

Package: CSOA (via r-universe)

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Type Package

Title Calculate per-cell gene signature scores in scRNA-seq data using cell set overlaps

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Description Cell Set Overlap Analysis (CSOA) is a tool for calculating per-cell gene signature scores in an scRNA-seq dataset. CSOA constructs a set for each gene in the signature, consisting of the cells that highly express the gene. Next, all overlaps of pairs of cell sets are computed, ranked, filtered and scored. The CSOA per-cell score is calculated by summing up all products of the overlap scores and the min-max-normalized expression of the two involved genes. CSOA can run on a Seurat object, a SingleCellExperiment object, a matrix and a dgCMMatrix.

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Imports dplyr, ggplot2, henna, kerntools, methods, paletteer, qs2, reshape2, rlang, Seurat, SeuratObject, SummarizedExperiment, spatstat.utils, stats, textshape

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attachCellScores.default

Attach CSOA scores to object

Description

This function attaches the data frame of CSOA scores to the input object.

Usage

```
## Default S3 method:
attachCellScores(scObj, scoreDF, ...)
```

```
## S3 method for class 'Seurat'
attachCellScores(scObj, scoreDF, ...)
```

```
## S3 method for class 'SingleCellExperiment'
attachCellScores(scObj, scoreDF, ...)

## S3 method for class 'matrix'
attachCellScores(scObj, scoreDF, ...)

## S3 method for class 'dgCMatrix'
attachCellScores(scObj, scoreDF, ...)

attachCellScores(scObj, ...)
```

Arguments

scObj	A Seurat object, SingleCellExperiment object, or expression matrix.
scoreDF	Data frame of CSOA scores.
...	Additional arguments.

Details

If the input object is of the Seurat or SingleCellExperiment class, it will be returned with added CSOA scores. Otherwise, a list containing the expression matrix and the CSOA scores data frame will be returned.

Value

A Seurat object with CSOA scores added to metadata.
 A SingleCellExperiment object with CSOA scores added to colData.
 A list containing the expression matrix and the CSOA scores data frame.
 A list containing the expression matrix and the CSOA scores data frame.

Examples

```
library(Seurat)
mat <- matrix(0, 500, 300)
rownames(mat) <- paste0('G', seq(500))
colnames(mat) <- paste0('C', seq(300))
mat[sample(8000)] <- sample(20, 8000, TRUE)
seuratObj <- CreateSeuratObject(mat)
seuratObj <- NormalizeData(seuratObj)
scores <- data.frame(CSOA = runif(300))
seuratObj <- attachCellScores(seuratObj, scores)
head(seuratObj$CSOA)
```

basicHeatmap	<i>Plot a simple heatmap</i>
--------------	------------------------------

Description

This function plots a simple heatmap, with clustering but no dendograms.

Usage

```
basicHeatmap(  
  mat,  
  aesNames = c("x", "y", "Score"),  
  title = "Heatmap",  
  axisTextSize = 7,  
  palette = paletteer_c("grDevices::Plasma", 30),  
  ...  
)
```

Arguments

mat	A matrix.
aesNames	A character vector of length 3 representing the y, x and fill aes elements.
title	Plot title.
axisTextSize	Axis text size.
palette	Color palette.
...	Other arguments passed to <code>henna::centerTitle</code> .

Value

A ggplot object.

Examples

```
mat <- matrix(0, 10, 20)  
mat[sample(length(mat), 50)] <- runif(50, max = 2.5)  
basicHeatmap(mat)
```

breakWeakTies	<i>Remove overlap pairs with low Jaccard scores</i>
---------------	-----------------------------------------------------

Description

This function iteratively removes all overlap pairs with neighbor Jaccard score below a fixed cutoff until no overlap pairs can be removed. Subsequently, overlap ranks are recalculated.

Usage

```
breakWeakTies(  
  overlapDF,  
  cutoff = 1/3,  
  doConnComp = FALSE,  
  mtMethod = c("BY", "BH")  
)
```

Arguments

overlapDF	An overlap data frame.
cutoff	A cutoff used in the filtering of edges with low Jaccard scores.
doConnComp	Whether to calculate the connected components.
mtMethod	Multiple testing correction method. Choose between Benjamini-Yekutieli ('BY') and Benjamini-Hochberg('BH'). Default is 'BY'.

Details

The functions removes overlaps for which the two involved genes record too few shared neighbors—genes whose cell set significantly overlaps with those of both overlap genes.

Value

An overlap data frame in which edges with low Jaccard scores have been removed.

Examples

```
overlapDF <- data.frame(gene1=paste0('G', c(1, 3, 7, 6, 8, 2, 4, 3, 4, 5)),  
  gene2=paste0('G', c(2, 7, 2, 5, 4, 5, 1, 2, 2, 8)),  
  ratio=runif(10, 2, 10),  
  pval=runif(10, 0, 1e-10))  
breakWeakTies(overlapDF, cutoff=0.1)
```

cellDistribution	<i>Show the distribution of cell sets among cells</i>
------------------	-------------------------------------------------------

Description

This function returns a logical matrix that shows the representation of cell sets among all cells.

Usage

```
cellDistribution(cellSets, allCells)
```

Arguments

cellSets	A list of character vectors.
allCells	Names of all cells in the dataset.

Value

A logical matrix with genes as rows and cells as columns.

Examples

```
cellSets <- list(c('A', 'H', 'J'),  
c('B', 'D', 'E', 'F', 'J'),  
c('C', 'I', 'L'))  
allCells <- LETTERS[seq(15)]  
cellDistribution(cellSets, allCells)
```

cellSetsOverlaps	<i>Calculates the significance of overlaps of pairs of cells sets</i>
------------------	-----------------------------------------------------------------------

Description

This function computes the statistical significance of overlaps of pairs of cell sets.

Usage

```
cellSetsOverlaps(cellSets, nCells, pairs = NULL, overlapFileName = NULL)
```

Arguments

cellSets	A list of character arrays.
nCells	The total number of cells in the Seurat object.
pairs	Pairs of cell sets to be assessed. If NULL (as default), all pairs will be assessed.
overlapFileName	The name of the file where the overlap data frame will be saved. This option can be used to save time when performing exploratory analyses such as trying different jaccardCutoff parameters in breakWeakTies. Default is NULL (the overlap data frame will not be saved).

Value

A data frame listing statistics for all cell set overlaps: cell set sizes, recorded and expected shared cells, the recorded-over-expected ratio and the hypergeometric p-value.

Examples

```
cellSets <- list(G1 = c('A', 'H', 'J'),
                G2 = c('B', 'D', 'E', 'F', 'J'),
                G3 = c('C', 'I', 'L'))
cellSetsOverlaps(cellSets, 40)
```

 expMat

Extracts the data expression matrix from object

Description

This function extracts the data expression matrix from object as a non-sparse matrix. Selected genes can be specified as input.

Usage

```
expMat(scObj, ...)

## Default S3 method:
expMat(scObj, genes = NULL, ...)

## S3 method for class 'Seurat'
expMat(scObj, ...)

## S3 method for class 'SingleCellExperiment'
expMat(scObj, ...)

## S3 method for class 'dgMatrix'
expMat(scObj, ...)
```

```
## S3 method for class 'matrix'
expMat(scObj, ...)
```

Arguments

scObj A Seurat object, SingleCellExperiment object, or expression matrix.
 ... Additional arguments.
 genes Genes retained in the expression matrix. If NULL, all genes will be retained

Value

An expression matrix.

Examples

```
library(Seurat)
mat <- matrix(0, 6, 4)
mat[sample(length(mat), 7)] <- sample(3, 7, TRUE)
seuratObj <- CreateSeuratObject(counts = mat)
seuratObj <- NormalizeData(seuratObj)
expMat(seuratObj)
```

featureWes

A feature plot with a more distinctive color scheme.

Description

This function customizes the appearance of `Seurat::FeaturePlot` for improved distinctiveness and aesthetics.

Usage

```
featureWes(
  seuratObj,
  feature,
  title = feature,
  idClass = NULL,
  labelSize = 3.5,
  titleSize = 12,
  palette = paletteer_d("wesanderson::Royal1")[c(3, 2)],
  ...
)
```

Arguments

seuratObj	A Seurat object.
feature	Seurat feature.
title	Plot title.
idClass	Column to be used for labelling. If NULL, no column-based labels will be generated.
labelSize	Size of labels. Ignored if idClass is NULL.
titleSize	Title size.
palette	Color palette.
...	Additional arguments passed to <code>Seurat::FeaturePlot</code> .

Value

A ggplot object.

Examples

```
library(Seurat)
mat <- matrix(0, 3000, 800)
mat[sample(length(mat), 90000)] <- sample(8, 90000, TRUE)
seuratObj <- CreateSeuratObject(counts = mat)
seuratObj <- FindVariableFeatures(seuratObj, nfeatures=200)
seuratObj <- NormalizeData(seuratObj)
seuratObj <- ScaleData(seuratObj)
seuratObj <- RunPCA(seuratObj, verbose=FALSE)
seuratObj <- RunUMAP(seuratObj, dims=1:20, verbose=FALSE)
featureWes(seuratObj, 'Feature3')
```

geneRadialPlot

Radial plot for an overlap data frame

Description

This function draws a radial plot for an overlap data frame to illustrate gene participation in top overlaps.

Usage

```
geneRadialPlot(
  overlapObj,
  title = "Top overlap genes plot",
  degreeLegendTitle = "Number of top overlaps",
  groupLegendTitle = "Group",
  extraCircles = 2,
  groupNames = NULL,
```

```

    cutoff = NULL,
    ...
  )

```

Arguments

<code>overlapObj</code>	An overlap data frame or list of overlap data frames.
<code>title</code>	Plot title.
<code>degreeLegendTitle</code>	The title of the degree legend.
<code>groupLegendTitle</code>	The title of the group legend. If NULL, no groups will be distinguished.
<code>extraCircles</code>	Number of extra circles to be displayed on the plot.
<code>groupNames</code>	Names of groups. If provided, must be a vector of the same length as the list of overlap data frames.
<code>cutoff</code>	Number of retained edges from each overlap data frame after refiltering. If NULL (as default), no refiltering will be performed.
<code>...</code>	Additional parameters passed to <code>henna::radialPlot</code> .

Details

The function can separate genes by groups. The groups can be, for instance, different gene sets, or different connected components of the same overlap data frame. A wrapper around `henna::radialPlot`

Value

A ggplot object.

Examples

```

edgesDF <- data.frame(gene1 = paste0('G', c(1, 2, 3, 4, 7, 8, 10,
11, 11, 10, 10, 10)),
gene2 = paste0('G', c(2, 5, 1, 8, 4, 9, 12,
13, 14, 13, 16, 14)))
edgesDF <- henna::connectedComponents(edgesDF, 'group')
geneRadialPlot(edgesDF, groupLegendTitle='Component', extraCircles=1)

```

generateOverlaps

Generate overlaps of cell sets for input genes

Description

This function constructs, for each gene in the expression matrix, a set of cells expressing the gene at or above the input percentile. Subsequently, overlaps of pairs of the constructed cell sets are assessed for statistical significance.

Usage

```
generateOverlaps(
  geneSetExp,
  percentile = 90,
  pairs = NULL,
  overlapFileName = NULL
)
```

Arguments

geneSetExp A gene expression non-sparse matrix with the rows restricted to the genes for which cell sets will be computed.

percentile A positive number under 100.

pairs Pairs of cell sets to be assessed. If NULL (as default), all pairs will be assessed.

overlapFileName The name of the file where the overlap data frame will be saved. This option can be used to save time when performing exploratory analyses such as trying different `jaccardCutoff` parameters in `breakWeakTies`. Default is NULL (the overlap data frame will not be saved).

Details

Wrapper around `percentileSets` and `cellSetsOverlaps`.

Value

A data frame listing statistics for all cell set overlaps

Examples

```
mat <- matrix(0, 2000, 500)
rownames(mat) <- paste0('G', seq(2000))
colnames(mat) <- paste0('C', seq(500))
mat[sample(length(mat), 270000)] <- sample(50, 270000, TRUE)
mat <- mat[paste0('G', sample(2000, 5)), ]
generateOverlaps(mat)
```

getPairs

Get all unordered pairs of two elements from a vector

Description

This function returns all unordered pairs of two elements from a vector.

Usage

```
getPairs(v)
```

Arguments

`v` A vector.

Value

A list of vectors of length 2.

Examples

```
v <- c('ASD', 'VBN', 'HJKL')
getPairs(v)
```

overlapCutoffPlot *Plot the selection of overlaps*

Description

This function illustrates the process of selecting the overlap rank cutoff by plotting rank frequencies against ranks and showcasing the convex hull of the rank-frequency points.

Usage

```
overlapCutoffPlot(
  overlapDF,
  title = "Overlap cutoff plot",
  palette = c("purple", "yellow"),
  hullWidth = 0.8,
  xLab = "Overlap rank",
  yLab = "Frequency",
  legendLabs = c("Accepted overlaps", "Discarded overlaps"),
  pointShape = 24,
  ...
)
```

Arguments

<code>overlapDF</code>	Processed overlap data frame created with <code>processOverlaps</code> .
<code>title</code>	Plot title.
<code>palette</code>	Color palette. Must have two colors, the first one representing accepted overlaps and the other representing discarded overlaps.
<code>hullWidth</code>	Width of the convex hull.
<code>xLab</code>	x axis label.
<code>yLab</code>	y axis label.
<code>legendLabs</code>	Legend labels.
<code>pointShape</code>	Point shape.
<code>...</code>	Additional arguments passed to <code>henna::hullPlot</code> .

Details

A wrapper around `henna::hullPlot`.

Value

A ggplot object.

Examples

```
overlapDF <- data.frame(gene1=paste0('G', c(1, 3, 7, 6, 8, 2, 4, 3, 4, 5)),
  gene2=paste0('G', c(2, 7, 2, 5, 4, 5, 1, 2, 2, 8)),
  rank=c(1, 2, 3, 4, 4, 6, 7, 7, 7, 10))
overlapCutoffPlot(overlapDF)
```

overlapGenes

Get all genes from an overlap data frame

Description

This function gets all genes from an overlap data frame.

Usage

```
overlapGenes(overlapDF, components = NULL)
```

Arguments

overlapDF	Overlap data frame.
components	A numeric vector representing the connected components of the overlap data frame graph.

Value

A character vector of genes.

Examples

```
overlapDF <- data.frame(gene1 = paste0('G', c(1, 2, 3)),
  gene1 = paste0('G', c(2, 7, 8)))
overlapGenes(overlapDF)
```

overlapNetworkPlot *Plot the overlaps as a network*

Description

This function plots the graph of the overlap data frame, with genes as vertices and overlaps as edges.

Usage

```
overlapNetworkPlot(  
  overlapDF,  
  title = "Top overlaps network plot",  
  nodeColor = "orange",  
  edgeColor = "green4",  
  ...  
)
```

Arguments

overlapDF	Overlap data frame.
title	Plot title.
nodeColor	The color of nodes. If NULL, the default henna::networkPlot color scheme will be used, which uses different colors for nodes belonging to different connected components.
edgeColor	The color of edges.
...	Additional parameters passed to henna::networkPlot.

Details

A thin wrapper around henna::networkPlot.

Value

An overlap network plot.

Examples

```
overlapDF <- data.frame(gene1 = paste0('G', c(1, 2, 5, 6, 7, 17)),  
  gene2 = paste0('G', c(2, 5, 8, 11, 11, 11)),  
  rank = c(1, 1, 3, 3, 3, 3))  
overlapNetworkPlot(overlapDF)
```

overlapPairs	<i>Extract gene pairs from overlap data frame</i>
--------------	---------------------------------------------------

Description

This function extracts the gene pairs from an overlap data frame.

Usage

```
overlapPairs(overlapDF)
```

Arguments

overlapDF Overlap data frame.

Value

A list of gene pairs.

Examples

```
overlapDF <- data.frame(gene1 = paste0('G', c(1, 2, 3)),
  gene2 = paste0('G', c(2, 7, 8)))
overlapPairs(overlapDF)
```

percentileSets	<i>Generates cell expressing input genes at an input percentile</i>
----------------	---------------------------------------------------------------------

Description

This function constructs, for each gene in the expression matrix, a set of cells expressing the gene at or above the input percentile.

Usage

```
percentileSets(geneSetExp, percentile = 90)
```

Arguments

geneSetExp A gene expression non-sparse matrix with the rows restricted to the genes for which cell sets will be computed.

percentile A positive number under 100.

Value

A named list of character vectors of length equaling the number of input genes. Each vector stores the cells expressing the gene at or above the input percentile.

Examples

```
mat <- matrix(0, 1000, 500)
rownames(mat) <- paste0('G', seq(1000))
colnames(mat) <- paste0('C', seq(500))
mat[sample(length(mat), 70000)] <- sample(50, 70000, TRUE)
mat <- mat[paste0('G', sample(1000, 3)), ]
percentileSets(mat)
```

processOverlaps

Process data frame of overlaps of cell sets

Description

This function filters, ranks and scores previously generated overlaps of cell sets.

Usage

```
processOverlaps(
  overlapDF,
  mtMethod = c("BY", "BH"),
  jaccardCutoff = NULL,
  osMethod = c("log", "minmax"),
  ...
)
```

Arguments

overlapDF	Overlap data frame.
mtMethod	Multiple testing correction method. Choose between Benjamini-Yekutieli ('BY') and Benjamini-Hochberg('BH'). Default is 'BY'.
jaccardCutoff	A cutoff used in the filtering of edges with low Jaccard scores. If NULL (as default), no filtering of such edges will be performed.
osMethod	Method used to compute overlap scores. Options are "log" and "minmax".
...	Additional arguments passed to mtCorrectDF.

Details

Wrapper around byCorrectDF, rankOverlaps, prepareFiltering, filterOverlaps and scoreOverlaps. If jaccardCutoff is not NULL, it also calls breakWeakTies between filterOverlaps and scoreOverlaps.

Value

A data frame consisting of filtered, ranked and scored cell sets overlaps

Examples

```
overlapDF <- data.frame(gene1=paste0('G',
c(1, 3, 7, 6, 8, 2, 4, 3, 4, 5)),
gene2=paste0('G',
c(2, 7, 2, 5, 4, 5, 1, 2, 2, 8)),
ratio=runif(10, 2, 10),
pval=runif(10, 0, 1e-10))
processOverlaps(overlapDF)
```

qGrab

Read and delete a .qs2 file

Description

This functions reads a .qs2 file, deletes it, and returns its content.

Usage

```
qGrab(qs2File)
```

Arguments

qs2File Name of .qs2 file with path.

Value

The content of the .qs2 file.

Examples

```
library(qs2)
qs_save(c(1, 2, 3), 'temp.qs2')
qGrab('temp.qs2')
```

runCSOA *Run the CSOA pipeline*

Description

This function generates cell set overlaps for input gene sets based on percentiles of gene expression, computes the significance of these overlaps, ranks, filters and scores the overlaps, and builds a per-cell score by summing the products of overlap scores and the min-max-normalized expression of the corresponding pairs of genes.

Usage

```
runCSOA(
  scObj,
  geneSets,
  percentile = 90,
  mtMethod = c("BY", "BH"),
  jaccardCutoff = NULL,
  osMethod = c("log", "minmax"),
  overlapFileName = NULL,
  pairFileTemplate = NULL,
  keepOverlapOrder = FALSE,
  ...
)
```

Arguments

scObj	A Seurat object, SingleCellExperiment object, or expression matrix.
geneSets	Named list of character vectors of which each must contain at least two genes.
percentile	A positive number under 100.
mtMethod	Multiple testing correction method. Choose between Benjamini-Yekutieli ('BY') and Benjamini-Hochberg('BH'). Default is 'BY'.
jaccardCutoff	A cutoff used in the filtering of edges with low Jaccard scores. If NULL (as default), no filtering of such edges will be performed.
osMethod	Method used to compute overlap scores. Options are "log" and "minmax".
overlapFileName	The name of the file where the overlap data frame will be saved. This option can be used to save time when performing exploratory analyses such as trying different jaccardCutoff parameters in breakWeakTies. Default is NULL (the overlap data frame will not be saved).
pairFileTemplate	Character object used in the naming of the files where the pair data frames will be saved. Default is NULL (the pair data frames will not be saved).
keepOverlapOrder	Keep the rank-based order of overlaps in the pair score file, as opposed to changing it to a pair score-based order. Ignored if pairFileTemplate is NULL.

... Additional arguments.

Details

Wrapper around expMat, generateOverlaps, scoreCells and attachCellScores.

Value

An object of the same class as scObj with per-gene-set CSOA scores assigned for each cell.

Examples

```
mat <- matrix(0, 500, 300)
rownames(mat) <- paste0('G', seq(500))
colnames(mat) <- paste0('C', seq(300))
mat[sample(8000)] <- runif(8000, max=13)
genes <- paste0('G', seq(200))
mat[genes, 20:50] <- matrix(runif(200 * 31, min = 14, max = 15),
nrow = 200, ncol = 31)
geneSet1 <- paste0('G', seq(1, 150))
geneSet2 <- paste0('G', seq(50, 200))
df <- runCSOA(mat, list(a = geneSet1, b = geneSet2))
head(df)
```

scoreCells

Generate CSOA scores from overlap data frame and list of pairs

Description

This function scores an overlap data frame using its associated list of pairs. The overlap data frame is split based on the overlaps corresponding to each gene set and scored, and the output is rejoined as a data frame.

Usage

```
scoreCells(
  geneSetExp,
  overlapDF,
  setPairs,
  geneSetNames,
  mtMethod = c("BY", "BH"),
  jaccardCutoff = NULL,
  osMethod = c("log", "minmax"),
  pairFileTemplate = NULL,
  keepOverlapOrder = FALSE,
  ...
)
```

Arguments

geneSetExp	A gene expression non-sparse matrix with the rows restricted to the genes for which cell sets will be computed.
overlapDF	Overlap data frame.
setPairs	A list of overlaps corresponding to each input gene set.
geneSetNames	Character vector of names of gene sets.
mtMethod	Multiple testing correction method. Choose between Benjamini-Yekutieli ('BY') and Benjamini-Hochberg('BH'). Default is 'BY'.
jaccardCutoff	A cutoff used in the filtering of edges with low Jaccard scores. If NULL (as default), no filtering of such edges will be performed.
osMethod	Method used to compute overlap scores. Options are "log" and "minmax".
pairFileTemplate	Character object used in the naming of the files where the pair data frames will be saved. Default is NULL (the pair data frames will not be saved).
keepOverlapOrder	Keep the rank-based order of overlaps in the pair score file, as opposed to changing it to a pair score-based order. Ignored if pairFileTemplate is NULL.
...	Additional arguments passed to mtCorrectDF.

Details

This function calls `scoreCells` to score each gene set data frame split from the full overlap data frame.

Value

A data frame whose columns correspond to the CSOA scores of the input gene sets.

Examples

```
mat <- matrix(0, 500, 300)
rownames(mat) <- paste0('G', seq(500))
colnames(mat) <- paste0('C', seq(300))
mat[sample(8000)] <- runif(8000, max=13)
genes <- paste0('G', seq(200))
mat[genes, 20:50] <- matrix(runif(200 * 31, min=14, max=15),
  nrow=200, ncol=31)
geneSet1 <- paste0('G', seq(1, 150))
geneSet2 <- paste0('G', seq(50, 200))
geneSets <- list(geneSet1, geneSet2)
geneSets <- lapply(geneSets, sort)
setPairs <- lapply(geneSets, getPairs)
pairs <- Reduce(union, setPairs)
genes <- union(geneSet1, geneSet2)
mat <- mat[genes, ]
overlapDF <- generateOverlaps(mat, pairs=pairs)
scoreDF <- scoreCells(mat, overlapDF, setPairs, c('set1', 'set2'))
head(scoreDF)
```

scoreModules	<i>Run CSOA separately on the connected components of the overlap graph</i>
--------------	-----------------------------------------------------------------------------

Description

This function runs CSOA on the connected components of the graph having the filtered overlaps as edges.

Usage

```
scoreModules(  
  scObj,  
  networkDF,  
  components,  
  colStrTemplate = "CSOA_component",  
  ...  
)
```

Arguments

scObj	A Seurat object, SingleCellExperiment object, or expression matrix.
networkDF	A data frame with gene1, gene2 and component columns.
components	A numeric vector representing the connected components of the overlap data frame graph.
colStrTemplate	Character used in the naming of the component gene sets.
...	Additional parameters passed to runCSOAMultiple.

Value

An object of the same class as scObj with CSOA scores corresponding to the genes defining each connected components assigned for each cell.

Examples

```
mat <- matrix(0, 500, 300)  
rownames(mat) <- paste0('G', seq(500))  
colnames(mat) <- paste0('C', seq(300))  
mat[sample(8000)] <- runif(8000, max=13)  
genes1 <- paste0('G', seq(100))  
mat[genes1, 20:50] <- matrix(runif(100 * 31, min = 14, max = 15),  
  nrow = 100, ncol = 31)  
genes2 <- paste0('G', seq(101, 200))  
mat[genes2, 70:100] <- matrix(runif(100 * 31, min = 14, max = 15),  
  nrow = 100, ncol = 31)  
genes <- union(genes1, genes2)  
mat <- mat[genes, ]
```

```
overlapDF <- generateOverlaps(mat)
overlapDF <- processOverlaps(overlapDF)
overlapDF <- henna::connectedComponents(overlapDF)
df <- scoreModules(mat, overlapDF, unique(overlapDF$component))[[2]]
head(df)
```

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