

Package: **bridger2** (via r-universe)

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Title Genome-Wide RNA Degradation Analysis Using BRIC-Seq Data

Version 0.1.0

Description BRIC-seq is a genome-wide approach for determining RNA stability in mammalian cells. This package provides a series of functions for performing quality check of your BRIC-seq data, calculation of RNA half-life for each transcript and comparison of RNA half-lives between two conditions.

Depends R (>= 3.3.1)

Imports data.table, ggplot2, shiny, shinydashboard, plotly, BSDA, outliers

Suggests testthat

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Repository <https://imamachi-n.r-universe.dev>

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BridgeRCore	<i>BridgeR basic function for calculating RNA half-life from BRIC-seq data</i>
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Description

BridgeRCore is a basic function for calculating RNA half-life BRIC-seq data and a wrapper of the other individual bridger2 functions.

Usage

```
BridgeRCore(inputFile, inforColumn = 4, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), RPKMcutoff = 0.1, cutoffBelow = 0.1,
  YMin = -2, YMax = 2, downsamplingFig = 0.2, makeFig = FALSE,
  cutoffQuantile = 0.975, inforHKGenesRow = "symbol", HKGenes = c("GAPDH",
  "PGK1", "PPIA", "EN01", "ATP5B", "ALDOA"), CutoffTimePointNumber = 4,
  R2_criteria = 0.9, TimePointRemoval1 = c(1, 2), TimePointRemoval2 = c(8,
  12), ThresholdHalfLife1 = 3, ThresholdHalfLife2 = 12, save = TRUE,
  outputPrefix = "BridgeR", normalization = "default", method = "default")
```

Arguments

inputFile	The vector of tab-delimited matrix file.
inforColumn	The number of information columns.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
RPKMcutoff	Cutoff value of RPKM at 0hr.
cutoffBelow	Cutoff value of RPKM at all time points.
YMin	Y-axis min.
YMax	Y-axis max.
downsamplingFig	the factor for downsampling.
makeFig	Whether to save the figure of normalization factor.

cutoffQuantile cutoff value of quantile.#' @param save Whether to save the output matrix file.
 inforHKGenesRow The column number of house-keeping gene information.
 HKGenes The vector of house-keeping genes.
 CutoffTimePointNumber The number of minimum time points for calc.
 R2_criteria The cutoff of R2 for R2 selection.
 TimePointRemoval1 The candidate_1 of time point removal.
 TimePointRemoval2 The candidate_2 of time point removal.
 ThresholdHalfLife1 The cutoff of TimePointRemoval1.
 ThresholdHalfLife2 The cutoff of TimePointRemoval2.
 save Whether to save the output matrix file.
 outputPrefix The prefix for the name of the output.
 normalization select "default" (percentile method) or "house_keeping_genes"
 method select "default" (R2 selection/1st-order) or "3models".

Value

data.table object including RNA half-life, R2 and the selected fitting model.

Examples

```

halflife_table <- BridgeRCore(RNA_half-life_comparison[1:30,],
                             save = FALSE)
halflife_table <- BridgeRCore(RNA_half-life_comparison_HK[177:206],
                             save = FALSE,
                             normalization = "house_keeping_genes",
                             method = "3models")
  
```

BridgeRDatasetChecker *BRIC-seq Dataset checker*

Description

BridgeRDatasetChecker returns several BRIC-seq dataset information. This function is used for checking your BRIC-seq dataset quality.

Usage

```
BridgeRDatasetChecker(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), inforColumn = 4, percentile = c(0.99, 0.95,
  0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, 0.1, 0.05), save = T,
  outputPrefix = "BridgeR_2_raw")
```

Arguments

inputFile	Input matrix object.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
inforColumn	The number of information columns.
percentile	Percentile numbers.
save	Whether to save the output fig file.
outputPrefix	The prefix for the name of the output.

Value

list object about ggplot2 fig data.

Examples

```
library(data.table)
normalized_table <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(1.00, 1.00, 1.00),
  CTRL_1_1h = c(1.00, 0.86, 0.96),
  CTRL_1_2h = c(1.00, 0.96, 0.88),
  CTRL_1_4h = c(1.00, 0.74, 0.85),
  CTRL_1_8h = c(1.00, 0.86, 0.68),
  CTRL_1_12h = c(1.01, 0.65, 0.60),
  gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  KD_1_0h = c(1.00, 1.00, 1.00),
  KD_1_1h = c(1.01, 0.73, 0.71),
  KD_1_2h = c(1.01, 0.77, 0.69),
  KD_1_4h = c(1.01, 0.72, 0.67),
  KD_1_8h = c(1.01, 0.64, 0.38),
  KD_1_12h = c(1.00, 0.89, 0.63))
group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
fig_list_norm <- BridgeRDatasetChecker(inputFile = normalized_table,
  save = FALSE)
```

`BridgeRDataSetFromMatrix`*Calculate relative RPKM expression from data.table format.*

Description

`BridgeRDataSetFromMatrix` calculates the relative RPKM values compared with 0hr, importing `data.table` format.

Usage

```
BridgeRDataSetFromMatrix(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), cutoff = 0.1, cutoffBelow = 0.1,
  inforColumn = 4, save = T, outputPrefix = "BridgeR_1")
```

Arguments

<code>inputFile</code>	The vector of tab-delimited matrix file.
<code>group</code>	The vector of group names.
<code>hour</code>	The vector of time course about BRIC-seq experiment.
<code>cutoff</code>	Cutoff value of RPKM at 0hr.
<code>cutoffBelow</code>	Cutoff value of RPKM at all time points.
<code>inforColumn</code>	The number of information columns.
<code>save</code>	Whether to save the output matrix file.
<code>outputPrefix</code>	The prefix for the name of the output.

Value

`data.table` object about relative RPKM values.

Examples

```
library(data.table)
rpkm_matrix <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(41, 5, 5),
  CTRL_1_1h = c(48, 7, 6),
  CTRL_1_2h = c(56, 10, 6),
  CTRL_1_4h = c(87, 12, 10),
  CTRL_1_8h = c(124, 20, 11),
  CTRL_1_12h = c(185, 22, 15),
  gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
```

```

        locus = c("chr12", "chr12", "chr4"),
        KD_1_0h = c(21, 10, 3),
        KD_1_1h = c(33, 11, 3),
        KD_1_2h = c(42, 15, 4),
        KD_1_4h = c(60, 20, 5),
        KD_1_8h = c(65, 37, 6),
        KD_1_12h = c(70, 42, 6))
group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
test_table <- BridgeRDataSetFromMatrix(inputFile = rpkm_matrix,
                                       group = group,
                                       hour = hour,
                                       cutoff = 0.1,
                                       inforColumn = 4,
                                       save = FALSE)

```

BridgeRDataSetFromRaw *Calculate relative RPKM expression from raw data.*

Description

BridgeRDataSetFromRaw calculates the relative RPKM values compared with 0hr, importing tab-delimited txt file.

Usage

```

BridgeRDataSetFromRaw(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), cutoff = 0.1, cutoffBelow = 0.1,
  inforColumn = 4, save = T, outputPrefix = "BridgeR_1")

```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
cutoff	Cutoff value of RPKM at 0hr.
cutoffBelow	Cutoff value of RPKM at all time points.
inforColumn	The number of information columns.
save	Whether to save the output matrix file.
outputPrefix	The prefix for the name of the output.

Value

data.table object about relative RPKM values.

 BridgeReport

Shinyapp reporting for drawing RNA decay curve.

Description

BridgeReport returns a shinyapp object to draw RNA decay curve. You can easily check RNA half-life and RNA decay fitting curve on your web browser.

Usage

```
BridgeReport(inputFile, group = c("Control", "Knockdown"), hour = c(0, 1, 2,
  4, 8, 12), comparisonFile = c("Control", "Knockdown"),
  searchRowName = "symbol", inforColumn = 4, color = c("black", "red"),
  TimePointRemoval1 = c(1, 2), TimePointRemoval2 = c(8, 12))
```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
comparisonFile	The vector of group names.
searchRowName	Row name for searching.
inforColumn	The number of information columns.
color	color of line graph for two decay curve.
TimePointRemoval1	The candidate_1 of time point removal.
TimePointRemoval2	The candidate_2 of time point removal.

Value

shiny.appobj object for searching and showing RNA decay curve for each gene.

Examples

```
library(data.table)
normalized_rpk_matrix <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(1.00, 1.00, 1.00),
  CTRL_1_1h = c(1.00, 0.86, 0.96),
  CTRL_1_2h = c(1.00, 0.96, 0.88),
  CTRL_1_4h = c(1.00, 0.74, 0.85),
  CTRL_1_8h = c(1.00, 0.86, 0.68),
  CTRL_1_12h = c(1.01, 0.65, 0.60),
```

```

        gr_id = c(8, 9, 14),
        symbol = c("AAAS", "AACS", "AADAT"),
        accession_id = c("NM_015665", "NM_023928", "NM_182662"),
        locus = c("chr12", "chr12", "chr4"),
        KD_1_0h = c(1.00, 1.00, 1.00),
        KD_1_1h = c(1.01, 0.73, 0.71),
        KD_1_2h = c(1.01, 0.77, 0.69),
        KD_1_4h = c(1.01, 0.72, 0.67),
        KD_1_8h = c(1.01, 0.64, 0.38),
        KD_1_12h = c(1.00, 0.89, 0.63))

group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
halflife_table <- BridgeRHalfLifeCalcR2Select(normalized_rpk_matrix,
                                             group = group,
                                             hour = hour,
                                             save = FALSE)
pvalue_table <- BridgeRPvalueEvaluation(halflife_table,
                                       save = FALSE)
shiny_test <- BridgeReport(pvalue_table)

```

BridgeRGrubbsTest

RNA half-life Grubbs test.

Description

BridgeRGrubbsTest calculates the p-value for each gene using grubbs test. The estimation is based on the standard deviation of RNA half-lives in control conditions.

Usage

```

BridgeRGrubbsTest(controlFile, compFile, hour = c(0, 1, 2, 4, 8, 12),
                  controlGroup = c("CTRL_PUM1", "CTRL_PUM2", "CTRL_DKD"), inforColumn = 4,
                  compIndex = 2, save = T, outputPrefix = "BridgeR_8")

```

Arguments

controlFile	The dataframe of halflife table.
compFile	The dataframe of RPKM table.
hour	The vector of time course about BRIC-seq experiment.
controlGroup	The vector of group names.
inforColumn	The number of information columns.
compIndex	The number of information columns.
save	Whether to save the output matrix file.
outputPrefix	The prefix for the name of the output.

Value

data.table object about Grabbs test result.

Examples

```
group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
half_sd_table <- CalcHalfLifeDeviation(halflife_table,
                                       RNA_halflife_grubbs_test,
                                       group = c("CTRL_1",
                                                "CTRL_2",
                                                "CTRL_3"),
                                       save = FALSE)
grubbs_table <- BridgeRGrubbsTest(half_sd_table,
                                  halflife_table,
                                  compIndex = 4,
                                  controlGroup = c("CTRL_1",
                                                  "CTRL_2",
                                                  "CTRL_3"),
                                  save = FALSE)
```

BridgeRHalfLifeCalc3models

Calculate RNA half-life for each gene using 3model method.

Description

BridgeRHalfLifeCalc3models calculates RNA half-life for each gene using 3 models methods (older version).

Usage

```
BridgeRHalfLifeCalc3models(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), inforColumn = 4, CutoffTimePointNumber = 4,
  save = T, outputPrefix = "BridgeR_5")
```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
inforColumn	The number of information columns.
CutoffTimePointNumber	The number of minimum time points for calc.
save	Whether to save the output matrix file.
outputPrefix	The prefix for the name of the output.

Value

data.table object about RNA half-life, R2 and fitting model.

Examples

```
library(data.table)
normalized_rpk_matrix <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(1.00, 1.00, 1.00),
  CTRL_1_1h = c(1.00, 0.86, 0.96),
  CTRL_1_2h = c(1.00, 0.96, 0.88),
  CTRL_1_4h = c(1.00, 0.74, 0.85),
  CTRL_1_8h = c(1.00, 0.86, 0.68),
  CTRL_1_12h = c(1.01, 0.65, 0.60),
  gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  KD_1_0h = c(1.00, 1.00, 1.00),
  KD_1_1h = c(1.01, 0.73, 0.71),
  KD_1_2h = c(1.01, 0.77, 0.69),
  KD_1_4h = c(1.01, 0.72, 0.67),
  KD_1_8h = c(1.01, 0.64, 0.38),
  KD_1_12h = c(1.00, 0.89, 0.63))

group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
halflife_table <- BridgeRHalfLifeCalc3models(normalized_rpk_matrix,
  group = group,
  hour = hour,
  save = FALSE)
```

BridgeRHalfLifeCalcR2Select

Calculate RNA half-life for each gene using R2 selection method.

Description

BridgeRHalfLifeCalcR2Select calculates RNA half-life for each gene using R2 selection method (default version).

Usage

```
BridgeRHalfLifeCalcR2Select(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), inforColumn = 4, CutoffTimePointNumber = 4,
  R2_criteria = 0.9, TimePointRemoval1 = c(1, 2), TimePointRemoval2 = c(8,
  12), ThresholdHalfLife1 = 3, ThresholdHalfLife2 = 12, save = T,
  outputPrefix = "BridgeR_5")
```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
inforColumn	The number of information columns.
CutoffTimePointNumber	The number of minimum time points for calc.
R2_criteria	The cutoff of R2 for R2 selection.
TimePointRemoval1	The candidate_1 of time point removal.
TimePointRemoval2	The candidate_2 of time point removal.
ThresholdHalfLife1	The cutoff of TimePointRemoval1.
ThresholdHalfLife2	The cutoff of TimePointRemoval2.
save	Whether to save the output matrix file.
outputPrefix	The prefix for the name of the output.

Value

data.table object about RNA half-life, R2 and fitting model.

Examples

```
library(data.table)
normalized_rpk_matrix <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(1.00, 1.00, 1.00),
  CTRL_1_1h = c(1.00, 0.86, 0.96),
  CTRL_1_2h = c(1.00, 0.96, 0.88),
  CTRL_1_4h = c(1.00, 0.74, 0.85),
  CTRL_1_8h = c(1.00, 0.86, 0.68),
  CTRL_1_12h = c(1.01, 0.65, 0.60),
  gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  KD_1_0h = c(1.00, 1.00, 1.00),
  KD_1_1h = c(1.01, 0.73, 0.71),
  KD_1_2h = c(1.01, 0.77, 0.69),
  KD_1_4h = c(1.01, 0.72, 0.67),
  KD_1_8h = c(1.01, 0.64, 0.38),
  KD_1_12h = c(1.00, 0.89, 0.63))

group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
```

```

halflife_table <- BridgeRHalfLifeCalcR2Select(normalized_rpk_matrix,
                                             group = group,
                                             hour = hour,
                                             save = FALSE)

```

BridgeRNormalization *Calculate the normalized RPKM for BRIC-seq dataset.*

Description

BridgeRNormalization calculates the normalized RPKM values.

Usage

```

BridgeRNormalization(inputFile, normFactorFile, group = c("Control",
"Knockdown"), hour = c(0, 1, 2, 4, 8, 12), inforColumn = 4, save = T,
outputPrefix = "BridgeR_4")

```

Arguments

inputFile	The vector of tab-delimited matrix file.
normFactorFile	The vector of tab-delimited normalization factor file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
inforColumn	The number of information columns.
save	Whether to save the output matrix file.
outputPrefix	The prefix for the name of the output.

Value

data.table object about normalized RPKM values.

Examples

```

library(data.table)
rpk_matrix <- data.table(gr_id = c(8, 9, 14),
                        symbol = c("AAAS", "AACS", "AADAT"),
                        accession_id = c("NM_015665", "NM_023928", "NM_182662"),
                        locus = c("chr12", "chr12", "chr4"),
                        CTRL_1_0h = c(41, 5, 5),
                        CTRL_1_1h = c(48, 7, 6),
                        CTRL_1_2h = c(56, 10, 6),
                        CTRL_1_4h = c(87, 12, 10),
                        CTRL_1_8h = c(124, 20, 11),
                        CTRL_1_12h = c(185, 22, 15),
                        gr_id = c(8, 9, 14),

```

```

symbol = c("AAAS", "AACS", "AADAT"),
accession_id = c("NM_015665", "NM_023928", "NM_182662"),
locus = c("chr12", "chr12", "chr4"),
KD_1_0h = c(21, 10, 3),
KD_1_1h = c(33, 11, 3),
KD_1_2h = c(42, 15, 4),
KD_1_4h = c(60, 20, 5),
KD_1_8h = c(65, 37, 6),
KD_1_12h = c(70, 42, 6))
group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
rpkm_list <- BridgeRDataSetFromMatrix(inputFile = rpkm_matrix,
                                     group = group,
                                     hour = hour,
                                     cutoff = 0.1,
                                     inforColumn = 4,
                                     save = FALSE)

raw_table <- rpkm_list[[1]]
test_table <- rpkm_list[[2]]
factor_table <- BridgeRNormalizationFactors(test_table,
                                           save = FALSE)
normalized_table <- BridgeRNormalization(test_table,
                                         factor_table,
                                         save = FALSE)

```

BridgeRNormalizationFactors

Calculate normalization factors for BRIC-seq datasets.

Description

BridgeRNormalizationFactors calculates the normalization factors for BRIC-seq datasets.

Usage

```

BridgeRNormalizationFactors(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), inforColumn = 4, save = T, YMin = -2,
  YMax = 2, downsamplingFig = 0.2, makeFig = FALSE,
  cutoffQuantile = 0.975, figOutputPrefix = "BridgeR_3_fig",
  factorOutputPrefix = "BridgeR_3")

```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
inforColumn	The number of information columns.

save Whether to save the output matrix file.
YMin Y-axis min.
YMax Y-axis max.
downsamplingFig the factor for downsampling.
makeFig Whether to save the figure of normalization factor.
cutoffQuantile cutoff value of quantile.
figOutputPrefix The prefix for the name of figure output.
factorOutputPrefix The prefix for the name of factor output.

Value

data.table object about normalization factors calculated by quantile method.

Examples

```

library(data.table)
rpkm_matrix <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(41, 5, 5),
  CTRL_1_1h = c(48, 7, 6),
  CTRL_1_2h = c(56, 10, 6),
  CTRL_1_4h = c(87, 12, 10),
  CTRL_1_8h = c(124, 20, 11),
  CTRL_1_12h = c(185, 22, 15),
  gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  KD_1_0h = c(21, 10, 3),
  KD_1_1h = c(33, 11, 3),
  KD_1_2h = c(42, 15, 4),
  KD_1_4h = c(60, 20, 5),
  KD_1_8h = c(65, 37, 6),
  KD_1_12h = c(70, 42, 6))
group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
rpkm_list <- BridgeRDataSetFromMatrix(inputFile = rpkm_matrix,
  group = group,
  hour = hour,
  cutoff = 0.1,
  inforColumn = 4,
  save = FALSE)

raw_table <- rpkm_list[[1]]
test_table <- rpkm_list[[2]]
factor_table <- BridgeRNormalizationFactors(test_table,

```

```
save = FALSE)
```

```
BridgeRNormalizationFactorsHK
```

```
Calculate normalization factors from house-keeping genes.
```

Description

BridgeRNormalizationFactorsHK calculates the normalization factors from house-keeping genes.

Usage

```
BridgeRNormalizationFactorsHK(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), inforColumn = 4,
  inforHKGenesRow = "symbol", HKGenes = c("GAPDH", "PGK1", "PPIA", "ENO1",
  "ATP5B", "ALDOA"), save = T, factorOutputPrefix = "BridgeR_3")
```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
inforColumn	The number of information columns.
inforHKGenesRow	The column number of house-keeping gene information.
HKGenes	The vector of house-keeping genes.
save	Whether to save the output matrix file.
factorOutputPrefix	The prefix for the name of factor output.

Value

data.table object about normalization factor calculated by house-keeping genes.

Examples

```
library(data.table)
rpkm_matrix <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(41, 5, 5),
  CTRL_1_1h = c(48, 7, 6),
  CTRL_1_2h = c(56, 10, 6),
  CTRL_1_4h = c(87, 12, 10),
  CTRL_1_8h = c(124, 20, 11),
```

```

CTRL_1_12h = c(185, 22, 15),
gr_id = c(8, 9, 14),
symbol = c("AAAS", "AACS", "AADAT"),
accession_id = c("NM_015665", "NM_023928", "NM_182662"),
locus = c("chr12", "chr12", "chr4"),
KD_1_0h = c(21, 10, 3),
KD_1_1h = c(33, 11, 3),
KD_1_2h = c(42, 15, 4),
KD_1_4h = c(60, 20, 5),
KD_1_8h = c(65, 37, 6),
KD_1_12h = c(70, 42, 6)

group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
rpkm_list <- BridgeRDataSetFromMatrix(inputFile = rpkm_matrix,
                                     group = group,
                                     hour = hour,
                                     cutoff = 0.1,
                                     inforColumn = 4,
                                     save = FALSE)

raw_table <- rpkm_list[[1]]
test_table <- rpkm_list[[2]]
factor_table <- BridgeRNormalizationFactorsSHK(test_table,
                                               save = FALSE)

```

BridgeRPvalueEvaluation

Calculate Fold-change of RNA half-life and p-value.

Description

BridgeRPvalueEvaluation calculates the fold-change of RNA half-life and p-value between two conditions.

Usage

```

BridgeRPvalueEvaluation(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), comparisonFile = c("Control", "Knockdown"),
  inforColumn = 4, CutoffTimePointNumber = 4, calibration = FALSE,
  save = TRUE, outputPrefix = "BridgeR_6")

```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
comparisonFile	The vector of group names.
inforColumn	The number of information columns.

CutoffTimePointNumber	The number of minimum time points for calc.
calibration	Calibration of RNA half-life.
save	Whether to save the output matrix file.
outputPrefix	The prefix for the name of the output.

Value

data.table object about Fold-change of RNA half-lives, p-value.

Examples

```
library(data.table)
normalized_rpk_matrix <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(1.00, 1.00, 1.00),
  CTRL_1_1h = c(1.00, 0.86, 0.96),
  CTRL_1_2h = c(1.00, 0.96, 0.88),
  CTRL_1_4h = c(1.00, 0.74, 0.85),
  CTRL_1_8h = c(1.00, 0.86, 0.68),
  CTRL_1_12h = c(1.01, 0.65, 0.60),
  gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  KD_1_0h = c(1.00, 1.00, 1.00),
  KD_1_1h = c(1.01, 0.73, 0.71),
  KD_1_2h = c(1.01, 0.77, 0.69),
  KD_1_4h = c(1.01, 0.72, 0.67),
  KD_1_8h = c(1.01, 0.64, 0.38),
  KD_1_12h = c(1.00, 0.89, 0.63))

group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
halflife_table <- BridgeRHalfLifeCalcR2Select(normalized_rpk_matrix,
  group = group,
  hour = hour,
  save = FALSE)

pvalue_table <- BridgeRPvalueEvaluation(halflife_table,
  group = group,
  hour = hour,
  save = FALSE)
```

Description

BridgeRResultChecker returns several BRIC-seq result information. This function is used for checking the distribution of genome-wide RNA half-lives.

Usage

```
BridgeRResultChecker(inputFile, group = c("Control", "Knockdown"),
  hour = c(0, 1, 2, 4, 8, 12), inforColumn = 4, save = T,
  outputPrefix = "BridgeR_9")
```

Arguments

inputFile	The vector of tab-delimited matrix file.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
inforColumn	The number of information columns.
save	Whether to save the output fig file.
outputPrefix	The prefix for the name of the output.

Value

list object about ggplot2 fig data.

Examples

```
library(data.table)
normalized_table <- data.table(gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  CTRL_1_0h = c(1.00, 1.00, 1.00),
  CTRL_1_1h = c(1.00, 0.86, 0.96),
  CTRL_1_2h = c(1.00, 0.96, 0.88),
  CTRL_1_4h = c(1.00, 0.74, 0.85),
  CTRL_1_8h = c(1.00, 0.86, 0.68),
  CTRL_1_12h = c(1.01, 0.65, 0.60),
  gr_id = c(8, 9, 14),
  symbol = c("AAAS", "AACS", "AADAT"),
  accession_id = c("NM_015665", "NM_023928", "NM_182662"),
  locus = c("chr12", "chr12", "chr4"),
  KD_1_0h = c(1.00, 1.00, 1.00),
  KD_1_1h = c(1.01, 0.73, 0.71),
  KD_1_2h = c(1.01, 0.77, 0.69),
  KD_1_4h = c(1.01, 0.72, 0.67),
  KD_1_8h = c(1.01, 0.64, 0.38),
  KD_1_12h = c(1.00, 0.89, 0.63))
group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
half-life_table <- BridgeRHalfLifeCalcR2Select(normalized_table,
```

```

                                group = group,
                                hour = hour,
                                save = FALSE)
pvalue_table <- BridgeRPvalueEvaluation(halfLife_table,
                                group = group,
                                hour = hour,
                                save = FALSE)
result_fig <- BridgeRResultChecker(pvalue_table,
                                save = FALSE)

```

CalcHalfLifeDeviation *Calculate RNA half-life SD.*

Description

BridgeRHalfLifeCalcR2Select calculates RPKM SD and RNA half-life SD for each gene.

Usage

```

CalcHalfLifeDeviation(inputFile, rawFile, group = c("CTRL_PUM1", "CTRL_PUM2",
  "CTRL_DKD"), hour = c(0, 1, 2, 4, 8, 12), save = T, figSave = F,
  inforColumn = 4, outputPrefix = "BridgeR_7")

```

Arguments

inputFile	The dataframe of halfLife table.
rawFile	The dataframe of RPKM table.
group	The vector of group names.
hour	The vector of time course about BRIC-seq experiment.
save	Whether to save the output matrix file.
figSave	Whether to save the output fig file.
inforColumn	The number of information columns.
outputPrefix	The prefix for the name of the output.

Value

data.table object about RNA half-life SD.

Examples

```

group <- c("Control", "Knockdown")
hour <- c(0, 1, 2, 4, 8, 12)
half_sd_table <- CalcHalfLifeDeviation(halfLife_table,
                                RNA_halfLife_grubbs_test,
                                group = c("CTRL_1",
                                "CTRL_2",

```

```

"CTRL_3"),
save = FALSE)

```

halflife_table	<i>BRIC-seq result dataset for p-value estimation using grubbs test</i>
----------------	---

Description

A dataset containing the RPKM for each time point, information column, RNA half-life, R2 and fitting model about 200 genes. The variables are as follows:

Usage

```
halflife_table
```

Format

A data frame with 200 rows and 52 variables:

gr_id Group id
symbol Gene symbol
accession_id Gene accession id (RefSeq)
locus Genome locus
T00_1 RPKM value at 0h in control condition
T01_1 RPKM value at 1h in control condition
T02_1 RPKM value at 2h in control condition
T04_1 RPKM value at 4h in control condition
T08_1 RPKM value at 8h in control condition
T12_1 RPKM value at 12h in control condition
Model RNA decay fitting model
R2 R2 for fitting curve
half_life RNA half-life
gr_id Group id
symbol Gene symbol
accession_id Gene accession id (RefSeq)
locus Genome locus
T00_2 RPKM value at 0h in control condition
T01_2 RPKM value at 1h in control condition
T02_2 RPKM value at 2h in control condition
T04_2 RPKM value at 4h in control condition

T08_2 RPKM value at 8h in control condition

T12_2 RPKM value at 12h in control condition

Model RNA decay fitting model

R2 R2 for fitting curve

half_life RNA half-life

gr_id Group id

symbol Gene symbol

accession_id Gene accession id (RefSeq)

locus Genome locus

T00_3 RPKM value at 0h in control condition

T01_3 RPKM value at 1h in control condition

T02_3 RPKM value at 2h in control condition

T04_3 RPKM value at 4h in control condition

T08_3 RPKM value at 8h in control condition

T12_3 RPKM value at 12h in control condition

Model RNA decay fitting model

R2 R2 for fitting curve

half_life RNA half-life

gr_id Group id

symbol Gene symbol

accession_id Gene accession id (RefSeq)

locus Genome locus

T00_4 RPKM value at 0h in knockdown condition

T01_4 RPKM value at 1h in knockdown condition

T02_4 RPKM value at 2h in knockdown condition

T04_4 RPKM value at 4h in knockdown condition

T08_4 RPKM value at 8h in knockdown condition

T12_4 RPKM value at 12h in knockdown condition

Model RNA decay fitting model

R2 R2 for fitting curve

half_life RNA half-life

RNA_half-life_comparison

test BRIC-seq dataset for RNA half-life comparison

Description

A dataset containing the RPKM for each time point and information column about 200 genes. The variables are as follows:

Usage

RNA_half-life_comparison

Format

A data frame with 200 rows and 20 variables:

gr_id Group id

symbol Gene symbol

accession_id Gene accession id (RefSeq)

locus Genome locus

CTRL_1_0h RPKM value at 0h in control condition

CTRL_1_1h RPKM value at 1h in control condition

CTRL_1_2h RPKM value at 2h in control condition

CTRL_1_4h RPKM value at 4h in control condition

CTRL_1_8h RPKM value at 8h in control condition

CTRL_1_12h RPKM value at 12h in control condition

gr_id Group id

symbol Gene symbol

accession_id Gene accession id (RefSeq)

locus Genome locus

KD_1_0h RPKM value at 0h in knockdown condition

KD_1_1h RPKM value at 1h in knockdown condition

KD_1_2h RPKM value at 2h in knockdown condition

KD_1_4h RPKM value at 4h in knockdown condition

KD_1_8h RPKM value at 8h in knockdown condition

KD_1_12h RPKM value at 12h in knockdown condition

RNA_half-life_comparison_HK

test BRIC-seq dataset for RNA half-life comparison using House-keeping genes.

Description

A dataset containing the RPKM for each time point and information column about 200 genes + house-keeping genes. The variables are as follows:

Usage

RNA_half-life_comparison_HK

Format

A data frame with 200 rows and 20 variables:

gr_id Group id

symbol Gene symbol

accession_id Gene accession id (RefSeq)

locus Genome locus

CTRL_1_0h RPKM value at 0h in control condition

CTRL_1_1h RPKM value at 1h in control condition

CTRL_1_2h RPKM value at 2h in control condition

CTRL_1_4h RPKM value at 4h in control condition

CTRL_1_8h RPKM value at 8h in control condition

CTRL_1_12h RPKM value at 12h in control condition

gr_id Group id

symbol Gene symbol

accession_id Gene accession id (RefSeq)

locus Genome locus

KD_1_0h RPKM value at 0h in knockdown condition

KD_1_1h RPKM value at 1h in knockdown condition

KD_1_2h RPKM value at 2h in knockdown condition

KD_1_4h RPKM value at 4h in knockdown condition

KD_1_8h RPKM value at 8h in knockdown condition

KD_1_12h RPKM value at 12h in knockdown condition

 RNA_half-life_grubbs_test

test BRIC-seq dataset for p-value estimation using grubbs test

Description

A dataset containing the RPKM for each time point and information column about 200 genes. The variables are as follows:

Usage

RNA_half-life_grubbs_test

Format

A data frame with 200 rows and 40 variables:

gr_id Group id
symbol Gene symbol
accession_id Gene accession id (RefSeq)
locus Genome locus
CTRL_1_0h RPKM value at 0h in control condition
CTRL_1_1h RPKM value at 1h in control condition
CTRL_1_2h RPKM value at 2h in control condition
CTRL_1_4h RPKM value at 4h in control condition
CTRL_1_8h RPKM value at 8h in control condition
CTRL_1_12h RPKM value at 12h in control condition
gr_id Group id
symbol Gene symbol
accession_id Gene accession id (RefSeq)
locus Genome locus
CTRL_2_0h RPKM value at 0h in control condition
CTRL_2_1h RPKM value at 1h in control condition
CTRL_2_2h RPKM value at 2h in control condition
CTRL_2_4h RPKM value at 4h in control condition
CTRL_2_8h RPKM value at 8h in control condition
CTRL_2_12h RPKM value at 12h in control condition
gr_id Group id
symbol Gene symbol
accession_id Gene accession id (RefSeq)

locus Genome locus

CTRL_3_0h RPKM value at 0h in control condition

CTRL_3_1h RPKM value at 1h in control condition

CTRL_3_2h RPKM value at 2h in control condition

CTRL_3_4h RPKM value at 4h in control condition

CTRL_3_8h RPKM value at 8h in control condition

CTRL_3_12h RPKM value at 12h in control condition

gr_id Group id

symbol Gene symbol

accession_id Gene accession id (RefSeq)

locus Genome locus

KD_1_0h RPKM value at 0h in knockdown condition

KD_1_1h RPKM value at 1h in knockdown condition

KD_1_2h RPKM value at 2h in knockdown condition

KD_1_4h RPKM value at 4h in knockdown condition

KD_1_8h RPKM value at 8h in knockdown condition

KD_1_12h RPKM value at 12h in knockdown condition

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