Package ‘attract’

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Type Package

Title Methods to Find the Gene Expression Modules that Represent the Drivers of Kauffman’s Attractor Landscape

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Description This package contains the functions to find the gene expression modules that represent the drivers of Kauffman’s attractor landscape. The modules are the core attractor pathways that discriminate between different cell types of groups of interest. Each pathway has a set of synexpression groups, which show transcriptionally-coordinated changes in gene expression.

License LGPL (>= 2.0)


Depends R (>= 3.4.0), AnnotationDbi

Imports Biobase, limma, cluster, GOstats, graphics, stats, reactome.db, KEGGREST, org.Hs.eg.db, utils, methods

Suggests illuminaHumanv1.db

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attract-package  Methods to find the Gene Expression Modules that Represent the Drivers of Kauffman's Attractor Landscape

Description

This package contains functions used to determine the gene expression modules that represent the drivers of Kauffman’s attractor landscape.

Details

Package: attract
Type: Package
Version: 1.33.2
Date: 2018-06-29
License:
LazyLoad: yes
The method can be summarized in the following key steps: (1) Determine core KEGG or reactome pathways that discriminate the most strongly between celltypes or experimental groups of interest (see findAttractors). (2) Find the different synexpression groups that are present within a core attractor pathway (see findSynexprs). (3) Find sets of genes that show highly similar profiles to the synexpression groups within an attractor pathway module (see findCorrPartners). (4) Test for functional enrichment for each of the synexpression groups to detect any potentially shared biological themes (see calcFuncSynexprs).

Author(s)
Jessica Mar <jess@jimmy.harvard.edu>

References

Examples
```r
## Not run:
data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", nperm=10, annotation="illuminaHumanv1.db")remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)mapk.syn <- findSynexprs("04010", attractor.states, remove.these.genes)mapk.cor <- findCorrPartners(mapk.syn, subset.loring.eset, remove.these.genes)mapk.func <- calcFuncSynexprs(mapk.syn, attractor.states, "CC", annotation="illuminaHumanv1.db")
## End(Not run)
```

---

**AttractorModuleSet-class**

**Class AttractorModuleSet**

**Description**

This is a class representation for storing the output of the findAttractors function.

**Objects from the Class**

Objects are output by the function `findAttractors`. Objects can also be created by using `new("AttractorModuleSet", ...)`. 

---
Slots

eSet: ExpressionSet which primarily stores the expression data and the phenotype/sample data sets.

cellTypeTag: character string of the tag which stores the group membership information for the samples. Must be a column name of the data frame pData(eset).

incidenceMatrix: incidence matrix used as input to GSEAlm.

rankedPathways: Data frame of significantly enriched pathways, ranked first by significance and then by size.

Methods

No methods have yet been defined with class "AttractorModuleSet" in the signature.

Note

This class is better describe in the vignette.

Author(s)

Jessica Mar <jess@jimmy.harvard.edu>

Examples

```r
## Not run:
new.attractmodule <- new("AttractorModuleSet", eSet=new("ExpressionSet"), cellTypeTag=character(1), incidenceMatrix=matrix(0), rankedPathways=data.frame())
## End(Not run)
```

buildCorMatrix

`Internal function - builds the correlation matrix between an average transcriptional module expression profile and a set of other genes.`

Description

Internal function - builds the correlation matrix between an average transcriptional module expression profile and a set of other genes.

Usage

```r
buildCorMatrix(dat.fr, module.genes, cor.cutoff)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dat.fr</td>
<td>a matrix object of gene expression values.</td>
</tr>
<tr>
<td>module.genes</td>
<td>character vector specifying genes that belong in this pathway module.</td>
</tr>
<tr>
<td>cor.cutoff</td>
<td>numeric value specifying the correlation cut-off.</td>
</tr>
</tbody>
</table>
buildCustomIncidenceMatrix

Details
This function is called internally by findCorrPartners which is easier for the user to call since findCorrPartners uses the SynExpressionSet and ExpressionSet class objects directly.

Value
A character vector of genes that meet the correlation cut-off.

Author(s)
Jessica Mar

Examples
```r
## Not run:
data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", nperm=10, annotation="illuminaHumanv1.db")
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)
mapk.syn <- findSynexprs("04010", attractor.states, remove.these.genes)
cormat <- buildCorMatrix(exprs(subset.loring.eset), mapk.syn, 0.95)
## End(Not run)
```

buildCustomIncidenceMatrix
This function builds an incidence matrix for custom gene sets.

Description
This function builds an incidence matrix for custom gene sets.

Usage
```r
buildCustomIncidenceMatrix(geneSetFrame, geneNames, databaseGeneFormat, expressionSetGeneFormat, geneSetNames)
```

Arguments
- `geneSetFrame`: a dataframe where rows are gene sets and columns are genes.
- `geneNames`: a vector of all the genes in the geneSetFrame dataframe
- `databaseGeneFormat`: a character string specifying the type of identifier for a gene in a database (KEGG, reactome, MsigDB) gene set. The default value is NULL. (ex. SYMBOL, ENTREZID, REFSEQ, ENSEMBL)
- `expressionSetGeneFormat`: a character string specifying the type of identifier for a gene in your expression data set. The default value is NULL. (ex. SYMBOL, ENTREZID, REFSEQ, ENSEMBL)
- `geneSetNames`: a vector of the name of the custom gene sets.
Details
This function creates an incidence matrix from a dataframe where the rows are the names of gene sets and the columns are genes.

Value
A matrix object with 0 and 1 entries where 1 denotes membership of a gene in a custom gene set, 0 denotes non-membership.

Author(s)
Jessica Mar

References

Usage
buildKeggIncidenceMatrix(kegg.ids, gene.ids, annotation, database, analysis, envPos, expressionSetGeneFormat)

Arguments
kegg.ids character vector of KEGG pathway ids.
gene.ids character vector of gene ids.
aputation character string that denotes which annotation package to be used, eg. illuminaHumanv1.db.
database a character string specifying what pathway database you would like to use.
analysis a character string specifying what type of experiment you performed, microarray or RNAseq.
enPos the position of the annotation package in the R search path.
expressionSetGeneFormat a character string specifying the type of identifier for a gene in your expression data set. The default value is NULL. (ex. SYMBOL, ENTREZID, REFSEQ, ENSEMBL)
calcFuncSynexprs

Details

This function is called internally by findAttractors.

Value

A matrix object with 0 and 1 entries where 1 denotes membership of a gene in a KEGG or reactome pathway, 0 denotes non-membership.

Author(s)

Jessica Mar

References


Examples

```r
## Not run:
# this takes a long time!
require("illuminaHumanv2.db", character.only=TRUE)
loadNamespace("illuminaHumanv2.db")
envPos <- match(paste("package:", "illuminaHumanv2.db", sep=""), search())
kegg.ids <- ls(illuminaHumanv2PATH2PROBE)
gene.ids <- ls(illuminaHumanv2PATH)
database <- "KEGG"
analysis <- "microarray"
imat <- buildKeggIncidence(kegg.ids, gene.ids, illuminaHumanv2.db, database, analysis, envPos)
## End(Not run)
```

---

calcFuncSynexprs  
**Functional enrichmental analysis for a set of synexpression groups.**

Description

This function performs functional enrichment for a given set of synexpression groups.

Usage

calcFuncSynexprs(mySynExpressionSet, myAttractorModuleSet, ontology = "BP", min.pvalue = 0.05, min.pwaysize = 5, annotation = "illuminaHumanv2.db", analysis="microarray", expressionSetGeneFormat=NULL, ...)

```r
## Not run:
# this takes a long time!
require("illuminaHumanv2.db", character.only=TRUE)
loadNamespace("illuminaHumanv2.db")
envPos <- match(paste("package:", "illuminaHumanv2.db", sep=""), search())
kegg.ids <- ls(illuminaHumanv2PATH2PROBE)
gene.ids <- ls(illuminaHumanv2PATH)
database <- "KEGG"
analysis <- "microarray"
imat <- buildKeggIncidence(kegg.ids, gene.ids, illuminaHumanv2.db, database, analysis, envPos)
## End(Not run)
```
calcFuncSynexprs

Arguments

mySynExpressionSet
    SynExpressionSet object.
myAttractorModuleSet
    AttractorModuleSet object.
ontology
    character string specifying which GO ontology to use, either "MF", "BP", or "CC"; defaults to "BP".
min.pvalue
    numeric value specifying adjusted P-value cut-off to use, categories with P-values <= min.pvalue will be reported.
min.pwaysize
    integer specifying minimum size of the pathway or category to consider for enrichment analysis.
annotation
    character string specifying the annotation package that corresponds to the chip platform the data was generated from.
analysis
    a character string specifying what type of experiment you performed, microarray or RNAseq.
expressionSetGeneFormat
    a character string specifying the type of identifier for a gene in your expression data set. The default value is NULL. (ex. SYMBOL, ENTREZID, REFSEQ, ENSEMBL)

... additional arguments.

Details

This function performs a functional enrichment analysis on each synexpression group using the hyperGTest from the GOstats package. P-values are adjusted using the Benjamini-Hochberg correction method. Results are returned only if they satisfy the minimum P-value level, as specified by the min.pvalue argument.

Value

A list object.

Author(s)

Jessica Mar

References


Examples

data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", nperm=10, annotation="illuminaHumanv1.db", analysis="microarray")
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)
mapk.syn <- findSynexprs("04010", attractor.states, remove.these.genes)
mapk.func <- calcFuncSynexprs(mapk.syn, attractor.states, "CC", annotation="illuminaHumanv1.db", analysis="microarray")
calcInform

Function calculates the informativeness metric (average MSS) for a set of cluster assignments.

Description

Function calculates the informativeness metric (average MSS) for a set of cluster assignments.

Usage

calcInform(exprs.dat, cl, class.vector)

Arguments

exprs.dat a matrix of gene expression values.
cl a vector of cluster assignments.
class.vector a vector specifying the group membership of the samples.

Details

This function is also called internally by findSynexprs.

Value

A numeric value representing the average MSS value (informativeness metric) for a set of cluster assignments. For an informative cluster, the RSS values should be very small relative to those produced by the informativeness metric (the MSS values).

Author(s)

Jessica Mar

References


Examples

```r
## Not run:
library(cluster)
data(subset.loring.eset)
clustObj <- agnes(as.dist(1-t(cor(exprs(subset.loring.eset)))))
cinform.vals <- NULL
for( i in 1:10 ){
cinform.vals <- c(cinform.vals, calcInform(exprs(subset.loring.eset), cutree(clustObj,i), pData(subset.loring.eset)) )
}
k <- (1:10)[cinform.vals==max(cinform.vals)] # gives the optimal number of clusters
```
calcModfstat  

*Function calculates a modified F-statistic for a set of cluster assignments.*

## Description

Function calculates a modified F-statistic for a set of cluster assignments.

## Usage

```r
calcModfstat(exprs.dat, cl, class.vector)
```

## Arguments

- `exprs.dat`: a matrix of gene expression values.
- `cl`: a vector of cluster assignments.
- `class.vector`: a vector specifying group membership of the samples.

## Details

This function is called internally by `findSynexprs`.

## Value

A modified F-statistic (average MSS/average RSS) value for a set of cluster assignments.

## Author(s)

Jessica Mar

## Examples

```r
## Not run:
library(cluster)
data(subset.loring.eset)
clustObj <- agnes(as.dist(1-t(cor(exprs(subset.loring.eset)))))
cfmod.vals <- NULL
for( i in 1:10 ){
cfmod.vals <- c(cfmod.vals, calcModfstat(exprs(subset.loring.eset), cutree(clustObj,i), pData(subset.loring.eset)$celltype))
}
k <- (1:10)[cfmod.vals==max(cfmod.vals)]
## End(Not run)
```
Function calculates the average RSS for a set of cluster assignments.

Usage

calcRss(exprs.dat, cl, class.vector)

Arguments

exprs.dat  a matrix of gene expression values.
cl  a vector of cluster assignments.
class.vector  a vector specifying the group membership of the samples.

Details

This function is called internally by findSynexprs. For an informative cluster, the RSS values should be very small relative to those produced by the informativeness metric (the MSS values).

Value

A numeric value representing the average RSS value for this set of cluster assignments.

Author(s)

Jessica Mar

Examples

## Not run:
library(cluster)
data(subset.loring.eset)
clustObj <- agnes(as.dist(1-t(cor(exprs(subset.loring.eset)))))
crss.vals <- NULL
for( i in 1:10 ){
crss.vals <- c(crss.vals, calcRss(exprs(subset.loring.eset), cutree(clustObj,i), pData(subset.loring.eset)$celltype))
}
# The RSS values are expected to be smaller than the informativeness metric values in the presence of genuine clusters.

## End(Not run)
**Description**

This is a matrix object containing published gene expression data from Mueller et al. (NCBI GEO accession id GSE11508). The data set contains 11044 probes for 68 samples. From the original data set, we have selected four cell lines giving a total of 68 samples - embryonic stem cells (12 samples), neural progenitors (31 samples), neural stem cells (8 samples) and teratoma-differentiated cells (17 samples). The lines have also been restricted based on Illumina BeadChip platform, and only those collected using the WG-6 version have been used.

We also applied a quality filter to the original gene expression data where a probe was retained if it passed a 0.99 detection score in 75

**Usage**

```r
data(exprs.dat)
```

**Format**

A matrix with normalized log2 expression intensities for 11044 probes on 68 samples (representing 4 different cell types).

**Value**

A matrix object containing published gene expression data from Mueller et al. (NCBI GEO accession id GSE11508). The data set contains 11044 probes for 68 samples.

**References**


**See Also**

`samp.info, loring.eset`

**Examples**

```r
data(exprs.dat)
```
filterDataSet

This function filters our lowly expressed genes in RNAseq data.

Description

This function filters our lowly expressed genes in RNAseq data.

Usage

filterDataSet(data, filterPerc = 0.75)

Arguments

data  A dataset with genes as rows and samples as columns.
filterPerc  a number specifying the percent of expression values that are not equal to 0 for a gene.

Details

This function removes any genes in a dataset that have an expression value of 0 for a specified percentage of samples.

Value

A data frame is returned.

Author(s)

Jessica Mar

Examples

data(exprs.dat)
exprs.filtered.dat <- filterDataSet(exprs.dat)

findAttractors

Infers the set of cell-lineage specific gene expression modules using GSEAIm and KEGG.

Description

The function infers a set of KEGG pathways that correspond to the cell-lineage specific gene expression modules, as determined using GSEA. These pathways represent those that show the greatest discrimination between the different cell types or tissues in the expression data set supplied.
findAttractors

Usage

findAttractors(myEset, cellTypeTag, min.pwaysize = 5, annotation = "illuminaHumanv2.db", database="KEGG", analysis="microarray", databaseGeneFormat=NULL, expressionSetGeneFormat=NULL, ...)

Arguments

myEset  
ExpressionSet object.

cellTypeTag  
character string of the variable name which stores the cell-lineages or experimental groups of interest for the samples in the data set (this string should be one of the column names of pData(myEset)).

min.pwaysize  
integer specifying the minimum size of the KEGG or reactome pathways to consider in the analysis.

annotation  
character string specifying the annotation package that corresponds to the chip platform or organism (for RNAseq data) the data was generated from.

database  
a character string specifying what pathway database you would like to use.

analysis  
a character string specifying what type of experiment you performed, microarray or RNAseq.

databaseGeneFormat  
a character string specifying the type of identifier for a gene in a database (KEGG, REACTOME, MsigDB) gene set. The default value is NULL. (ex. SYMBOL, ENTREZID, REFSEQ, ENSEMBL)

expressionSetGeneFormat  
a character string specifying the type of identifier for a gene in your expression data set. The default value is NULL. (ex. SYMBOL, ENTREZID, REFSEQ, ENSEMBL)

...  
additional arguments.

Details

This function subsets the expression data so that only those genes with annotations in KEGG or reactome are used for the downstream gene set enrichment analysis. This subset is stored in the eSet slot of the AttractorModuleSet output object.

The GSEAlm algorithm finds the KEGG or reactome pathway modules which discriminate between the celltypes or experimental groups of interest. It also ranks the results of the GSEAlm step by significance of these pathway modules, as stored in rankedPathways.

The output object of the findAttractors function also contains the incidence matrix that was built for the KEGG or reactome pathways, stored in the slot incidenceMatrix and the character string denoting which column of the sample data represents the cell type or experimental groups of interest, as stored in the slot cellTypeTag.

Value

An AttractorModuleSet object.
findCorrPartners

Author(s)
Jessica Mar

References

Examples
data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", annotation="illuminaHumanv1.db", database="KEGG", MSigDBpath <- system.file("extdata","c4.cgn.v5.0.entrez.gmt",package="attract")
attractor.states.cutsom <- findAttractors(subset.loring.eset, "celltype", annotation="illuminaHumanv1.db", database=MSigDBpath, analysis="microarray", databaseGeneFormat="ENTREZID", expressionSetGeneFormat="PROBEID")

findCorrPartners

Determines Genes with Highly Correlated Expression Profiles to a Synexpression Group

Description
This function finds genes with expression profiles highly correlated to a synexpression group.

Usage
findCorrPartners(mySynExpressionSet, myEset, removeGenes = NULL, cor.cutoff = 0.85, ...)

Arguments
mySynExpressionSet
SynExpressionSet object.
myEset
ExpressionSet object.
removeGenes
vector of probes that specify those genes who demonstrate little variability across the different celltypes and thus should be removed from downstream analysis.
cor.cutoff
numeric value specifying the correlation cut-off.
...
additional arguments.

Details
Genes with highly correlated profiles to the synexpression groups (e.g. R > 0.85) are also likely to be integral in maintaining cell type-specific differences, however due to their lack of inclusion in resources like KEGG, would not have been picked up by the first GSEA step using findAttractors.
findOnepwaySynexprs

Value

A SynExpressionSet object which stores the genes that are highly correlated with the synexpression group provided, and their average expression profile.

Author(s)

Jessica Mar

Examples

data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", annotation="illuminaHumanv1.db")
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)
mapk.syn <- findSynexprs("04010", attractor.states, remove.these.genes)
mapk.cor <- findCorrPartners(mapk.syn, subset.loring.eset, remove.these.genes)

findOnepwaySynexprs

Internal function - finds the synexpression groups for a single given pathway.

Description

Internal function - finds the synexpression groups for a single given pathway.

Usage

findOnepwaySynexprs(myIDs, myDataSet, cellTypeTag, min.clustersize = 5, removeGenes = NULL, ...)

Arguments

myIDs a single character string denoting the KEGG or reactome ID of the pathway module to be analyzed or a character codevector of gene names of a pathway.
myDataSet AttractorModuleSet object, output of the findAttractors step. This could also be an ExpressionSet object.
cellTypeTag character string of the variable name which stores the cell-lineages or experimental groups of interest for the samples in the data set (this string should be one of the column names of pData(myEset)).
min.clustersize integer specifying the minimum number of genes that must be present in clusters that are inferred.
removeGenes vector of probes that specify those genes who demonstrate little variability across the different celltypes and thus should be removed from downstream analysis.
... additional arguments.
Details

This function is called internally by calcFuncSynexprs. Users should use calcFuncSynexprs rather than calling findOnepwaySynexprs directly.

Value

A SynExpressionSet object is returned.

Author(s)

Jessica Mar

Examples

## Not run:
data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", nperm=10, annotation="illuminaHumanv1.db")
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)
map.syn <- findOnepwaySynexprs("04010", attractor.states, "celltype", removeGenes=remove.these.genes)
vec.geneid <- c("GI_17999531-S","GI_17978503-A")
custom.syn <- findSynexprs(vec.geneid, subset.loring.eset, "celltype", removeGenes=remove.these.genes)
## End(Not run)
removeGenes vector of gene names that specify those genes who demonstrate little variability across the different celltypes and thus should be removed from downstream analysis.

min.clustersize integer specifying the minimum number of genes that must be present in clusters that are inferred.

Details
This function performs a hierarchical cluster analysis of the genes in a core attractor pathway module, and uses an informativeness metric to determine the number of optimal clusters (syenexpression groups) that describe the data.

Value
If a single KEGG or reactome ID is specified in pwayIds, then a SynExpressionSet object is returned. If a multiple KEGG or reactome IDs are specified, then an environment object is returned where the keys are labeled "pwayIDsynexprs" (e.g. for MAPK KEGGID = 04010, the key is pway04010synexprs). The value associated with each key is a SynExpressionSet object.

Author(s)
Jessica Mar

References

Examples
```r
data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", annotation="illuminaHumanv1.db")
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)
mapk.syn <- findSynexprs("04010", attractor.states, "celltype", remove.these.genes)
top5.syn <- findSynexprs(attractor.states@rankedPathways[1:5,1], attractor.states, "celltype", removeGenes=remove.these.genes)
vec.geneid <- c("GI_17999531-S","GI_17978503-A")
custom.syn <- findSynexprs(vec.geneid, subset.loring.eset, "celltype", removeGenes=remove.these.genes)
```

flagPwayExists \hspace{1cm} Internal function - flags a gene if it exists in a pathway.

Description
Internal function - flags a gene if it exists in a pathway.
getCustomGenes

Usage
flagPwayExists(x)

Arguments
x A vector of pathway ids.

Details
This function is called internally by the findAttractors function. Function returns TRUE if the probe exists in at least one pways, FALSE if there are no pway annotations.

Value
A logical value.

Author(s)
Jessica Mar

Examples
## Not run:
library(illuminaHumanv2.db)
flag.check <- flagPwayExists(ls(illuminaHumanv2PATH2PROBE))
## End(Not run)

getCustomGenes Function removes genes from the custom pathway that demonstrate little variation across the cell types.

Description
Function removes genes from the custom pathway that demonstrate little variation across the cell types.

Usage
getCustomGenes(vec.geneid, removeGenes = NULL)

Arguments
vec.geneid a vector of character strings denoting a custom gene set.
removeGenes vector of gene names that specify those genes who demonstrate little variability across the different cell types and thus should be removed from downstream analysis.
getPwayGenes

Function removes genes from the chosen pathway that demonstrate little variation across the cell types.

Description
Function removes genes from the chosen pathway that demonstrate little variation across the cell types.

Usage
getPwayGenes(pathwayIds, myAttractorModuleSet, removeGenes = NULL)

Arguments
- pathwayIds: a single character string denoting the KEGG or reactome ID of the pathway module to be analyzed.
- myAttractorModuleSet: AttractorModuleSet object, output of the findAttractors step.
- removeGenes: vector of probes or gene IDs (RNAseq) that specify those genes who demonstrate little variability across the different celltypes and thus should be removed from downstream analysis.
loring.eset

Details

This function is also called internally by \texttt{findSynexprs}.

Value

A vector of gene names that have variable expression across the different cell types in a pathway.

Author(s)

Jessica Mar

References


Examples

```r
## Not run:
data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", nperm=10, annotation="illuminaHumanv1.db")
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)
map.syn <- getPwayGenes("04010", attractor.states, removeGenes=remove.these.genes)
## End(Not run)
```

loring.eset

An ExpressionSet Object containing published data from M?ller et al.

Description

This is an ExpressionSet object containing the published data from M?ller et al. (NCBI GEO accession id GSE11508). The expression data set contains 11044 probes for 68 samples.

Usage

data(loring.eset)

Format

An ExpressionSet object.

Value

An ExpressionSet object containing the published data from M?ller et al. (NCBI GEO accession id GSE11508). The expression data set contains 11044 probes for 68 samples.
References


See Also

exprs.dat, samp.info

Examples

data(loring.eset)
exprs.dat <- exprs(loring.eset) # gene expression matrix

plotsynexprs

Visualizing the Average Expression Profile of a Synexpression Group.

Description

This function plots the average expression profile for a specific synexpression group.

Usage

plotsynexprs(mySynExpressionSet, tickMarks, tickLabels, vertLines, index=1, ...)

Arguments

mySynExpressionSet
    SynExpressionSet object.
tickMarks
    numeric vector of specifying the location of the tick marks along the x-axis. There should be one tick for each cell type or group.
tickLabels
    character vector specifying the labels to be appear underneath the tick marks on the x-axis. These should correspond to the cell type or group names.
vertLines
    numeric vector specifying the location of the vertical lines that indicate the cell type or group-specific regions along the x-axis.
index
    numeric value specifying which synexpression group should be plotted.
...
    additional arguments.

Details

Generic plotting parameters can be passed to this function to create a more sophisticated plot, e.g col="blue", main="Synexpression Group 1".

Value

A plot showing the average expression profile for the synexpression group specified.
removeFlatGenes

Author(s)
Jessica Mar

Examples

data(subset.loring.eset)
attractor.states <- findAttractors(subset.loring.eset, "celltype", nperm=10, annotation="illuminaHumanv1.db")
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)
mapk.syn <- findSynexprs("04010", attractor.states, remove.these.genes)
par(mfrow=c(2,2))
pretty.col <- rainbow(3)
for( i in 1:3 ){
plotsynexprs(mapk.syn, tickMarks=c(6, 28, 47, 60), tickLabels=c("ESC", "PRO", "NSC", "TER"), vertLines=c(12.5, 43.5),
main=paste("Synexpression Group ", i, sep=""), col=pretty.col[i])
}

removeFlatGenes Flags a set of genes which demonstrates little variation across the cell-types or experimental groups of interest.

Description
This function uses a linear model set up in limma to assess the degree of association between celltype and a gene’s expression profile. In this way, we can flag those genes whose profiles show very little change across different celltype groups, or in other words are "flat".

Usage
removeFlatGenes(eSet, cellTypeTag, contrasts = NULL, limma.cutoff = 0.05, ...)

Arguments
eSet ExpressionSet object.
cellTypeTag character string of the variable name which stores the cell-lineages or experimental groups of interest for the samples in the data set (this string should be one of the column names of pData(myEset)).
contrasts optional vector of contrasts that specify the comparisons of interest. By default, all comparisons between the different groups are generated.
limma.cutoff numeric specifying the P-value cutoff. Genes with P-values greater than this value are considered "flat" and will be included in the set of flat genes.
...
additional arguments.

Details
Flat genes are removed from the analysis after the core attractor pathway modules are first inferred (i.e. the findAttractors step).
Value

A vector with gene names (as defined in the eset) of those genes with expression profiles that hardly vary across different celltype or experimental groups.

Author(s)

Jessica Mar

References

limma package.

Examples

data(subset.loring.eset)
remove.these.genes <- removeFlatGenes(subset.loring.eset, "celltype", contrasts=NULL, limma.cutoff=0.05)

Description

This is sample information data frame for the samples in the Mueller data set (NCBI GEO accession id GSE11508). The data frame contains the cell type groups for the 68 samples.

Usage

data(samp.info)

Format

A data.frame object with one column of sample IDs (these are the column IDs of the exprs.dat expression matrix object) and second column indicating which cell type each sample represents.

ChipID A vector of sample IDs.
celltype A vector denoting the cell type a sample represents.

Value

A sample data frame for the samples in the Mueller data set (NCBI GEO accession id GSE11508). The data frame contains the cell type groups for the 68 samples.
subset.loring.eset

References

See Also
exprs.dat, loring.eset

Examples
data(samp.info)

subset.loring.eset  An ExpressionSet Object containing published data from Müller et al.

Description
This is an ExpressionSet object containing a subset of the published data from Müller et al. (NCBI GEO accession id GSE11508). The expression data set contains 5522 probes for 68 samples. This ExpressionSet object was created specifically to demonstrate the functions in this package. If you're looking for the full Müller data set, see loring.eset.

Usage
data(subset.loring.eset)

Format
An ExpressionSet object.

Value
An ExpressionSet object containing a subset of the published data from Müller et al. (NCBI GEO accession id GSE11508). The expression data set contains 5522 probes for 68 samples.

References

See Also
exprs.dat, samp.info, loring.eset

Examples
data(subset.loring.eset)
subset.exprs.dat <- exprs(subset.loring.eset) # gene expression matrix
SynExpressionSet-class

Class `SynExpressionSet`

Description

This is a class representation for storing synexpression group information.

Objects from the Class

Objects are output by the function `findSynexprs`. Objects can also be created by using `new("SynExpressionSet", ...)`.

Slots

groups: A list object denoting the probes or gene IDs (rnaseq) belonging to each synexpression group.

profiles: A matrix of average expression profiles for each synexpression group, each profile is stored as a row.

Methods

No methods have yet been defined with class "SynExpressionSet" in the signature.

Note

This class is described in more detail in the vignette.

Author(s)

Jessica Mar <jess@jimmy.harvard.edu>

Examples

```r
new.synexpressionset <- new("SynExpressionSet", groups=list(), profiles=matrix(0))
```
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