Package 'Hiiragi2013'

November 10, 2026

Type Package

Title Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages

Version 1.48.1

Description This package contains the experimental data and a complete executable transcript (vignette) of the statistical analysis presented in the paper ``Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages" by Y. Ohnishi, W. Huber, A. Tsumura, M. Kang, P. Xenopoulos, K. Kurimoto, A. K. Oles, M. J. Arauzo-Bravo, M. Saitou, A.-K. Hadjantonakis and T. Hiiragi; Nature Cell Biology (2014) 16(1): 27-37. doi: 10.1038/ncb2881."

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LazyLoad true

Depends R (>= 4.0.0), Biobase

Imports MASS, RColorBrewer, cluster, gplots, grid, lattice, latticeExtra, genefilter

Suggests affy, BiocStyle, boot, clue, geneplotter, gtools, KEGGREST, mouse4302.db, xtable

biocViews ExperimentData, MicroarrayData, qPCRData, ReproducibleResearch

git_url https://git.bioconductor.org/packages/Hiiragi2013

git_branch RELEASE_3_23

git_last_commit 586aff9

git_last_commit_date 2026-06-22

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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`getDifferentialExpressedGenes`
Find Differentially Expressed Genes

Description

Returns differentially expressed genes between two conditions.

Usage

```
getDifferentialExpressedGenes(x, groups, g1, g2, theta = 0.5, FDRcutoff = 0.05)
```

Arguments

`x`	an `ExpressionSet` containing a matrix of expression values with rows representing features and columns samples
`groups`	list of integer vectors specifying the grouping of samples
`g1`	character string specifying the name of the first tested group from `groups`
`g2`	character string specifying the name of the second tested group from `groups`
`theta`	numeric, probability with values in [0,1] used for quantile filtering of variance
`FDRcutoff`	numeric, p-value cutoff

Details

Differentially expressed features are selected based on a t-test with the adjusted p-value cutoff specified by `FDRcutoff`.

The filtering selects only features whose variance is greater than the quantile defined by the probability `theta`.

Value

Integer vector containing indices of differentially expressed features from `x`.

Author(s)

Wolfgang Huber, 2013

Examples

```
data(x)
groups = with(pData(x), list(
  "E3.25"       = which(genotype=="WT" & Embryonic.day=="E3.25"),
  "E3.5 (EPI)"  = which(genotype=="WT" & Embryonic.day=="E3.5" & lineage=="EPI"),
  "E3.5 (PE)"   = which(genotype=="WT" & Embryonic.day=="E3.5" & lineage=="PE")))

# get a list of differentially expressed genes along the transition from E3.25 to E3.5
de = union(
  getDifferentialExpressedGenes(x, groups, "E3.25", "E3.5 (EPI)"),
  getDifferentialExpressedGenes(x, groups, "E3.25", "E3.5 (PE)"))
fData(x[de,])$symbol
```

`MDSplot` *Multidimensional Scaling Plots*

Description

Visualization of data similarity using non-metric multidimensional scaling.

Usage

```
MDSplot(
  x,
  mask,
  flip = integer(0),
  rotation = 0,
  cex = 2,
  col = x$sampleColour,
  panellabel,
  pointlabel
)
```

Arguments

`x`	an `ExpressionSet` containing a matrix of expression values with rows representing features and columns samples
`mask`	a logical vector specifying the masking of data points; if missing all points are drawn
`flip`	an integer vector containing indices of columns of the distance matrix whose sign should be flipped
`rotation`	numeric, angle in radians by which the plot should be rotated

cex	numeric, the value giving the amount by which text and symbols should be scaled relative to the current setting
col	character vector specifing the colors of points
panellabel	character, the label of the figure panel
pointlabel	character vector containing labels corresponding to samples; if specified labels are drawn instead of points

Value

The result of the function is a plot.

Author(s)

Wolfgang Huber, 2013

Examples

```
## data preparation
data(x)
y = x[, with(pData(x), Embryonic.day=="E3.25")]

## define colours for plotting
colours = setNames(RColorBrewer::brewer.pal(10, "Paired")[c(9, 7)], c("WT", "FGF4-KO"))[y$genotype]
stopifnot(!any(is.na(colours)))

## select 100 most variable genes for plotting
selMDS = order(genefilter::rowVars(exprs(y)), decreasing=TRUE)[seq_len(100)]
MDSplot(y[selMDS,], col=colours)
```

---

myHeatmap *Plot Heatmaps*

Description

Plots a heatmap with features (rows) and samples (columns) reordered according to hierarchical clustering.

Usage

```
myHeatmap(x, collapseDuplicateFeatures = FALSE, haveColDend = FALSE)
```

Arguments

x	an ExpressionSet containing a matrix of expression values with rows representing features and columns samples
collapseDuplicateFeatures	logical, if TRUE multiple features per gene will be averaged
haveColDend	logical, if TRUE displays the grouping of samples using a dendrogram

Value

The result of the function is a plot.

Author(s)

Wolfgang Huber, 2013

See Also

myHeatmap2

Examples

```
data(x)
groups = with(pData(x), list(
  "E3.25"       = which(genotype=="WT" & Embryonic.day=="E3.25"),
  "E3.5 (EPI)"  = which(genotype=="WT" & Embryonic.day=="E3.5" & lineage=="EPI"),
  "E3.5 (PE)"   = which(genotype=="WT" & Embryonic.day=="E3.5" & lineage=="PE")))
samples = unlist(groups)

# heatmap of differentially expressed genes along the transition from E3.25 to E3.5
de = union(
  getDifferentialExpressedGenes(x, groups, "E3.25", "E3.5 (EPI)"),
  getDifferentialExpressedGenes(x, groups, "E3.25", "E3.5 (PE)"))
myHeatmap(x[de, samples], collapseDuplicateFeatures=TRUE)
```

---

myHeatmap2 *Plot Heatmaps*

Description

Plots a heatmap with clustering of rows and columns specified by the `rowGroups` and `colGroups`, respectively.

Usage

```
myHeatmap2(
  x,
  rowGroups = factor(rep(1, nrow(x))),
  colGroups = factor(rep(1, ncol(x))),
  keeprownames = TRUE,
  colors = colorRampPalette(brewer.pal(9, "Blues")[-1])(100),
  ...
)
```

Arguments

x	an ExpressionSet containing a matrix of expression values with rows representing features and columns samples
rowGroups	factor which length aligns with rows of x
colGroups	factor which length aligns with columns of x
keeprownames	logical, if TRUE displays row names
colors	color palette used to plot the heatmap
...	arguments passed to the internal ordermat function

Value

The result of the function is a plot.

Author(s)

Wolfgang Huber, 2013

See Also

myHeatmap

Examples

```
## The function is currently defined as
function (x, rowGroups = factor(rep(1, nrow(x))), colGroups = factor(rep(1, ncol(x))),
   keeprownames = TRUE, colors = colorRampPalette(brewer.pal(9, "Blues")[-1])(100), ...) {
    x = ordermat(x, rowGroups, ...)
    x = ordermat(t(x), colGroups, ...)
    if (!keeprownames)
        colnames(x) = NULL
    print(levelplot(x, aspect = "fill", xlab = "", ylab = "",
        scales = list(x = list(rot = 90), raster = TRUE), col.regions = colors,
        colorkey = list(space = "left", height = 0.15, useRaster = TRUE)))
  }
```

---

pamCluster *Clustering of Most Variable Genes*

Description

The function pamCluster selects the ngenes most variable genes and performs their clustering using the partitioning around medoids method pam.

Usage

```
pamCluster(ngenes, x, k = 2)
```

Arguments

ngenes	numeric, the number of most variable genes to select
x	ExpressionSet containing gene expression values
k	positive integer specifying the number of clusters

Value

Integer vector specifying the clustering.

Author(s)

Wolfgang Huber

See Also

pam

Examples

```
data("x")
y = x[, x$Embryonic.day=="E3.5"]

## perform the clustering
pc = pamCluster(50, y, k=3)

## display clustering vs. sample lineage
plot(as.factor(pData(y)$lineage), pc, yaxt="n", xlab="lineage", ylab="cluster")
```

---

plotProjection *Overview of the Sample Expression*

Description

Plots a projection of sample expression profiles on the differential expression signature.

Usage

```
plotProjection(projection, label, col, colourMap)
```

Arguments

projection	a vector of scalar products between each sample's expression profile and differential expression signature
label	character vector of sample names
col	sample colour palette
colourMap	sample colour map

Value

The result of the function is a plot.

Author(s)

Wolfgang Huber, 2013

Examples

```
## For illustration of use please see the package vignette
```

---

x *Normalized Microarray Data*

Description

An ExpressionSet object containing the RMA normalized dataset in the assayData and annotation in the phenoData.

Usage

```
data(x)
```

Format

```
Formal class 'ExpressionSet' [package "Biobase"] with 7 slots
  ..@ experimentData   :Formal class 'MIAME' [package "Biobase"] with 13 slots
  .. .. ..@ name             : chr ""
  .. .. ..@ lab              : chr ""
  .. .. ..@ contact          : chr ""
  .. .. ..@ title            : chr ""
  .. .. ..@ abstract         : chr ""
  .. .. ..@ url              : chr ""
  .. .. ..@ pubMedIds        : chr ""
  .. .. ..@ samples          : list()
  .. .. ..@ hybridizations   : list()
  .. .. ..@ normControls     : list()
  .. .. ..@ preprocessing    :List of 2
 .. .. .. ..$ filenames  : chr [1:101] "/tmp/RtmpI5T6yy/1_C32_IN.CEL" "/tmp/RtmpI5T6yy/2_C32_IN.CEL" "/
  .. .. .. ..$ affyversion: chr NA
  .. .. ..@ other            :List of 1
  .. .. .. ..$ : chr ""
 .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
  .. .. .. .. ..@ .Data:List of 2
  .. .. .. .. .. ..$ : int [1:3] 1 0 0
  .. .. .. .. .. ..$ : int [1:3] 1 1 0
  ..@ assayData        :<environment: 0x167aa270>
```

```
..@ phenoData      :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
 .. .. ..@ varMetadata      :'data.frame':  5 obs. of  1 variable:
 .. .. .. ..$ labelDescription: chr [1:5] NA NA NA NA ...
 .. .. ..@ data             :'data.frame': 101 obs. of  5 variables:
.. .. .. ..$ File.name         : chr [1:101] "1_C32_IN" "2_C32_IN" "3_C32_IN" "4_C32_IN" ...
.. .. .. ..$ Embryonic.day     : Factor w/ 3 levels "E3.25","E3.5",..: 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..$ Total.number.of.cells: Factor w/ 11 levels "32","33","34",..: 1 1 1 1 1 1 1 1 1 1 ...
 .. .. .. ..$ lineage              : chr [1:101] "" "" "" "" ...
.. .. .. ..$ genotype         : Factor w/ 2 levels "FGF4-KO","WT": 2 2 2 2 2 2 2 2 2 2 ...
 .. .. ..@ dimLabels        : chr [1:2] "sampleNames" "sampleColumns"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
 .. .. .. .. ..@ .Data:List of 1
 .. .. .. .. .. ..$ : int [1:3] 1 1 0
..@ featureData    :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
 .. .. ..@ varMetadata      :'data.frame': 3 obs. of  1 variable:
 .. .. .. ..$ labelDescription: chr [1:3] NA NA NA
 .. .. ..@ data             :'data.frame': 45101 obs. of  3 variables:
 .. .. .. ..$ symbol  : chr [1:45101] "Copg1" "Atp6v0d1" "Golga7" "Psph" ...
.. .. .. ..$ genename: chr [1:45101] "coatomer protein complex, subunit gamma 1" "ATPase, H+ transporti
.. .. .. ..$ ensembl : chr [1:45101] "ENSMUSG00000030058" "ENSMUSG00000013160" "ENSMUSG00000015341" "E
 .. .. ..@ dimLabels        : chr [1:2] "featureNames" "featureColumns"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
 .. .. .. .. ..@ .Data:List of 1
 .. .. .. .. .. ..$ : int [1:3] 1 1 0
 ..@ annotation       : chr "mouse4302"
..@ protocolData   :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
 .. .. ..@ varMetadata      :'data.frame': 1 obs. of  1 variable:
 .. .. .. ..$ labelDescription: chr NA
 .. .. ..@ data             :'data.frame': 101 obs. of  1 variable:
.. .. .. ..$ ScanDate: chr [1:101] "2011-03-16T04:33:05Z" "2011-03-16T04:42:32Z" "2011-03-16T04:51:54
 .. .. ..@ dimLabels        : chr [1:2] "sampleNames" "sampleColumns"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
 .. .. .. .. ..@ .Data:List of 1
 .. .. .. .. .. ..$ : int [1:3] 1 1 0
 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
 .. .. ..@ .Data:List of 4
 .. .. .. ..$ : int [1:3] 3 0 2
 .. .. .. ..$ : int [1:3] 2 22 0
 .. .. .. ..$ : int [1:3] 1 3 0
 .. .. .. ..$ : int [1:3] 1 0 0
```

References

Ohnishi et al., 2014

See Also

xq, xql

Examples

```
data(x)
x
pData(x)
```

---

xq *qPCR Gene Expression*

Description

An ExpressionSet object containing single-cell gene expression levels measured by qPCR.

Usage

```
data(xq)
```

Format

```
Formal class 'ExpressionSet' [package "Biobase"] with 7 slots
  ..@ experimentData   :Formal class 'MIAME' [package "Biobase"] with 13 slots
  .. .. ..@ name             : chr ""
  .. .. ..@ lab              : chr ""
  .. .. ..@ contact          : chr ""
  .. .. ..@ title            : chr ""
  .. .. ..@ abstract         : chr ""
  .. .. ..@ url              : chr ""
  .. .. ..@ pubMedIds        : chr ""
  .. .. ..@ samples          : list()
  .. .. ..@ hybridizations   : list()
  .. .. ..@ normControls     : list()
  .. .. ..@ preprocessing    : list()
  .. .. ..@ other            : list()
 .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
  .. .. .. .. ..@ .Data:List of 2
  .. .. .. .. .. ..$ : int [1:3] 1 0 0
  .. .. .. .. .. ..$ : int [1:3] 1 1 0
  ..@ assayData        :<environment: 0xb12e938>
 ..@ phenoData      :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
  .. .. ..@ varMetadata      :'data.frame':  4 obs. of  1 variable:
  .. .. .. ..$ labelDescription: chr [1:4] NA NA NA NA
  .. .. ..@ data             :'data.frame': 137 obs. of  4 variables:
  .. .. .. ..$ Sample.ID    : chr [1:137] "34c_2" "34c_3" "34c_4" "34c_5" ...
  .. .. .. ..$ Embryonic.day: chr [1:137] "E3.25" "E3.25" "E3.25" "E3.25" ...
  .. .. .. ..$ Cell.type     : chr [1:137] "ICM" "ICM" "ICM" "ICM" ...
  .. .. .. ..$ sampleGroup   : chr [1:137] "E3.25" "E3.25" "E3.25" "E3.25" ...
  .. .. ..@ dimLabels        : chr [1:2] "sampleNames" "sampleColumns"
 .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
```

```
.. .. .. .. ..@ .Data:List of 1
.. .. .. .. .. ..$ : int [1:3] 1 1 0
..@ featureData    :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata      :'data.frame': 1 obs. of  1 variable:
.. .. .. ..$ labelDescription: chr NA
.. .. ..@ data             :'data.frame': 38 obs. of  1 variable:
.. .. .. ..$ symbol: chr [1:38] "Fgf4" "Tom1l1" "Tdgf1" "Cldn4" ...
.. .. ..@ dimLabels        : chr [1:2] "featureNames" "featureColumns"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. .. .. ..@ .Data:List of 1
.. .. .. .. .. ..$ : int [1:3] 1 1 0
..@ annotation       : chr "single cell qPCR"
..@ protocolData   :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata      :'data.frame': 0 obs. of  1 variable:
.. .. .. ..$ labelDescription: chr(0)
.. .. ..@ data             :'data.frame': 137 obs. of  0 variables
.. .. ..@ dimLabels        : chr [1:2] "sampleNames" "sampleColumns"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. .. .. ..@ .Data:List of 1
.. .. .. .. .. ..$ : int [1:3] 1 1 0
..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ .Data:List of 4
.. .. .. ..$ : int [1:3] 2 15 0
.. .. .. ..$ : int [1:3] 2 16 0
.. .. .. ..$ : int [1:3] 1 3 0
.. .. .. ..$ : int [1:3] 1 0 0
```

References

Ohnishi et al., 2014

See Also

x, xql

Examples

```
data(xq)
xq
pData(xq)
```

---

xql *Position-dependent Gene Expression*

Description

An ExpressionSet object containing single-cell gene expression measured by qPCR, with cells facing the blastocyst cavity labelled fluorescently.

Usage

```
data(xql)
```

Format

```
Formal class 'ExpressionSet' [package "Biobase"] with 7 slots
  ..@ experimentData   :Formal class 'MIAME' [package "Biobase"] with 13 slots
  .. .. ..@ name             : chr ""
  .. .. ..@ lab              : chr ""
  .. .. ..@ contact          : chr ""
  .. .. ..@ title            : chr ""
  .. .. ..@ abstract         : chr ""
  .. .. ..@ url              : chr ""
  .. .. ..@ pubMedIds        : chr ""
  .. .. ..@ samples          : list()
  .. .. ..@ hybridizations   : list()
  .. .. ..@ normControls     : list()
  .. .. ..@ preprocessing    : list()
  .. .. ..@ other            : list()
 .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
  .. .. .. .. ..@ .Data:List of 2
  .. .. .. .. .. ..$ : int [1:3] 1 0 0
  .. .. .. .. .. ..$ : int [1:3] 1 1 0
  ..@ assayData        :<environment: 0x7fe9c10>
 ..@ phenoData     :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
  .. .. ..@ varMetadata      :'data.frame':  2 obs. of  1 variable:
  .. .. .. ..$ labelDescription: chr [1:2] NA NA
  .. .. ..@ data             :'data.frame': 43 obs. of  2 variables:
  .. .. .. ..$ Embryonic.day: chr [1:43] "E4.5" "E4.5" "E4.5" "E4.5" ...
  .. .. .. ..$ Label        : chr [1:43] "High" "High" "Low" "Low" ...
  .. .. ..@ dimLabels        : chr [1:2] "sampleNames" "sampleColumns"
 .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
  .. .. .. .. ..@ .Data:List of 1
  .. .. .. .. .. ..$ : int [1:3] 1 1 0
 ..@ featureData    :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
  .. .. ..@ varMetadata      :'data.frame': 1 obs. of  1 variable:
  .. .. .. ..$ labelDescription: chr NA
  .. .. ..@ data             :'data.frame': 10 obs. of  1 variable:
  .. .. .. ..$ symbol: chr [1:10] "Fgf4" "Cubn" "Sox17" "Lama1" ...
  .. .. ..@ dimLabels        : chr [1:2] "featureNames" "featureColumns"
 .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
  .. .. .. .. ..@ .Data:List of 1
  .. .. .. .. .. ..$ : int [1:3] 1 1 0
  ..@ annotation       : chr "single cell qPCR"
 ..@ protocolData   :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
  .. .. ..@ varMetadata      :'data.frame': 0 obs. of  1 variable:
  .. .. .. ..$ labelDescription: chr(0)
  .. .. ..@ data             :'data.frame': 43 obs. of  0 variables
```

```
.. .. ..@ dimLabels        : chr [1:2] "sampleNames" "sampleColumns"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. .. .. ..@ .Data:List of 1
.. .. .. .. .. ..$ : int [1:3] 1 1 0
..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ .Data:List of 4
.. .. .. ..$ : int [1:3] 3 0 1
.. .. .. ..$ : int [1:3] 2 20 1
.. .. .. ..$ : int [1:3] 1 3 0
.. .. .. ..$ : int [1:3] 1 0 0
```

References

Ohnishi et al., 2014

See Also

x, xq

Examples

```
data(xql)
xql
pData(xql)
```

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