### Examples

```
if(!require(SummarizedExperiment)){
  suppressPackageStartupMessages(library(SummarizedExperiment))
}
data(stats_minimal)
dataframe_summary_events(data = stats_minimal,
  data_annotation = metadata(stats_minimal)$annot[[1]])
```

---

```
dataframe_summary_events_HL_int
%
```

---

### **dataframe\_summary\_events\_HL\_int**

*dataframe\_summary\_events\_HL\_int creates one table with all events between the segments*

---

### Description

The dataframe\_summary\_events\_HL\_int creates one table with the following columns: event, features, p\_value, event\_position, position, region, gene, locus\_tag, strand, TU, segment\_1, segment\_2, length, FC\_HL, FC\_intensity, FC\_HL/FC\_intensity.



**Usage**

```
dataframe_summary_events_HL_int(data, data_annotation)
```

**Arguments**

**data** SummarizedExperiment: the input data frame with correct format.  
**data\_annotation** dataframe: dataframe from processed gff3 file.

**Value**

**event:** String, event type.  
**p\_value:** Integer, p\_value of the event.  
**p\_adjusted:** Integer, p\_value adjusted.  
**FC\_HL:** Integer, the fold change value of 2 HL fragments.  
**FC\_intensity:** Integer, the fold change value of 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.  
**FC\_HL\_FC\_intensity:** Fold change of half-life/ fold change of intensity.  
**feature\_type:** 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 (+/-).  
**TU:** String, The overarching transcription unit.  
**segment\_1:** String, the first segment of the event, includes the segment, TU, delay fragment in case of ps or iTSS\_I. The rest of the events include HL fragment and could be extended intensity fragment.  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis.  
**event\_duration:** Integer, the difference (min) between 2 delay fragment when ps or iTSS\_I happen.  
**gap\_fragments:** Integer, length in position (nt), calculated by the difference between the last position of the first fragment and the first position of the second fragment.  
**features:** Integer, number of fragments involved on the event

**Examples**

```
if(!require(SummarizedExperiment)){
  suppressPackageStartupMessages(library(SummarizedExperiment))
}
data(stats_minimal)
dataframe_summary_events_HL_int(data = stats_minimal,
data_annotation = metadata(stats_minimal)$annot[[1]])
```

---

```
dataframe_summary_events_ps_itss
%
```

```
=====
dataframe_summary_events_ps_itss
```

```
dataframe_summary_events_ps_itss creates one table with all
events between the segments.
```

---

### Description

The `dataframe_summary_events_ps_itss` creates one table with the following columns: `event`, `features`, `p_value`, `event_position`, `event_duration`, `position`, `region`, `gene`, `locus_tag`, `strand`, `TU`, `segment_1`, `segment_2`, `length`, `velocity_ratio`.

### Usage

```
dataframe_summary_events_ps_itss(data, data_annotation)
```

### Arguments

```
data          SummarizedExperiment: the input data frame with correct format.
data_annotation
              dataframe: dataframe from processed gff3 file.
```

### Value

**event:** String, event type.

**p\_value:** Integer, p\_value of the event.

**p\_adjusted:** Integer, p\_value adjusted.

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

**velocity\_ratio:** Integer, the ratio value of velocity from 2 delay fragments.

**feature\_type:** 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 (+/-).

**TU:** String, The overarching transcription unit.

**segment\_1:** String, the first segment of the event, includes the segment, TU, delay fragment in case of ps or iTSS\_I. The rest of the events include HL fragment and could be extended intensity fragment.

**segment\_2:** String, the second fragment of the two of fragments subjected to analysis.

**event\_duration:** Integer, the difference (min) between 2 delay fragment when ps or iTSS\_I happen.

**gap\_fragments:** Integer, length in position (nt), calculated by the difference between the last position of the first fragment and the first position of the second fragment.

**features:** Integer, number of fragments involved on the event

**Examples**

```

data(stats_minimal)
if(!require(SummarizedExperiment)){
  suppressPackageStartupMessages(library(SummarizedExperiment))
}
dataframe_summary_events_ps_itss(data = stats_minimal,
  data_annotation = metadata(stats_minimal)$annot[[1]])

```

---

```

dataframe_summary_events_velocity
%
```

```

=====
dataframe_summary_events_velocity
```

```

dataframe_summary_events_velocity creates one table with all
events between the segments.
```

---

**Description**

The `dataframe_summary_events_velocity` creates one table with the following columns: `event`, `features`, `p_value`, `event_position`, `event_duration`, `position`, `region`, `gene`, `locus_tag`, `strand`, `TU`, `segment_1`, `segment_2`, `length`, `velocity_ratio`.

**Usage**

```
dataframe_summary_events_velocity(data, data_annotation)
```

**Arguments**

`data` SummarizedExperiment: the input data frame with correct format.  
`data_annotation` dataframe: dataframe from processed gff3 file.

**Value**

**event:** String, event type.  
**p\_value:** Integer, p\_value of the event.  
**p\_adjusted:** Integer, p\_value adjusted.  
**event\_position:** Integer, the position of event, calculated dividing the last position of the first fragment and the first position of the next fragment on 2.  
**velocity\_ratio:** Integer, the ratio value of velocity from 2 delay fragments  
**feature\_type:** 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 (+/-).  
**TU:** String, The overarching transcription unit.

**segment\_1:** String, the first segment of the event, includes the segment, TU, delay fragment in case of ps or iTSS\_I. The rest of the events include HL fragment and could be extended intensity fragment.

**segment\_2:** String, the second fragment of the two of fragments subjected to analysis

**event\_duration:** Integer, the difference (min) between 2 delay fragment when ps or iTSS\_I happen.

**gap\_fragments:** Integer, length in position (nt), calculated by the difference between the last position of the first fragment and the first position of the second fragment.

**features:** Integer, number of fragments involved on the event.

## Examples

```
if(!require(SummarizedExperiment)){
  suppressPackageStartupMessages(library(SummarizedExperiment))
}
data(stats_minimal)
dataframe_summary_events_velocity(data = stats_minimal,
  data_annotation = metadata(stats_minimal)$annot[[1]])
```

---

```
dataframe_summary_TI %
```

---

### **dataframe\_summary\_TI**

*dataframe\_summary\_TI creates one table with all TI fragments, p\_value and the coordinates*

---

## Description

The dataframe\_summary creates one table with the following columns: event, TI\_fragment, TI\_factor, TI\_fragments\_TU, p\_value, feature\_type, gene, locus\_tag, strand, TU, features, event\_position, position\_1 and position\_2.

## Usage

```
dataframe_summary_TI(data, input)
```

## Arguments

data	SummarizedExperiment: the input data frame with correct format.
input	dataframe: dataframe from event_dataframe function.

## Value

**event:** String, event type, transcription interference.

**TI\_fragment:** String, the fragment with TI.

**TI\_termination\_factor:** String, the factor of TI fragment.

**p\_value:** Integer, p\_value of the event.

**p\_adjusted:** Integer, p\_value adjusted.

**feature\_type:** 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 (+/-).

**TU:** String, The overarching transcription unit.

**Features:** Integer, The number of segments within the TI.

**event\_position:** Integer, the position middle between 2 TI fragments.

**position\_1:** String, the first position of TI fragment, if 2 fragments, first position is from the first fragment.

**position\_2:** String, the last position of TI fragment, if 2 fragments, last position is from the second fragment.

WIP

## Examples

```
data(stats_minimal)
data(res_minimal)
dataframe_summary_TI(data = stats_minimal, input = res_minimal)
```

---

```
event_dataframe      %
```

```
=====
event_dataframe
```

```
event_dataframe creates a dataframe only with events
```

---

## Description

event\_dataframe creates a dataframe connecting segments, events and the annotation.

## Usage

```
event_dataframe(data, data_annotation)
```

## Arguments

data                    dataframe: the probe based data frame.

data\_annotation        dataframe: the coordinates are extracted from gff3

## Details

The functions used are:

`position_function`: adds the specific position of ps or iTSS event.

`annotation_function_event`: adds the events to the annotated genes.

annotation file needs to be supplied. Strand is indicated in case of stranded data The `event_dataframe` selects columns with statistical features. ID, position, strand and TU columns are required.

## Value

A dataframe with unique intensity fragments

**feature\_type**: 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 (+/-)

**TU**: String, The overarching transcription unit

**position**: Integer, position of the bin/probe on the genome

**segment**: String, the bin/probe segment on the genome

**FC\_fragment\_intensity**: String, the fragments subjected to fold change

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

**p\_value\_intensity**: Integer, p\_value of the FC\_intensity

**FC\_fragment\_HL**: String, the fragments subjected to fold change

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

**p\_value\_HL**: Integer, p\_value of the FC\_HL

**FC\_HL\_FC\_intensity\_fragment**: String, fragments subjected to FC\_HL/FC\_intensity

**FC\_HL\_FC\_intensity**: Integer, the value of FC\_HL/FC\_intensity

**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

**p\_value\_manova**: Integer, p\_value of the event FC\_HL/FC\_intensity

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

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

**pausing\_site**: Boolean, presence or absence of pausing\_site event (ps)

**iTSS\_I**: Boolean, presence or absence of internal starting site event (iTSS\_I)

**ps\_ts\_fragment**: String, fragments involved on the event ps or iTSS\_I

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

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

**delay**: Integer, the delay value of the bin/probe

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

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

**delay\_frg\_slope**: Integer, the slope value of the fit through the respective delay fragment

**p\_value\_slope**: Integer, the p\_value added to the inp

## Examples

```
if(!require(SummarizedExperiment)){
  suppressPackageStartupMessages(library(SummarizedExperiment))
}
data(stats_minimal)
event_dataframe(data = stats_minimal,
  data_annotation = metadata(stats_minimal)$annot[[1]])
```

---

example\_input\_e\_coli *An example SummarizedExperiment from E. coli An example SummarizedExperiment from RNA-seq containing information about the intensities at all time points (assay). Seqnames, IRanges and strand columns (rowRanges)and colData with time point series and replicates.*

---

## Description

An example SummarizedExperiment from E. coli An example SummarizedExperiment from RNA-seq containing information about the intensities at all time points (assay). Seqnames, IRanges and strand columns (rowRanges)and colData with time point series and replicates.

## Usage

```
data(example_input_e_coli)
```

## Format

A assay:

- 0:** relative intensities at 0 min
- 1:** relative intensities at 1 min
- 10:** relative intensities at 10 min
- 15:** relative intensities at 15 min
- 2:** relative intensities at 2 min
- 20:** relative intensities at 20 min
- 3:** relative intensities at 3 min
- 4:** relative intensities at 4 min
- 5:** relative intensities at 5 min
- 6:** relative intensities at 6 min
- 8:** relative intensities at 8 min

## Source

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

---

`example_input_minimal` *An artificial example SummarizedExperiment An example SummarizedExperiment containing information about the intensities at all time points (assay). Seqnames, IRanges and strand columns (rowRanges) and colData with time point series and replicates.*

---

### Description

An artificial example SummarizedExperiment An example SummarizedExperiment containing information about the intensities at all time points (assay). Seqnames, IRanges and strand columns (rowRanges) and colData with time point series and replicates.

### Usage

```
data(example_input_minimal)
```

### Format

An object of class RangedSummarizedExperiment with 4 rows and 33 columns.

### Source

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

---

`example_input_synechocystis_6803` *An example input data frame from Synechocystis PCC 6803 A SummarizedExperiment from microarrays data containing information about the intensities at all time points (assay), Seqnames, IRanges and strand columns (rowRanges) and colData with time point series and averaged replicates.*

---

### Description

An example input data frame from Synechocystis PCC 6803 A SummarizedExperiment from microarrays data containing information about the intensities at all time points (assay), Seqnames, IRanges and strand columns (rowRanges) and colData with time point series and averaged replicates.

### Usage

```
data(example_input_synechocystis_6803)
```



**Format**

Assay with 3000 rows and 10 variables:

- 0:** relative intensities at 0 min
- 2:** relative intensities at 2 min
- 4:** relative intensities at 4 min
- 8:** relative intensities at 8 min
- 16:** relative intensities at 16 min
- 32:** relative intensities at 32 min
- 64:** relative intensities at 64 min

**Source**

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

---

finding\_PDD                    %

=====

**finding\_PDD**

*finding\_PDD* Flags potential candidates for post transcription decay

---

**Description**

'finding\_PDD' uses 'score\_fun\_linear\_PDD' to make groups by the difference to the slope. The slope is further checked for steepness to decide for PDD. 'PDD' is added to the 'flag' column. Post transcription decay is characterized by a strong decrease of intensity by position. The rowRanges need to contain at least 'ID', 'intensity', 'position' and 'position\_segment'!

**Usage**

```
finding_PDD(inp, cores = 1, pen = 2, pen_out = 1, thrsh = 0.001)
```

**Arguments**

- |         |  |
|---------|--|
| inp     | SummarizedExperiment: the input.   |
| cores   | integer: the number of assigned cores for the task   |
| pen     | numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Advised to be kept at 2. Default is 2.  |
| pen_out | numeric: an internal parameter for the dynamic programming. Higher values result in fewer possible outliers. Advised to be kept at 1. Default is 1.  |
| thrsh   | numeric: an internal parameter that allows fragments with slopes steeper than the thrsh to be flagged with 'PDD'. Higher values result in fewer candidates. Advised to be kept at 0.001. Default is 0.001. |

**Value**

The SummarizedExperiment object: with "PDD" added to the flag column.

**Examples**

```
data(preprocess_minimal)
finding_PDD(inp = preprocess_minimal, cores = 2, pen = 2,
pen_out = 1, thrsh = 0.001)
```

---

finding_TI	%
------------	---

---

**finding\_TI**

*finding\_TI flags potential candidates for transcription interference*

---

**Description**

finding\_TI uses 'score\_fun\_ave' to make groups by the mean of "probe\_TI". "TI" is added to the "flag" column. TI is characterized by relative intensities at time points later than "0". The rowRanges need to contain at least "ID", "probe\_TI" and "position\_segment"!

**Usage**

```
finding_TI(inp, cores, pen = 10, thrsh = 0.5, add = 1000)
```

**Arguments**

inp	SummarizedExperiment: the input.
cores	integer: the number of assigned cores for the task
pen	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Advised to be kept at 10. Default is 10.
thrsh	numeric: an internal parameter that allows fragments with a certain amount of IDs with higher relative intensities at time points later than "0" to be flagged as "TI". Higher values result in fewer candidates. -0.5 is 25 %, 0 is 50%, 0.5 is 75%. Advised to be kept at 0.5. Default is 0.5.
add	integer: range of nucleotides before and after a potential TI event wherein IDs are fitted with the TI fit.

**Value**

The SummarizedExperiment object: with "TI" added to the flag column.

**Examples**

```
data(preprocess_minimal)
finding_TI(inp = preprocess_minimal, cores = 2, pen = 10, thrsh = 0.5,
add = 1000)
```

---

fit_e_coli	<i>The result of rifi_fit for E.coli example data A SummarizedExperiment containing the output from rifi_fit as an extension of rowRanges and metadata.</i>
------------	---

---

## Description

The result of rifi\_fit for E.coli example data A SummarizedExperiment containing the output from rifi\_fit as an extension of rowRanges and metadata.

## Usage

```
data(fit_e_coli)
```

## Format

Three data frames with 290 rows and 10 variables, 155 rows and 5 variables, and 135 rows and 9 variables are generated. The columns of the first data frame are added to the rowRanges and the rest are added as metadata.

**inp:** The SummarizedExperiment:

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

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

**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

**postion\_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:** String, the factor of TI fragment

**fit\_obj\_STD:** the fit object for the standard fit:

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

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

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

**inty\_S0:** The relative intensity at time point 0

**intyf:** The background value of the fit

**fit\_obj\_TI:** the fit object for the TI fit:

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

**ti\_delay:** The ti-delay value of the bin/probe

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

**ti\_value:** The ti-value of the bin/probe

**TI\_termination\_factor:** String, the factor of TI fragment

**synthesis\_rate:** The synthesis rate of the bin/probe

**TI\_background:** The background value of the fit

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

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

**Source**

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

---

fit_minimal	<i>The artificial result of rifi_fit for artificial example data A SummarizedExperiment containing the output from rifi_fit.</i>
-------------	--

---

**Description**

The artificial result of rifi\_fit for artificial example data A SummarizedExperiment containing the output from rifi\_fit.

**Usage**

```
data(fit_minimal)
```

**Format**

An object of class RangedSummarizedExperiment with 4 rows and 33 columns.

**Source**

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

---

fit_synechocystis_6803	<i>The result of rifi_fit for Synechocystis 6803 example data A SummarizedExperiment containing the output from rifi_fit as an extension of rowRanges and metadata.</i>
------------------------	---

---

**Description**

The result of rifi\_fit for Synechocystis 6803 example data A SummarizedExperiment containing the output from rifi\_fit as an extension of rowRanges and metadata.

**Usage**

```
data(fit_synechocystis_6803)
```

**Format**

Three data frames with 3000 rows and 10 variables, 2811 rows and 5 variables, and 189 rows and 9 variable are generated. The columns of the first data frame are added to the rowRanges and the rest are added as metadata.

**inp:** the SummarizedExperiment:

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

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

**strand:** The bin/probe specific strand

**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  
**postion\_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:** String, the factor of TI fragment  
**fit\_obj\_STD:** the fit object for the standard fit:  
**ID:** The bin/probe specific ID  
**delay:** The delay value of the bin/probe  
**half\_life:** The half-life of the bin/probe  
**inty\_S0:** The relative intensity at time point 0  
**intyf:** The background value of the fit  
**fit\_obj\_TI:** the fit object for the TI fit:  
**delay:** The delay value of the bin/probe  
**ti\_delay:** The ti-delay value of the bin/probe  
**half\_life:** The half-life of the bin/probe  
**ti\_value:** The ti-value of the bin/probe  
**TI\_termination\_factor:** String, the factor of TI fragment  
**synthesis\_rate:** The synthesis rate of the bin/probe  
**TI\_background:** The background value of the fit  
**position:** The bin/probe specific position  
**ID:** The bin/probe specific ID

### Source

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

---

fold_change	%
-------------	---

---

### fold\_change

*fold\_change sets a fold-change ratio between the neighboring fragments of Half-life (HL) and intensity*

---

### Description

fold\_change sets fold change on intensity and fold change HL fragments of two successive fragments. Two intensity fragments could belong to one HL fragment. This function sets first the borders using the position and applies the fold change ratio between the neighboring fragments of HL and those from intensity  $\log_2(\text{intensity frgA}/\text{intensity frgB}/\text{half-life frgA}/\text{half-life frgB})$ . All grapped fragments are from the same TU excluding outliers.

### Usage

fold\_change(inp)

## Arguments

**inp** SummarizedExperiment: the input data frame with correct format.

## Details

The function used is: `synthesis_r_Function`: assigns events depending on the ratio between HL and intensity of two consecutive fragments.  $\text{intensity}(\text{int}) = \text{synthesis rate}(k)/\text{decay}(\text{deg})$  (steady state),  $\text{int1}/\text{int2} = k1/\text{deg1} * \text{deg2}/k2 \text{ int1} * (\text{deg1}/\text{int2}) * \text{deg2} = k1/k2 \Rightarrow$  synthesis ratio. In case of synthesis ratio is: synthesis ratio  $> 0 \rightarrow$  New start synthesis ratio  $< 0 \rightarrow$  Termination

## Value

the SummarizedExperiment with the columns regarding statistics:

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

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

**strand:** The bin/probe specific strand.

**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:** String, the factor of TI fragment.

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

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

**p\_value\_slope:** Integer, the p\_value added to the inp.

**delay\_frg\_slope:** Integer, the slope value of the fit through the respective delay fragment.

**velocity\_ratio:** Integer, the ratio value of velocity from 2 delay fragments.

**event\_position:** Integer, position of the event added to the input.

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

**FC\_fragment\_HL:** String, the fragments corresponding to HL fold change.

**p\_value\_HL:** Integer, the p\_value added to the input of 2 HL fragments.

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

**FC\_fragment\_intensity:** String, the fragments corresponding to intensity fold change.

**p\_value\_intensity:** Integer, the p\_value added to the input of 2 intensity fragments.

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

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

**FC\_HL\_intensity:** Integer, the value corresponding to HL and intensity fold change.

**FC\_HL\_intensity\_fragment:** String, the fragments corresponding to intensity and HL fold change.

**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.

### Examples

```
data(stats_minimal)
fold_change(inp = stats_minimal)
```

---

fragmentation_e_coli	<i>The result of rfi_fragmentation for E.coli example data A SummarizedExperiment containing the output from rfi_fragmentation as an extension of rowRanges</i>
----------------------	---

---

### Description

The result of rfi\_fragmentation for E.coli example data A SummarizedExperiment containing the output from rfi\_fragmentation as an extension of rowRanges

### Usage

```
data(fragmentation_e_coli)
```

### Format

rowRanges of the SummarizedExperiment with 290 rows and 22 variables:

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

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

**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:** String, the factor of TI fragment  
**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

### Source

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

---

fragmentation\_minimal *The result of rifi\_fragmentation for artificial example data A SummarizedExperiment containing the output from rifi\_fragmentation as an extension of rowRanges and metadata.*

---

### Description

The result of rifi\_fragmentation for artificial example data A SummarizedExperiment containing the output from rifi\_fragmentation as an extension of rowRanges and metadata.

### Usage

```
data(fragmentation_minimal)
```

### Format

An object of class RangedSummarizedExperiment with 24 rows and 33 columns.

### Source

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



---

fragmentation\_synechocystis\_6803

*The result of rifi\_fragmentation for Synechocystis 6803 example data A SummarizedExperiment containing the output from rifi\_fragmentation as an extension fo rowRanges*

---

## Description

The result of rifi\_fragmentation for Synechocystis 6803 example data A SummarizedExperiment containing the output from rifi\_fragmentation as an extension fo rowRanges

## Usage

```
data(fragmentation_synechocystis_6803)
```

## Format

rowRanges of the SummarizedExperiment:

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

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

**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:** String, the factor of TI fragment

**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

## Source

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

---

fragment_delay	%
----------------	---

---

### **fragment\_delay**

*fragment\_delay performs the delay fragmentation*

---

#### **Description**

fragment\_delay makes delay\_fragments based on position\_segments and assigns all gathered information to the SummarizedExperiment object. The columns "delay\_fragment", "velocity\_fragment", "intercept" and "slope" are added. fragment\_delay makes delay\_fragments, assigns slopes, which are 1/velocity at the same time, and intercepts for the TU calculation. The function used is: score\_fun\_linear the input is the SummarizedExperiment object. pen is the penalty for new fragments in the dynamic programming, pen\_out is the outlier penalty.

#### **Usage**

```
fragment_delay(inp, cores = 1, pen, pen_out)
```

#### **Arguments**

inp	SummarizedExperiment: the input data frame with correct format.
cores	cores: integer: the number of assigned cores for the task.
pen	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.
pen_out	numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.

#### **Value**

the SummarizedExperiment object:

ID:	The bin/probe specific ID.
position:	The bin/probe specific position.
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:	String, the factor of TI fragment.
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.

### Examples

```
data(fragmentation_minimal)
fragment_delay(inp = fragmentation_minimal, cores = 2, pen = 2, pen_out = 1)
```

---

fragment\_HL %

=====

### **fragment\_HL**

*fragment\_HL performs the half\_life fragmentation*

---

### Description

fragment\_HL makes HL\_fragments based on delay\_fragments and assigns all gathered information to the SummarizedExperiment object.

### Usage

```
fragment_HL(inp, cores = 1, pen, pen_out)
```

### Arguments

inp SummarizedExperiment: the input data frame with correct format.  
 cores integer: the number of assigned cores for the task.  
 pen numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.  
 pen\_out numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.

### Details

The columns "HL\_fragment" and "HL\_mean\_fragment" are added.

fragment\_HL makes half-life\_fragments and assigns the mean of each fragment.

The function used is:

.score\_fun\_ave.

The input the SummarizedExperiment object.

pen is the penalty for new fragments in the dynamic programming, pen\_out is the outlier penalty.

**Value**

The SummarizedExperiment object:

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

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

**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:** String, the factor of TI fragment

**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

**Examples**

```
data(fragmentation_minimal)
fragment_HL(inp = fragmentation_minimal, cores = 2, pen = 2, pen_out = 1)
```

---

```
fragment_inty      %
```

```
=====
fragment_inty
```

```
fragment_inty performs the intensity fragmentation
```

---

**Description**

fragment\_inty makes intensity\_fragments based on HL\_fragments and assigns all gathered information to the SummarizedExperiment object.

**Usage**

```
fragment_inty(inp, cores = 1, pen, pen_out)
```

**Arguments**

inp	SummarizedExperiment: the input data frame with correct format.
cores	cores: integer: the number of assigned cores for the task.
pen	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.
pen_out	numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.

**Details**

The columns "intensity\_fragment" and "intensity\_mean\_fragment" are added.  
fragment\_inty makes intensity\_fragments and assigns the mean of each fragment.

The function used is:

.score\_fun\_ave.

The input is the the SummarizedExperiment object.

pen is the penalty for new fragments in the dynamic programming, pen\_out is the outlier penalty.

**Value**

The SummarizedExperiment object:

ID:	The bin/probe specific ID
position:	The bin/probe specific position
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:	String, the factor of TI fragment
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

**Examples**

```
data(fragmentation_minimal)
fragment_inty(inp = fragmentation_minimal, cores = 2, pen = 2, pen_out = 1)
```

---

```
fragment_TI      %
```

```
=====
fragment_TI
```

```
fragment_TI performs the TI fragmentation
```

---

**Description**

fragment\_TI makes TI\_fragments based on TUs and assigns all gathered information to the SummarizedExperiment object. The columns "TI\_termination\_fragment" and the "TI\_mean\_termination\_factor" are added.

**Usage**

```
fragment_TI(inp, cores = 1, pen, pen_out)
```

**Arguments**

inp	SummarizedExperiment: the input data frame with correct format.
cores	cores: integer: the number of assigned cores for the task.
pen	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.
pen_out	numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.

**Details**

The function used is:

```
.score_fun_ave.
```

The input is the SummarizedExperiment object.

pen is the penalty for new fragments in the dynamic programming, pen\_out is the outlier penalty.

**Value**

The SummarizedExperiment object:

ID:	The bin/probe specific ID
position:	The bin/probe specific position
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:     String, the factor of TI fragment  
 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  
 TI\_termination\_fragment:   The TI fragment the bin belongs to  
 TI\_mean\_termination\_factor: The mean termination factor of the respective TI fragment

### Examples

```

data(fragmentation_minimal)
fragment_TI(inp = fragmentation_minimal, cores = 2, pen = 2, pen_out = 1)
  
```

---

```

gff3_preprocess            %
  
```

---

### **gff3\_preprocess**

*gff3\_preprocess process gff3 file from database for multiple usage*

---

### Description

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

### Usage

```
gff3_preprocess(path)
```

**Arguments**

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

**Details**

The resulting dataframe contains region, positions, strand, gene and locus\_tag.

**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_e_coli.gff3.gz", package = "rifi"))
)
```

---

```
make_df %
```

```
=====
make_df
```

```
make_df adds important columns to the SummarizedExperiment
object
```

---

**Description**

'make\_df' adds to the SummarizedExperiment object with the columns: "intensity", "probe\_TI" and "flag".

**Usage**

```
make_df(inp, cores = 1, bg = 0, rm_FLT = TRUE)
```

**Arguments**

inp SummarizedExperiment: the (checked) input.  
cores integer: the number of assigned cores for the task.  
bg numeric: threshold over which the last timepoint has to be fitted with the above background mode.  
rm\_FLT logical: remove IDs where all replicates are marked as filtered. Default is FALSE.



**Details**

The replicates are collapsed into their respective means.

"intensity" is the mean intensity from time point 0.

"probe\_TI" is a value needed for the distribution for the different fitting models.

"flag" contains information on the distribution for the different fitting models.

Probes that don't reach the background level expression are flagged as "ABG" ("above background"). This is only needed for microarray data and is controlled by the bg parameter. The default for bg = 0, resulting in all probes to be above background (0 is advised for RNAseq data).

Probes where all replicates were filtered in the optional filtration step can be fully removed by rm\_FLT = TRUE! If you wish to keep all information in the assay set to FALSE!

**Value**

the SummarizedExperiment object: with intensity, probe\_TI and flag added to the rowRanges.

**Examples**

```
data(preprocess_minimal)
make_df(inp = preprocess_minimal, cores = 2, bg = 0, rm_FLT = TRUE)
```

---

```
make_pen          %
```

```
=====
make_pen
```

```
make_pen assigns automatically a penalties
```

---

**Description**

'make\_pen' calls one of four available penalty functions to automatically assign penalties for the dynamic programming.

**Usage**

```
make_pen(
  inp,
  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

inp	SummarizedExperiment: the input data frame with correct format.
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. Default is 2.
smp1_min	integer: the smaller end of the sampling size. Default is 10.
smp1_max	integer: the larger end of the sampling size. Default is 100.
sta_pen	numeric: the lower starting penalty. Default is 0.5.
end_pen	numeric: the higher starting penalty. Default is 4.5.
rez_pen	numeric: the number of penalties iterated within the penalty range. Default is 9.
sta_pen_out	numeric: the lower starting outlier penalty. Default is 0.5.
end_pen_out	numeric: the higher starting outlier penalty. Default is 3.5.
rez_pen_out	numeric: the number of outlier penalties iterated within the outlier penalty range. Default is 7.

## Details

The four functions to be called are:

1. fragment\_delay\_pen
2. fragment\_HL\_pen
3. fragment\_inty\_pen
4. fragment\_TI\_pen

These functions 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. Returns a penalty object (list of 4 objects) the first being the logbook.

## Value

A list with 4 items:

**logbook:** Integer, the logbook vector containing all penalty information

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

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

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

**Examples**

```

data(fit_minimal)
make_pen(
  inp = fit_minimal, FUN = rifi:::fragment_HL_pen, cores = 2,
  logs = as.numeric(rep(NA, 8)), dpt = 1, smp1_min = 10, smp1_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
)

```

---

```
nls2_fit          %
```

```
=====
nls2_fit
```

```
nls2_fit estimates decay for each probe or bin
```

---

**Description**

nls2\_fit uses nls2 function to fit a probe or bin using intensities of the time series data from different time point. nls2 uses different starting values through expand grid and selects the best fit. Different filters could be applied prior fitting to the model.

**Usage**

```

nls2_fit(
  inp,
  cores = 1,
  decay = seq(0.01, 0.11, by = 0.02),
  delay = seq(0, 10, by = 0.1),
  k = seq(0.1, 1, 0.2),
  bg = 0.2
)

```

**Arguments**

inp	SummarizedExperiment: the input with correct format.
cores	integer: the number of assigned cores for the task.
decay	numeric vector: A sequence of starting values for the decay. Default is seq(.08, 0.11, by=.02)
delay	numeric vector: A sequence of starting values for the delay. Default is seq(0,10, by=.1)
k	numeric vector: A sequence of starting values for the synthesis rate. Default is seq(0.1,1,0.2)
bg	numeric vector: A sequence of starting values. Default is 0.2.

## Details

To apply `nls2_fit` function, prior filtration could be applied.

1. `generic_filter_BG`: filter probes with intensities below background using threshold. Those probes are filtered.
2. `filtration_below_backg`: additional functions exclusive to microarrays could be applied. It is very strict to the background (not recommended in usual case).
3. `filtration_above_backg`: selects probes with a very high intensity and above the background (recommended for special transcripts). Probes are flagged with "ABG". Those transcripts are usually related to a specific function in bacteria. This filter selects all probes with the same ID, the mean is applied, the last time point is selected and compared to the threshold.

The model used estimates the delay, decay, intensity of the first time point (synthesis rate/decay) and the background. The coefficients are gathered in vectors with the corresponding IDs. Absence of the fit or a very bad fit are assigned with NA. In case of probes with very high intensities and above the background, the model used makes abstinence of background coefficient. The output of all coefficients is saved in the metadata. The fits are plotted using the function `plot_fit.r` through `rifi_fit`.

## Value

the `SummarizedExperiment` object: with delay and decay added to the `rowRanges`. The full fit data is saved in the metadata as "fit\_STD".

**delay**: Integer, the delay value of the bin/probe

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

## Examples

```
data(preprocess_minimal)
nls2_fit(inp = preprocess_minimal, cores = 2)
```

---

<code>penalties_e_coli</code>	<i>The result of <code>rifi_penalties</code> for E.coli example data. A <code>SummarizedExperiment</code> containing the output from <code>rifi_penalties</code> including the logbook and the four penalty objects as metadata.</i>
-------------------------------	--

---

## Description

The result of `rifi_penalties` for E.coli example data. A `SummarizedExperiment` containing the output from `rifi_penalties` including the logbook and the four penalty objects as metadata.

## Usage

```
data(penalties_e_coli)
```

**Format**

A list with 5 items:

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

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

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

**delay\_penalties:** a vector with the delay penalty and delay outlier penalty

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

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

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

**logbook:** The logbook vector containing all 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

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

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

**inty\_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

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

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

**TI\_penalties:** a vector with the TI penalty and TI outlier penalty

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

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

**Source**

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

---

penalties_minimal	<i>The result of rifi_penalties for artificial example data A Summarized-Experiment containing the output from rifi_penalties including the logbook and the four penalty objects as metadata.</i>
-------------------	---

---

**Description**

The result of rifi\_penalties for artificial example data A SummarizedExperiment containing the output from rifi\_penalties including the logbook and the four penalty objects as metadata.

**Usage**

```
data(penalties_minimal)
```

**Format**

An object of class RangedSummarizedExperiment with 24 rows and 33 columns.

**Source**

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

---

penalties\_synechocystis\_6803

*The result of rfi\_penalties for Synechocystis 6803 example data. A SummarizedExperiment containing the output from rfi\_penalties including the logbook and the four penalty objects as metadata.*

---

### Description

The result of rfi\_penalties for Synechocystis 6803 example data. A SummarizedExperiment containing the output from rfi\_penalties including the logbook and the four penalty objects as metadata.

### Usage

```
data(penalties_synechocystis_6803)
```

### Format

A list with 5 items:

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

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

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

**delay\_penalties:** a vector with the delay penalty and delay outlier penalty

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

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

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

**logbook:** The logbook vector containing all 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

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

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

**inty\_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

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

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

**TI\_penalties:** a vector with the TI penalty and TI outlier penalty

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

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

### Source

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

---

predict\_ps\_itss            %

=====

**predict\_ps\_itss**

*predict\_ps\_itss predicts pausing sites (ps) and internal starting sites (ITSS) between delay fragments.*

---

### Description

predict\_ps\_itss predicts ps and ITSS within the same TU. Neighboring delay segments are compared to each other by positioning the intercept of the second segment into the first segment using slope and intercept coefficients.

### Usage

```
predict_ps_itss(inp, maxDis = 300)
```

### Arguments

inp                      SummarizedExperiment: the input data frame with correct format.

maxDis                  integer: the maximal distance allowed between two successive fragments.

### Details

predict\_ps\_itss uses 3 steps to identify ps and ITSS:

1. select unique TU.
2. select from the input dataframe the columns: ID, position, strand, delay. delay fragment, TU and slope coordinates, velocity\_fragment and intercept.
3. select delay segments in the TU.
4. loop into all delay segments and estimate the coordinates of the last point of the first segment using the coefficients of the second segment and vice versa. We get two predicted positions, the difference between them is compared to the threshold.

In case the strand is "-", additional steps are added:

The positions of both segments are ordered from the last position to the first one.

All positions are merged in one column and subtracted from the maximum position. the column is split in 2. The first and second correspond to the positions of the first and second segments respectively.

Both segments are subjected to lm fit and the positions predicted are used on the same way as the opposite strand.

If the difference between the positions predicted is lower than negative threshold, ps is assigned otherwise, and if the difference is higher than the positive threshold, ITSS is assigned.

**Value**

The SummarizedExperiment with the columns regarding statistics:

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

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

**strand:** The bin/probe specific strand.

**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:** String, the factor of TI fragment.

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

**Examples**

```
data(fragmentation_minimal)
predict_ps_itss(inp = fragmentation_minimal, maxDis = 300)
```



---

preprocess_e_coli	<i>The result of rifi_preprocess for E.coli example data A SummarizedExperiment containing the output from rifi_penalties including the logbook and the four penalty objects as metadata. A list containing the output from rifi_preprocess, including the inp and the modified input_df.</i>
-------------------	---

---

## Description

The result of rifi\_preprocess for E.coli example data A SummarizedExperiment containing the output from rifi\_penalties including the logbook and the four penalty objects as metadata. A list containing the output from rifi\_preprocess, including the inp and the modified input\_df.

## Usage

```
data(preprocess_e_coli)
```

## Format

A SummarizedExperiment:

**inp:** the SummarizedExperiment:

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

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

**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

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

**fit\_obj\_TI:** the fit object for the TI fit:

**0:** relative intensities at 0 min

**1:** relative intensities at 1 min

**10:** relative intensities at 10 min

**15:** relative intensities at 15 min

**2:** relative intensities at 2 min

**20:** relative intensities at 20 min

**3:** relative intensities at 3 min

**4:** relative intensities at 4 min

**5:** relative intensities at 5 min

**6:** relative intensities at 6 min

**8:** relative intensities at 8 min

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

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

**filtration:** indicator whether the replicate is filtered or not

## Source

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

---

preprocess_minimal	<i>The result of rifi_preprocess for artificial example data A Summarized-Experiment containing the output from rifi_preprocess</i>
--------------------	---

---

### Description

The result of rifi\_preprocess for artificial example data A SummarizedExperiment containing the output from rifi\_preprocess

### Usage

```
data(preprocess_minimal)
```

### Format

An object of class RangedSummarizedExperiment with 4 rows and 33 columns.

### Source

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

---

preprocess_synechocystis_6803	<i>The result of rifi_preprocess for Synechocystis 6803 example data is a A SummarizedExperiment containing the output of rifi_preprocess as an extention to rowRanges</i>
-------------------------------	--

---

### Description

The result of rifi\_preprocess for Synechocystis 6803 example data is a A SummarizedExperiment containing the output of rifi\_preprocess as an extention to rowRanges

### Usage

```
data(preprocess_synechocystis_6803)
```

### Format

A SummarizedExperiment:

**inp:** the SummarizedExperiment:

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

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

**strand:** The bin/probe specific strand

**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

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

**fit\_obj\_TI:** the fit object for the TI fit:

**0:** relative intensities at 0 min  
**2:** relative intensities at 2 min  
**4:** relative intensities at 4 min  
**8:** relative intensities at 8 min  
**16:** relative intensities at 16 min  
**32:** relative intensities at 32 min  
**64:** relative intensities at 64 min  
**ID:** The bin/probe specific ID  
**position:** The bin/probe specific position  
**filtration:** indicator whether the replicate is filtered or not

### Source

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

---

res_minimal	<i>The result of event_dataframe for E.coli artificial example. A data frame combining the processed genome annotation and a SummarizedExperiment data from rifi_stats. The dataframe is</i>
-------------	--

---

### Description

The result of event\_dataframe for E.coli artificial example. A data frame combining the processed genome annotation and a SummarizedExperiment data from rifi\_stats. The dataframe is

### Usage

```
data(res_minimal)
```

### Format

A list with 2 items:

**region:** the region from the gff file  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** the strand of the annotation  
**TU:** The overarching transcription unit  
**position:** The bin/probe specific position  
**FC\_fragment\_intensity:** String, fragments involved in fold change between 2 intensity fragments  
**FC\_intensity:** Integer, the fold change value of 2 intensity fragments  
**p\_value\_intensity:** p\_value of the fold change of intensity fragments  
**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\_HL\_intensity\_fragment:** fragments involved on ratio of fold change between 2 half-life fragments and fold change between 2 intensity fragments

**FC\_HL\_intensity:** 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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

## Source

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

---

rifi\_fit %

=====  
**rifi\_fit**

*rifi\_fit wraps conveniently all fitting steps*

---

## Description

rifi\_fit wraps the functions:

1. nls2\_fit
2. TI\_fit
3. plot\_nls2\_function
4. plot\_singleProbe\_function

**Usage**

```
rifi_fit(
  inp,
  cores = 1,
  viz = FALSE,
  restr = 0.2,
  decay = seq(0.08, 0.11, by = 0.02),
  delay = seq(0, 10, by = 0.1),
  k = seq(0.1, 1, 0.2),
  bg = 0.2,
  TI_k = seq(0, 1, by = 0.5),
  TI_decay = c(0.05, 0.1, 0.2, 0.5, 0.6),
  TI = seq(0, 1, by = 0.5),
  TI_delay = seq(0, 2, by = 0.5),
  TI_rest_delay = seq(0, 2, by = 0.5),
  TI_bg = 0
)
```

**Arguments**

inp	SummarizedExperiment: the input with correct format.
cores	integer: the number of assigned cores for the task.
viz	logical: whether to visualize the output.
restr	numeric: a parameter that restricts the freedom of the fit to avoid wrong TI-term_factors, ranges from 0 to 0.2
decay	numeric vector: A sequence of starting values for the decay. Default is seq(.08, 0.11, by=.02)
delay	numeric vector: A sequence of starting values for the delay. Default is seq(0,10, by=.1)
k	numeric vector: A sequence of starting values for the synthesis rate. Default is seq(0.1,1,0.2)
bg	numeric vector: A sequence of starting values. Default is 0.2.
TI_k	numeric vector: A sequence of starting values for the synthesis rate. Default is seq(0, 1, by = 0.5).
TI_decay	numeric vector: A sequence of starting values for the decay. Default is c(0.05, 0.1, 0.2, 0.5, 0.6).
TI	numeric vector: A sequence of starting values for the TI. Default is seq(0, 1, by = 0.5).
TI_delay	numeric vector: A sequence of starting values for the delay. Default is seq(0, 2, by = 0.5).
TI_rest_delay	numeric vector: A sequence of starting values. Default is seq(0, 2, by = 0.5).
TI_bg	numeric vector: A sequence of starting values. Default is 0.

**Value**

the SummarizedExperiment object: with delay, decay and TI\_termination\_factor added to the rowRanges. The full fit data is saved in the metadata as "fit\_STD" and "fit\_TI". A plot is given if viz = TRUE.

**See Also**

nls2\_fit  
 TI\_fit  
 plot\_nls2  
 plot\_singleProbe

**Examples**

```
data(preprocess_minimal)
rifi_fit(
  inp = preprocess_minimal,
  cores = 1, viz = FALSE, restr = 0.1,
  decay = seq(.08, 0.11, by = .02),
  delay = seq(0, 10, by = .1), k = seq(0.1, 1, 0.2), bg = 0.2,
  TI_k = seq(0, 1, by = 0.5), TI_decay = c(0.05, 0.1, 0.2, 0.5, 0.6),
  TI = seq(0, 1, by = 0.5), TI_delay = seq(0, 2, by = 0.5),
  TI_rest_delay = seq(0, 2, by = 0.5), TI_bg = 0
)
```

---

```
rifi_fragmentation %
```

```
=====
```

**rifi\_fragmentation**

*rifi\_fragmentation wraps conveniently all fragmentation steps*

---

**Description**

rifi\_fragmentation is wrapper of the following functions:

1. fragment\_delay
2. fragment\_HL
3. fragment\_inty
4. TUgether
5. fragment\_TI

**Usage**

```
rifi_fragmentation(
  inp,
  cores = 1,
  pen_delay = NULL,
  pen_out_delay = NULL,
  pen_HL = NULL,
  pen_out_HL = NULL,
  pen_inty = NULL,
  pen_out_inty = NULL,
```

```

    pen_TU = NULL,
    pen_TI = NULL,
    pen_out_TI = NULL
)

```

### Arguments

inp	SummarizedExperiment: the input data frame with correct format.
cores	integer: the number of assigned cores for the task.
pen_delay	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.
pen_out_delay	numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.
pen_HL	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.
pen_out_HL	numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.
pen_inty	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.
pen_out_inty	numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.
pen_TU	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default -0.75.
pen_TI	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default is the auto generated value.
pen_out_TI	numeric: an internal parameter for the dynamic programming. Higher values result in fewer allowed outliers. Default is the auto generated value.

### Value

the SummarizedExperiment object: with delay\_fragment, HL\_fragment, intensity\_fragment, TI\_termination\_fragment and TU, and the respective values added to the rowRanges.

### See Also

```

fragment_delay
fragment_HL
fragment_inty
TUgether
fragment_TI

```

### Examples

```

data(penalties_minimal)
rifi_fragmentation(inp = penalties_minimal, cores = 2)

```

---

```
rifi_penalties      %
```

```
=====
```

**rifi\_penalties**

*rifi\_penalties wraps conveniently all penalty steps*

---

### Description

rifi\_penalties wraps the functions:

1. make\_pen,
2. viz\_pen\_obj

### Usage

```
rifi_penalties(  
  inp,  
  details = FALSE,  
  viz = FALSE,  
  top_i = 25,  
  cores = 1,  
  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 = 4.5,  
  rez_pen_out = 9  
)
```

### Arguments

inp	SummarizedExperiment: the input data frame with correct format.
details	logical: whether to return the penalty objects or just the logbook.
viz	logical: whether to visualize the output or not. Default is FALSE
top_i	integer: the number of top results visualized. Default is all.
cores	integer: the number of assigned cores for the task.
dpt	integer: the number of times a full iteration cycle is repeated with a more narrow range based on the previous cycle. Default is 2.
smpl_min	integer: the smaller end of the sampling size. Default is 10.
smpl_max	integer: the larger end of the sampling size. Default is 100.
sta_pen	numeric: the lower starting penalty. Default is 0.5.
end_pen	numeric: the higher starting penalty. Default is 4.5.
rez_pen	numeric: the number of penalties iterated within the penalty range. Default is 9.



sta_pen_out	numeric: the lower starting outlier penalty. Default is 0.5.
end_pen_out	numeric: the higher starting outlier penalty. Default is 3.5.
rez_pen_out	numeric: the number of outlier penalties iterated within the outlier penalty range. Default is 7.

### Value

The SummarizedExperiment object: with the penalties in the logbook added to the metadata. Also adds logbook\_details if details is TRUE, and plots the penalties if viz is TRUE.

### See Also

make\_pen  
viz\_pen\_obj

### Examples

```
data(fit_minimal)
rifi_penalties(
  inp = fit_minimal, details = FALSE, viz = FALSE,
  top_i = 25, cores = 2, 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 = 4.5, rez_pen_out = 9
)
```

---

```
rifi_preprocess      %
```

---

```
=====
rifi_preprocess
```

```
rifi_preprocess wraps conveniently all pre-processing steps
```

---

### Description

rifi\_preprocess wraps the functions:

1. check\_input
2. make\_df
3. function\_seg
4. finding\_PDD
5. finding\_TI

**Usage**

```

rifi_preprocess(
  inp,
  cores,
  FUN_filter = function(x) { FALSE },
  bg = 0,
  rm_FLT = FALSE,
  thrsh_check = 0,
  dista = 300,
  run_PDD = FALSE,
  pen_PDD = 2,
  pen_out_PDD = 1,
  thrsh_PDD = 0.001,
  pen_TI = 10,
  thrsh_TI = 0.5,
  add = 1000
)

```

**Arguments**

inp	SummarizedExperiment: the input.
cores	integer: the number of assigned cores for the task.
FUN_filter	function: A function of x, returning a logical. x is the numeric vector of the intensity from all time points for a specific replicate.
bg	numeric: threshold over which the last time point has to be fitted with the above background mode.
rm_FLT	logical: remove IDs where all replicates are marked as filtered by the background check. Default is FALSE.
thrsh_check	numeric: the minimal allowed intensity for time point "0". Advised to be kept at 0! Default is 0.
dista	integer: the amount of nucleotides defining the gap. Default is 300.
run_PDD	logical: running the PDD flag function
pen_PDD	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Advised to be kept at 2. Default is 2.
pen_out_PDD	numeric: an internal parameter for the dynamic programming. Higher values result in fewer possible outliers. Advised to be kept at 1. Default is 1.
thrsh_PDD	numeric: an internal parameter that allows fragments with slopes steeper than the threshold to be flagged with "PDD". Higher values result in fewer candidates. Advised to be kept at 0.001. Default is 0.001.
pen_TI	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Advised to be kept at 10. Default is 10.
thrsh_TI	numeric: an internal parameter that allows fragments with a certain amount of IDs with higher relative intensities at time points later than "0" to be flagged as "TI". Higher values result in fewer candidates. -0.5 is 25 %, 0 is 50%, 0.5 is 75%. Advised to be kept at 0.5. Default is 0.5.
add	integer: range of nucleotides before a potential TI event where in IDs are fitted with the TI fit.

### Details

rifi\_preprocess allows for the optional integration of filter functions. Filter functions mark replicates with TRUE. Those are then not considered in the fit! FUN\_filter is a general filter usually to exclude probes with low expression or "bad" patterns.

### Value

The SummarizedExperiment object: checked, and with position, ID, intensity, probe\_TI, position\_segment, flag and filtration added to the rowRanges.

### See Also

check\_input  
make\_df  
segment\_pos  
finding\_PDD  
finding\_TI

### Examples

```
data(example_input_minimal)
rifi_preprocess(
  inp = example_input_minimal, cores = 2, bg = 100, rm_FLT = FALSE,
  thrsh_check = 0, dista = 300, run_PDD = FALSE
)
```

---

rifi\_stats

*rifi\_stats wraps all statistical prediction steps conveniently*

---

### Description

rifi\_stats wraps the functions:

1. predict\_ps\_itss
2. apply\_Ttest\_delay
3. apply\_ancova
4. apply\_event\_position
5. apply\_t\_test
6. fold\_change
7. apply\_manova
8. apply\_t\_test\_ti
9. gff3\_preprocess

### Usage

```
rifi_stats(inp, dista = 300, path)
```

**Arguments**

inp	SummarizedExperiment: the input data frame with correct format.
dista	integer: the maximal distance allowed between two successive fragments. Default is the auto generated value.
path	path: to the directory containing the gff3 file.

**Value**

The SummarizedExperiment object: 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, TI\_fragments\_p\_value

**See Also**

predict\_ps\_itss  
 apply\_Ttest\_delay  
 apply\_ancova  
 apply\_event\_position  
 apply\_t\_test  
 fold\_change  
 apply\_manova  
 apply\_t\_test\_ti  
 gff3\_preprocess

**Examples**

```
data(fragmentation_minimal)
rifi_stats(inp = fragmentation_minimal, dista = 300,
path = gzfile(system.file("extdata", "gff_e_coli.gff3.gz",
package = "rifi")))
```

---

```
rifi_summary %
```

```
=====
rifi_summary
```

```
rifi_summary wraps conveniently and summarize all rifi outputs
```

---

**Description**

rifi\_summary wraps the functions:

1. event\_dataframe
2. dataframe\_summary
3. dataframe\_summary\_events
4. dataframe\_summary\_events\_HL\_int
5. dataframe\_summary\_events\_ps\_itss
6. dataframe\_summary\_events\_velocity
7. dataframe\_summary\_TI

**Usage**

```
rifi_summary(inp, data_annotation = metadata(inp)$annot[[1]])
```

**Arguments**

inp                    SummarizedExperiment: the input data frame with correct format.  
data\_annotation        dataframe: gff3 dataframe after processing.

**Value**

WIP

**See Also**

event\_dataframe  
dataframe\_summary  
dataframe\_summary\_events  
dataframe\_summary\_events\_HL\_int  
dataframe\_summary\_events\_ps\_itss  
dataframe\_summary\_events\_velocity  
dataframe\_summary\_TI

**Examples**

```
data(stats_minimal)
if(!require(SummarizedExperiment)){
  suppressPackageStartupMessages(library(SummarizedExperiment))
}
rifi_summary(inp = stats_minimal, data_annotation =
  metadata(stats_minimal)$annot[[1]])
```

---

```
rifi_visualization %
```

```
=====
```

**rifi\_visualization**

*rifi\_visualization plots all the data with fragments and events from both strands*

---

## Description

rifi\_visualization plots the whole genome with genes, transcription units (TUs), delay, half-life (HL), intensity fragments, features, events, velocity, annotation, coverage if available.

## Usage

```
rifi_visualization(
  data,
  genomeLength,
  annot,
  coverage = 0,
  chr_fwd = NA,
  chr_rev = NA,
  region = c("CDS", "asRNA", "5'UTR", "ncRNA", "3'UTR", "tRNA"),
  color_region = c("grey0", "red", "blue", "orange", "yellow", "green", "white",
    "darkseagreen1", "grey50", "black"),
  color_text.1 = "grey0",
  color_text.2 = "black",
  color_TU = "blue",
  Alpha = 0.5,
  size_tu = 1.6,
  size_locusTag = 1.6,
  size_gene = 1.6,
  Limit = 10,
  shape = 22,
  col_outlier = "grey50",
  col_coverage = "grey",
  shape_outlier = 13,
  limit_intensity = NA,
  face = "bold",
  tick_length = 0.3,
  arrow.color = "darkseagreen1",
  minVelocity = 3000,
  medianVelocity = 6000,
  col_above20 = "#00FFFF",
  fontface = "plain",
  shape_above20 = 14,
  col_outlierabove10 = "darkorchid",
  shape_outlierabove10 = 5,
  axis_text_y_size = 3,
  axis_title_y_size = 6,
```

```

TI_threshold = 1.1,
termination_threshold = -0.5,
iTSS_threshold = 0.5,
p_value_int = 0.05,
p_value_event = 0.05,
p_value_h1 = 0.05,
p_value_TI = 0.05,
p_value_manova = 0.05,
event_duration_ps = 1,
event_duration_itss = -1,
HL_threshold_1 = log2(1.5),
HL_threshold_2 = -log2(1.5),
vel_threshold = 200,
HL_threshold_color = "black",
vel_threshold_color = "grey52",
ps_color = "orange",
iTSS_I_color = "blue"
)

```

### Arguments

data	SummarizedExperiment: the input data frame with correct format.
genomeLength	integer: genome length output of gff3_preprocess function and element of meta-data of SummarizedExperiment.
annot	dataframe: the annotation file, output of gff3_preprocess function and element of metadata of SummarizedExperiment.
coverage	integer: in case the coverage is available.
chr_fwd	string object: coverage of the forward strand.
chr_rev	string object: coverage of the reverse strand.
region	dataframe: gff3 features of the genome.
color_region	string vector: vector of colors.
color_text.1	string: TU color text
color_text.2	string: genes color text
color_TU	string: TU color
Alpha	integer: color transparency degree.
size_tu	integer: TU size
size_locusTag	integer: locus_tag size
size_gene	integer: font size for gene annotation.
Limit	integer: value for y-axis limit.
shape	integer: value for shape.
col_outlier	string: outlier color.
col_coverage	integer: color for coverage plot.
shape_outlier	integer: value for outlier shape.
limit_intensity	integer: intensity limit if applicable.
face	string: label font.

tick\_length integer: value for ticks.  
 arrow.color string: arrows color.  
 minVelocity integer: threshold to fix the minimum of velocity.  
 medianVelocity integer: threshold to fix the maximum of velocity.  
 col\_above20 string: color for probes/bin above value 20.  
 fontface integer: font type  
 shape\_above20 integer: shape for probes/bins above value 20.  
 col\_outlierabove10 string: color for probes/bin outliers between 10 and 20,  
 shape\_outlierabove10 integer: shape for probes/bin outliers between 10 and 20,  
 axis\_text\_y\_size integer: text size for y-axis.  
 axis\_title\_y\_size integer: title size for y-axis.  
 TI\_threshold integer: threshold for TI between two fragments in case the TI termination factor drops from the first segment to the second, default 1.1. If threshold is reached a line is drawn to separates the two TI segments.  
 termination\_threshold integer: threshold for termination to plot, default .8.  
 iTSS\_threshold integer: threshold for iTSS\_II selected to plot, default 1.2.  
 p\_value\_int integer: p\_value of intensity fragments fold-change to plot, default 0.05.  
 p\_value\_event integer: p\_value of t-test from pausing site and iTSS\_I events to plot, default 0.05.  
 p\_value\_hl integer: p\_value of half\_life fragments fold-change to plot, default 0.05.  
 p\_value\_TI integer: p\_value of TI fragments selected to be plotted, default 0.05.  
 p\_value\_manova integer: p\_value of manova test fragments to plot, default 0.05.  
 event\_duration\_ps integer: threshold for pausing sites selected to plot, default -2.  
 event\_duration\_itss integer: threshold for iTSS\_I selected to plot, default 2.  
 HL\_threshold\_1 integer: threshold for log2FC(HL) selected to plot, default log2(1.5). log2FC(HL)  $\geq$  log2(1.5) are indicated by black color. If p\_value  $\leq$  p\_value\_hl (default 0.05), log2FC(HL) is indicated by HL\* otherwise HL.  
 HL\_threshold\_2 integer: threshold for log2FC(HL) selected to plot, default -log2(1.5). log2FC(HL)  $\leq$  -log2(1.5) are indicated by green color. If p\_value  $\leq$  p\_value\_hl (default 0.05), log2FC(HL) is indicated by HL\* otherwise HL. In case of p\_value is significant and the log2FC(HL) is between -log2FC(1.5) and log2FC(1.5), FC is assigned by green color and HL\*.  
 vel\_threshold integer: threshold for velocity ratio selected to plot, default 200.  
 HL\_threshold\_color string: color for HL fold change plot.  
 vel\_threshold\_color string: color for velocity ratio plot.  
 ps\_color string: color for pausing site plot.  
 iTSS\_I\_color string: color for iTSS\_I plot.



## Details

rifi\_visualization uses several functions to plot the genes including as-RNA and ncRNA and TUs as segments. The function plots delay, HL and intensity fragments with statistical t-test between the neighboring fragment, significant t-test is assigned with '. *t-test and Manova statistical test are also depicted as* '.

The functions used are:

1. annotation\_plot: plots the corresponding annotation.
2. positive\_strand\_function: plots delay, HL, intensity and events of positive strand.
3. negative\_strand\_function: plots delay, HL, intensity and events of negative strand.
4. empty\_data\_positive: plots empty boxes in case no data is available for positive strand.
5. empty\_data\_negative: plots empty boxes in case no data is available for negative strand.
6. strand\_selection: check if data is stranded and arrange by position.
7. splitGenome\_function: splits the genome into fragments.
8. indice\_function: assign a new column to the data to distinguish between fragments, outliers from delay or HL or intensity.
9. TU\_annotation: designs the segments border for the genes and TUs annotation
10. 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.
11. label\_log2\_function: used to add log scale to intensity values.
12. label\_square\_function: used to add square scale to coverage values.
13. coverage\_function: this function is used only in case of coverage is available.
14. 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.
15. outlier\_plot: plot the outliers with half-life between 10 and 30 on the maximum of the yaxis.
16. add\_genomeBorders: when the annotated genes are on the borders, they can not be plotted, therefore the region was split in 2 adding the row corresponding to the split part to the next annotation (i + 1) except for the first page.
17. my\_arrow: creates an arrow for the annotation.
18. arrange\_byGroup: selects the last row for each segment and add 40 nucleotides in case of negative strand for a nice plot.
19. regr: plots the predicted delay from linear regression if the data is on negative strand.
20. meanPosition: assign a mean position for the plot.
21. delay\_mean: adds a column in case of velocity is NA or equal to 60. The mean of the delay is calculated outliers.
22. my\_segment\_T: plots terminals and pausing sites labels.
23. my\_segment\_NS: plots internal starting sites 'iTSS'.
24. min\_value: returns minimum value for event plots in intensity plot.
25. velocity\_fun: function for velocity plot.
26. limit\_function: for values above 10 or 20 in delay and hl. Limit of the axis is set differently. y-axis limit is applied only if we have more than 3 values above 10 and lower or equal to 20. An exception is added in case a dataframe has less than 3 rows and 1 or more values are above 10, the rest of the values above 20 are adjusted to 20 on "secondaryAxis" function.

27. `empty_boxes`: used only in case the dataframe from the positive strand is not empty, the TU are annotated.
28. `function_TU_arrow`: used to avoid plotting arrows when a TU is split into two pages.
29. `terminal_plot_lm`: draws a linear regression line when terminal outliers have an intensity above a certain threshold and are consecutive. Usually are smallRNA (ncRNA, asRNA).
30. `slope_function`: replaces slope lower than 0.0009 to 0.
31. `velo_function`: replaces infinite velocity with NA.
32. plot the coverage of RNA\_seq in exponential phase growth

### Value

The visualization plot.

### Examples

```
data(stats_minimal)
if(!require(SummarizedExperiment)){
  suppressPackageStartupMessages(library(SummarizedExperiment))
}
rifi_visualization(data = stats_minimal,
  genomeLength = metadata(stats_minimal)$annot[[2]],
  annot = metadata(stats_minimal)$annot[[1]])
```

---

```
rifi_wrapper %
```

---

### **rifi\_wrapper**

*rifi\_wrapper wraps conveniently all functions included on rifi workflow*

---

### Description

`rifi_wrapper` wraps the functions:

1. `rifi_preprocess`
2. `rifi_fit`
3. `rifi_penalties`
4. `rifi_fragmentation`
5. `rifi_stats`
6. `rifi_summary`
7. `rifi_visualization`.

### Usage

```
rifi_wrapper(inp, cores, path, bg, restr)
```

**Arguments**

inp	data frame: the input data frame with correct format.
cores	integer: the number of assigned cores for the task.
path	path: path to an annotation file in gff format.
bg	numeric: threshold over which the last time point has to be fitted with the above background mode.
restr	numeric: a parameter that restricts the freedom of the fit to avoid wrong TI-term_factors, ranges from 0 to 0.2

**Value**

All intermediate objects

**See Also**

rifi\_preprocess  
 rifi\_fit  
 rifi\_penalties  
 rifi\_fragmentation  
 rifi\_stats  
 rifi\_summary  
 rifi\_visualization

**Examples**

```
data(example_input_minimal)
rifi_wrapper(inp = example_input_minimal, cores = 2, path =
  gzfile(system.file("extdata", "gff_e_coli.gff3.gz", package = "rifi")),
  bg = 0, restr = 0.01)
```

---

```
segment_pos      %
```

```
=====
segment_pos
```

```
segment_pos divides all IDs by position into position_segments
```

---

**Description**

segment\_pos adds the column "position\_segment" to the rowRanges. To reduce run time, the data is divided by regions of no expression larger than "dist" nucleotides.

**Usage**

```
segment_pos(inp, dista = 300)
```

**Arguments**

inp	SummarizedExperiment: the input.
dista	integer: the amount of nucleotides defining the gap. Default is 300.

**Value**

The SummarizedExperiment object:

<b>ID:</b>	The bin/probe specific ID
<b>position:</b>	The bin/probe specific position
<b>intensity:</b>	The relative intensity at time point 0
<b>probe_TI:</b>	An internal value to determine which fitting model is applied
<b>flag:</b>	Information on which fitting model is applied
<b>position_segment:</b>	The position based segment

**Examples**

```
data(preprocess_minimal)
segment_pos(inp = preprocess_minimal, dista = 300)
```

---

stats_e_coli	<i>The result of rfi_stats for E.coli example data A SummarizedExperiment containing the output from rfi_stats</i>
--------------	--

---

**Description**

The result of rfi\_stats for E.coli example data A SummarizedExperiment containing the output from rfi\_stats

**Usage**

```
data(stats_e_coli)
```

**Format**

A SummarizedExperiment:

<b>ID:</b>	The bin/probe specific ID
<b>position:</b>	The bin/probe specific position
<b>strand:</b>	The bin/probe specific strand
<b>intensity:</b>	The relative intensity at time point 0
<b>probe_TI:</b>	An internal value to determine which fitting model is applied
<b>flag:</b>	Information on which fitting model is applied
<b>position_segment:</b>	The position based segment
<b>delay:</b>	The delay value of the bin/probe
<b>half_life:</b>	The half-life of the bin/probe

**TI\_termination\_factor:** String, the factor of TI fragment  
**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

#### Source

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

---

stats_minimal	<i>The result of rifi_stats for artificial example data A SummarizedExperiment containing the output of rifi_stats as an extension to rowRanges and metadata (gff file processed, see gff file documentation)</i>
---------------	---

---

### Description

The result of rifi\_stats for artificial example data A SummarizedExperiment containing the output of rifi\_stats as an extension to rowRanges and metadata (gff file processed, see gff file documentation)

### Usage

```
data(stats_minimal)
```

### Format

A rowRanges of SummarizedExperiment with 24 rows and 45 variables:

**ID:** The bin/probe specific ID  
**position:** The bin/probe specific position  
**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:** String, the factor of TI fragment  
**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

### Source

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

---

stats\_synechocystis\_6803

*The result of rifi\_stats for Synechocystis 6803 example data A SummarizedExperiment containing the output of rifi\_stats as an extension to rowRanges*

---

### Description

The result of rifi\_stats for Synechocystis 6803 example data A SummarizedExperiment containing the output of rifi\_stats as an extension to rowRanges

### Usage

```
data(stats_synechocystis_6803)
```

**Format**

The rowRanges of SummarizedExperiment:

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

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

**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:** String, the factor of TI fragment

**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

## Source

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

---

summary_e_coli	<i>The result of rifi_summary for E.coli example data A SummarizedExperiment containing the output of rifi_stats as an extension to rowRanges</i>
----------------	---

---

## Description

The result of rifi\_summary for E.coli example data A SummarizedExperiment containing the output of rifi\_stats as an extension to rowRanges

## Usage

```
data(summary_e_coli)
```

## Format

The rowRanges of SummarizedExperiment:

**bin\_df:** all information regarding bins:

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

**feature\_type:** String, region annotation covering the fragments

**gene:** String, gene annotation covering the fragments

**locus\_tag:** String, locus\_tag annotation covering the fragments

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

**strand:** The bin/probe specific strand

**segment:** The segment the bin/probe belongs to

**TU:** The overarching transcription unit

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

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

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

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

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

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

**flag:** The flag of the bin/probe(TI, PDD)

**TI\_termination\_factor:** String, the factor of TI fragment

**frag\_df:** all information regarding fragments:

**feature\_type:** String, region annotation covering the fragments

**gene:** String, gene annotation covering the fragments

**locus\_tag:** String, locus\_tag annotation covering the fragments

**first\_position\_frg:** The first position of the fragment on the genome

**last\_position\_frg:** The last position of the fragment on the genome

**strand:** The bin/probe specific strand

**TU:** The overarching transcription unit

**segment:** The segment the fragment belongs to

**delay\_fragment:** The delay fragment of the fragment

**HL\_fragment:** The half-life fragment of the fragment

**half\_life:** The half-life mean of the fragment

**HL\_SD:** The half-life standard deviation of the fragment

**HL\_SE:** The half-life standard error of the fragment

**intensity\_fragment:** The intensity\_fragment of the fragment

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

**intensity\_SD:** The intensity standard deviation of the fragment

**intensity\_SE:** The intensity standard error of the fragment

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

**event\_df:** all information regarding events:

**event:** String, event type

**p\_value:** Integer, p\_value of the event

**p\_adjusted:** Integer, p\_value adjusted

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

**FC\_intensity:** Fold change of intensity

**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

**FC\_HL\_FC\_intensity:** Fold change of half-life/ fold change of intensity

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

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

**feature\_type:** String, region annotation covering the fragments

**gene:** String, gene annotation covering the fragments

**locus\_tag:** String, locus\_tag annotation covering the fragments

**strand:** The bin/probe specific strand

**TU:** The overarching transcription unit

**segment\_1:** String, the first fragment of the two of fragments subjected to analysis

**segment\_2:** String, the second fragment of the two of fragments subjected to analysis

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

**gap\_fragments:** Integer, the distance between two delay fragments

**features:** Integer, number of fragments involved on the event

**events\_HL\_int\_df:** all information regarding events related to half-life and intensity:

**event:** String, event type

**p\_value:** Integer, p\_value of the event

**p\_adjusted:** Integer, p\_value adjusted  
**FC\_HL:** Integer, the fold change value of 2 HL fragments  
**FC\_intensity:** Integer, the fold change value of 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  
**FC\_HL\_FC\_intensity:** Fold change of half-life/ fold change of intensity  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragementes involved on the event  
**events\_ps\_itss\_df:** all information regarding events related to pausing sites and iTSS\_I:  
**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay 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  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragementes involved on the event  
**events\_velocity\_df:** all information regarding events related to velocity:  
**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand

**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragementes involved on the event

**TI\_df:** all information regarding TI:

**event:** String, event type  
**TI\_fragment:** String, the fragment with TI  
**TI\_termination\_factor:** String, the factor of TI fragment  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**features:** Integer, number of fragementes involved on the event  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**position\_1:** the first position of TI fragment, if 2 fragments, first position is from the first fragment  
**position\_2:** the last position of TI fragment, if 2 fragments, last position is from the second fragment.

### Source

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

---

summary_minimal	<i>The result of rifi_summary for artificial example data A Summarized-Experiment with the output from rifi_summary as metadata</i>
-----------------	---

---

### Description

The result of rifi\_summary for artificial example data A SummarizedExperiment with the output from rifi\_summary as metadata

### Usage

```
data(summary_minimal)
```

### Format

A list of 7 data frames with 290 rows and 11 variables, 36 rows and 11 variables, 57 rows and 18 variables, and 8 rows and 14 variables:

**bin\_df:** all information regarding bins:

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

**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**position:** The bin/probe specific position  
**strand:** The bin/probe specific strand  
**segment:** The segment the bin/probe belongs to  
**TU:** The overarching transcription unit  
**delay\_fragment:** The delay fragment the bin/probe belongs to  
**delay:** The delay of the bin/probe  
**HL\_fragment:** The half-life fragment the bin/probe belongs to  
**half\_life:** The half-life of the bin/probe  
**intensity\_fragment:** The intensity fragment the bin/probe belongs to  
**intensity:** The relative intensity at time point 0  
**flag:** The flag of the bin/probe(TI, PDD)  
**TI\_termination\_factor:** String, the factor of TI fragment

**frag\_df:** all information regarding fragments:

**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**first\_position\_frg:** The first position of the fragment on the genome  
**last\_position\_frg:** The last position of the fragment on the genome  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment:** The segment the fragment belongs to  
**delay\_fragment:** The delay fragment of the fragment  
**HL\_fragment:** The half-life fragment of the fragment  
**half\_life:** The half-life mean of the fragment  
**HL\_SD:** The half-life standard deviation of the fragment  
**HL\_SE:** The half-life standard error of the fragment  
**intensity\_fragment:** The intensity\_fragment of the fragment  
**intensity:** The relative intensity at time point 0  
**intensity\_SD:** The intensity standard deviation of the fragment  
**intensity\_SE:** The intensity standard error of the fragment  
**velocity:** The velocity value of the respective delay fragment

**event\_df:** all information regarding events:

**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**FC\_HL:** Integer, the fold change value of 2 HL fragments  
**FC\_intensity:** Fold change of intensity  
**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  
**FC\_HL\_FC\_intensity:** Fold change of half-life/ fold change of intensity  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments

**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragement involved on the event

**events\_HL\_int\_df:** all information regarding events related to half-life and intensity:

**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**FC\_HL:** Integer, the fold change value of 2 HL fragments  
**FC\_intensity:** Integer, the fold change value of 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  
**FC\_HL\_FC\_intensity:** Fold change of half-life/ fold change of intensity  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragement involved on the event

**events\_ps\_itss\_df:** all information regarding events related to pausing sites and iTSS\_I:

**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay 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  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis

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

**gap\_fragments:** Integer, the distance between two delay fragments

**features:** Integer, number of fragments involved on the event

**events\_velocity\_df:** all information regarding events related to velocity:

**event:** String, event type

**p\_value:** Integer, p\_value of the event

**p\_adjusted:** Integer, p\_value adjusted

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

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

**feature\_type:** String, region annotation covering the fragments

**gene:** String, gene annotation covering the fragments

**locus\_tag:** String, locus\_tag annotation covering the fragments

**strand:** The bin/probe specific strand

**TU:** The overarching transcription unit

**segment\_1:** String, the first fragment of the two of fragments subjected to analysis

**segment\_2:** String, the second fragment of the two of fragments subjected to analysis

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

**gap\_fragments:** Integer, the distance between two delay fragments

**features:** Integer, number of fragments involved on the event

**TI\_df:** all information regarding TI:

**event:** String, event type

**TI\_fragment:** String, the fragment with TI

**TI\_termination\_factor:** String, the factor of TI fragment

**p\_value:** Integer, p\_value of the event

**p\_adjusted:** Integer, p\_value adjusted

**feature\_type:** String, region annotation covering the fragments

**gene:** String, gene annotation covering the fragments

**locus\_tag:** String, locus\_tag annotation covering the fragments

**strand:** The bin/probe specific strand

**TU:** The overarching transcription unit

**features:** Integer, number of fragments involved on the event

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

**position\_1:** the first position of TI fragment, if 2 fragments, first position is from the first fragment

**position\_2:** the last position of TI fragment, if 2 fragments, last position is from the second fragment.

## Source

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

---

summary\_synechocystis\_6803

*The result of rfi\_summary for Synechocystis 6803 example data A list containing the output from rfi\_summary, including the fragment based data frame, bin based data frame, event data frame and the TI dataframe.*

---

## Description

The result of rfi\_summary for Synechocystis 6803 example data A list containing the output from rfi\_summary, including the fragment based data frame, bin based data frame, event data frame and the TI dataframe.

## Usage

```
data(summary_synechocystis_6803)
```

## Format

A list of 4 data frames with 3000 rows and 11 variables, 297 rows and 11 variables, 486 rows and 18 variables, and 10 rows and 14 variables:

**bin\_df:** all information regarding bins:

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

**feature\_type:** String, region annotation covering the fragments

**gene:** String, gene annotation covering the fragments

**locus\_tag:** String, locus\_tag annotation covering the fragments

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

**strand:** The bin/probe specific strand

**segment:** The segment the bin/probe belongs to

**TU:** The overarching transcription unit

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

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

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

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

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

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

**flag:** The flag of the bin/probe(TI, PDD)

**TI\_termination\_factor:** String, the factor of TI fragment

**frag\_df:** all information regarding fragments:

**feature\_type:** String, region annotation covering the fragments

**gene:** String, gene annotation covering the fragments

**locus\_tag:** String, locus\_tag annotation covering the fragments

**first\_position\_frg:** The first position of the fragment on the genome

**last\_position\_frg:** The last position of the fragment on the genome

**strand:** The bin/probe specific strand

**TU:** The overarching transcription unit



**segment:** The segment the fragment belongs to  
**delay\_fragment:** The delay fragment of the fragment  
**HL\_fragment:** The half-life fragment of the fragment  
**half\_life:** The half-life mean of the fragment  
**HL\_SD:** The half-life standard deviation of the fragment  
**HL\_SE:** The half-life standard error of the fragment  
**intensity\_fragment:** The intensity\_fragment of the fragment  
**intensity:** The relative intensity at time point 0  
**intensity\_SD:** The intensity standard deviation of the fragment  
**intensity\_SE:** The intensity standard error of the fragment  
**velocity:** The velocity value of the respective delay fragment

**event\_df:** all information regarding events:

**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**FC\_HL:** Integer, the fold change value of 2 HL fragments  
**FC\_intensity:** Fold change of intensity  
**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  
**FC\_HL\_FC\_intensity:** Fold change of half-life/ fold change of intensity  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragments involved on the event

**events\_HL\_int\_df:** all information regarding events related to half-life and intensity:

**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**FC\_HL:** Integer, the fold change value of 2 HL fragments  
**FC\_intensity:** Integer, the fold change value of 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  
**FC\_HL\_FC\_intensity:** Fold change of half-life/ fold change of intensity  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments

**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragement involved on the event

**events\_ps\_itss\_df:** all information regarding events related to pausing sites and iTSS\_I:

**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay 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  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragement involved on the event

**events\_velocity\_df:** all information regarding events related to velocity:

**event:** String, event type  
**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**velocity\_ratio:** Integer, ratio of velocity between 2 delay fragments  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**segment\_1:** String, the first fragment of the two of fragments subjected to analysis  
**segment\_2:** String, the second fragment of the two of fragments subjected to analysis  
**event\_duration:** Integer, the duration between two delay fragments  
**gap\_fragments:** Integer, the distance between two delay fragments  
**features:** Integer, number of fragement involved on the event

**TI\_df:** all information regarding TI:

**event:** String, event type  
**TI\_fragment:** String, the fragment with TI  
**TI\_termination\_factor:** String, the factor of TI fragment

**p\_value:** Integer, p\_value of the event  
**p\_adjusted:** Integer, p\_value adjusted  
**feature\_type:** String, region annotation covering the fragments  
**gene:** String, gene annotation covering the fragments  
**locus\_tag:** String, locus\_tag annotation covering the fragments  
**strand:** The bin/probe specific strand  
**TU:** The overarching transcription unit  
**features:** Integer, number of fragements involved on the event  
**event\_position:** Integer, the position middle between 2 fragments with an event  
**position\_1:** the first position of TI fragment, if 2 fragments, first position is from the first fragment  
**position\_2:** the last position of TI fragment, if 2 fragments, last position is from the second fragment.

### Source

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

---

TI\_fit %

---

#### TI\_fit

*TI\_fit estimates transcription interference and termination factor using nls function for probe or bin flagged as "TI".*

---

### Description

TI\_fit uses nls2 function to fit the flagged probes or bins with "TI" found using finding\_TI.r. It estimates the transcription interference level (referred later to TI) as well as the transcription factor fitting the probes/bins with nls function looping into several starting values.

### Usage

```

TI_fit(
  inp,
  cores = 1,
  restr = 0.2,
  k = seq(0, 1, by = 0.5),
  decay = c(0.05, 0.1, 0.2, 0.5, 0.6),
  ti = seq(0, 1, by = 0.5),
  ti_delay = seq(0, 2, by = 0.5),
  rest_delay = seq(0, 2, by = 0.5),
  bg = 0
)
  
```

**Arguments**

<code>inp</code>	SummarizedExperiment: the input with correct format.
<code>cores</code>	integer: the number of assigned cores for the task.
<code>restr</code>	numeric: a parameter that restricts the freedom of the fit to avoid wrong TI-term_factors, ranges from 0 to 0.2.
<code>k</code>	numeric vector: A sequence of starting values for the synthesis rate. Default is <code>seq(0, 1, by = 0.5)</code> .
<code>decay</code>	numeric vector: A sequence of starting values for the decay Default is <code>c(0.05, 0.1, 0.2, 0.5, 0.6)</code> .
<code>ti</code>	numeric vector: A sequence of starting values for the delay. Default is <code>seq(0, 1, by = 0.5)</code> .
<code>ti_delay</code>	numeric vector: A sequence of starting values for the delay. Default is <code>seq(0, 2, by = 0.5)</code> .
<code>rest_delay</code>	numeric vector: A sequence of starting values. Default is <code>seq(0, 2, by = 0.5)</code> .
<code>bg</code>	numeric vector: A sequence of starting values. Default is 0.

**Details**

To determine TI and termination factor, `TI_fit` function is applied to the flagged probes and to the probes localized 1000 nucleotides upstream. Before applying `TI_fit` function, some probes/bins are filtered out if they are below the background using `generic_filter_BG`. The model loops into a dataframe containing sequences of starting values and the coefficients are extracted from the fit with the lowest residuals. When many residuals are equal to 0, the lowest residual can not be determined and the coefficients extracted could be wrong. Therefore, a second filter was developed. First we loop into all starting values, we collect `nls` objects and the corresponding residuals. They are sorted and residuals non equal to 0 are collected in a vector. If the first residuals are not equal to 0, 20 % of the best residuals are collected in `tmp_r_min` vector and the minimum termination factor is selected. In case the first residuals are equal to 0 then values between 0 to 20% of the values collected in `tmp_r_min` vector are gathered. The minimum termination factor coefficient is determined and saved. The coefficients are gathered in `res` vector and saved as an object.

**Value**

the SummarizedExperiment object: with `delay`, `decay` and `TI_termination_factor` added to the `rowRanges`. The full fit data is saved in the metadata as "fit\_TI".

**Examples**

```
data(preprocess_minimal)
TI_fit(inp = preprocess_minimal, cores=2, restr=0.01)
```

---

TUgether %

=====

**TUgether**

*TUgether combines delay fragments into TUs*

---

### Description

TUgether combines delay fragments into TUs. The column "TU" is added. It uses score fun\_increasing on the start and end points of delay\_fragments.

### Usage

```
TUgether(inp, cores = 1, pen = -0.75)
```

### Arguments

inp	SummarizedExperiment: the input data frame with correct format.
cores	cores: integer: the number of assigned cores for the task.
pen	numeric: an internal parameter for the dynamic programming. Higher values result in fewer fragments. Default -0.75.

### Details

The function used is: .score\_fun\_increasing

The input is the SummarizedExperiment object. pen is the penalty for new fragments in the dynamic programming. Since high scores are aimed, pen is negative.

### Value

The SummarizedExperiment with the columns regarding the TU:

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

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

**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:** String, the factor of TI fragment.

**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.

### Examples

```
data(fragmentation_minimal)
TUgether(inp = fragmentation_minimal, cores = 2, pen = -0.75)
```

---

```
viz_pen_obj          %
```

```
=====
viz_pen_obj
```

```
viz_pen_obj visualizes penalty objects
```

---

### Description

viz\_pen\_obj provides an optional visualization of any penalty object created by make\_pen. the function can be customized to show only the n = top\_i top results.

### Usage

```
viz_pen_obj(obj, top_i = nrow(obj[[3]][[1]]) * ncol(obj[[3]][[1]]))
```

### Arguments

obj                    object: penalty object(make\_pen output)

top\_i                  integer: the number of top results visualized. Default is all.

### Value

A visualization of the penalty object

### Examples

```
data(penalties_e_coli)
viz_pen_obj(penalties_e_coli$pen_obj_delay, 25)
```

---

wrapper_e_coli	<i>The result of rifi_wrapper for E.coli example data A list of SummarizedExperiment containing the output of rifi_wrapper. The list contains 6 elements of SummarizedExperiment output of rifi_preprocess, rifi_fit, rifi_penalties, rifi_fragmentation, rifi_stats and rifi_summary. The plot is generated from rifi_visualization. for more detail, please refer to each function separately.</i>
----------------	--

---

### Description

The result of rifi\_wrapper for E.coli example data A list of SummarizedExperiment containing the output of rifi\_wrapper. The list contains 6 elements of SummarizedExperiment output of rifi\_preprocess, rifi\_fit, rifi\_penalties, rifi\_fragmentation, rifi\_stats and rifi\_summary. The plot is generated from rifi\_visualization. for more detail, please refer to each function separately.

### Usage

```
data(wrapper_e_coli)
```

### Format

An object of class list of length 6.

### Source

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

---

wrapper_minimal	<i>The result of rifi_wrapper for E.coli artificial example. A list of SummarizedExperiment containing the output of rifi_wrapper. The list contains 6 elements of SummarizedExperiment output of rifi_preprocess, rifi_fit, rifi_penalties, rifi_fragmentation, rifi_stats and rifi_summary. The plot is generated from rifi_visualization. for more detail, please refer to each function separately.</i>
-----------------	---

---

### Description

The result of rifi\_wrapper for E.coli artificial example. A list of SummarizedExperiment containing the output of rifi\_wrapper. The list contains 6 elements of SummarizedExperiment output of rifi\_preprocess, rifi\_fit, rifi\_penalties, rifi\_fragmentation, rifi\_stats and rifi\_summary. The plot is generated from rifi\_visualization. for more detail, please refer to each function separately.

### Usage

```
data(wrapper_minimal)
```

### Format

An object of class list of length 6.

**Source**

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

---

wrapper\_summary\_synechocystis\_6803

*The result of rifi\_wrapper for summary\_synechocystis\_6803 example data A list of SummarizedExperiment containing the output of rifi\_wrapper. The list contains 6 elements of SummarizedExperiment output of rifi\_preprocess, rifi\_fit, rifi\_penalties, rifi\_fragmentation, rifi\_stats and rifi\_summary. The plot is generated from rifi\_visualization. for more detail, please refer to each function separately.*

---

**Description**

The result of rifi\_wrapper for summary\_synechocystis\_6803 example data A list of SummarizedExperiment containing the output of rifi\_wrapper. The list contains 6 elements of SummarizedExperiment output of rifi\_preprocess, rifi\_fit, rifi\_penalties, rifi\_fragmentation, rifi\_stats and rifi\_summary. The plot is generated from rifi\_visualization. for more detail, please refer to each function separately.

**Usage**

```
data(wrapper_summary_synechocystis_6803)
```

**Format**

An object of class list of length 6.

**Source**

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



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