# Package ‘BcDiag’

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**Title** Diagnostics Plots for Bicluster Data

**License** GPL-3

**Depends** R (>= 2.10)

**Suggests** biclust, isa2

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**Description** Diagnostic tools based on two-way anova and median-polish residual plots for Bicluster output obtained from packages; ``biclust'' by Kaiser et al.(2008),``isa2'' by Csardi et al. (2010) and ``fabia'' by Hochreiter et al. (2010). Moreover, It provides visualization tools for bicluster output and corresponding non-bicluster rows- or columns outcomes. It has also extended the idea of Kaiser et al.(2008) which is, extracting bicluster output in a text format, by adding two bicluster methods from the fabia and isa2 R packages.

**Imports** fabia, methods, graphics, stats

**NeedsCompilation** no

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## Contents

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## `BcDiag-package` *The BCDiag package*

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### Description

Bicluster Diagnostics plots

### Introduction

The Bicluster Diagnostics plots(BcDiag) package is a visualization technique, for profiling and summarizing Bicluster data, particularly for gene expression level data. Target data matrix are bicluster genes(rows) and conditions(columns) versus clustered genes or conditions.

### Main task

A BicDiag is a package of visualaization bicluster data, which is a subset matrix that have similar characterstics in terms of row(genes) and columns(conditions).

It has used three different types of bicluster algorithms to extract the biculsterd data; 'biclust','isa2' and 'fabia'. plots such as boxplot,histogram, line plot,3D plot are some of the plots that have used to visualize the data.

Major taskes of the package can be categorized in to three sections;

1. profiling and summarizing the biclustered vs. the clustered simultaneously
2. profiling and summarizing only the biclusterd data.
3. exploring the biclusterd data using anova and median polish techniques.

### Author(s)

Mengsteab Aregay <`mycs.zab@gmail.com`>

### References

Hochreiter, S., Bodenhofer, U., Heusel, M.*et al.* (2010).FABIA: factor analysis for bicluster acquisition. *Bioinformatices*, 26, 1520-1527.

Kaiser S. and Leisch F. (2008). A Toolbox for Bicluster Analysis in R. *Ludwigstrasse.* 33.

Csardi G., Kutalik Z., and Bergmann S.(2010). Modular analysis of gene expression data with R. *Bioinformatics,* 26, 1376-7

### See Also

The Bicluster algorithms in the packages **biclust**,**fabia** and **isa2**.

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`anomedOnlybic` *The anomedOnlybic function*

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## Description

Provides ANOVA and median polish residual plots for biclustered data.

## Usage

```
anomedOnlybic(dset, bres, fit="boxplot", mname="biclust", bnum=1,
fabia.thresZ=0.5,fabia.thresL=NULL)
```

## Arguments

| | |
|---|---|
| `dset` | data matrix. |
| `bres` | bicluster result. |
| `fit` | a string value to fit a plot; 'aplot','mplot','anovbplot','mpolishbplot','boxplot'. |
| `mname` | method name; 'biclust', 'isa2', 'fabia' or 'bicare'. |
| `bnum` | existing biclusters; '1','2'... |
| `fabia.thresZ` | Bicluster threshold for `mname="fabia"`. Threshold for sample belonging to bicluster; default 0.5. |
| `fabia.thresL` | Bicluster threshold for `mname="fabia"`. Threshold for loading belonging to bicluster (if not given it is estimated). |

## Details

A function provides residuals plots for biclustered data based on ANOVA and median polish.

The function checks the required parameter values and fit the plot according to the user requirements.

Note that the `"biclust"` option for `mname` will also accept results from the packages **iBBiG** and **rqubic**.

## Value

Residual plots or residual box plots.

## Author(s)

Mengsteab Aregay <`mycs.zab@gmail.com`>

## References

Van't Veer, L.J., Dai, H., van de Vijver, M.J., He, Y.D., Hart, A.A. et al. (2002). Gene expression profiling predicts clinical outcome of breast cancer,*Nature*, 415, 530-536.

Kaiser S. and Leisch F. (2008). A Toolbox for Bicluster Analysis in R. *Ludwigstrasse.* 33.

### Examples

```
data(breastc)
library(biclust)
# find bicluster using one of biclust algorithms

bic <- biclust(breastc, method=BCPlaid())
# fit residual boxplot from ANOVA
anomedOnlybic(dset=breastc,bres=bic,fit="boxplot",mname="biclust")
```

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## `breastc` *Gene Expression Data Example*

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### Description

Microarray data set of van't Veer breast cancer.

### Usage

```
data(breastc)
```

### Format

A data matrix with 1213 genes and 97 samples.

### References

Van't Veer, L.J., Dai, H., van de Vijver, M.J., He, Y.D., Hart, A.A. et al. (2002). Gene expression profiling predicts clinical outcome of breast cancer,*Nature*, 415, 530-536.

### Examples

```
data(breastc)

head(breastc)
```

---

## `dlbcl` *Gene Expression Data Example*

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### Description

Log transformed Microarray data set of Rosenwald diffuse large-B-cell lymphoma.

### Usage

```
data(dlbcl)
```

## Format

A data matrix with 661 genes and 141 samples.

## References

Rosenwald, A., Wright, G., Chan, W.C., Connors, J.M., Campo, E. et al. (2002). The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma, *New Engl. J. Med.*, 346. 1937-1947.

## Examples

```
data(dlbcl)

head(dlbcl)
```

---

## `exploreBic` *The exploreBic function*

## Description

Provides exploratory plots for biclustered and clustered data.

## Usage

```
exploreBic(dset, bres, gby ="genes", pfor ="mean", mname ="biclust", bnum =1,
fabia.thresZ=0.5,fabia.thresL=NULL)
```

## Arguments

| | |
|---|---|
| `dset` | data matrix. |
| `bres` | bicluster result. |
| `gby` | dimension to plot; 'genes' or 'conditions'. |
| `pfor` | plot for 'mean', 'median', 'variance', 'mad', 'all', or 'quant' (quantile). |
| `mname` | method name; 'biclust', 'isa2', 'fabia' or 'bicare' |
| `bnum` | existing biclusters; '1','2'... |
| `fabia.thresZ` | Bicluster threshold for `mname="fabia"`. Threshold for sample belonging to bicluster; default 0.5. |
| `fabia.thresL` | Bicluster threshold for `mname="fabia"`. Threshold for loading belonging to bicluster (if not given it is estimated). |

## Details

The exploreBic function is mainly used for exploratory data analysis. It provides summary plots for mean, median, variance, MAD and quantile plot.

The `exploreBic` function checks if the parameters are appropriately submitted and then identifies the biclusters submatrix and calculates its summary statistics. Finally, the results are displayed on the required plot.

Note that the `"biclust"` option for `mname` will also accept results from the packages **iBBiG** and **rqubic**.

## Value

Summary plot will display according to the user specification.

## Author(s)

Mengsteab Aregay <`mycs.zab@gmail.com`>

## References

Van't Veer, L.J., Dai, H., van de Vijver, M.J., He, Y.D., Hart, A.A. et al. (2002). Gene expression profiling predicts clinical outcome of breast cancer,*Nature*, 415, 530-536.

Hochreiter, S., Bodenhofer, U., Heusel, M.*et al.* (2010).FABIA: factor analysis for bicluster acquisition. *Bioinformatices*, 26, 1520-1527.

## See Also

`exploreOnlybic`

## Examples

```
data(breastc)
# find bicluster using biclust package
library(biclust)
bic <- biclust(breastc,method=BCPlaid())
# Plot the mean of biclusterd and clustered genes parallely.
exploreBic(dset=breastc,bres=bic,gby="conditions",pfor="mean",mname="biclust")
```

---

# `exploreOnlybic` *The exploreOnlybic function*

## Description

Provides exploratory plots only for biclustering results.

## Usage

```
exploreOnlybic(dset, bres, pfor= "all", gby= "genes", mname="biclust",bnum=1,
fabia.thresZ=0.5,fabia.thresL=NULL)
```

### Arguments

| | |
|---|---|
| `dset` | data matrix. |
| `bres` | biclustering result. |
| `gby` | group bicluster; 'genes' or 'conditions'. |
| `pfor` | fit a plot for 'mean', 'median', 'variance', 'mad', 'all', or 'quant' (quantile). |
| `mname` | method name; 'biclust', 'isa2', 'fabia' or 'bicare'. |
| `bnum` | existing biclusters; '1','2'... |
| `fabia.thresZ` | Bicluster threshold for `mname="fabia"`. Threshold for sample belonging to bicluster; default 0.5. |
| `fabia.thresL` | Bicluster threshold for `mname="fabia"`. Threshold for loading belonging to bicluster (if not given it is estimated). |

### Details

The exploreOnlybic function has similar function with `exploreBic`. The only difference is that it provides exploratory plots only for biclustered data.

### Value

Summary plot will display only for biclustered data.

Note that the `"biclust"` option for `mname` will also accept results from the packages **iBBiG** and **rqubic**.

### Author(s)

Mengsteab Aregay <`mycs.zab@gmail.com`>

### References

Van't Veer, L.J., Dai, H., van de Vijver, M.J., He, Y.D., Hart, A.A. et al. (2002). Gene expression profiling predicts clinical outcome of breast cancer,*Nature*, 415, 530-536.

Hochreiter, S., Bodenhofer, U., Heusel, M.*et al.* (2010).FABIA: factor analysis for bicluster acquisition. *Bioinformatices*, 26, 1520-1527.

### See Also

`exploreBic`

### Examples

```
data(breastc)
# find bicluster using biclust algorithm
library(biclust)
bic <- biclust(breastc,method=BCPlaid())
# Plot the median of biclusterd data.
exploreOnlybic(dset=breastc, bres=bic, pfor="all", gby="genes", mname="biclust", bnum=1)
```

---

`profileBic` *The profileBic function.*

---

## Description

Provides profile plots for biclustered and clustered data.

## Usage

```
profileBic(dset, bres, mname = c("fabia", "isa2", "biclust","bicare"), bplot = "all",
gby = "genes", bnum = 1, teta = 120, ph = 30, fabia.thresZ=0.5,fabia.thresL=NULL,
BClabel=TRUE,gene.lines=NULL,condition.lines=NULL)
```

## Arguments

| | |
|---|---|
| `dset` | data matrix. |
| `bres` | biclustering result. |
| `mname` | method name; 'biclust', 'isa2', 'fabia' or 'bicare'. |
| `bplot` | types of plots; 'all','lines', 'boxplot', 'histogram' or '3D'. |
| `gby` | grouped by; 'genes', or 'conditions'. |
| `bnum` | Existing biclusters; '1','2',... |
| `teta` | numerical value to rotate the 3D; 0, 90, 180,... |
| `ph` | numerical value to rotate the 3D; 0, 90, 180,... |
| `fabia.thresZ` | Bicluster threshold for `mname="fabia"`. Threshold for sample belonging to bicluster; default 0.5. |
| `fabia.thresL` | Bicluster threshold for `mname="fabia"`. Threshold for loading belonging to bicluster (if not given it is estimated). |
| `BClabel` | `TRUE`/`FALSE` to show BC labels on the lines plot. |
| `gene.lines` | Vector of indices or names of genes inside of Bicluster `bnum`. These gene profiles will be highlighted in the line plot (`bplot='lines'`). |
| `condition.lines` | Vector of indices or names of conditions inside of Bicluster `bnum`. These condition profiles will be highlighted in the line plot (`bplot='lines'`). |

## Details

The profile.bic function checks if all parameters are correctly submitted and then identifies the biclustered and clustered data.

Note that the `"biclust"` option for `mname` will also accept results from the packages **iBBiG** and **rqubic**.

## Value

profile.bic(dset, bres, mname="biclust", bplot="all", gby="genes", bnum=1, teta=120, ph=30)

## Author(s)

Mengsteab Aregay <`mycs.zab@gmail.com`>

## References

Van't Veer, L.J., Dai, H., van de Vijver, M.J., He, Y.D., Hart, A.A. et al. (2002). Gene expression profiling predicts clinical outcome of breast cancer,*Nature*, 415, 530-536.

Kaiser S. and Leisch F. (2008). A Toolbox for Bicluster Analysis in R. *Ludwigstrasse.* 33.

## Examples

```
# create the biclustering result
data(breastc)
library(biclust)
bic<- biclust(breastc, method=BCPlaid())
# 3 biclusters found

# 3D profile plot for biclustered and clustered data.
profileBic(dset=breastc,bres=bic,mname="biclust",
bplot="3D",gby="genes",teta=-30,ph=50,bnum=1)
```

---

# `writeBic` *The writeBic function*

## Description

Provides a summary output in a text format, extracted from 'biclust','isa2' and 'fabia' bicluster algorithms.

## Usage

```
writeBic(dset, fileName, bicResult, bicname,
mname = c("fabia", "isa2", "biclust","bicare"), append = TRUE, delimiter = " ",
fabia.thresZ=0.5,fabia.thresL=NULL)
```

## Arguments

| | |
|---|---|
| `dset` | data matrix |
| `fileName` | the name of the bicluster file to be saved. |
| `bicResult` | bicluster result obtained from 'biclust','isa2' or 'fabia' |
| `bicname` | the title to be given for the biclustered data. |
| `mname` | method name; 'biclust', 'isa2', 'fabia' or 'bicare' |
| `append` | logical value; TRUE as default |
| `delimiter` | delimiter in created output file; default value is " ". |
| `fabia.thresZ` | Bicluster threshold for `mname="fabia"`. Threshold for sample belonging to bicluster; default 0.5. |
| `fabia.thresL` | Bicluster threshold for `mname="fabia"`. Threshold for loading belonging to bicluster (if not given it is estimated). |

### Details

The original function was developed in 'biclust' package by Kaiser *et.al* (2008). We extend the function to be used for further bicluster algorithms, such as; 'isa2', 'fabia' and 'bicare'.

Note that the `"biclust"` option for `mname` will also accept results from the packages **iBBiG** and **rqubic**.

### Value

Biclustered text file with title, total number of biclustered, dimension and name of the biclustered genes(rows) or conditions(columns).

### Author(s)

Mengsteab Aregay

`<mycs.zab@gmail.com>`

### References

Van't Veer, L.J., Dai, H., van de Vijver, M.J., He, Y.D., Hart, A.A. et al. (2002). Gene expression profiling predicts clinical outcome of breast cancer,*Nature*, 415, 530-536.

Kaiser S. and Leisch F. (2008). A Toolbox for Bicluster Analysis in R. *Ludwigstrasse.* 33.

Csardi G., Kutalik Z., and Bergmann S.(2010). Modular analysis of gene expression data with R. *Bioinformatics,* 26, 1376-7

### See Also

**biclust**

### Examples

```
# create the biclustering result
data(breastc)
library(fabia)
fab<- fabia(breastc)
# write the biclustering result into a text file
writeBic(dset=breastc,fileName="fabiabreast.txt",
bicResult=fab, bicname="Biclust results for fabia",
mname="fabia")
```

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