Package ‘BloodGen3Module’

November 7, 2025

Type Package

Title This R package for performing module repertoire analyses and generating fingerprint representations

Version 1.19.0

Date 2020-11-05

Description The BloodGen3Module package provides functions for R user performing module repertoire analyses
and generating fingerprint representations. Functions can perform group comparison or
individual sample analysis and visualization by fingerprint grid plot or fingerprint heatmap.
Module repertoire analyses typically involve determining the percentage of the constitutive genes
for each module that are significantly increased or decreased.
As we describe in details;https://www.biorxiv.org/content/10.1101/525709v2 and https://pubmed.ncbi.nlm.nih.gov/33624743/,
the results of module repertoire analyses can be represented in a fingerprint format,
where red and blue spots indicate increases or decreases in module activity.
These spots are subsequently represented either on a grid,
with each position being assigned to a given module,
or in a heatmap where the samples are arranged in columns and the modules in rows.

Depends R (>= 4.1)

License GPL-2

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Imports SummarizedExperiment, ExperimentHub, methods, grid, graphics, stats, grDevices, circlize, testthat, ComplexHeatmap(>= 1.99.8), ggplot2, matrixStats, gtools, reshape2, preprocessCore, randomcoloR, V8, limma

biocViews Software, Visualization, GeneExpression

Suggests RUnit, devtools, BiocGenerics, knitr, rmarkdown

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/BloodGen3Module

git_branch devel

git_last_commit 825e116

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-07

Author Darawan Rinchai [aut, cre] (ORCID: <https://orcid.org/0000-0001-8851-7730>)

Maintainer Darawan Rinchai <drinchai@gmail.com>

Contents

`color` *Color for fingerprint visulization*

Description

Character vector of color for fingerprint grid plot

Usage

```
color
```

Format

A vector of 1134 character

`fingerprintplot` *Individual fingerprint visualization The fingerprintplot function will generate fingerprint heatmap plots as a pdf file. The file will be saved in the working directory specified for the analysis. The default cut off for visualization is set at 15%, it can be changed to any value between 0-100%.*

Description

Individual fingerprint visualization The fingerprintplot function will generate fingerprint heatmap plots as a pdf file. The file will be saved in the working directory specified for the analysis. The default cut off for visualization is set at 15%, it can be changed to any value between 0-100%.

Usage

```
fingerprintplot(
  Individual_df,
  sample_info = NULL,
  cutoff = NULL,
  rowSplit = TRUE,
  Ref_group = NULL,
  show_ref_group = FALSE,
  Group_column = NULL,
  Aggregate = NULL,
  filename = NULL,
  height = NULL,
  width = NULL
)
```

Arguments

`Individual_df`	Dataframe with output generated after running the 'Individualcomparison' function
`sample_info`	A dataframe with sample annotation.
`cutoff`	Numeric value specifying the percentage cut off used for fingerprint visualization (0 to 100).
`rowSplit`	Logical operator (TRUE/FALSE) to indicate if rows of the heatmaps should be split by each aggregate
`Ref_group`	Characters name of reference group or samples that considered as control
`show_ref_group`	Character vector specifying value within the group column that will be used as Reference group
`Group_column`	Name of the columns for the groups used for the analysis
`Aggregate`	Character vector specifying name of specific module aggregates for heatmap fingerprint plot
`filename`	Character vector with a name for saving file

`height`	Sets the height of the graphics region in inches. The default values are 28
`width`	Sets the width of the graphics region in inches. The default values are 17

Value

A heatmap of % of module response in each single sample

Author(s)

Darawan Rinchai drinchai@gmail.com

Examples

```
## data could be downloaded from ExperimentHub("GSE13015")
library(ExperimentHub)
library(SummarizedExperiment)
dat = ExperimentHub()
res = query(dat , "GSE13015")
GSE13015 = res[["EH5429"]]
Individual_df = Individualcomparison(GSE13015, sample_info = NULL,
                                    FC = 1.5, DIFF = 10, Group_column = "Group_test",
                                    Ref_group = "Control")
fingerprintplot(Individual_df, sample_info = NULL,
               cutoff = 15, rowSplit = TRUE, Ref_group = "Control",
               show_ref_group = FALSE, Group_column = "Group_test",
               Aggregate = c("A28"), filename = tempfile(), height = 5,
               width = 10)
```

`fold_change` *calculation of Fold-Change*

Description

A function to calculate fold-change between group comparison; "Test_group" vs "Ref_group"

Usage

```
fold_change(
  df_raw = df_raw,
  sample_info = sample_info,
  Group_column = Group_column,
  Test_group = Test_group,
  Ref_group = Ref_group
)
```

Arguments

`df_raw`	Matrix of normalized expression data (not Log2 transformed). Genes should be in rows and Sample ID in columns. Row names are required to be valid Gene Symbols
`sample_info`	A dataframe with sample annotation. Sample_info dataframe requires two columns: 1) a column specifying Sample ID (exactly matching Sample ID of data.matrix) and 2) a column specifying group names
`Group_column`	Character vector identical to the column name from sample_info dataframe that specifies group annotation used for the analysis
`Test_group`	Character vector specifying values within the group column (Group_column) that will be used as Test group (samples considered as cases or “intervention” group).
`Ref_group`	Character vector specifying value within the group column (Group_column) that will be used as Reference group

Value

A matrix of the fold change comparison between "Test_group" vs ""Ref_group"

Author(s)

Darawan Rinchai drinchai@gmail.com

Examples

```
## data could be downloaded from ExperimentHub("GSE13015")
library(ExperimentHub)
library(SummarizedExperiment)
dat = ExperimentHub()
res = query(dat , "GSE13015")
GSE13015 = res[["EH5429"]]
data_matrix = assay(GSE13015)
sample_ann = data.frame(colData(GSE13015))

FCgroup = fold_change(df_raw = data_matrix[c(1:5),],
                      sample_info = sample_ann,
                      Group_column = "Group_test",
                      Test_group="Sepsis",
                      Ref_group="Control")
```

`Gen3_ann` *Functional annotation for visulization*

Description

A dataframe contain module identifer, functional annotation and color in each specific module

Usage

```
Gen3_ann
```

Format

A data.frame with 5 variables: `Modules: Module identifier`, `Function: Functional annotation`, `Position: position on fingerprint grid plot`, `Module_color: specific color of each module for visulization`, `Cluster: Module cluster membership`

`gridplot` *Fingerprint grid visualization*

Description

The gridplot function will generate a grid plot as a pdf file. Specific working directory for the analysis need to be specified for saving the file. The result of the plot should be return in the same working directory. The default cut off for visualization is set at 15%, it can be changed to any value between 0-100%.

Usage

```
gridplot(Group_df, cutoff = NULL, Ref_group = NULL, filename = NULL)
```

Arguments

`Group_df`	Dataframe with output generated after running the'Groupcomparison' function
`cutoff`	Numeric value specifying the percentage cut off used for fingerprint visualization (from 0 to 100)
`Ref_group`	Character vector specifying value within the group column that will be used as Reference group
`filename`	Character vector with a name for saving file

Value

```
A pdf file of grid plot
```

Author(s)

Darawan Rinchai drinchai@gmail.com

Examples

```
## data could be downloaded from ExperimentHub("GSE13015")
library(ExperimentHub)
library(SummarizedExperiment)
dat = ExperimentHub()
res = query(dat , "GSE13015")
GSE13015 = res[["EH5429"]]
Group_df = Groupcomparison(GSE13015, sample_info = NULL,
                          FC = 0, pval = 0.1, FDR = TRUE, Test_group = "Sepsis",
                          Group_column = "Group_test", Ref_group = "Control")
gridplot(Group_df, cutoff = 15,
         Ref_group = "Control",
         filename= tempfile())
```

`Groupcomparison` *Group comparison analysis*

Description

The Groupcomparison function will perform group comparison analyses and the results are expressed “at the module level” as percent of genes increased or decreased.

- Expression matrix and sample annotation files are required to perform this analysis.
- The sample annotation file must be loaded using a specific name = "sample_info".
- The names of the columns for the conditions used in the analysis must be specified.

Usage

```
Groupcomparison(
  data.matrix,
  sample_info = NULL,
  FC = NULL,
  pval = NULL,
  FDR = TRUE,
  Group_column = NULL,
  Test_group = "Test_group",
  Ref_group = "Control",
  SummarizedExperiment = TRUE
)
```

Arguments

`data.matrix`	Matrix of normalized expression data (not Log2 transformed).Row names are required to be valid Gene Symbols. Columns names are sample IDs or data.matrix can also be given a summarizedexperiment object and assigned data.matrix and sample_info accordingly from the object.

`sample_info`	A dataframe with sample annotation. Sample_info dataframe requires two columns: 1) a column specifying Sample ID (exactly matching the Sample ID of data.matrix) and 2) a column specifying group names
`FC`	Numeric value specifying the foldchange cut off that will be applied to define increase or decrease of a given transcript compared to the reference group
`pval`	Numeric value specifying p-value cut off or False discovery rate when FDR = TRUE
`FDR`	Logical operator to specify whether False discovery rate cut off (using BH-method) should be used
`Group_column`	Character vector identical to the column name from sample_info dataframe that specifies group annotation used for the analysis
`Test_group`	Character vector specifying values within the group column (Group_column) that will be used as Test group (samples considered as cases or “intervention” group).
`Ref_group`	Character vector specifying value within the group column (Group_column) that will be used as Reference group
`SummarizedExperiment`	Output data as the SummarizedExperiment class when SummarizedExperiment = TRUE

Value

```
A matrix of the percentahe of module response in each group comparison
```

Author(s)

Darawan Rinchai drinchai@gmail.com

Examples

```
## data could be downloaded from ExperimentHub("GSE13015")
library(ExperimentHub)
library(SummarizedExperiment)
dat = ExperimentHub()
res = query(dat , "GSE13015")
GSE13015 = res[["EH5429"]]
Group_df = Groupcomparison(GSE13015, sample_info = NULL,
                          FC = 0, pval = 0.1, FDR = TRUE, Test_group = "Sepsis",
                          Group_column = "Group_test", Ref_group = "Control")
```

`Groupcomparisonlimma` *Group comparison analysis using limma*

Description

The Groupcomparisonlimma function will perform group comparison analyses using "limma" function from "limma R package" and the results are expressed “at the module level” as percent of genes increased or decreased.

- Expression matrix and sample annotation files are required to perform this analysis.
- The sample annotation file must be loaded using a specific name = "sample_info".
- The names of the columns for the conditions used in the analysis must be specified.

Usage

```
Groupcomparisonlimma(
  data.matrix,
  sample_info = NULL,
  FC = NULL,
  pval = NULL,
  FDR = TRUE,
  Group_column = NULL,
  Test_group = "Test_group",
  Ref_group = "Control",
  SummarizedExperiment = TRUE
)
```

Arguments

`data.matrix`	Matrix of normalized expression data (not Log2 transformed).Row names are required to be valid Gene Symbols. Columns names are sample IDs or data.matrix can also be given a summarizedexperiment object and assigned data.matrix and sample_info accordingly from the object.
`sample_info`	A dataframe with sample annotation.
`FC`	Numeric value specifying the foldchange cut off that will be applied to define increase or decrease of a given transcript compared to the reference group
`pval`	Numeric value specifying p-value cut off or False discovery rate when FDR = TRUE
`FDR`	Logical operator to specify whether False discovery rate cut off (using BH-method) should be used
`Group_column`	Character vector identical to the column name from sample_info dataframe that specifies group annotation used for the analysis
`Test_group`	Character vector specifying value within the group column that will be used as Test group

`Ref_group`	Character vector specifying value within the group column that will be used as Reference group
`SummarizedExperiment`	Output data as the SummarizedExperiment class when SummarizedExperiment = TRUE

Value

```
A matrix of the percentahe of module response in each group comparison
```

Author(s)

Darawan Rinchai drinchai@gmail.com

Examples

```
## data could be downloaded from ExperimentHub("GSE13015")
library(ExperimentHub)
library(SummarizedExperiment)
dat = ExperimentHub()
res = query(dat , "GSE13015")
GSE13015 = res[["EH5429"]]
Group_limma <- Groupcomparisonlimma(GSE13015, sample_info = NULL,
FC = 1.5, pval = 0.1, FDR = TRUE, Group_column = "Group_test",
Test_group = "Sepsis", Ref_group = "Control")
```

`Individualcomparison` *Individual single sample analysis*

Description

The Individualcomparison function will perform individual sample comparison analysis in reference to a control sample or group of samples, with the results are expressed “at the module level” as percent of genes increased or decreased.

Usage

```
Individualcomparison(
  data.matrix,
  sample_info = NULL,
  FC = NULL,
  DIFF = NULL,
  Group_column = NULL,
  Ref_group = NULL,
  SummarizedExperiment = TRUE
)
```

Arguments

`data.matrix`	Matrix of normalized expression data (not Log2 transformed).Row names are required to be valid Gene Symbols. Columns names are sample IDs or data.matrix can also be given a summarizedexperiment object and assigned data.matrix and sample_info accordingly from the object.
`sample_info`	A dataframe with sample annotation.
`FC`	Numeric value specifying the foldchange cut off that will be applied to define increase or decrease of a given transcript compared to the reference group
`DIFF`	Numeric value specifying the difference cut off that will be applied to define increase or decrease of a given transcript compared to the reference group
`Group_column`	Character vector identical to the column name from sample_info dataframe that specifies group annotation used for the analysis
`Ref_group`	Character vector specifying value within the group column that will be used as Reference group
`SummarizedExperiment`	Output data as the SummarizedExperiment class when SummarizedExperiment = TRUE

Details

- Expression matrix and sample annotation file are required in order to perform this analysis.
- The sample annotation file must be loaded using a specific name = "sample_info".
- The names of the columns for the conditions used in the analysis must be specified
- The default cutoff is set at FC =1.5 and DIFF =10

Value

```
A matrix of the percentahe of module response at individual level and SummarizedExperiment object
```

Author(s)

Darawan Rinchai drinchai@gmail.com

Examples

```
## data could be downloaded from ExperimentHub("GSE13015")
library(ExperimentHub)
library(SummarizedExperiment)
dat = ExperimentHub()
res = query(dat , "GSE13015")
GSE13015 = res[["EH5429"]]
Individual_df = Individualcomparison(GSE13015, sample_info = NULL,
                                    FC = 1.5, DIFF = 10, Group_column = "Group_test",
                                    Ref_group = "Control")
```

`Module_listGen3` *Module identifer and list membership in each module*

Description

A dataframe contain gene member of 3rd generantion of blood module repertoire construction

Usage

```
Module_listGen3
```

Format

A data.frame with 14168 rows by 5 variables: `Module`: `Module identifier`, `Gene symbol`: `gene membership`, `Module_gene`: `gene specific module membership`, `Function`: `Functional annotation`, `position`: `position on fingerprint grid plot`

Index