Package ‘bridger2’

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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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`BridgeRCore` *BridgeR basic function for calculating RNA half-life from BRIC-seq data*

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", "ENO1", "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 candicate_1 of time point removal.
`TimePointRemoval2`	The candicate_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_halflife_comparison[1:30,],
                              save = FALSE)
halflife_table <- BridgeRCore(RNA_halflife_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

`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.

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 candicate_1 of time point removal.
`TimePointRemoval2`	The candicate_2 of time point removal.

Value

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

Examples

```
library(data.table)
normalized_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(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_rpkm_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_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(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_rpkm_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 candicate_1 of time point removal.
`TimePointRemoval2`	The candicate_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_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(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_rpkm_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)
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)
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 <- BridgeRNormalizationFactorsHK(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_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(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_rpkm_matrix,
                                              group = group,
                                              hour = hour,
                                              save = FALSE)
pvalue_table <- BridgeRPvalueEvaluation(halflife_table,
                                        group = group,
                                        hour = hour,
                                        save = FALSE)
```

`BridgeRResultChecker` *BRIC-seq result checker*

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)
halflife_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` *BRIC-seq result dataset for p-value estimation using grubbs test*

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_halflife_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_halflife_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_halflife_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_halflife_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_halflife_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_halflife_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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