Package ‘clusterExperiment’

May 1, 2024

Title Compare Clusterings for Single-Cell Sequencing

Version 2.24.0

Description Provides functionality for running and comparing many different clusterings of single-cell sequencing data or other large mRNA Expression data sets.

BugReports https://github.com/epurdom/clusterExperiment/issues

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'makeBlankData.R' 'makeConsensus.R' 'makeDendrogram.R'
'makeFilterStats.R' 'makeReducedDims.R' 'mergeClusters.R'
'plotBarplot.R' 'plotClusters.R' 'plotClustersTable.R'
'plotClustersWorkflow.R' 'plotContrastHeatmap.R'
'plotDendrogram.R' 'plotFeatureBoxplot.R'
'plotFeatureScatter.R' 'plotHeatmap.R' 'plotReduceDim.R'
'plottingHelpers.R' 'rsec.R' 'seqCluster.R' 'subsampleLoop.R'
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addClusterings

Description

Function for adding new clusterings in form of vector (single clustering) or matrix (multiple clusterings) to an existing ClusterExperiment object.

Usage

```r
## S4 method for signature 'ClusterExperiment, matrix'
addClusterings(
  x,
  y,
  clusterTypes = "User",
  clusterLabels = NULL,
  clusterLegend = NULL
)

## S4 method for signature 'ClusterExperiment, ClusterExperiment'
addClusterings(x, y, transferFrom = c("x", "y"), mergeCEObjects = FALSE)

## S4 method for signature 'ClusterExperiment, vector'
addClusterings(x, y, makePrimary = FALSE, ...)
```

Index

addClusterings  Add clusterings to ClusterExperiment object
**Arguments**

- **x**: a ClusterExperiment object
- **y**: additional clusters to add to x. Can be a ClusterExperiment object or a matrix/vector of clusters.
- **clusterTypes**: a string describing the nature of the clustering. The values 'clusterSingle', 'clusterMany', 'mergeClusters', 'makeConsensus' are reserved for the clustering coming from the package workflow and should not be used when creating a new object with the constructor.
- **clusterLabels**: label(s) for the clusters being added. If y a matrix, the column names of that matrix will be used by default, if clusterLabels is not given.
- **clusterLegend**: a list giving the cluster legend for the clusters added.
- **transferFrom**: If x and y are both ClusterExperiment objects indicates from which object the clustering info should be taken (regarding merging, dendrogram, etc). Does not affect the order of the clusterings, which will always be the clusterings of x, followed by those of y (along with slots 'clusterType', 'clusterInfo', 'clusterLegend')
- **mergeCEObjects**: logical If x and y are both ClusterExperiment objects indicates as to whether should try to grab in the information missing from x from y (or vice versa if transferFrom=y).
- **makePrimary**: whether to make the added cluster the primary cluster (only relevant if y is a vector)
- ...
  For addClusterings, passed to signature ClusterExperiment, matrix. For [ (subsetting), passed to SingleCellExperiment subsetting function.

**Details**

addClusterings adds y to x, and is thus not symmetric in the two arguments. In particular, the primaryCluster, all of the dendrogram information, the merge information, coClustering, and orderSamples are all kept from the x object, even if y is a ClusterExperiment.

**Value**

A ClusterExperiment object.

**Examples**

data(simData)

cl1 <- clusterSingle(simData, subsample=FALSE, sequential=FALSE, mainClusterArgs=list(clusterArgs=list(k=3), clusterFunction="pam"))
cl2 <- clusterSingle(simData, subsample=FALSE, sequential=FALSE, mainClusterArgs=list(clusterArgs=list(k=3), clusterFunction="pam"))

addClusterings(cl1, cl2)
assignUnassigned

Assign unassigned samples to nearest cluster

Description

Assigns the unassigned samples in a cluster to the nearest cluster based on distance to the medians of the clusters.

Usage

```r
## S4 method for signature 'ClusterExperiment'
assignUnassigned(
  object,
  whichCluster = "primary",
  clusterLabel = NULL,
  makePrimary = TRUE,
  whichAssay = 1,
  reduceMethod = "none",
  ...
)
```

Arguments

- `object`: A Cluster Experiment object
- `whichCluster`: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.
- `clusterLabel`: if missing, the current cluster label of the cluster will be appended with the string "_AllAssigned".
- `makePrimary`: whether to make the added cluster the primary cluster (only relevant if `y` is a vector)
- `whichAssay`: which assay to use to calculate the median per cluster and take dimensionality reduction (if requested)
- `reduceMethod`: character. A method (or methods) for reducing the size of the data, either by filtering the rows (genes) or by a dimensionality reduction method. Must either be 1) must match the name of a built-in method, in which case if it is not already existing in the object will be passed to `makeFilterStats` or `link(makeReducedDims)`, or 2) must match a stored filtering statistic or dimensionality reduction in the object
- `...`: arguments passed to `getReducedData` specifying the dimensionality reduction (if any) to be taken of the data for calculating the medians of the clusters
clusterContrasts

Create contrasts for testing DE of a cluster

Description

Uses clustering to create different types of contrasts to be tested that can then be fed into DE testing programs.
Usage

```r
## S4 method for signature 'ClusterExperiment'
clusterContrasts(cluster, contrastType, ...)

## S4 method for signature 'vector'
clusterContrasts(
    cluster,
    contrastType = c("Dendro", "Pairs", "OneAgainstAll"),
    dendro = NULL,
    pairMat = NULL,
    outputType = c("limma", "MAST"),
    removeUnassigned = TRUE
)
```

Arguments

- `cluster`: Either a vector giving contrasts assignments or a ClusterExperiment object
- `contrastType`: What type of contrast to create. ‘Dendro’ traverses the given dendrogram and does contrasts of the samples in each side, ‘Pairs’ does pair-wise contrasts based on the pairs given in pairMat (if pairMat=NULL, does all pairwise), and ‘OneAgainstAll’ compares each cluster to the average of all others.
- `...`: arguments that are passed to from the ClusterExperiment version to the most basic numeric version.
- `dendro`: The dendrogram to traverse if contrastType="Dendro". Note that this should be the dendrogram of the clusters, not of the individual samples, either of class "dendrogram" or "phylo4"
- `pairMat`: matrix giving the pairs of clusters for which to do pair-wise contrasts (must match to elements of cl). If NULL, will do all pairwise of the clusters in cluster (excluding "-1" categories). Each row is a pair to be compared and must match the names of the clusters in the vector cluster.
- `outputType`: character string. Gives format for the resulting contrast matrix. Currently the two options are the format appropriate for limma and MAST package.
- `removeUnassigned`: logical, whether to remove negative valued clusters from the design matrix. Appropriate to pick TRUE (default) if design will be input into linear model on samples that excludes -1.

Details

The input vector must be numeric clusters, but the external commands that make the contrast matrix (e.g. makeContrasts) require syntactically valid R names. For this reason, the names of the levels will be "X1" instead of "1". And negative values (if removeUnassigned=FALSE) will be "X.1","X.2", etc.

Value

List with components:
• contrastMatrix Contrast matrix, the form of which depends on outputType. If outputType="limma", the result of running makeContrasts: a matrix with number of columns equal to the number of contrasts, and rows equal to the number of levels of the factor that will be fit in a linear model.

• contrastNames A vector of names for each of the contrasts. NULL if no such additional names.

Author(s)

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References


Examples

```r
## Not run:
data(simData)
cl <- clusterMany(simData,nReducedDims=c(5,10,50),
  reduceMethod="PCA", makeMissingDiss=TRUE,
  clusterFunction="pam", ks=2:4, findBestK=c(FALSE), removeSil=TRUE,
  subsample=FALSE)
# Pairs:
clusterContrasts(cl,contrastType="Pairs")
# Dendrogram
cl<-makeDendrogram(cl)
clusterContrasts(cl,contrastType="Pairs")
## End(Not run)
```

Description

These functions are for accessing and manipulating the dendrograms stored in a ClusterExperiment object. We also document the required format of these dendrograms here.
## Usage

```r
## S4 method for signature 'ClusterExperiment'
clusterDendrogram(x)
```

```r
## S4 method for signature 'ClusterExperiment'
sampleDendrogram(x)
```

```r
## S4 method for signature 'ClusterExperiment'
nInternalNodes(x)
```

```r
## S4 method for signature 'ClusterExperiment'
nTips(x)
```

```r
## S4 method for signature 'ClusterExperiment'
nNodes(x)
```

```r
## S4 replacement method for signature 'ClusterExperiment'
nodeLabels(x, ...) <- value
```

```r
## S4 method for signature 'ClusterExperiment,phylo4d,phylo4d'
checkDendrogram(x, dendroCluster, dendroSample, whichCluster = "dendro")
```

```r
## S4 method for signature 'ClusterExperiment'
nodeLabels(x)
```

```r
## S4 method for signature 'ClusterExperiment'
nodeIds(x, type = c("all", "internal", "tip"))
```

```r
## S4 method for signature 'ClusterExperiment'
convertToDendrogram(x)
```

### Arguments

- **x**
  - a `ClusterExperiment` object

- **...**
  - additional options passed to `nodeLabels<-(...)`

- **value**
  - replacement value for `nodeLabels`. See details.

- **dendroCluster**
  - a `phylo4d` to be check as for being cluster hierarchy

- **dendroSample**
  - a `phylo4d` to be check as for being cluster hierarchy

- **whichCluster**
  - argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.

- **type**
  - the type of node to return results from. One of "all", "internal", and "tip".

### Details

Two dendrograms are stored in a `ClusterExperiment` object. One is a dendrogram that describes the hierarchy between the clusters (`@dendro_clusters`), and the other is a dendrogram that extends...
that hierarchy to include the clusters (@dendro_samples). The clustering that is used to make these hierarchies is saved in as well (@dendro_index).

The dendrograms stored in a ClusterExperiment object are required to be a phylo4d-class from the package phylolbase (which uses the basic format of the S3 class phylo in the ape package to store the edges; phylolbase makes it a $S4$ class with some useful helpers). This class allows storage of a data.frame of information corresponding to information on each node (see tdata).

Additional requirements are made of these dendrograms to be a valid for the slots of the ClusterExperiment class, described below, regarding the data that must be stored with it and the labels which can be assigned. Possible dendrograms can be checked for validity with the function checkDendrogram. The reason for the restrictions on the labels is so as to not duplicate storage of the names, see below descriptions for where to save user-defined names.

- **Labels** The cluster dendrogram can only have labels on the internal nodes. Labels on the internal nodes of the cluster dendrogram can be set by the user (the function nodeLabels<- is defined to work on a ClusterExperiment object to make this easy). The tips of the cluster dendrogram, corresponding to the clusters, cannot have labels; users can set the labels (e.g. for plotting, etc) in the clusterLegend slot using the function renameClusters.

- **Data** The cluster hierarchy must have data stored with it that has the following columns (additional ones are allowed):
  - NodeId The permanent node id for the node. Must be of the format "NodeIdX" where "X" is a integer.
  - Position The type of node, in terms of its position. The internal nodes should have the values "cluster hierarchy node" while the tips should have "cluster hierarchy tip".
  - ClusterIdDendro Only for tips of dendrogram, should have the id that corresponds to its cluster in the clustering of the @dendro_index. Of the form "ClusterIdX", where "X" is the internal cluster id (see clusterLegend). Internal nodes should have NA values.
  - ClusterIdMerge The id that corresponds to the cluster in the clustering of the @merge_index, if it exists. Of the form "ClusterIdX", where "X" is the internal cluster id (see clusterLegend).

- **Labels** The sample dendrogram is not allowed to have ANY labels. The names for those nodes that correspond to the cluster hierarchy will be pulled from the names in the cluster hierarchy for plotting, etc. and should be set there (see above). Sample names for the tips of the tree will be pulled from colnames of the object and should be set there.

- **Data** The cluster hierarchy must have data stored with it that has the following columns (additional ones are allowed):
  - NodeId For those nodes that correspond to a node in the cluster hierarchy, should have its permanent node id in this column. Other nodes should be NA.
  - Position The type of node, in terms of its position. The internal nodes should have the values "cluster hierarchy node" while the tips should have "cluster hierarchy tip".
  - SampleIndex Only for tips of dendrogram, the index of the sample at that tip to the samples in the object.

For setting the node labels of the cluster dendrogram via nodeLabels<-, the replacement value has to have names that match the internal ids of the cluster dendrogram (the NodeId column).
Value

clusterDendrogram returns the dendrogram describing the clustering hierarchy.
sampleDendrogram returns the dendrogram that expands the cluster hierarchy to the samples.
nInternalNodes returns the number of internal nodes of the cluster hierarchy.
nTips returns the number of tips of the cluster hierarchy (same as number of non-negative clusters in the dendrogram clustering)
nNodes returns the number of total nodes of the cluster hierarchy
nodeLabels<- sets the node labels of the cluster dendrogram
checkClusterDendrogram checks if a phylo4d objects are valid for the cluster and sample dendrogram slots of the given ClusterExperiment object. Returns TRUE if there are no problems. Otherwise creates error.
nodeLabels returns the node labels of the cluster dendrogram
nodeIds returns the internal (permanent) node ids of the cluster dendrogram
convertToDendrogram returns the sample dendrogram converted to a dendrogram class.

The Stored Dendrograms

NA

Cluster Hierarchy

NA

Sample Hierarchy

NA

Helper Functions

NA

See Also

makeDendrogram, phylo4d-class, phylo
dendrogram

Examples

data(rsecFluidigm)
# retrieve the dendrogram of the clusters:
head(clusterDendrogram(rsecFluidigm),5)
# retrieve the dendrogram of the samples:
head(sampleDendrogram(rsecFluidigm),5)
# Return # internal nodes from cluster hierarchy
nInternalNodes(rsecFluidigm)
# Return # tips from cluster hierarchy (i.e. # clusters)
nTips(rsecFluidigm)
# Return internal node ids
nodeIds(rsecFluidigm, type="internal")

# Labels assigned to internal nodes
nodeLabels(rsecFluidigm)

# Assign new labels to the internal nodes of the cluster hierarchy
l1 <- paste("A", 1:nInternalNodes(rsecFluidigm), sep=":")
names(l1) <- nodeIds(rsecFluidigm, type="internal")
nodeLabels(rsecFluidigm) <- l1
nodeLabels(rsecFluidigm)

ClusterExperiment-class

Class ClusterExperiment

Description

ClusterExperiment is a class that extends SingleCellExperiment and is used to store the data and clustering information.

In addition to the slots of the SingleCellExperiment class, the ClusterExperiment object has the additional slots described in the Slots section.

There are several methods implemented for this class. The most important methods (e.g., clusterMany, makeConsensus, ...) have their own help page. Simple helper methods are described in the Methods section. For a comprehensive list of methods specific to this class see the Reference Manual.

The constructor ClusterExperiment creates an object of the class ClusterExperiment. However, the typical way of creating these objects is the result of a call to clusterMany or clusterSingle.

Note that when subsetting the data, the co-clustering and dendrogram information are lost.

Usage

ClusterExperiment(object, clusters, ...)

## S4 method for signature 'matrixOrHDF5,ANY'
ClusterExperiment(object, clusters, ...)

## S4 method for signature 'SummarizedExperiment,ANY'
ClusterExperiment(object, clusters, ...)

## S4 method for signature 'SingleCellExperiment,numeric'
ClusterExperiment(object, clusters, ...)

## S4 method for signature 'SingleCellExperiment,character'
ClusterExperiment(object, clusters, ...)

## S4 method for signature 'SingleCellExperiment,factor'
ClusterExperiment(object, clusters, ...)
## S4 method for signature 'SingleCellExperiment,matrix'
ClusterExperiment(
  object,
  clusters,
  transformation = function(x) {
    x
  },
  primaryIndex = 1,
  clusterTypes = "User",
  clusterInfo = NULL,
  orderSamples = seq_len(ncol(object)),
  dendro_samples = NULL,
  dendro_index = NA_real_,
  dendro_clusters = NULL,
  coClustering = NULL,
  merge_index = NA_real_,
  merge_cutoff = NA_real_,
  merge_dendrocluster_index = NA_real_,
  merge_nodeProp = NULL,
  merge_nodeMerge = NULL,
  merge_method = NA_character_,
  merge_demethod = NA_character_,
  clusterLegend = NULL,
  checkTransformAndAssay = TRUE
)

### Arguments

- **object**: a matrix or SummarizedExperiment or SingleCellExperiment containing the data that was clustered.
- **clusters**: can be either a numeric or character vector, a factor, or a numeric matrix, containing the cluster labels.
- **transformation**: a function to transform the data before performing steps that assume normal-like data (i.e. constant variance), such as the log.
- **primaryIndex**: integer. Sets the 'primaryIndex' slot (see Slots).
- **clusterTypes**: a string describing the nature of the clustering. The values 'clusterSingle', 'clusterMany', 'mergeClusters', 'makeConsensus' are reserved for the clustering coming from the package workflow and should not be used when creating a new object with the constructor.
- **clusterInfo**: a list with information on the clustering (see Slots).
- **orderSamples**: a vector of integers. Sets the 'orderSamples' slot (see Slots).
- **dendro_samples**: phylo4 object. Sets the 'dendro_samples' slot (see Slots).
- **dendro_index**: numeric. Sets the dendro_index slot (see Slots).
dendro_clusters
phylo4 object. Sets the ‘dendro_clusters’ slot (see Slots).
coClustering matrix. Sets the coClustering slot (see Slots).
merge_index integer. Sets the merge_index slot (see Slots)
merge_cutoff numeric. Sets the merge_cutoff slot (see Slots)
merge_dendrocluster_index integer. Sets the merge_dendrocluster_index slot (see Slots)
merge_nodeProp data.frame. Sets the merge_nodeProp slot (see Slots)
merge_nodeMerge data.frame. Sets the merge_nodeMerge slot (see Slots)
merge_method character. Sets the merge_method slot (see Slots)
merge_demethod character. Sets the merge_demethod slot (see Slots)
clusterLegend list. Sets the clusterLegend slot (see details).
checkTransformAndAssay logical. Whether to check the content of the assay and given transformation function for whether they are valid.

Details
The clusterLegend argument to ClusterExperiment must be a valid clusterLegend format and match the values in clusters, in that the "clusterIds" column must matches the value in the clustering matrix clusters. If names(clusterLegend)==NULL, it is assumed that the entries of clusterLegend are in the same order as the columns of clusters. Generally, this is not a good way for users to set the clusterLegend slot.

The ClusterExperiment constructor function gives clusterLabels based on the column names of the input matrix/SingleCellExperiment. If missing, will assign labels "cluster1","cluster2", etc.

Note that the validity check when creating a new ClusterExperiment object with new is less extensive than when using ClusterExperiment function with checkTransformAndAssay=TRUE (the default). Users are advised to use ClusterExperiment to create new ClusterExperiment objects.

Value
A ClusterExperiment object.

Slots
transformation function. Function to transform the data by when methods that assume normal-like data (e.g. log)
clusterMatrix matrix. A matrix giving the integer-valued cluster ids for each sample. The rows of the matrix correspond to clusterings and columns to samples. The integer values are assigned in the order that the clusters were found, if found by setting sequential=TRUE in clusterSingle. "-1" indicates the sample was not clustered.
primaryIndex numeric. An index that specifies the primary set of labels.
clusterInfo list. A list with info about the clustering. If created from clusterSingle, clusterInfo will include the parameter used for the call, and the call itself. If sequential = TRUE it will also include the following components.
ClusterExperiment-class

- **clusterInfo** if sequential=TRUE and clusters were successfully found, a matrix of information regarding the algorithm behavior for each cluster (the starting and stopping K for each cluster, and the number of iterations for each cluster).
- **whyStop** if sequential=TRUE and clusters were successfully found, a character string explaining what triggered the algorithm to stop.

**merge_index**  index of the current merged cluster

**merge_cutoff**  value for the cutoff used to determine whether to merge clusters

**merge_dendrocluster_index**  index of the cluster merged with the current merge

**merge_nodeMerge**  data.frame of information about nodes merged in the current merge. See `mergeClusters`

**merge_nodeProp**  data.frame of information of proportion estimated non-null at each node of dendrogram. See `mergeClusters`

**merge_method**  character indicating method used for merging. See `mergeClusters`

**merge_demethod**  character indicating the DE method used for merging. See `mergeClusters`

**clusterTypes**  character vector with the origin of each column of clusterMatrix.

**dendro_samples**  phylo4d object. A dendrogram containing the cluster relationship (leaves are samples; see `clusterDendrogram` for details).

**dendro_clusters**  phylo4d object. A dendrogram containing the cluster relationship (leaves are clusters; see `sampleDendrogram` for details).

**dendro_index**  numeric. An integer giving the cluster that was used to make the dendrograms. NA_real_value if no dendrograms are saved.

**coClustering**  One of

- NULL, i.e. empty
- a numeric vector, signifying the indices of the clusterings in the clusterMatrix that were used for makeConsensus. This allows for the recreation of the distance matrix (using hamming distance) if needed for function plotClusters but doesn’t require storage of full NxN matrix.
- a `sparseMatrix` object – a sparse representation of the NxN matrix with the cluster co-occurrence information; this can either be based on subsampling or on co-clustering across parameter sets (see `clusterMany`). The matrix is a square matrix with number of rows/columns equal to the number of samples.

**clusterLegend**  a list, one per cluster in clusterMatrix. Each element of the list is a matrix with nrows equal to the number of different clusters in the clustering, and consisting of at least two columns with the following column names: "clusterId" and "color".

**orderSamples**  a numeric vector (of integers) defining the order of samples to be used for plotting of samples. Usually set internally by other functions.

See Also

sparseMatrix phylo4d
Examples

```r
sce <- matrix(data=rnorm(200), ncol=10)
labels <- gl(5, 2)
cc <- ClusterExperiment(sce, as.numeric(labels), transformation =
function(x){x}(x))
```

Description

These functions are provided for compatibility with older versions of ‘clusterExperiment’ only, and will be defunct at the next release.

Usage

```r
## S4 method for signature 'ANY'
combineMany(x, ...)
```

Arguments

- `x`: any object
- `...`: additional arguments

Details

The following functions are deprecated and will be made defunct; use the replacement indicated below:

- `combineMany`: `makeConsensus`
- `removeUnclustered`: `removeUnassigned`

Description

This is a collection of helper methods for the ClusterExperiment class.
Usage

## S4 method for signature 'ClusterExperiment'
show(object)

## S4 method for signature 'ClusterExperiment'
transformation(x)

## S4 replacement method for signature 'ClusterExperiment,function'
transformation(object) <- value

## S4 method for signature 'ClusterExperiment'
nClusterings(x)

## S4 method for signature 'ClusterExperiment'
nClusters(x, ignoreUnassigned = TRUE)

## S4 method for signature 'ClusterExperiment'
nFeatures(x)

## S4 method for signature 'ClusterExperiment'
nSamples(x)

## S4 method for signature 'ClusterExperiment'
clusterMatrixNamed(x, whichClusters = "all")

## S4 method for signature 'ClusterExperiment'
clusterMatrixColors(x, whichClusters = "all")

## S4 method for signature 'ClusterExperiment'
clusterMatrix(x, whichClusters)

## S4 method for signature 'ClusterExperiment'
primaryCluster(x)

## S4 method for signature 'ClusterExperiment'
primaryClusterIndex(x)

## S4 method for signature 'ClusterExperiment'
primaryClusterLabel(x)

## S4 method for signature 'ClusterExperiment'
primaryClusterNamed(x)

## S4 method for signature 'ClusterExperiment'
primaryClusterType(x)

## S4 replacement method for signature 'ClusterExperiment,numeric'
primaryClusterIndex(object) <- value
```r
## S4 method for signature 'ClusterExperiment'
dendroClusterIndex(x)

## S4 method for signature 'ClusterExperiment'
corClustering(x)

## S4 replacement method for signature 'ClusterExperiment,matrix'
corClustering(object) <- value

## S4 replacement method for signature 'ClusterExperiment,dsCMatrix'
corClustering(object) <- value

## S4 replacement method for signature 'ClusterExperiment,numeric'
corClustering(object) <- value

## S4 method for signature 'ClusterExperiment'
clusterTypes(x)

## S4 method for signature 'ClusterExperiment'
clusteringInfo(x)

## S4 method for signature 'ClusterExperiment'
clusterLabels(x)

## S4 replacement method for signature 'ClusterExperiment,character'
clusterLabels(object) <- value

## S4 method for signature 'ClusterExperiment'
clusterLegend(x)

## S4 replacement method for signature 'ClusterExperiment,list'
clusterLegend(object) <- value

## S4 method for signature 'ClusterExperiment'
orderSamples(x)

## S4 replacement method for signature 'ClusterExperiment,numeric'
orderSamples(object) <- value

## S4 replacement method for signature 'ClusterExperiment,character'
clusterTypes(object) <- value

## S4 method for signature 'ClusterExperiment'
addToColData(object, ...)

## S4 method for signature 'ClusterExperiment'
colDataClusters(
```
Arguments

- **x, object**
  a ClusterExperiment object.

- **value**
  The value to be substituted in the corresponding slot. See the slot descriptions in `ClusterExperiment` for details on what objects may be passed to these functions.

- **ignoreUnassigned**
  logical. If true, ignore the clusters with -1 or -2 assignments in calculating the number of clusters per clustering.

- **whichClusters**
  argument that can be either numeric or character vector indicating the clusterings to be used. See details of `getClusterIndex`.

- **...**
  For `addToColData`, arguments passed to `colDataClusters`.

- **useNames**
  for `tableClusters`, whether the output should be tabled with names (`useNames=TRUE`) or ids (`useNames=FALSE`)

- **makeFactor**
  logical for `colDataClusters`. If TRUE the clustering will be added to the `colData` slot as a factor. If FALSE, the clustering will be added to the `colData` slot as a character vector if `useNames=TRUE` and as a numeric vector if `useNames=FALSE`.

Details

Note that redefining the transformation function via `transformation(x) <-` will check the validity of the transformation on the data assay. If the assay is large, this may be time consuming. Consider using a call to `ClusterExperiment`, which has the option as to whether to check the validity of the transformation.

Value

- `transformation` prints the function used to transform the data prior to clustering.
- `nClusterings` returns the number of clusterings (i.e., `ncol` of `clusterMatrix`).
- `nClusters` returns the number of clusters per clustering
- `nFeatures` returns the number of features (same as `nrow`).
- `nSamples` returns the number of samples (same as `ncol`).
- `clusterMatrixNamed` returns a matrix with cluster labels.
- `clusterMatrixColors` returns the matrix with all the clusterings, using the internally stored colors for each cluster.
- `clusterMatrix` returns the matrix with all the clusterings.
- `primaryCluster` returns the primary clustering (as numeric).
primaryClusterIndex returns/sets the primary clustering index (i.e., which column of clusterMatrix corresponds to the primary clustering).

primaryClusterIndex returns/sets the primary clustering index (i.e., which column of clusterMatrix corresponds to the primary clustering).

primaryClusterNamed returns the primary cluster (using cluster labels).

primaryClusterIndex returns/sets the primary clustering index (i.e., which column of clusterMatrix corresponds to the primary clustering).

dendroClusterIndex returns/sets the clustering index of the clusters used to create dendrogram (i.e., which column of clusterMatrix corresponds to the clustering).

coclustering returns/sets the co-clustering matrix.

clusterTypes returns/sets the clusterTypes slot.

clusteringInfo returns the clusterInfo slot.

clusterLabels returns/sets the column names of the clusterMatrix slot.

clusterLegend returns/sets the clusterLegend slot.

orderSamples returns/sets the orderSamples slot.

addToColData returns a ClusterExperiment object with the clusterings in clusterMatrix slot added to the colData slot.

colDataClusters returns a DataFrame object that has the clusterings in clusterMatrix slot added to the DataFrame in the colData slot.

Examples

```r
# load data:
data(rsecFluidigm)
show(rsecFluidigm)
# Number of clusterings
nClusterings(rsecFluidigm)
# Number of clusters per clustering
nClusters(rsecFluidigm)
# Number of features/samples
nSamples(rsecFluidigm)
nFeatures(rsecFluidigm)
# retrieve all clustering assignments
# (either as cluster ids, cluster names or cluster colors)
head(clusterMatrix(rsecFluidigm)[,1:5])
head(clusterMatrixNamed(rsecFluidigm)[,1:5])
head(clusterMatrixColors(rsecFluidigm)[,1:5])
# clustering Types/Labels
clusterTypes(rsecFluidigm)
clusterLabels(rsecFluidigm)
# Add a clustering assignment to the colData of the object
# (useful if working with function that relies on colData)
colData(rsecFluidigm)
test<-addToColData(rsecFluidigm,whichCluster="primary")
colData(test)
```
ClusterFunction-methods

*Helper methods for the ClusterFunction class*

**Description**

This is a collection of helper methods for the ClusterExperiment class.

**Usage**

```r
## S4 method for signature 'character'
requiredArgs(object)

## S4 method for signature 'ClusterFunction'
requiredArgs(object, genericOnly = FALSE)

## S4 method for signature 'list'
requiredArgs(object)

## S4 method for signature 'character'
requiredArgs(object)

## S4 method for signature 'character'
requiredArgs(object)

## S4 method for signature 'factor'
requiredArgs(object)

## S4 method for signature 'ClusterFunction'
algorithmType(object)

## S4 method for signature 'character'
algorithmType(object)

## S4 method for signature 'factor'
algorithmType(object)

## S4 method for signature 'list'
algorithmType(object)

## S4 method for signature 'ClusterFunction'
inputType(object)

## S4 method for signature 'list'
inputType(object)

## S4 method for signature 'character'
```
inputType(object)
## S4 method for signature 'factor'
inputType(object)

Arguments

table

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>input to the method, either a ClusterFunction class or a character describing</td>
</tr>
<tr>
<td></td>
<td>a built-in ClusterFunction object. Can also be a list of ClusterFunction</td>
</tr>
<tr>
<td></td>
<td>objects, in which case the list must have names for each function.</td>
</tr>
<tr>
<td>genericOnly</td>
<td>logical If TRUE, return only the generic required arguments (i.e. those</td>
</tr>
<tr>
<td></td>
<td>required by the algorithm type) and not the arguments specific to that</td>
</tr>
<tr>
<td></td>
<td>clustering found in the slot requiredArgs. If FALSE both sets of arguments</td>
</tr>
<tr>
<td></td>
<td>are returned.</td>
</tr>
</tbody>
</table>

Details

Note that when subsetting the data, the dendrogram information and the co-clustering matrix are lost.

Value

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>requiredArgs</td>
<td>returns a list of the required args of a function (via a call to requiredArgs)</td>
</tr>
<tr>
<td>algorithmType</td>
<td>returns a character value giving the type of clustering function (&quot;01&quot; or &quot;K&quot;)</td>
</tr>
<tr>
<td>inputType</td>
<td>returns a character value giving the input type of the object</td>
</tr>
</tbody>
</table>

Description

Given a range of parameters, this function will return a matrix with the clustering of the samples across the range, which can be passed to plotClusters for visualization.

Usage

```r
# S4 method for signature 'matrixOrHDF5'
clusterMany(
  x,
  reduceMethod = "none",
  nReducedDims = NA,
  transFun = NULL,
  isCount = FALSE,
  ...
)
```

```r
# S4 method for signature 'SingleCellExperiment'
clusterMany(
```
clusterMany

x,
ks = NA,
clusterFunction,
reduceMethod = "none",
nFilterDims = defaultNDims(x, reduceMethod, type = "filterStats"),
nReducedDims = defaultNDims(x, reduceMethod, type = "reducedDims"),
alphas = 0.1,
findBestK = FALSE,
sequential = FALSE,
removeSil = FALSE,
subsample = FALSE,
silCutoff = 0,
distFunction = NA,
betas = 0.9,
minSizes = 1,
transFun = NULL,
isCount = FALSE,
verbose = TRUE,
parameterWarnings = FALSE,
mainClusterArgs = NULL,
subsampleArgs = NULL,
seqArgs = NULL,
whichAssay = 1,
makeMissingDiss = if (ncol(x) < 1000) TRUE else FALSE,
ncores = 1,
random.seed = NULL,
run = TRUE,
...
)

## S4 method for signature 'ClusterExperiment'
clusterMany(
  x,
  reduceMethod = "none",
nFilterDims = defaultNDims(x, reduceMethod, type = "filterStats"),
nReducedDims = defaultNDims(x, reduceMethod, type = "reducedDims"),
  eraseOld = FALSE,
  ...
)

## S4 method for signature 'SummarizedExperiment'
clusterMany(x, ...)

## S4 method for signature 'data.frame'
clusterMany(x, ...)

Arguments

x  
the data matrix on which to run the clustering. Can be object of the following classes: matrix (with genes in rows), SummarizedExperiment, SingleCellExperiment or ClusterExperiment.

reduceMethod  
character A character identifying what type of dimensionality reduction to perform before clustering. Options are 1) "none", 2) one of listBuiltInReducedDims() or listBuiltInFilterStats OR 3) stored filtering or reducedDim values in the object.

nReducedDims  
vector of the number of dimensions to use (when reduceMethod gives a dimensionality reduction method).

transFun  
a transformation function to be applied to the data. If the transformation applied to the data creates an error or NA values, then the function will throw an error. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

isCount  
if transFun=NULL, then isCount=TRUE will determine the transformation as defined by function(x){log2(x+1)}, and isCount=FALSE will give a transformation function function(x){x}. Ignored if transFun=NULL. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

...  
For signature matrix, arguments to be passed on to mclapply (if ncores>1). For all the other signatures, arguments to be passed to the method for signature matrix.

ks  
the range of k values (see details for the meaning of k for different choices of other parameters).

clusterFunction  
function used for the clustering. This must be either 1) a character vector of built-in clustering techniques, or 2) a named list of ClusterFunction objects. Current functions can be found by typing listBuiltInFunctions() into the command-line.

nFilterDims  
vector of the number of the most variable features to keep (when "var", "absCV", or "mad" is identified in reduceMethod).

alphas  
values of alpha to be tried. Only used for clusterFunctions of type '01'. Determines tightness required in creating clusters from the dissimilarity matrix. Takes on values in [0,1]. See documentation of ClusterFunction.

findBestK  
logical, whether should find best K based on average silhouette width (only used when clusterFunction of type "K").

sequential  
logical whether to use the sequential strategy (see details of seqCluster). Can be used in combination with subsample=TRUE or FALSE.

removeSil  
logical as to whether remove when silhouette < silCutoff (only used if clusterFunction of type "K")

subsample  
logical as to whether to subsample via subsampleClustering. If TRUE, clustering in mainClustering step is done on the co-occurrence between clusterings in the subsampled clustering results. If FALSE, the mainClustering step will be run directly on x/diss
silCutoff  Requirement on minimum silhouette width to be included in cluster (only for combinations where removeSil=TRUE).

distFunction  a vector of character strings that are the names of distance functions found in the global environment. See the help pages of clusterSingle for details about the required format of distance functions. Currently, this distance function must be applicable for all clusterFunction types tried. Therefore, it is not possible in clusterMany to intermix type "K" and type "01" algorithms if you also give distances to evaluate via distFunction unless all distances give 0-1 values for the distance (and hence are possible for both type "01" and "K" algorithms).

betas  values of beta to be tried in sequential steps. Only used for sequential=TRUE. Determines the similarity between two clusters required in order to deem the cluster stable. Takes on values in [0,1]. See documentation of seqCluster.

minSizes  the minimum size required for a cluster (in the mainClustering step). Clusters smaller than this are not kept and samples are left unassigned.

verbose  logical. If TRUE it will print informative messages.

parameterWarnings  logical, as to whether warnings and comments from checking the validity of the parameter combinations should be printed.

mainClusterArgs  list of arguments to be passed for the mainClustering step, see help pages of mainClustering.

subsampleArgs  list of arguments to be passed to the subsampling step (if subsample=TRUE), see help pages of subsampleClustering.

seqArgs  list of arguments to be passed to seqCluster.

whichAssay  numeric or character specifying which assay to use. See assay for details.

makeMissingDiss  logical. Whether to calculate necessary distance matrices needed when input is not "diss". If TRUE, then when a clustering function calls for a inputType "diss", but the given matrix is of type "X", the function will calculate a distance function. A dissimilarity matrix will also be calculated if a post-processing argument like findBestK or removeSil is chosen, since these rely on calculating silhouette widths from distances.

ncores  the number of threads

random.seed  a value to set seed before each run of clusterSingle (so that all of the runs are run on the same subsample of the data). Note, if 'random.seed' is set, argument 'ncores' should NOT be passed via subsampleArgs; instead set the argument 'ncores' of clusterMany directly (which is preferred for improving speed anyway).

run  logical. If FALSE, doesn’t run clustering, but just returns matrix of parameters that will be run, for the purpose of inspection by user (with rownames equal to the names of the resulting column names of clMat object that would be returned if run=TRUE). Even if run=FALSE, however, the function will create the dimensionality reductions of the data indicated by the user input.

eraseOld  logical. Only relevant if input x is of class ClusterExperiment. If TRUE, will erase existing workflow results (clusterMany as well as mergeClusters and
makeConsensus). If FALSE, existing workflow results will have "_i" added to the clusterTypes value, where \( i \) is one more than the largest such existing workflow clusterTypes.

**Details**

Some combinations of these parameters are not feasible. See the documentation of `clusterSingle` for important information on how these parameter choices interact.

While the function allows for multiple values of clusterFunction, the code does not reuse the same subsampling matrix and try different clusterFunctions on it. This is because if sequential=TRUE, different subsample clusterFunctions will create different sets of data to subsample so it is not possible; if sequential=FALSE, we have not implemented functionality for this reuse. Setting the random.seed value, however, should mean that the subsampled matrix is the same for each, but there is no gain in computational complexity (i.e. each subsampled co-occurrence matrix is recalculated for each set of parameters).

The argument `ks` is interpreted differently for different choices of the other parameters. When/if sequential=TRUE, `ks` defines the argument `k0` of `seqCluster`. Otherwise, `ks` values are the `k` values for both the mainClustering and subsampling step (i.e. assigned to the subsampleArgs and mainClusterArgs that are passed to `mainClustering` and `subsampleClustering` unless `k` is set appropriately in subsampleArgs. The passing of these arguments via subsampleArgs will only have an effect if `subsample=TRUE`. Similarly, the passing of `mainClusterArgs["k"]` will only have an effect when the clusterFunction argument includes a clustering algorithm of type "K". When/if "findBestK=TRUE", `ks` also defines the `kRange` argument of `mainClustering` unless `kRange` is specified by the user via the `mainClusterArgs`; note this means that the default option of setting `kRange` that depends on the input `k` (see `mainClustering`) is not available in `clusterMany`, only in `clusterSingle`.

If the input is a `ClusterExperiment` object, current implementation is that existing orderSamples, coClustering or the many dendrogram slots will be retained.

If run=FALSE, the function will still calculate reduced dimensions or filter statistics if not already calculated and saved in the object. Moreover the results of these calculations will not be save. Therefore, if these steps are lengthy for large datasets it is recommended to do them before calling the function.

The given `reduceMethod` values must either be all precalculated filtering/dimensionality reduction stored in the appropriate location, or must all be character values giving a built-in filtering/dimensionality reduction methods to be calculated. If some of the filtering/dimensionality methods are already calculated and stored, but not all, then they will all be recalculated (and if they are not all built-in methods, this will give an error). So to save computational time with pre-calculated dimensionality reduction, the user must make sure they are all precalculated. Also, user-defined values (i.e. not built-in functions) cannot be mixed with built-in functions unless they have already been precalculated (see `makeFilterStats` or `makeReducedDims`).

**Value**

If run=TRUE will return a `ClusterExperiment` object, where the results are stored as clusterings with clusterTypes `clusterMany`. Depending on eraseOld argument above, this will either delete existing such objects, or change the clusterTypes of existing objects. See argument eraseOld above. Arbitrarily the first clustering is set as the primaryClusteringIndex.
If run=FALSE a list with elements:

- paramMatrix a matrix giving the parameters of each clustering, where each column is a possible parameter set by the user and passed to clusterSingle and each row of paramMatrix corresponds to a clustering in clMat
- mainClusterArgs a list of (possibly modified) arguments to mainClusterArgs
- seqArgs seqArgs a list of (possibly modified) arguments to seqArgs
- subsampleArgs subsampleArgs a list of (possibly modified) arguments to subsampleArgs

Examples

```r
## Not run:
data(simData)

# Example: clustering using pam with different dimensions of pca and different
# k and whether remove negative silhouette values
# check how many and what runs users choices will imply:
checkParams <- clusterMany(simData, reduceMethod="PCA", makeMissingDiss=TRUE,
                         nReducedDims=c(5,10,50), clusterFunction="pam", isCount=FALSE,
                         ks=2:4, findBestK=c(TRUE, FALSE), removeSil=c(TRUE, FALSE), run=FALSE)
print(head(checkParams$paramMatrix))

# Now actually run it
cl <- clusterMany(simData, reduceMethod="PCA", nReducedDims=c(5,10,50), isCount=FALSE,
                  clusterFunction="pam", ks=2:4, findBestK=c(TRUE, FALSE), makeMissingDiss=TRUE,
                  removeSil=c(TRUE, FALSE))
print(cl)
head(colnames(clusterMatrix(cl)))

# make names shorter for plotting
clNames <- clusterLabels(cl)
clNames <- gsub("TRUE", "T", clNames)
clNames <- gsub("FALSE", "F", clNames)
clNames <- gsub("k=NA,"", ",", clNames)

par(mar=c(2, 10, 1, 1))
plotClusters(cl, axisLine=-2, clusterLabels=clNames)

# following code takes around 1+ minutes to run because of the subsampling
# that is redone each time:

system.time(clusterTrack <- clusterMany(simData, ks=2:15,
                                        alphas=c(0.1,0.2,0.3), findBestK=c(TRUE,FALSE), sequential=c(FALSE),
                                        subsample=c(FALSE), removeSil=c(TRUE), clusterFunction="pam",
                                        makeMissingDiss=TRUE,
                                        mainClusterArgs=list(minSize=5, kRange=2:15), ncores=1, random.seed=48120))

## End(Not run)
```
clusterSingle

*General wrapper method to cluster the data*

**Description**

Given input data, this function will find clusters, based on a single specification of parameters.

**Usage**

```r
## S4 method for signature 'SummarizedExperiment'
clusterSingle(inputMatrix, ...)

## S4 method for signature 'ClusterExperiment'
clusterSingle(inputMatrix, ...)

## S4 method for signature 'SingleCellExperiment'
clusterSingle(
  inputMatrix,
  reduceMethod = "none",
  nDims = defaultNDims(inputMatrix, reduceMethod),
  whichAssay = 1,
  ...
)

## S4 method for signature 'matrixOrHDF5OrNULL'
clusterSingle(
  inputMatrix,
  inputType = "X",
  subsample = FALSE,
  sequential = FALSE,
  distFunction = NA,
  mainClusterArgs = NULL,
  subsampleArgs = NULL,
  seqArgs = NULL,
  isCount = FALSE,
  transFun = NULL,
  reduceMethod = "none",
  nDims = defaultNDims(inputMatrix, reduceMethod),
  makeMissingDiss = if (ncol(inputMatrix) < 1000) TRUE else FALSE,
  clusterLabel = "clusterSingle",
  saveSubsamplingMatrix = FALSE,
  checkDiss = FALSE,
  warnings = TRUE
)
```
Arguments

inputMatrix  numerical matrix on which to run the clustering or a SummarizedExperiment, SingleCellExperiment, or ClusterExperiment object.

...  arguments to be passed on to the method for signature matrix.

reduceMethod  character A character identifying what type of dimensionality reduction to perform before clustering. Options are 1) "none", 2) one of listBuiltInReduced-Dims() or listBuiltInFilterStats OR 3) stored filtering or reducedDim values in the object.

nDims  integer An integer identifying how many dimensions to reduce to in the reduction specified by reduceMethod. Defaults to output of defaultNDims

whichAssay  numeric or character specifying which assay to use. See assay for details.

inputType  a character vector defining what type of input is given in the inputMatrix argument. Must consist of values "diss","X", or "cat" (see details). "X" and "cat" should be indicate matrices with features in the row and samples in the column; "cat" corresponds to the features being numerical integers corresponding to categories, while "X" are continuous valued features. "diss" corresponds to an inputMatrix that is a NxN dissimilarity matrix. "cat" is largely used internally for clustering of sets of clusterings.

subsample  logical as to whether to subsample via subsampleClustering. If TRUE, clustering in mainClustering step is done on the co-occurrence between clusterings in the subsampled clustering results. If FALSE, the mainClustering step will be run directly on x/diss

sequential  logical whether to use the sequential strategy (see details of seqCluster). Can be used in combination with subsample=TRUE or FALSE.

distFunction  a distance function to be applied to inputMatrix. Only relevant if inputType="X". See details of clusterSingle for the required format of the distance function.

mainClusterArgs  list of arguments to be passed for the mainClustering step, see help pages of mainClustering.

subsampleArgs  list of arguments to be passed to the subsampling step (if subsample=TRUE), see help pages of subsampleClustering.

seqArgs  list of arguments to be passed to seqCluster.

isCount  if transFun=NULL, then isCount=TRUE will determine the transformation as defined by function(x){log2(x+1)}, and isCount=FALSE will give a transformation function function(x){x}. Ignored if transFun=NULL. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

transFun  a transformation function to be applied to the data. If the transformation applied to the data creates an error or NA values, then the function will throw an error. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

makeMissingDiss  logical. Whether to calculate necessary distance matrices needed when input is not "diss". If TRUE, then when a clustering function calls for a inputType
clusterSingle

"diss", but the given matrix is of type "X", the function will calculate a distance function. A dissimilarity matrix will also be calculated if a post-processing argument like findBestK or removeSil is chosen, since these rely on calculating silhouette widths from distances.

clusterLabel: a string used to describe the clustering. By default it is equal to "clusterSingle", to indicate that this clustering is the result of a call to clusterSingle.

saveSubsamplingMatrix: logical. If TRUE, the co-clustering matrix resulting from subsampling is returned in the coClustering slot (and replaces any existing coClustering object in the slot coClustering if input object is a ClusterExperiment object.)

checkDiss: logical. Whether to check whether the dissimilarities matrices are valid (whether given by the user or calculated because makeMissingDiss=TRUE).

warnings: logical. Whether to print out the many possible warnings and messages regarding checking the internal consistency of the parameters.

Details

clusterSingle is an 'expert-oriented' function, intended to be used when a user wants to run a single clustering and/or have a great deal of control over the clustering parameters. Most users will find clusterMany more relevant. However, clusterMany makes certain assumptions about the intention of certain combinations of parameters that might not match the user's intent; similarly clusterMany does not directly take a dissimilarity matrix but only a matrix of values x (though a user can define a distance function to be applied to x in clusterMany).

Unlike clusterMany, most of the relevant arguments for the actual clustering algorithms in clusterSingle are passed to the relevant steps via the arguments mainClusterArgs, subsampleArgs, and seqArgs. These arguments should be named lists with parameters that match the corresponding functions: mainClustering, subsampleClustering, and seqCluster. These three functions are not meant to be called by the user, but rather accessed via calls to clusterSingle. But the user can look at the help files of those functions for more information regarding the parameters that they take.

Only certain combinations of parameters are possible for certain choices of sequential and subsample. These restrictions are documented below.

• clusterFunction for mainClusterArgs: The choice of subsample=TRUE also controls what algorithm type of clustering functions can be used in the mainClustering step. When subsample=TRUE, then resulting co-clustering matrix from subsampling is converted to a dissimilarity (specifically 1-co-clustering values) and is passed to diss of mainClustering. For this reason, the ClusterFunction object given to mainClustering via the argument mainClusterArgs must take input of the form of a dissimilarity. When subsample=FALSE and sequential=TRUE, the clusterFunction passed in clusterArgs element of mainClusterArgs must define a ClusterFunction object with algorithmType 'K'. When subsample=FALSE and sequential=FALSE, then there are no restrictions on the ClusterFunction and that clustering is applied directly to the input data.

• clusterFunction for subsampleArgs: If the ClusterFunction object given to the clusterArgs of subsamplingArgs is missing the algorithm will use the default for subsampleClustering (currently "pam"). If sequential=TRUE, this ClusterFunction object must be of type 'K'.

• Setting k for subsampling: If subsample=TRUE and sequential=TRUE, the current K of the sequential iteration determines the 'k' argument passed to subsampleClustering so setting
'k=' in the list given to the subsampleArgs will not do anything and will produce a warning to that effect (see documentation of seqCluster).

- Setting k for mainClustering step: If sequential=TRUE then the user should not set k in the clusterArgs argument of mainClusterArgs because it must be set by the sequential code, which has an iterative resetting of the parameters. Specifically if subsample=FALSE, then the sequential method iterates over choices of k to cluster the input data. And if subsample=TRUE, then the k in the clustering of mainClustering step (assuming the clustering function is of type 'K') will use the k used in the subsampling step to make sure that the k used in the mainClustering step is reasonable.

- Setting findBestK in mainClusterArgs: If sequential=TRUE and subsample=FALSE, the user should not set 'findBestK=TRUE' in mainClusterArgs. This is because in this case the sequential method changes k; an error message will be given if this combination of options are set. However, if sequential=TRUE and subsample=TRUE, then passing either 'findBestK=TRUE' or 'findBestK=FALSE' via mainClusterArgs will function as expected (assuming the clusterFunction argument passed to mainClusterArgs is of type 'K'). In particular, the sequential step will set the number of clusters k for clustering of each subsample. If findBestK=FALSE, that same k will be used for mainClustering step that clusters the resulting co-occurrence matrix after subsampling. If findBestK=TRUE, mainClustering will search for best k. Note that the default 'kRange' over which mainClustering searches when findBestK=TRUE depends on the input value of k which is set by the sequential method if sequential=TRUE), see above. The user can change kRange to not depend on k and to be fixed across all of the sequential steps by setting kRange explicitly in the mainClusterArgs list.

To provide a distance matrix via the argument distFunction, the function must be defined to take the distance of the rows of a matrix (internally, the function will call distFunction(t(x)). This is to be compatible with the input for the dist function. as.matrix will be performed on the output of distFunction, so if the object returned has a as.matrix method that will convert the output into a symmetric matrix of distances, this is fine (for example the class dist for objects returned by dist have such a method). If distFunction=NA, then a default distance will be calculated based on the type of clustering algorithm of clusterFunction. For type "K" the default is to take dist as the distance function. For type "01", the default is to take the (1-cor(x))/2.

Value

A ClusterExperiment object if inputType is of type "X".

If input was not of type "X", then the result is a list with values

- clustering: The vector of clustering results
- clusterInfo: A list with information about the parameters run in the clustering
- coClusterMatrix: (only if saveSubsamplingMatrix=TRUE, NxB set of clusterings obtained after B subsamples.

See Also

clusterMany to compare multiple choices of parameters, and mainClustering, subsampleClustering, and seqCluster for the underlying functions called by clusterSingle.
Examples

data(simData)

## Not run:
# following code takes some time.
# use clusterSingle to do sequential clustering
# (same as example in seqCluster only using clusterSingle ...)
set.seed(44261)
clustSeqHier_v2 <- clusterSingle(simData,
  sequential=TRUE, subsample=TRUE,
  subsampleArgs=list(resamp.n=100, samp.p=0.7,
    clusterFunction="kmeans", clusterArgs=list(nstart=10)),
  seqArgs=list(beta=0.8, k0=5), mainClusterArgs=list(minSize=5,
    clusterFunction="hierarchical01", clusterArgs=list(alpha=0.1)))

## End(Not run)

# use clusterSingle to do just clustering k=3 with no subsampling
clustObject <- clusterSingle(simData,
  subsample=FALSE, sequential=FALSE,
  mainClusterArgs=list(clusterFunction="pam", clusterArgs=list(k=3)))
# compare to standard pam
pamOut<-cluster::pam(t(simData),k=3,cluster.only=TRUE)
all(pamOut==primaryCluster(clustObject))

---

**fluidigmData**

*Subset of fluidigm data*

Description

Subset of fluidigm data

Format

subset of fluidigm data used in vignette package.

Details

`fluidigmData` and `fluidigmColData` are portions of the `fluidigm` data distributed in the package `scRNAseq` package. We have subsetted to only the cells sequenced under high depth, and limited our selves to only two of the four gene estimates provided by `scRNAseq` ("tophat_counts" and "rsem_tpm").

Author(s)

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See Also

`fluidigm`
Examples

```r
#code used to create objects:
## Not run:
library(scRNAseq)
if(packageVersion("scRNAseq")>="1.11.0") fluidigm <- ReprocessedFluidigmData() else data(fluidigm)
fluidSubset <- fluidigm[,colData(fluidigm)[,"Coverage_Type"] == "High"]
fluidigmData <- assays(fluidSubset)[c("tophat_counts","rsem_tpm")]
fluidigmColData <- as.data.frame(colData(fluidSubset))
usethis::use_data(fluidigmData, fluidigmColData, overwrite=FALSE)

## End(Not run)
```

getBestFeatures

Function for finding best features associated with clusters

Description

Calls limma on input data to determine features most associated with found clusters (based on an F-statistic, pairwise comparisons, or following a tree that clusters the clusters).

Usage

```r
## S4 method for signature 'matrixOrHDF5'
getBestFeatures(
  x,
  cluster,
  contrastType = c("F", "Dendro", "Pairs", "OneAgainstAll"),
  dendro = NULL,
  pairMat = NULL,
  weights = NULL,
  contrastAdj = c("All", "PerContrast", "AfterF"),
  DEMethod = c("edgeR", "limma", "limma-voom"),
  dgeArgs = NULL,
  ...
)

## S4 method for signature 'ClusterExperiment'
getBestFeatures(
  x,
  contrastType = c("F", "Dendro", "Pairs", "OneAgainstAll"),
  whichCluster = "primary",
  whichAssay = 1,
  DEMethod,
  weights = if ("weights" %in% assayNames(x)) "weights" else NULL,
  ...
)
```
Arguments

**x**
- data for the test. Can be a numeric matrix or a ClusterExperiment.

**cluster**
- A numeric vector with cluster assignments. “-1” indicates the sample was not assigned to a cluster.

**contrastType**
- What type of test to do. ‘F’ gives the omnibus F-statistic, ‘Dendro’ traverses the given dendrogram and does contrasts of the samples in each side, ‘Pairs’ does pair-wise contrasts based on the pairs given in pairMat (if pairMat=NULL, does all pairwise), and ‘OneAgainstAll’ compares each cluster to the average of all others. Passed to clusterContrasts.

**dendro**
- The dendrogram to traverse if contrastType="Dendro". Note that this should be the dendrogram of the clusters, not of the individual samples, either of class "dendrogram" or "phylo4".

**pairMat**
- matrix giving the pairs of clusters for which to do pair-wise contrasts (must match to elements of cl). If NULL, will do all pairwise of the clusters in cluster (excluding "-1" categories). Each row is a pair to be compared and must match the names of the clusters in the vector cluster.

**weights**
- weights to use in by edgeR. If x is a matrix, then weights should be a matrix of weights, of the same dimensions as x. If x is a ClusterExperiment object weights can be a either a matrix, as previously described, or a character or numeric index to an assay in x that contains the weights. We recommend that weights be stored as an assay with name "weights" so that the weights will also be used with mergeClusters, and this is the default. Setting weights=NULL ensures that weights will NOT be used, and only the standard edgeR.

**contrastAdj**
- What type of FDR correction to do for contrasts tests (i.e. if contrastType=’Dendro’ or ’Pairs’).

**DEMethod**
- character vector describing how the differential expression analysis should be performed (replaces previous argument isCount. See details.

**dgeArgs**
- a list of arguments to pass to DGEList which is the starting point for both edgeR and limma-voom methods of DE. This includes normalization factors/total count values etc.

**...**
- If x is a matrix, these are options to pass to topTable (see limma package). If x is a ClusterExperiment object, these arguments can also be those to pass to the matrix version.

**whichCluster**
- argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of getClusterIndex.

**whichAssay**
- numeric or character specifying which assay to use. See assay for details.

Details

ggetBestFeatures returns the top ranked features corresponding to a cluster assignment. It uses either limma or edgeR to fit the models, and limma/edgeR functions topTable to find the best features. See the options of this function to put better control on what gets returned (e.g. only if significant, only if log-fc is above a certain amount, etc.). In particular, set ‘number=’ to define how many significant features to return (where number is per contrast for the ‘Pairs’ or ‘Dendro’ option).
DEMethod triggers what type of differential expression analysis will be performed. Three options are available: limma, edgeR, and limma with a voom corrections. The last two options are only appropriate for count data. If the input x is a ClusterExperiment object, and DEMethod="limma", then the data analyzed for DE will be after taking the transformation of the data (as given in the transformation slot of the object). For the options "limma-voom" and "edgeR", the transformation slot will be ignored and only the counts data (as specified by the whichAssay slot) will be passed to the programs. Note that for "limma-voom" this implies that the data will be transformed by voom with the function \(\log_2(x+0.5)\). If weights is not NULL, and DEMethod="edgeR", then the function glmWeightedF from the zinbwave package is run; otherwise glmLRT from edgeR.

Note that the argument DEMethod replaces the previous option isCount, to decide on the method of DE.

When ‘contrastType’ argument implies that the best features should be found via contrasts (i.e. ’contrastType’ is ‘Pairs’ or ‘Dendro’), then then ‘contrastAdj’ determines the type of multiple testing correction to perform. ‘PerContrast’ does FDR correction for each set of contrasts, and does not guarantee control across all the different contrasts (so probably not the preferred method). ‘All’ calculates the corrected p-values based on FDR correction of all of the contrasts tested. ‘AfterF’ controls the FDR based on a hierarchical scheme that only tests the contrasts in those genes where the omnibus F statistic is significant. If the user selects ‘AfterF’, the user must also supply an option ‘p.value’ to have any effect, and then only those significant at that p.value level will be returned. Note that currently the correction for ‘AfterF’ is not guaranteed to control the FDR; improvements will be added in the future.

Note that the default option for topTable is to not filter based on adjusted p-values (p.value = 1) and return only the top 10 most significant (number = 10) – these are options the user can change (these arguments are passed via the ... in getBestFeatures). In particular, it only makes sense to set requireF = TRUE if p.value is meaningful (e.g. 0.1 or 0.05); the default value of p.value = 1 will not result in any effect on the adjusted p-value otherwise.

Value

A data.frame in the same format as topTable, or topTags. The output differs between these two programs, mainly in the naming of columns. Furthermore, if weights are used, an additional column padjFilter is included as the result of running glmWeightedF with default option independentFiltering = TRUE. The following column names are the same between all of the DE methods.

- **Feature** This is the column called ‘ProbeID’ by topTable
- **IndexInOriginal** Gives the index of the feature to the original input dataset, x
- **Contrast** The contrast that the results corresponds to (if applicable, depends on contrastType argument)
- **ContrastName** The name of the contrast that the results corresponds to. For dendrogram searches, this will be the node of the tree of the dendrogram. If x is a ClusterExperiment object, this name will make use of the user defined names of the cluster or node in x.
- **InternalName** Only present if x is a ClusterExperiment object. In this case this column will give the name of the contrast using the internal ids of the clusters and nodes, not the user-defined names. This provides stability in matching the contrast if the user has changed the names since running getBestFeatures
- **P.Value** The unadjusted p-value (changed from PValue in topTags)
• adj.P.Val The adjusted p-value (changed from FDR or FWER in topTags)

References


See Also
glmLRT glmWeightedF topTable topTags

Examples

data(simData)

# create a clustering, for 8 clusters (truth was 4)
c1 <- clusterSingle(simData, subsample=FALSE, sequential=FALSE, mainClusterArgs=list(clusterFunction="pam", clusterArgs=list(k=8)))

# basic F test, return all, even if not significant:
testF <- getBestFeatures(c1, contrastType="F", number=nrow(simData), DEMethod="limma")

# Do all pairwise, only return significant, try different adjustments:
pairsPerC <- getBestFeatures(c1, contrastType="Pairs", contrastAdj="PerContrast", p.value=0.05, DEMethod="limma")
pairsAfterF <- getBestFeatures(c1, contrastType="Pairs", contrastAdj="AfterF", p.value=0.05, DEMethod="limma")
pairsAll <- getBestFeatures(c1, contrastType="Pairs", contrastAdj="All", p.value=0.05, DEMethod="limma")

# not useful for this silly example, but could look at overlap with Venn
allGenes <- paste("Row", 1:nrow(simData), sep="")
if(require(limma)){
  vennC <- vennCounts(cbind(PerContrast= allGenes %in% pairsPerC$Feature, AllJoint=allGenes %in% pairsAll$Feature, FHier=allGenes %in% pairsAfterF$Feature))
  vennDiagram(vennC, main="FDR Overlap")
}

# Do one cluster against all others
oneAll <- getBestFeatures(c1, contrastType="OneAgainstAll", contrastAdj="All", p.value=0.05, DEMethod="limma")

# Do dendrogram testing
hcl <- makeDendrogram(cl)
allDendro <- getBestFeatures(hcl, contrastType="Dendro", contrastAdj="All", number=ncol(simData), p.value=0.05,DEMethod="limma")

# do DE on counts using voom
# compare results to if used simData instead (not on count scale).
testFVoom <- getBestFeatures(simCount, primaryCluster(cl), contrastType="F", number=nrow(simData), DEMethod="limma-voom")
plot(testFVoom$P.Value[order(testFVoom$Index)], testFVoom$P.Value[order(testFVoom$Index)], log="xy")

# do DE on counts using edgeR, compare voom
testFEdge <- getBestFeatures(simCount, primaryCluster(cl), contrastType="F", n=nrow(simData), DEMethod="edgeR")
plot(testFVoom$P.Value[order(testFVoom$Index)], testFEdge$P.Value[order(testFEdge$Index)], log="xy")

description

definition

Finds index of clustering in clusterMatrix slot of object based on descriptions of clusters.

Usage

## S4 method for signature 'ClusterExperiment'
getClusterIndex(
  object,
  whichClusters,
  noMatch = c("silentlyRemove", "throwError")
)

## S4 method for signature 'ClusterExperiment'
getSingleClusterIndex(object, whichCluster, passedArgs = NULL, ...)

Arguments

object a ClusterExperiment object

whichClusters argument that can be either numeric or character vector indicating the clusterings to be used. See details of getClusterIndex.

noMatch how to handle if there is no match to a given value of whichClusters. "silentlyRemove" means that no error will be given, and the result will be just those that do match (resulting in a vector of length zero if there are none that match). "throwError" means that the function will stop with an error describing the problem with the match.
whichCluster  argument that can be a single numeric or character value indicating the\nclustering to be used. Giving values that result in more than one clustering will\nresult in an error. See details of `getClusterIndex`.

passedArgs  other arguments passed to the function (only used internally)
...
Not for user use. Argument allows function `getSingleClusterIndex` to catch\nthe wrong argument (the plural `whichClusters` argument rather than singular\n`whichCluster`).

Details

The function `getClusterIndex` is largely used internally to parse the argument `whichClusters`\nwhich is used as an argument extensively across functions in this package. Note that some func-
tions require the match return a single clustering, in which case those functions use the function\n`getSingleClusterIndex` with the singular argument `whichCluster` and returns an error if it indi-
cates more than one clustering. Furthermore `getSingleClusterIndex` does not allow for any mis-
matches (noMatch=\"throwError\". Otherwise the parsing of the two arguments `whichClusters`\nand `whichCluster` is the same, and is described in what follows.

If `whichClusters` is numeric, then the function just returns the numeric values of `whichClusters`,\nafter checking that they are valid. If any are invalid, they are silently removed if `silentlyRemove=TRUE`.
The values will be returned in the order given, so this argument can also be used to defined by func-
tions to give an ordering for the clusterings (as relevant).

If `whichClusters` is a character value, then it the function attempts to use the character value\nto identify the clustering. The value of the argument is first matched against a set of \"special\"\nvalues: \"workflow\", \"all\", \"none\", \"primaryCluster\", \"dendro\" using the argument `match.arg`, which\ndoes partial matching. If `whichClusters` is a vector of values, only the first value of the vector is\nmatched against these values and if it matches, the remaining values are ignored. If it matches one\nof these values, then the cluster indices are given as follows.

- \"workflow\" all clusterings in the current workflow (see `workflowClusters`)
- \"all\" all clusterings, with the primary clustering put first.
- \"none\" no clusterings
- \"primaryCluster\" the primary clustering index as given by `primaryClusterIndex`
- \"dendro\" the index of the clustering given to create the cluster dendrogram, if it exists

@details If `whichClusters` is a character value, but its first element does not match these predesig-
nated values, then all the values of `whichClusters` are attempted to be matched to the `clusterTypes`\nof the object. Note that there may be more than one clustering that matches a given type. For any\nentries that do not match a value in `clusterTypes(object)` are then matched based on the value\nof `clusterLabels` of the object.

Value

`getClusterIndex` returns a vector of all numeric indices that are indicated by the requested `whichClusters`.\nNote that there is not a one-to-one match between input values and returned values since there may\nbe more than one value for a given value of `whichClusters` or no value at all.
getClusterManyParams, ClusterExperiment-method

Examples

# load CE object
data(rsecFluidigm)
# get the cluster index from mergeClusters step
getClusterIndex(rsecFluidigm, whichClusters = "mergeClusters")
# get the cluster indices from mergeClusters step
getClusterIndex(rsecFluidigm, whichClusters = "clusterMany")

getClusterManyParams, ClusterExperiment-method

Get parameter values of clusterMany clusters

Description

Takes an input a ClusterExperiment object and returns the parameter values used in creating the clusters that were created by 'clusterMany'

Usage

## S4 method for signature 'ClusterExperiment'
getClusterManyParams(
  x,
  whichClusters = "clusterMany",
  searchAll = FALSE,
  simplify = TRUE
)

Arguments

x a ClusterExperiment object that contains clusterings from running clusterMany.

whichClusters argument that can be either numeric or character vector indicating the clusterings to be used. See details of getClusterIndex.

searchAll logical, indicating whether all clusterings with clusterMany label should be allowed (i.e. including those from previous ones with labels like clusterMany.1), or only limited to those in most recent workflow (default).

simplify logical. Whether to simplify the output so as to remove features that do not change across the clusterings.

Details

The method simply parses the clusterLabels of the indicated clusterings, relying on the specific format used by clusterMany to create labels. The function will only allow the parsing to be performed on those clusterings with a 'clusterMany' clusterType. If the user has manipulated the clusterLabels manually or manually identified the clusterType of a clustering as 'clusterMany', this function may create unexpected results or errors. Similarly, it cannot be used on 'clusterMany' results from an old iteration (e.g. that have type 'clusterMany.l')
Specifically, it splits the label of each clustering by the character ",", as indicating the different parameters; this should return a value of form "ABC=123". The function then pulls out the numeric value ('123') and associates that value as the value of the parameter ('ABC')

Value

Returns a data.frame where the column names are the parameter names, and the entries are the values of the parameter for the indicated clustering. The column 'clusteringIndex' identifies the index of the clustering in the full set of clusterings of the given ClusterExperiment object.

Examples

```r
## Not run:
data(simData)

cl <- clusterMany(simData, nReducedDims=c(5, 10), reduceMethod="PCA", 
  clusterFunction="pam", ks=2:4, findBestK=c(TRUE, FALSE), 
  makeMissingDiss=TRUE, removeSil=c(TRUE, FALSE))

getClusterManyParams(cl)

## End(Not run)
```

getReducedData,ClusterExperiment-method

Return matrix from ClusterExperiment with reduced dimensions

Description

Returns a matrix of data from a ClusterExperiment object based on the choices of dimensionality reduction given by the user.

Functions for calculating and manipulating either filtering statistics, stored in rowData, or the dimensionality reduction results, stored in reducedDims.

Usage

```r
## S4 method for signature 'ClusterExperiment'
getReducedData(
  object, 
  reduceMethod, 
  filterIgnoresUnassigned, 
  nDims = defaultNDims(object, reduceMethod), 
  whichCluster = "primary", 
  whichAssay = 1, 
  returnValue = c("object", "list"), 
  reducedDimName
)

## S4 method for signature 'SingleCellExperiment'
```
defaultNDims(object, reduceMethod, typeToShow)

## S4 method for signature 'matrixOrHDF5'
defaultNDims(object, ...)

## S4 method for signature 'SummarizedExperiment'
makeFilterStats(
  object,
  filterStats = listBuiltInFilterStats(),
  transFun = NULL,
  isCount = FALSE,
  filterNames = NULL,
  whichAssay = 1
)

## S4 method for signature 'matrixOrHDF5'
makeFilterStats(object, ...)

## S4 method for signature 'ClusterExperiment'
makeFilterStats(
  object,
  whichClusterIgnoreUnassigned = NULL,
  filterStats = listBuiltInFilterStats(),
  ...,
)

listBuiltInFilterStats()

## S4 method for signature 'SummarizedExperiment'
filterData(
  object,
  filterStats,
  cutoff,
  percentile,
  absolute = FALSE,
  keepLarge = TRUE,
  whichAssay = 1
)

## S4 method for signature 'SummarizedExperiment'
filterNames(object)

## S4 method for signature 'SingleCellExperiment'
makeReducedDims(
  object,
  reducedDims = "PCA",
  maxDims = 500,
  transFun = NULL,
getReducedData, ClusterExperiment-method

```r
isCount = FALSE,
whichAssay = 1
)
```

## S4 method for signature 'matrixOrHDF5'
makeReducedDims(object, ...)

## S4 method for signature 'SummarizedExperiment'
makeReducedDims(object, ...)

## S4 method for signature 'ClusterExperiment'
makeReducedDims(object, ...)

listBuiltInReducedDims()

### Arguments

- **object**: For `makeReducedDims, makeFilterStats`, defaultNDims either matrix-like, SingleCellExperiment, or ClusterExperiment object. For `getReducedData` only a ClusterExperiment object allowed.

- **reduceMethod**: character. A method (or methods) for reducing the size of the data, either by filtering the rows (genes) or by a dimensionality reduction method. Must either be 1) must match the name of a built-in method, in which case if it is not already existing in the object will be passed to `makeFilterStats` or `link(makeReducedDims)`, or 2) must match a stored filtering statistic or dimensionality reduction in the object.

- **filterIgnoresUnassigned**: logical. Whether filtering statistics should ignore the unassigned samples within the clustering. Only relevant if 'reduceMethod' matches one of built-in filtering statistics in `listBuiltInFilterStats()`, in which case the clustering identified in whichCluster is passed to `makeFilterStats` and the unassigned samples are excluded in calculating the statistic. See `makeFilterStats` for more details.

- **nDims**: The number of dimensions to keep from reduceMethod. If missing calls defaultNDims.

- **whichCluster**: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.

- **whichAssay**: numeric or character specifying which assay to use. See `assay` for details.

- **returnValue**: The format of output. Users will generally want to keep the default (see details)

- **reducedDimName**: The name given to the reducedDims slot storing result (if returnValue="object"). If missing, the function will create a default name: if reduceMethod is a dimensionality reduction, then reduceMethod will be given as the name; if a filtering statistic, "filteredBy_" followed by reduceMethod.

- **typeToShow**: character (optional). If given, should be one of “filterStats” or “reducedDims” to indicate of the values in the reduceMethod vector, only show those corresponding to “filterStats” or “reducedDims” options.
... 

filterStats character vector of statistics to calculate. Must be one of the character values given by listBuildInFilterStats().

transFun a transformation function to be applied to the data. If the transformation applied to the data creates an error or NA values, then the function will throw an error. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

isCount if transFun=NULL, then isCount=TRUE will determine the transformation as defined by function(x){log2(x+1)}, and isCount=FALSE will give a transformation function function(x){x}. Ignored if transFun=NULL. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

filterNames if given, defines the names that will be assigned to the filtering statistics in the rowData of the object. If missing, will be just the value of filterStats argument

whichClusterIgnoreUnassigned indicates clustering that should be used to filter out unassigned samples from the calculations. If NULL no filtering of samples will be done. See details for more information.

cutoff numeric. A value at which to filter the rows (genes) for the test statistic

percentile numeric. Either a number between 0,1 indicating what percentage of the rows (genes) to keep or an integer value indicated the number of rows (genes) to keep

absolute whether to take the absolute value of the filter statistic

keepLarge logical whether to keep rows (genes) with large values of the test statistic or small values of the test statistic.

reducedDims a vector of character values indicating the methods of dimensionality reduction to be performed. Currently only "PCA" is implemented.

maxDims Numeric vector of integer giving the number of PC dimensions to calculate. maxDims can also take values between (0,1) to indicate keeping the number of dimensions necessary to account for that proportion of the variance. maxDims should be of same length as reducedDims, indicating the number of dimensions to keep for each method (if maxDims is of length 1, the same number of dimensions will be used for each).

Details

getReducedData determines the matrix of values that can be used for computation based on the user’s choice of dimensionality methods. The methods can be either of the filtering kind or the more general dimensionality reduction. The function will first look at any stored ReducedDims or filtering statistics already present in the data, and if missing, will assume that reduceMethod is one of the built-in method provided by the package and calculate the necessary. Note that if reduceMethod is a filtering statistic, in addition to filtering the features, the function will also perform the stored transformation of the data.

Note that this is used internally by functions, but is mainly only of interest for the user if they want to have the filtered, transformed data available as a matrix for continual use.
If \( \text{returnValue} = \text{"object"} \), then the output is a single, updated \text{ClusterExperiment} object with the reduced data matrix stored as an element of the list in \text{reducedDims} slot (with name given by \text{reducedDimName} if given). If \( \text{"list"} \), then a list with one element that is the object and the other that is the reduced data matrix. Either way, the object returned in the list will be updated to contain with the filtering statistics or the dimensionality reduction. The only difference is that if \( \text{"list"} \), the reduced dimension matrix is NOT saved in the object (and so only really makes a difference if the \text{reduceMethod} argument is a filtering method). The option \( \text{"list"} \) is mainly for internal use, where we do not want to continually save subetsed datasets.

If \( \text{nDims} \) is missing, it will be given a default value depending on the value of \text{reduceMethod}. See \text{defaultNDims} for details.

If \text{filterIgnoresUnassigned} is missing, then it is set to \text{TRUE} unless: \text{reduceMethod} matches a stored filtering statistic in \text{rowData} AND does not match a built-in filtering method provided by the package.

For a \text{reduceMethod} that corresponds to a filtering statistics the current default is 1000 (or the length of the number of features, if less). For a dimensionality reduction saved in the \text{reducedDims} slot the default is 50 or the maximum number of dimensions if less than 50.

\text{reduceMethod} will first be checked to see if it corresponds with an existing saved filtering statistic or a dimensionality reduction to determine which of these two types it is. If it does not match either, then it will be checked against the built in functions provided by the package. @examples se<- \text{SingleCellExperiment(matrix(rnorm(5000*100),nrow=5000,ncol=100))} \text{defaultNDims}(se,\text{"PCA"}) \text{defaultNDims}(se,\text{"mad"})

\text{whichClusterIgnoreUnassigned} is only an option when applied to a \text{ClusterExperiment} class and indicates that the filtering statistics should be calculated based on samples that are unassigned by the designated clustering. The name given to the filter in this case is of the form \text{<filterStats>_<clusterLabel>}, i.e. the clustering label of the clustering is appended to the standard name for the filtering statistic.

Note that \text{filterData} returns a \text{SingleCellExperiment} object. To get the actual data out use either \text{assay} or \text{transformData} if transformed data is desired.

The PCA method uses either \text{prcomp} from the \text{stats} package or \text{svds} from the \text{RSpectra} package to perform PCA. Both are called on \text{t(assay(x))} with \text{center=TRUE} and \text{scale=TRUE} (i.e. the feature are centered and scaled), so that it is performing PCA on the correlation matrix of the features.

Note that this function does not check if such a \text{reduceDim} value already exists, and will recalculate (and overwrite) if it does.

\text{Value}

If \text{returnValue} = \text{"object"}, a \text{ClusterExperiment} object.

If \text{returnValue} = \text{"list"} a list with elements:

- \text{objectUpdate} object, potentially updated if had to calculate dimensionality reduction or filtering statistic
- \text{dataMatrix} the reduced dimensional matrix with the samples in columns, features in rows

\text{defaultNDims} returns a numeric vector giving the default dimensions the \text{methods} in \text{clusterExperiment} will use for reducing the size of the data. If \text{typeToShow} is missing, the resulting vector will be equal
makeFilterStats returns a `SummarizedExperiment` object with the requested filtering statistics will be added to the DataFrame in the rowData slot and given names corresponding to the filterStats values. Warning: the function will overwrite existing columns in rowData with the same name. Columns in the rowData slot with different names should not be affected.

filterData returns a `SingleCellExperiment` object with the rows (genes) removed based on filters

filterNames returns a vector of the columns of the rowData that are considered valid filtering statistics. Currently any numeric column in rowData is a valid filtering statistic.

makeReducedDims returns a `SingleCellExperiment` containing the calculated dimensionality reduction in the reduceDims with names corresponding to the name given in reducedDims.

**See Also**

`makeFilterStats`, `makeReducedDims`, `filterData`, `reducedDim`

**Examples**

data(simData)
listBuiltInFilterStats()
scf<-makeFilterStats(simData,filterStats=c("var","mad"))
scf
csfFiltered<-filterData(scf,filterStats="mad",percentile=10)
csfFiltered
assay(scfFiltered)[1:10,1:10]
data(simData)
listBuiltInReducedDims()
scf<-makeReducedDims(simData, reducedDims="PCA", maxDims=3)
scf

---

**internalFunctionCheck**

**Class ClusterFunction**

**Description**

ClusterFunction is a class for holding functions that can be used for clustering in the clustering algorithms in this package.

The constructor ClusterFunction creates an object of the class ClusterFunction.

**Usage**

`internalFunctionCheck(clusterFUN, inputType, algorithmType, outputType)`

ClusterFunction(clusterFUN, ...)

```r
## S4 method for signature 'function'
```
ClusterFunction(
    clusterFUN,
    inputType,
    outputType,
    algorithmType,
    inputClassifyType = NA_character_,
    requiredArgs = NA_character_,
    classifyFUN = NULL,
    checkFunctions = TRUE
)

Arguments

clusterFUN function passed to slot clusterFUN.
inputType character for slot inputType
algorithmType character for slot inputType
outputType character for slot outputType
... arguments passed to different methods of ClusterFunction
inputClassifyType character for slot inputClassifyType
requiredArgs character for slot requiredArgs
classifyFUN function for slot classifyFUN
checkFunctions logical for whether to check the input functions with internalFunctionCheck

Details

internalFunctionCheck is the function that is called by the validity check of the ClusterFunction constructor (if checkFunctions=TRUE). It is available as an S3 function for the user to be able to test their functions and debug them, which is difficult to do with a S4 validity function.

clusterFUN: The following arguments are required to be accepted for clusterFUN – higher-level code may pass these arguments (but the function can ignore them or just have be handled with a ...)

- "inputMatrix" will be the matrix of data
- "inputType" one of "X", "diss", or "cat". If "X", then inputMatrix is assumed to be nfeatures x nsamples (like assay(CEObj) would give). If "cat" then nfeatures x nsamples, but all entries should be categorical levels, encoded by positive integers, with -1/-2 types of NA (like a clusterMatrix slot, but with dimensions switched). If "diss", then inputMatrix should be a nxn dissimilarity matrix.
- "checkArgs" logical argument. If checkArgs=TRUE, the clusterFUN should check if the arguments passed in ... are valid and return an error if not; otherwise, no error will be given, but the check should be done and only valid arguments in ... passed along. This is necessary for the function to work with clusterMany which passes all arguments to all functions without checking.
• "cluster.only" logical argument. If `cluster.only=TRUE`, then `clusterFUN` should return only the vector of cluster assignments (or list if `outputType="list"`). If `cluster.only=FALSE`, then the `clusterFUN` should return a named list where one of the elements entitled `clustering` contains the vector described above (no list allowed!); anything else needed by the `classifyFUN` to classify new data should be contained in the output list as well. `cluster.only` is set internally depending on whether `classifyFUN` will be later used by subsampling or only for clustering the final product.

• "..." Any additional arguments specific to the algorithm used by `clusterFUN` should be passed via ... and NOT passed via arguments to `clusterFUN`.

• "Other required arguments" `clusterFUN` must also accept arguments required for its `algorithmType` (see Details below).

classifyFUN: The following arguments are required to be accepted for `classifyFUN` (if not NULL)

• `inputMatrix` the new data that will be classified into the clusters

• `inputType` the inputType of the new data (see above)

• `clusterResult` the result of running `clusterFUN` on the training data, when `cluster.only=FALSE`. Whatever is returned by `clusterFUN` is assumed to be sufficient for this function to classify new objects (e.g. could return the centroids of the clustering, if clustering based on nearest centroid).

algorithmType: Type "01" is for clustering functions that expect as an input a dissimilarity matrix that takes on 0-1 values (e.g. from subclustering) with 1 indicating more dissimilarity between samples. "01" algorithm types must also have `inputType` equal to "diss". It is also generally expected that "01" algorithms use the 0-1 nature of the input to set criteria as to where to find clusters. "01" functions must take as an argument `alpha` between 0 and 1 to determine the clusters, where larger values of `alpha` require less similarity between samples in the same cluster. "K" is for clustering functions that require an argument `k` (the number of clusters), but arbitrary `inputType`. On the other hand, "K" algorithms are assumed to need a predetermined 'k' and are also assumed to cluster all samples to a cluster. If not, the post-processing steps in `mainClustering` such as `findBestK` and `removeSil` may not operate correctly since they rely on silhouette distances.

Value

Returns a logical value of TRUE if there are no problems. If there is a problem, returns a character string describing the problem encountered.

A `ClusterFunction` object.

Slots

clusterFUN a function defining the clustering function. See details for required arguments.

inputType a character vector defining what type(s) of input `clusterFUN` takes. Must consist of values "diss", "X", or "cat" indicating the set of input values that the algorithm can handle (see details below).

algorithmType a character defining what type of clustering algorithm `clusterFUN` is. Must be one of either "01" or "K". `clusterFUN` must take the corresponding required arguments for its type (see details below).
classifyFUN a function that takes as input new data and the output of clusterFUN (where the output is from when cluster.only=FALSE) and results in cluster assignments of the new data. Used in subsampling clustering. Note that the function should assume that the data given to the inputMatrix argument is not the same samples that were input to the ClusterFunction (but does assume that it is the same number of features/columns). If slot classifyFUN is given value NULL then subsampling type can only be "InSample", see subsampleClustering.

inputClassifyType the input type for the classification function (if not NULL); like inputType, must be a vector containing "diss","X", or "cat"

outputType the type of output given by clusterFUN. Must either be "vector" or "list". If "vector" then the output should be a vector of length equal to the number of observations with integer-valued elements identifying them to different clusters; the vector assignments should be in the same order as the original input of the data. Samples that are not assigned to any cluster should be given a '-1' value. If "list", then it must be a list equal to the length of the number of clusters, and the elements of the list contain the indices of the samples in that cluster. Any indices not in any of the list elements are assumed to be -1. The main advantage of "list" is that it can preserve the order of the clusters if the clusterFUN desires to do so. In which case the orderBy argument of mainClustering can preserve this ordering (default is to order by size).

requiredArgs Any additional required arguments for clusterFUN (beyond those required of all clusterFUN, described in details). Will be used in checking that user provided necessary arguments.

checkFunctions logical. If TRUE, the validity check of the ClusterFunction object will check the clusterFUN with simple toy data using the function internalFunctionCheck.

Examples

#Use internalFunctionCheck to check possible function
goodFUN<-function(inputMatrix,k,cluster.only,...){
  cluster::pam(x=t(inputMatrix),k=k,cluster.only=cluster.only)
}
#passes internal check
internalFunctionCheck(goodFUN,inputType=c("X","diss"),
  algorithmType="K",outputType="vector")
myCF<-ClusterFunction(clusterFUN=goodFUN, inputType="X",
  algorithmType="K", outputType="vector")
#doesn't work, because haven't made results return vector when cluster.only=TRUE
badFUN<-function(inputMatrix,k,cluster.only,...){cluster::pam(x=inputMatrix,k=k)}
internalFunctionCheck(badFUN,inputType=c("X","diss"),
  algorithmType="K",outputType="vector")
listBuiltInFunctions

Usage

listBuiltInFunctions()

## S4 method for signature 'character'
getBuiltInFunction(object)

listBuiltInTypeK()

listBuiltInType01()

Arguments

object name of built in function.

Details

listBuiltInFunctions will return the character names of the built-in clustering functions available.

listBuiltInTypeK returns the names of the built-in functions that have type 'K'

listBuiltInType01 returns the names of the built-in functions that have type '01'

getBuiltInFunction will return the ClusterFunction object of a character value that corresponds to a built-in function.

algorithmType and inputType will return the algorithmType and inputType of the built-in clusterFunction corresponding to the character value.

Built-in clustering methods: The built-in clustering methods, the names of which can be accessed by listBuiltInFunctions() are the following:

- "pam" Based on pam in cluster package. Arguments to that function can be passed via clusterArgs. Input can be either "x" or "diss"; algorithm type is "K"
- "clara" Based on clara in cluster package. Arguments to that function can be passed via clusterArgs. Note that we have changed the default arguments of that function to match the recommendations in the documentation of clara (numerous functions are set to less than optimal settings for back-compatibility). Specifically, the following defaults are implemented samples=50, keep.data=FALSE, mediods.x=FALSE, rngR=TRUE, pamLike=TRUE, correct.d=TRUE. Input is "X"; algorithm type is "K".
- "kmeans" Based on kmeans in stats package. Arguments to that function can be passed via clusterArgs except for centers which is reencoded here to be the argument 'k'. Input is "X"; algorithm type is "K"
- "mbkmeans" mbkmeans runs mini-batch kmeans, a more computationally efficient version of kmeans.
- "hierarchical01" hclust in stats package is used to build hierarchical clustering. Arguments to that function can be passed via clusterArgs. The hierarchical01 cuts the hierarchical tree based on the parameter alpha. It does not use the cutree function, but instead transversing down the tree until getting a block of samples with whose summary of the values is greater than or equal to 1-alpha. Arguments that can be passed to "hierarchical01" are "evalClusterMethod" which determines how to summarize the samples' values of D[samples,samples]
for comparison to 1-alpha: "maximum" (default) takes the minimum of $D[samples,samples]$ and requires it to be less than or equal to 1-alpha; "average" requires that each row mean of $D[samples,samples]$ be less than or equal to 1-alpha. Additional arguments of hclust can also be passed via clusterArgs to control the hierarchical clustering of $D$. Input is "diss"; algorithm type is "01"

- "hierarchicalK" hclust in stats package is used to build hierarchical clustering and cutree is used to cut the tree into $k$ clusters. Input is "diss"; algorithm type is "K"

- "tight" Based on the algorithm in Tsang and Wong, specifically their method of picking clusters from a co-occurrence matrix after subsampling. The clustering encoded here is not the entire tight clustering algorithm, only that single piece that identifies clusters from the co-occurrence matrix. Arguments for the tight method are 'minSize.core' (default=2), which sets the minimum number of samples that form a core cluster. Input is "diss"; algorithm type is "01"

- "spectral" specc in kernlab package is used to perform spectral clustering. Note that spectral clustering can produce errors if the number of clusters ($K$) is not sufficiently smaller than the number of samples ($N$). $K < N$ is not always sufficient. Input is "X"; algorithm type is "K".

Value

listBuiltInFunctions returns a character vector of all the built-in cluster functions’ names.
getBuiltInFunction returns the ClusterFunction object that corresponds to the character name of a function.
listBuiltInTypeK returns a character vector of the names of built-in cluster functions that are of type "K".
listBuiltInType01 returns a character vector of the names of built-in cluster functions that are of type "01".

See Also

ClusterFunction, algorithmType, inputType

Examples

listBuiltInFunctions()
algorithmType(c("kmeans","pam","hierarchical01"))
inputType(c("kmeans","pam","hierarchical01"))
listBuiltInTypeK()
listBuiltInType01()

mainClustering  

Cluster distance matrix from subsampling

Description

Given input data, this function will try to find the clusters based on the given ClusterFunction object.
mainClustering

Usage

## S4 method for signature 'character'
mainClustering(clusterFunction, ...)

## S4 method for signature 'ClusterFunction'
mainClustering(
  clusterFunction,
  inputMatrix,
  inputType,
  clusterArgs = NULL,
  minSize = 1,
  orderBy = c("size", "best"),
  format = c("vector", "list"),
  returnData = FALSE,
  warnings = TRUE,
  ...
)

## S4 method for signature 'ClusterFunction'
getPostProcessingArgs(clusterFunction)

Arguments

clusterFunction

a ClusterFunction object that defines the clustering routine. See ClusterFunction for required format of user-defined clustering routines. User can also give a character value to the argument clusterFunction to indicate the use of clustering routines provided in package. Type listBuiltInFunctions at command prompt to see the built-in clustering routines. If clusterFunction is missing, the default is set to "pam".

... arguments passed to the post-processing steps of the clustering. The available post-processing arguments for a ClusterFunction object depend on it's algorithm type and can be found by calling getPostProcessingArgs. See details below for documentation.

inputMatrix

numerical matrix on which to run the clustering or a SummarizedExperiment, SingleCellExperiment, or ClusterExperiment object.

inputType

a character vector defining what type of input is given in the inputMatrix argument. Must consist of values "diss","X", or "cat" (see details). "X" and "cat" should be indicate matrices with features in the row and samples in the column; "cat" corresponds to the features being numerical integers corresponding to categories, while "X" are continuous valued features. "diss" corresponds to an inputMatrix that is a NxN dissimilarity matrix. "cat" is largely used internally for clustering of sets of clusterings.

clusterArgs

arguments to be passed directly to the clusterFUN slot of the ClusterFunction object

minSize

the minimum number of samples in a cluster. Clusters found below this size will be discarded and samples in the cluster will be given a cluster assignment
of ",-1" to indicate that they were not clustered.

**orderBy**

how to order the cluster (either by size or by maximum alpha value). If orderBy=",size" the numbering of the clusters are reordered by the size of the cluster, instead of by the internal ordering of the clusterFUN defined in the ClusterFunction object (an internal ordering is only possible if slot outputType of the ClusterFunction is "list").

**format**

whether to return a list of indices in a cluster or a vector of clustering assignments. List is mainly for compatibility with sequential part.

**returnData**

logical as to whether to return the diss or x matrix in the output. If FALSE only the clustering vector is returned.

**warnings**

logical as to whether should give warning if arguments given that don’t match clustering choices given. Otherwise, inapplicable arguments will be ignored without warning.

**Details**

mainClustering is not meant to be called by the user. It is only an exported function so as to be able to clearly document the arguments for mainClustering which can be passed via the argument mainClusterArgs in functions like clusterSingle and clusterMany.

Post-processing Arguments: For post-processing the clustering, currently only type 'K' algorithms have a defined post-processing. Specifically

- "findBestK"logical, whether should find best K based on average silhouette width (only used if clusterFunction of type "K").
- "kRange"vector of integers to try for k values if findBestK=TRUE. If k is given in clusterArgs, then default is k-2 to k+20, subject to those values being greater than 2; if not the default is 2:20. Note that default values depend on the input k, so running for different choices of k and findBestK=TRUE can give different answers unless kRange is set to be the same.
- "removeSil"logical as to whether remove the assignment of a sample to a cluster when the sample's silhouette value is less than silCutoff
- "silCutoff"Cutoff on the minimum silhouette width to be included in cluster (only used if removeSil=TRUE).

**Value**

If returnData=FALSE, mainClustering returns a vector of cluster assignments (if format=",vector") or a list of indices for each cluster (if format=",list"). Clusters less than minSize are removed. If returnData=TRUE, then mainClustering returns a list

- resultsThe clusterings of each sample.
- inputMatrixThe input matrix given to argument inputMatrix. Useful if input is result of subsampling, in which case input is the set of clusterings found over subsampling.

**Examples**

data(simData)
c11<-mainClustering(inputMatrix=simData, inputType="X",
**makeConsensus**

Find sets of samples that stay together across clusterings

### Description

Find sets of samples that stay together across clusterings in order to define a new clustering vector.

### Usage

```r
# S4 method for signature 'matrix'
makeConsensus(
  x, 
  proportion, 
  clusterFunction = "hierarchical01", 
  minSize = 5, 
  propUnassigned = 0.5, 
  whenUnassign = c("before", "after"), 
  clusterArgs = NULL
)
```

```r
class(makeConsensus) <- class
makeConsensus$setMethod(
  method = "matrix", 
  signature = signature,
  body = {
    proportion = x, 
    diss <- as.matrix(dist(t(simData), method = "manhattan")) 
    cl2 <- mainClustering(diss, inputType = "diss", clusterFunction = "hierarchical01", 
                        clusterArgs = list(alpha = 0.1)) 
    cl3 <- mainClustering(inputMatrix = diss, inputType = "diss", clusterFunction = "pam", 
                         clusterArgs = list(k = 3)) 
    # run hierarchical method for finding blocks, with method of evaluating 
    # coherence of block set to evalClusterMethod = "average", and the hierarchical 
    # clustering using single linkage:
    # (clustering function requires type 'diss'),
    clustSubHier <- mainClustering(diss, inputType = "diss", 
                                   clusterFunction = "hierarchical01", minSize = 5, 
                                   clusterArgs = list(alpha = 0.1, evalClusterMethod = "average", method = "single")) 
    # post-process results of pam -- must pass diss for silhouette calculation
    clustSubPamK <- mainClustering(simData, inputType = "X", clusterFunction = "pam", 
                                  silhouette = 0, minSize = 5, diss = diss, removeSil = TRUE, clusterArgs = list(k = 3)) 
    clustSubPamBestK <- mainClustering(simData, inputType = "X", clusterFunction = "pam", silhouette = 0, 
                                       minSize = 5, diss = diss, removeSil = TRUE, findBestK = TRUE, kRange = 2:10) 
    # note that passing the wrong arguments for an algorithm results in warnings
    # (which can be turned off with warnings = FALSE)
    clustSubTight_test <- mainClustering(diss, inputType = "diss", 
                                          clusterFunction = "tight", 
                                          clusterArgs = list(alpha = 0.1), minSize = 5, removeSil = TRUE) 
    clustSubTight_test2 <- mainClustering(diss, inputType = "diss", 
                                          clusterFunction = "tight", 
                                          clusterArgs = list(alpha = 0.1, evalClusterMethod = "average"))
  }
)
```

## S4 method for signature 'ClusterExperiment'
makeConsensus(
  x,
  whichClusters,
  eraseOld = FALSE,
  clusterLabel = "makeConsensus",
  ...)

### Arguments

- **x**: a matrix with samples on the rows and different clusterings on the columns or `ClusterExperiment` object.
- **proportion**: The proportion of times that two sets of samples should be together in order to be grouped into a cluster (if <1, passed to `mainClustering` via `alpha = 1 - proportion`).
- **clusterFunction**: the clustering function to use (passed to `mainClustering`); currently must be of type '01' and accept as input matrices of type "cat" (see details of ?ClusterFunction).
- **minSize**: minimum size required for a set of samples to be considered in a cluster because of shared clustering, passed to `mainClustering`.
- **propUnassigned**: samples with greater than this proportion of assignments equal to `-1` are assigned a `-1` cluster value as a last step (only if proportion < 1).
- **whenUnassign**: (provided for back compatibility with previous versions). Must be one of "before" or "after", indicating at what point are samples with a proportion of assignments of `-1` greater than `propUnassigned` forced to have a `-1` value. If "before", then these samples are removed and not used for clustering. If "after", these samples are included in the clustering step, but then the cluster values they receive are assigned a `-1`. These choices may result in different clusterings, because if these samples are included in the clustering (i.e. `whenUnassign="after"`), then these samples may affect the cluster assignments of other samples. The default is currently "before", but previous to version 2.5.4, there was no such option and the code internally set to "after", so for reproducibility with older results, users may need to set this option.
- **clusterArgs**: list of arguments to be passed to the call to `mainClustering` that is used to cluster the proportion overlap between samples.
- **whichClusters**: argument that can be either numeric or character vector indicating the clusterings to be used. See details of `getClusterIndex`.
- **eraseOld**: logical. Only relevant if input `x` is of class `ClusterExperiment`. If TRUE, will erase existing workflow results (clusterMany as well as mergeClusters and makeConsensus). If FALSE, existing workflow results will have "_i" added to the clusterTypes value, where `i` is one more than the largest such existing workflow clusterTypes.
clusterLabel: a string used to describe the type of clustering. By default it is equal to "makeConsensus", to indicate that this clustering is the result of a call to makeConsensus. However, a more informative label can be set (see vignette).

Arguments to be passed on to the method for signature matrix, missing.

Details

This function was previously called combineMany (versions <= 2.0.0). combineMany is still available, but is considered defunct and users should update their code accordingly.

The function tries to find a consensus cluster across many different clusterings of the same samples. It does so by creating a nSamples x nSamples matrix of the percentage of co-occurrence of each sample and then calling mainClustering to cluster the co-occurrence matrix. The function assumes that '-1' labels indicate clusters that are not assigned to a cluster. Co-occurrence with the unassigned cluster is treated differently than other clusters. The percent co-occurrence is taken only with respect to those clusterings where both samples were assigned. Then samples with more than propUnassigned values that are '-1' across all of the clusterings are assigned a '-1' regardless of their cluster assignment.

The method calls mainClustering on the proportion matrix with clusterFunction as the 01 clustering algorithm, alpha=1-proportion, minSize=minSize, and evalClusterMethod=c("average"). See help of mainClustering for more details.

Value

If x is a matrix, a list with values

- clustering vector of cluster assignments, with "-1" implying unassigned
- percentageShared a nSample x nSample matrix of the percent co-occurrence across clusters used to find the final clusters. Percentage is out of those not '-1'
- noUnassignedCorrection a vector of cluster assignments before samples were converted to '-1' because had >propUnassigned '-1' values (i.e. the direct output of the mainClustering output.)

If x is a ClusterExperiment, a ClusterExperiment object, with an added clustering of clusterTypes equal to makeConsensus and the percentageShared matrix stored in the coClustering slot.

Examples

```r
## Not run:
data(simData)
cl <- clusterMany(simData,nReducedDims=c(5,10,50), reduceMethod="PCA", clusterFunction="pam", ks=2:4, findBestK=c(FALSE), removeSil=TRUE, makeMissingDiss=TRUE, subsample=FALSE)
#make names shorter for plotting
cMat <- clusterMatrix(cl)
colnames(cMat) <- gsub("TRUE", "T", colnames(cMat))
colnames(cMat) <- gsub("FALSE", "F", colnames(cMat))
```
colnames(clMat) <- gsub("k=NA,"", ", colnames(clMat))

#require 100% agreement -- very strict
c1Common100 <- makeConsensus(clMat, proportion=1, minSize=10)

#require 70% agreement based on clustering of overlap
c1Common70 <- makeConsensus(clMat, proportion=0.7, minSize=10)

oldpar <- par(no.readonly = TRUE)
par(mar=c(1.1, 12.1, 1.1, 1.1))
plotClusters(cbind("70%Similarity"=clCommon70, clMat,
                   "100%Similarity"=clCommon100), axisLine=-2)

#method for ClusterExperiment object
c1Common <- makeConsensus(cl, whichClusters="workflow", proportion=0.7,
                           minSize=10)
plotClusters(c1Common)
par(oldpar)

## End(Not run)

makeDendrogram

Make hierarchy of set of clusters

Description

Makes a dendrogram of a set of clusters based on hclust on the medoids of the cluster.

Usage

## S4 method for signature 'ClusterExperiment'
makeDendrogram(
  x,
  whichCluster = "primaryCluster",
  reduceMethod = "mad",
  nDims = defaultNDims(x, reduceMethod),
  filterIgnoresUnassigned = TRUE,
  unassignedSamples = c("outgroup", "cluster"),
  whichAssay = 1,
  ...
)

## S4 method for signature 'dist'
makeDendrogram(
  x,
  cluster,
  unassignedSamples = c("outgroup", "cluster", "remove"),
  calculateSample = TRUE,
  ...
makeDendrogram

## S4 method for signature 'matrixOrHDF5'
makeDendrogram(
  x, 
  cluster, 
  unassignedSamples = c("outgroup", "cluster", "remove"), 
  calculateSample = TRUE, 
  ... 
)

### Arguments

- **x**: data to define the medoids from. Matrix and `ClusterExperiment` supported.
- **whichCluster**: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.
- **reduceMethod**: character A character identifying what type of dimensionality reduction to perform before clustering. Can be either a value stored in either of reducedDims or filterStats slot or a built-in dimensionality reduction/filtering. The option "co-Cluster" will use the co-Clustering matrix stored in the 'coClustering' slot of the `ClusterExperiment` object.
- **nDims**: The number of dimensions to keep from `reduceMethod`. If missing calls `defaultNDims`.
- **filterIgnoresUnassigned**: logical. Whether filtering statistics should ignore the unassigned samples within the clustering. Only relevant if `reduceMethod` matches one of built-in filtering statistics in `listBuiltInFilterStats()`, in which case the clustering identified in `whichCluster` is passed to `makeFilterStats` and the unassigned samples are excluded in calculating the statistic. See `makeFilterStats` for more details.
- **unassignedSamples**: how to handle unassigned samples("-1"); only relevant for sample clustering. See details.
- **whichAssay**: numeric or character specifying which assay to use. See `assay` for details.
- **...**: for `makeDendrogram`, if signature `matrix`, arguments passed to `hclust`; if signature `ClusterExperiment` passed to the method for signature `matrix`. For `plotDendrogram`, passed to `plot.dendrogram`.
- **cluster**: A numeric vector with cluster assignments. If `x` is a `ClusterExperiment` object, `cluster` is automatically the primaryCluster(`x`). "-1" indicates the sample was not assigned to a cluster.
- **calculateSample**: only relevant for `matrix` or `dist` version of function. Indicates whether to calculate the sample dendrogram.

### Details

The function returns two dendrograms (as a list if `x` is a matrix or in the appropriate slots if `x` is `ClusterExperiment`). The cluster dendrogram is created by applying `hclust` to the medoids of each
mergeClusters

Merge clusters based on dendrogram

Description

Takes an input of hierarchical clusterings of clusters and returns estimates of number of proportion of non-null and merges those below a certain cutoff.
mergeClusters

Usage

```r
## S4 method for signature 'matrixOrHDF5'
mergeClusters(
  x,
  cl,
  dendro = NULL,
  mergeMethod = c("none", "Storey", "PC", "adjP", "locfdr", "JC"),
  plotInfo = "none",
  nodePropTable = NULL,
  calculateAll = TRUE,
  showWarnings = FALSE,
  cutoff = 0.05,
  plot = TRUE,
  DEMethod,
  logFCcutoff = 0,
  weights = NULL,
  ...
)

## S4 method for signature 'ClusterExperiment'
mergeClusters(
  x,
  eraseOld = FALSE,
  mergeMethod = "none",
  plotInfo = "all",
  clusterLabel = "mergeClusters",
  leafType = c("samples", "clusters"),
  plotType = c("colorblock", "name", "ids"),
  plot = TRUE,
  whichAssay = 1,
  forceCalculate = FALSE,
  weights = if ("weights" %in% assayNames(x)) "weights" else NULL,
  DEMethod,
  ...
)

## S4 method for signature 'ClusterExperiment'
nodeMergeInfo(x)

## S4 method for signature 'ClusterExperiment'
mergeCutoff(x)

## S4 method for signature 'ClusterExperiment'
mergeMethod(x)

## S4 method for signature 'ClusterExperiment'
mergeClusterIndex(x)
```
## S4 method for signature 'ClusterExperiment'
eraseMergeInfo(x)

## S4 method for signature 'ClusterExperiment'
getMergeCorrespond(x, by = c("merge", "original"))

### Arguments

- **x**: data to perform the test on. It can be a matrix or a ClusterExperiment.
- **cl**: A numeric vector with cluster assignments to compare to. “-1” indicates the sample was not assigned to a cluster.
- **dendro**: dendrogram providing hierarchical clustering of clusters in cl. If x is a matrix, then the default is dendro=NULL and the function will calculate the dendrogram with the given (x, cl) pair using makeDendrogram. If x is a ClusterExperiment object, the dendrogram in the slot dendro_clusters will be used. In this case, this means that makeDendrogram needs to be called before mergeClusters.
- **mergeMethod**: method for calculating proportion of non-null that will be used to merge clusters (if 'none', no merging will be done). See details for description of methods.
- **plotInfo**: what type of information about the merging will be shown on the dendrogram. If 'all', then all the estimates of proportion non-null will be plotted at each node of the dendrogram; if 'mergeMethod', then only the value used in the mergeClusters command is plotted at each node. If 'none', then no proportions will be added to the dendrogram, though the dendrogram will be drawn. 'plotInfo' can also be one of the valid input to mergeMethod (even if that method is not the method chosen in mergeMethod argument). plotInfo can also show the information corresponding to "adjP" with a fold-change cutoff, by giving a value to this argument in the form of "adjP_2.0", for example.
- **nodePropTable**: Only for matrix version. Matrix of results from previous run of mergeClusters as returned by matrix version of mergeClusters. Useful if just want to change the cutoff. Not generally intended for user but used internally by package.
- **calculateAll**: logical. Whether to calculate the estimates for all methods. This reduces computation costs for any future calls to mergeClusters since the results can be passed to future calls of mergeClusters (and for ClusterExperiment objects this is done automatically).
- **showWarnings**: logical. Whether to show warnings given by the methods. The 'locfdr' method in particular frequently spits out warnings (which may indicate that its estimates are not reliable). Setting showWarnings=FALSE will suppress all warnings from all methods (not just "locfdr"). By default this is set to showWarnings=FALSE by default to avoid large number of warnings being produced by "locfdr", but users may want to be more careful to check the warnings for themselves.
- **cutoff**: minimum value required for NOT merging a cluster, i.e. two clusters with the proportion of DE below cutoff will be merged. Must be a value between 0, 1, where lower values will make it harder to merge clusters.
- **plot**: logical as to whether to plot the dendrogram with the merge results
- **DEMethod**: character vector describing how the differential expression analysis should be performed that will be used in the estimation of the percentage DE per node. See getBestFeatures for current options. See details.
logFCcutoff Relevant only if the mergeMethod selected is "adjP", in which case the calculation of the proportion of individual tests significant will also require that the estimated log-fold change of the features to be at least this large in absolute value. Value will be rounded to nearest tenth of an integer via `round(logFCcutoff,digits=1)`. For any other method, this parameter is ignored. Note that the logFC is based on log2 (the results of `getBestFeatures`).

weights weights to use in by edgeR. If x is a matrix, then weights should be a matrix of weights, of the same dimensions as x. If x is a ClusterExperiment object weights can be either a matrix, as previously described, or a character or numeric index to an assay in x that contains the weights. We recommend that weights be stored as an assay with name "weights" so that the weights will also be used with `mergeClusters`, and this is the default. Setting weights=NULL ensures that weights will NOT be used, and only the standard edgeR.

... for signature matrix, arguments passed to the `plot.phylo` function of ape that plots the dendrogram. For signature ClusterExperiment arguments passed to the method for signature matrix and then if do not match those arguments, will be passed onto `plot.phylo`.

eraseOld logical. Only relevant if input x is of class ClusterExperiment. If TRUE, will erase existing workflow results (clusterMany as well as mergeClusters and makeConsensus). If FALSE, existing workflow results will have "_i" added to the clusterTypes value, where i is one more than the largest such existing workflow clusterTypes.

clusterLabel a string used to describe the type of clustering. By default it is equal to "mergeClusters", to indicate that this clustering is the result of a call to mergeClusters (only if x is a ClusterExperiment object)

leafType if plotting, whether the leaves should be the clusters or the samples. Choosing 'samples' allows for visualization of how many samples are in the merged clusters (only if x is a ClusterExperiment object), which is the main difference between choosing "clusters" and "samples", particularly if `plotType="colorblock"`

plotType if plotting, then whether leaves of dendrogram should be labeled by rectangular blocks of color ("colorblock") or with the names of the leaves ("name") (only if x is a ClusterExperiment object).

whichAssay numeric or character specifying which assay to use. See `assay` for details.

forceCalculate This forces the function to erase previously saved merge results and recalculate the merging.

by indicates whether output from `getMergeCorrespond` should be a vector/list with elements corresponding to merge cluster ids or elements corresponding to the original clustering ids. See return value for details.

Details

of genes that are found significant based on a FDR adjusted p-values (method "BH") and a cutoff of 0.05. Previous versions offered the method "MB", a method of Meinshausen and Buhlmann (2005), but the package howmany is no longer supported for its implementation.

**Control of Plotting** If `mergeMethod` is not equal to 'none' then the plotting will indicate where the clusters will be merged by making dotted lines of edges that are merged together (assuming `plotInfo` is not 'none'). `plotInfo` controls simultaneously what information will be plotted on the nodes as well as whether the dotted lines will be shown for the merged cluster. Notice that the choice of `plotInfo` (as long as it is not 'none') has no effect on how the dotted edges are drawn – they are always drawn based on the `mergeMethod`. If you choose `plotInfo` to not be equal to the `mergeMethod`, then you will have a confusing picture where the dotted edges will be based on the clustering created by `mergeMethod` while the information on the nodes is based on a different method. Note that you can override `plotInfo` by setting `show.node.label=FALSE` (passed to `plot.phylo`), so that no information is plotted on the nodes, but the dotted edges are still drawn. If you just want plot of the dendrogram, with no merging performed nor demonstrated on the plot, see `plotDendrogram`.

**Saving and Reusing of results** By default, the function saves the results in the `ClusterExperiment` object and will not recalculate them if not needed. Note that by default `calculateAll=TRUE`, which means that regardless of the value of `mergeMethod`, all the methods will be calculated so that those results will be stored and if you change the `mergeMethod`, no additional calculations are needed. Since the computationally intensive step is the running the DE method on the genes, this is a big savings (all of the methods then calculate the proportion from those results). However, note that if `calculateAll=TRUE` and ANY of the methods returned NA for any value, the calculation will be redone. Thus if, for example, the `locfdr` function does not run successfully and returns NA, the function will always recalculate each time, even if you don’t specifically want the results of `locfdr`. In this case, it makes sense to turn `calculateAll=FALSE`.

If the dendrogram was made with option `unassignedSamples="cluster"` (i.e. unassigned were clustered in with other samples), then you cannot choose the option `leafType=′samples′`. This is because the current code cannot reliably link up the internal nodes of the sample dendrogram to the internal nodes of the cluster dendrogram when the unassigned samples are intermixed.

When the input is a `ClusterExperiment` object, the function attempts to update the merge information in that object. This is done by checking that the existing dendrogram stored in the object (and run on the clustering stored in the slot `dendro_index`) is the same clustering that is stored in the slot `merge_dendrocluster_index`. For this reason, new calls to `makeDendrogram` will erase the merge information saved in the object.

If `mergeClusters` is run with `mergeMethod="none"`, the function may still calculate the proportions per node if `plotInfo` is not equal to "none" or `calculateAll=TRUE`. If the input object was a `ClusterExperiment` object, the resulting information will be still saved, though no new clustering was created; if there was not an existing merge method, the slot `merge_dendrocluster_index` will be updated.

**Value**

If ‘x’ is a matrix, it returns (invisibly) a list with elements

- `clustering` a vector of length equal to `ncol(x)` giving the integer-valued cluster ids for each sample. "-1" indicates the sample was not clustered.
- `oldClToNew` A table of the old cluster labels to the new cluster labels.
nodeProp A table of the proportions that are DE on each node. This table is saved in the merge_nodeProp slot of a ClusterExperiment object and can be accessed along with the nodeMerge info with the nodeMergeInfo function.

nodeMerge A table of indicating for each node whether merged or not and the cluster id in the new clustering that corresponds to the node. Note that a node can be merged and not correspond to a node in the new clustering, if its ancestor node is also merged. But there must be some node that corresponds to a new cluster id if merging has been done. This table is saved in the merge_nodeMerge slot of a ClusterExperiment object and can be accessed along with the nodeProp info with the nodeMergeInfo function.

updatedClusterDendro The dendrogram on which the merging was based (based on the original clustering).

cutoff The cutoff value for merging.

If `x` is a ClusterExperiment, it returns a new ClusterExperiment object with an additional clustering based on the merging. This becomes the new primary clustering. Note that even if mergeMethod="none", the returned object will erase any old merge information, update the work flow numbering, and return the newly calculated merge information.

nodeMergeInfo returns information collected about the nodes during merging as a data.frame with the following entries:

- **Node** Name of the node
- **Contrast** The contrast compared at each node, in terms of the cluster ids
- **isMerged** Logical as to whether samples from that node which were merged into one cluster during merging
- **mergeClusterId** If a node corresponds to a new, merged cluster, gives the cluster id it corresponds to. Otherwise NA
- **...** The remaining columns give the estimated proportion of genes differentially expressed for each method. A column of NAs means that the method in question hasn’t been calculated yet.

mergeCutoff returns the cutoff used for the current merging.

mergeMethod returns the method used for the current merge.

mergeClusterIndex returns the index of the clustering used for the current merge.

eraseMergeInfo returns object with all previously saved merge info removed.

getMergeCorrespond returns the correspondence between the merged cluster and its originating cluster. If by="original" returns a named vector, where the names of the vector are the cluster ids of the originating cluster and the values of the vector are the cluster ids of the merged cluster. If by="merge" the results returned are organized by the merged clusters. This will generally be a list, with the names of the list equal to the clusterIds of the merge clusters and the entries the clusterIds of the originating clusters. However, if there was no merging done (so that the clusters are identical) the output will be a vector like with by="original".

References


See Also

makeDendrogram, plotDendrogram, getBestFeatures

Examples

data(simData)

#create a clustering, for 8 clusters (truth was 3)
c1<-clusterSingle(simData, subsample=FALSE, sequential=FALSE, mainClusterArgs=list(clusterFunction="pam", clusterArgs=list(k=8)))

#give more interesting names to clusters:
newNames<- paste("Cluster",clusterLegend(cl)[[1]][["name"],,,sep="")
clusterLegend(cl)[[1]][["name"]]<-newNames
#make dendrogram
c1 <- makeDendrogram(c1)

#plot showing the before and after clustering
#(Note argument 'use.edge.length' can improve readability)
merged <- mergeClusters(cl, plotInfo="all", mergeMethod="adjP", use.edge.length=FALSE, DEMethod="limma")

#Simpler plot with just dendrogram and single method
merged <- mergeClusters(cl, plotInfo="mergeMethod", mergeMethod="adjP", use.edge.length=FALSE, DEMethod="limma", leafType="clusters", plotType="name")

#compare merged to original
tableClusters(merged,whichClusters=c("mergeClusters","clusterSingle"))

numericalAsCharacter

Convert numeric values to character that sort correctly

Description

Small function that takes as input integer values (or values that can be converted to integer values) and converts them into character values that are 'padded' with zeros at the beginning of the numbers so that they will sort correctly.
Usage

electricalAsCharacter(values, prefix = "")

Arguments

values vector of values to be converted into sortable character values
prefix optional character string that will be added as prefix to the result

Details

The function determines the largest value and adds zeros to the front of smaller integers so that the resulting characters are the same number of digits. This allows standard sorting of the values to correctly sort.

The maximum number of zeros that will be added is 3. Input integers beyond that point will not be correctly fixed for sorting.

Negative integers will not be corrected, but left as-is

Value

A character vector

See Also

str_pad

Examples

electricalAsCharacter(c(-1, 5, 10, 20, 100))

Description

Make a barplot of sample's assignments to clusters for single clustering, or cross comparison for two clusterings.

Usage

## S4 method for signature 'ClusterExperiment'
plotBarplot(object, whichClusters = "primary", labels = c("names", "ids"), ...)

## S4 method for signature 'vector'
plotBarplot(object, ...)

## S4 method for signature 'matrix'
plotBarplot(
  object,
  xNames = NULL,
  legNames = NULL,
  legend = ifelse(ncol(object) == 2, TRUE, FALSE),
  xlab = NULL,
  legend.title = NULL,
  unassignedColor = "white",
  missingColor = "grey",
  colPalette = NULL,
  ...
)

Arguments

object A matrix of with each column corresponding to a clustering and each row a sample or a ClusterExperiment object.

whichClusters argument that can be either numeric or character vector indicating the clusterings to be used. See details of getClusterIndex.

labels if object is a ClusterExperiment object, then labels defines whether the clusters will be identified by their names values in clusterLegend (labels="names", the default) or by their clusterIds value in clusterLegend (labels="ids").

... for plotBarplot arguments passed either to the method of plotBarplot for matrices or ultimately to barplot.

xNames names for the clusters on x-axis (i.e. clustering given 1st). By default uses names of the 1st column of clusters matrix. See details.

legNames names for the clusters dividing up the 1st clusters (will appear in legend). By default uses names of the 2nd cluster of clusters matrix. If only one clustering, xNames and legNames refer to the same clustering. See details.

legend whether to plot the legend

xlab label for x-axis. By default or if equal NULL the column name of the 1st cluster of clusters matrix

legend.title label for legend. By default or if equal NULL the column name of the 2st cluster of clusters matrix

unassignedColor If "-1" in clusters, will be given this color (meant for samples not assigned to cluster).

missingColor If "-2" in clusters, will be given this color (meant for samples that were missing from the clustering, mainly when comparing clusterings run on different sets of samples)

colPalette a vector of colors used for the different clusters. See details.

Details

The first column of the cluster matrix will be on the x-axis and the second column (if present) will separate the groups of the first column.
All arguments of the matrix version can be passed to the ClusterExperiment version. As noted above, however, some arguments have different interpretations.

If whichClusters = "workflow", then the most recent two clusters of the workflow will be chosen where recent is based on the following order (most recent first): final, mergeClusters, makeConsensus, clusterMany.

xNames, legNames and colPalette should all be named vectors, with the names referring to the clusters they should match to (for ClusterExperiment objects, it is determined by the argument labels as to whether the names should match the cluster names or the clusterIds). colPalette and legNames must be same length of the number of clusters found in the second clustering, or if only a single clustering, the same length as the number of clusters in that clustering.

Value

A plot is produced, nothing is returned

Author(s)

Elizabeth Purdom

Examples

```r
## Not run:
#clustering using pam: try using different dimensions of pca and different k
data(simData)

c1 <- clusterMany(simData, nReducedDims=c(5, 10, 50), reduceMethod="PCA",
clusterFunction="pam", ks=2:4, findBestK=c(TRUE,FALSE),
removeSil=c(TRUE,FALSE), makeMissingDiss=TRUE)

plotBarplot(c1)
plotBarplot(c1,whichClusters=1:2)

## End(Not run)
```

---

plotClusters  
Visualize cluster assignments across multiple clusterings

Description

Align multiple clusterings of the same set of samples and provide a color-coded plot of their shared cluster assignments

Usage

```r
## S4 method for signature 'ClusterExperiment'
plotClusters(
  object,
  whichClusters,
```
existingColors = c("ignore", "all", "firstOnly"),
resetNames = FALSE,
resetColors = FALSE,
resetOrderSamples = FALSE,
colData = NULL,
clusterLabels = NULL,
...)

## S4 method for signature 'matrix'
plotClusters(
  object,
  orderSamples = NULL,
colData = NULL,
reuseColors = FALSE,
matchToTop = FALSE,
plot = TRUE,
unassignedColor = "white",
missingColor = "grey",
minRequireColor = 0.3,
startNewColors = FALSE,
colPalette = massivePalette,
input = c("clusters", "colors"),
clusterLabels = colnames(object),
add = FALSE,
xCoord = NULL,
ylim = NULL,
tick = FALSE,
ylab = "",
xlab = "",
axisLine = 0,
box = FALSE,
...)

Arguments

- **object**: A matrix of with each column corresponding to a clustering and each row a sample or a `ClusterExperiment` object. If a matrix, the function will plot the clusterings in order of this matrix, and their order influences the plot greatly.
- **whichClusters**: argument that can be either numeric or character vector indicating the clusterings to be used. See details of `getClusterIndex`.
- **existingColors**: how to make use of the exiting colors in the `ClusterExperiment` object. 'ignore' will ignore them and assign new colors. 'firstOnly' will use the existing colors of only the 1st clustering, and then align the remaining clusters and give new colors for the remaining only. 'all' will use all of the existing colors.
- **resetNames**: logical. Whether to reset the names of the clusters in `clusterLegend` to be the aligned integer-valued ids from `plotClusters`. 
resetColors logical. Whether to reset the colors in clusterLegend in the ClusterExperiment returned to be the colors from the plotClusters.

resetOrderSamples logical. Whether to replace the existing orderSamples slot in the ClusterExperiment object with the new order found.

colData If clusters is a matrix, colData gives a matrix of additional cluster/sample data on the samples to be plotted with the clusterings given in clusters. Values in colData will be added to the end (bottom) of the plot. NAs in the colData matrix will trigger an error. If clusters is a ClusterExperiment object, the input in colData refers to columns of the the colData slot of the ClusterExperiment object to be plotted with the clusters. In this case, colData can be TRUE (i.e. all columns will be plotted), or an index or a character vector that references a column or column name, respectively, of the colData slot of the ClusterExperiment object. If there are NAs in the colData columns, they will be encoded as ‘unassigned’ and receive the same color as ‘unassigned’ samples in the clustering.

clusterLabels names to go with the columns (clusterings) in matrix colorMat. If colData argument is not NULL, the clusterLabels argument must include names for the sample data too. If the user gives only names for the clusterings, the code will try to anticipate that and use the column names of the sample data, but this is fragile. If set to FALSE, then no labels will be plotted.

... for plotClusters arguments passed either to the method of plotClusters for matrices, or ultimately to plot (if add=FALSE).

orderSamples A predefined order in which the samples will be plotted. Otherwise the order will be found internally by aligning the clusters (assuming input=“clusters”)

reuseColors Logical. Whether each row should consist of the same set of colors. By default (FALSE) each cluster that the algorithm doesn’t identify to the previous rows clusters gets a new color.

matchToTop Logical as to whether all clusters should be aligned to the first row. By default (FALSE) each cluster is aligned to the ordered clusters of the row above it.

plot Logical as to whether a plot should be produced.

unassignedColor If “-1” in clusters, will be given this color (meant for samples not assigned to cluster).

missingColor If “-2” in clusters, will be given this color (meant for samples that were missing from the clustering, mainly when comparing clusterings run on different sets of samples)

minRequireColor In aligning colors between rows of clusters, require this percent overlap.

startNewColors logical, indicating whether in aligning colors between rows of clusters, should the colors restart at beginning of colPalette as long as colors are not in immediately proceeding row (the colors at the end of massivePalette are all of colors() and many will be indistinguishable, so this option can be useful if you have a large cluster matrix).
colPalette a vector of colors used for the different clusters. Must be as long as the maximum number of clusters found in any single clustering/column given in clusters or will otherwise return an error.

input indicate whether the input matrix is matrix of integer assigned clusters, or contains the colors. If input= "colors", then the object clusters is a matrix of colors and there is no alignment (this option allows the user to manually adjust the colors and replot, for example).

add whether to add to existing plot.

xCoord values on x-axis at which to plot the rows (samples).

ylim vector of limits of y-axis.

tick logical, whether to draw ticks on x-axis for each sample.

ylab character string for the label of y-axis.

xlab character string for the label of x-axis.

axisLine the number of lines in the axis labels on y-axis should be (passed to line = ... in the axis call).

box logical, whether to draw box around the plot.

Details

All arguments of the matrix version can be passed to the ClusterExperiment version. As noted above, however, some arguments have different interpretations.

If whichClusters = "workflow", then the workflow clusterings will be plotted in the following order: final, mergeClusters, makeConsensus, clusterMany.

Value

If clusters is a ClusterExperiment Object, then plotClusters returns an updated ClusterExperiment object, where the clusterLegend and/or orderSamples slots have been updated (depending on the arguments).

If clusters is a matrix, plotclusters returns (invisibly) the orders and other things that go into making the matrix. Specifically, a list with the following elements.

- orderSamples a vector of length equal to nrow(clusters) giving the order of the samples (rows) to use to get the original clusters matrix into the order made by plotClusters.

- colors matrix of color assignments for each element of original clusters matrix. Matrix is in the same order as original clusters matrix. The matrix colors[orderSamples,] is the matrix that can be given back to plotClusters to recreate the plot (see examples).

- alignedClusterIds a matrix of integer valued cluster assignments that match the colors. This is useful if you want to have cluster identification numbers that are better aligned than that given in the original clusters. Again, the rows/samples are in same order as original input matrix.

- clusterLegend list of length equal to the number of columns of input matrix. The elements of the list are matrices, each with three columns named "Original","Aligned", and "Color" giving, respectively, the correspondence between the original cluster ids in clusters, the aligned cluster ids in aligned, and the color.

- origClusters The original matrix of clusters given to plotClusters.
Author(s)

Elizabeth Purdom and Marla Johnson (based on the tracking plot in ConsensusClusterPlus by Matt Wilkerson and Peter Waltman).

References


See Also

The ConsensusClusterPlus package.

Examples

```r
## Not run:
# clustering using pam: try using different dimensions of pca and different K
data(simData)
cl <- clusterMany(simData, nReducedDims=c(5, 10, 50), reduceMethod="PCA", 
clustFunction="pam", ks=2:4, findBestK=c(TRUE,FALSE),
removeSil=c(TRUE,FALSE), makeMissingDiss=TRUE)

clusterLabels(cl)

# make names shorter for better plotting
x <- clusterLabels(cl)
x <- gsub("TRUE", "T", x)
x <- gsub("FALSE", "F", x)
x <- gsub("k=NA,"", ",", x)
x <- gsub("Features", "", x)
clusterLabels(cl) <- x

par(mar=c(2,10,1,1))
# this will make the choices of plotClusters
cl <- plotClusters(cl, axisLine=-1, resetOrderSamples=TRUE, resetColors=TRUE)

# see the new cluster colors
clusterLegend(cl)[1:2]

# We can also change the order of the clusterings. Notice how this
dramatically changes the plot!
c1Order <- c(3:6, 1:2, 7:ncol(clusterMatrix(cl)))
cl <- plotClusters(cl, whichClusters=c1Order, resetColors=TRUE, 
resetOrder=TRUE, axisLine=-2)

# We can manually switch the red ("#E31A1C") and green ("#33A02C") in the
# first cluster:

# see what the default colors are and their names
showPalette(wh=1:5)
```
#change "#E31A1C" to "#33A02C"
newColorMat <- clusterLegend(cl)[[clOrder[1]]]
newColorMat[2:3, "color"] <- c("#33A02C", "#E31A1C")
clusterLegend(cl)[[clOrder[1]]] <- newColorMat

# replot by setting 'input="colors"'
par(mfrow=c(1,2))
plotClusters(cl, whichClusters=clOrder, orderSamples=orderSamples(cl),
existingColors="all")
plotClusters(cl, whichClusters=clOrder, resetColors=TRUE, resetOrder=TRUE,
axisLine=-2)
par(mfrow=c(1,1))

# set some of clusterings arbitrarily to "-1", meaning not clustered (white),
# and "-2" (another possible designation getting gray, usually for samples not
# included in original clustering)
clMatNew <- apply(clusterMatrix(cl), 2, function(x) {
  wh <- sample(1:nSamples(cl), size=10)
  x[wh]<- -1
  wh <- sample(1:nSamples(cl), size=10)
  x[wh]<- -2
  return(x)
})

# make a new object
c12 <- ClusterExperiment(assay(cl), clMatNew,
transformation=transformation(cl))
plotClusters(c12)

## End(Not run)

---

### plotClustersTable

Plot heatmap of cross-tabs of 2 clusterings

#### Description

Plot heatmap of cross-tabulations of two clusterings

#### Usage

```
## S4 method for signature 'ClusterExperiment'
plotClustersTable(
  object, 
  whichClusters, 
  ignoreUnassigned = FALSE, 
  margin = NA, 
  ... 
)
```
plotClustersTable

## S4 method for signature 'table'
plotClustersTable(
  object,
  plotType = c("heatmap", "bubble"),
  main = "",
  xlab = NULL,
  ylab = NULL,
  legend = TRUE,
  cluster = FALSE,
  clusterLegend = NULL,
  sizeTable = NULL,
  ...
)

## S4 method for signature 'ClusterExperiment'
tableClusters(
  object,
  whichClusters = "primary",
  useNames = TRUE,
  tableMethod = c("intersect", "union"),
  ...
)

## S4 method for signature 'table,table'
bubblePlot(
  propTable,
  sizeTable,
  gridColor = rgb(0, 0, 0.05),
  maxCex = 8,
  cexFactor,
  ylab,
  xlab,
  propLabel = "Value of %",
  legend = TRUE,
  las = 2,
  colorScale = RColorBrewer::brewer.pal(11, "Spectral")[-6]
)

Arguments

object ClusterExperiment object (or matrix with table result)
whichClusters argument that can be either numeric or character vector indicating the clusterings to be used. See details of getClusterIndex.
ignoreUnassigned logical as to whether to ignore unassigned clusters in the plotting. This means they will also be ignored in the calculations of the proportions (if margin not NA).
margin if NA, the actual counts from tableClusters will be plotted. Otherwise, prop.table
will be called and the argument margin will be passed to prop.table to determine whether proportions should be calculated. If '1', then the proportions in the rows sum to 1, if '2' the proportions in the columns sum to 1. If 'NULL' then the proportion across the entire matrix will sum to 1. An additional option has been added so that if you set margin=0, the entry displayed in each cell will be the proportion equal to the size of the intersection over the size of the union of the clusters (a Jaccard similarity between the clusters), in which case each entry is a value between 0 and 1 but no combination of the entries sum to 1.

... arguments passed on to plotHeatmap or bubblePlot depending on choice of plotType. Note that these functions take different arguments so that switching from one to the other may not take all arguments. In particular bubblePlot calls plot while plotHeatmap calls NMF(ahetmap).

plotType type of plot. If "heatmap", then a heatmap will be created of the values of the contingency table of the two clusters (calculated as determined by the argument "margin") using plotHeatmap. If "bubble", then a plot will be created using bubblePlot, which will create circles for each cell of the contingency table whose size corresponds to the number of samples shared and the color based on the value of the proportion (as chosen by the argument margin).

main title of plot, passed to plotHeatmap or to the argument propLabel in bubblePlot
xlab label for labeling clustering on the x-axis. If NULL, will determine names. If set to NA no label for clustering on the x-axis will be plotted (to turn off legend of the clusterings in heatmap, set legend=FALSE).

ylab label for labeling clustering on the y-axis. If NULL, will determine names. If set to NA no label for clustering on the y-axis will be plotted (to turn off legend of the clusterings in heatmap, set legend=FALSE).

legend whether to draw legend along top (bubble plot) or the color legend (heatmap)

cluster logical, whether to cluster the rows and columns of the table. Passed to arguments clusterFeatures AND clusterSamples of plotHeatmap.

clusterLegend list in clusterLegend format that gives colors for the clusters tabulated.

sizeTable table of sizes (only for use in bubblePlot or plotType="bubble"). See details.

useNames for tableClusters, whether the output should be tabled with names (useNames=TRUE) or ids (useNames=FALSE)

tableMethod the type of table calculation to perform. "intersect" refers to the standard contingency table (table), where each entry of the resulting table is the number of objects in both clusters. "union" instead gives for each entry the number of objects that are in the union of both clusters.

propTable table of proportions (bubblePlot))

gridColor color for grid lines (bubblePlot))

maxCex largest value of cex for any point (others will scale proportionally smaller) (bubblePlot).

cexFactor factor to multiply by to get values of circles. If missing, finds value automatically, namely by using the maxCex value default. Overrides value of maxCex. (bubblePlot))

propLabel the label to go with the legend of the color of the bubbles/circles
**plotClustersTable**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>las</td>
<td>the value for the las value in the call to <code>axis</code> in labeling the clusters in the bubble plot. Determines whether parallel or perpendicular labels to the axis (see <code>par</code>).</td>
</tr>
<tr>
<td>colorScale</td>
<td>the color scale for the values of the proportion table</td>
</tr>
</tbody>
</table>

**Details**

For `plotClustersTable` applied to the class `table`, `sizeTable` is passed to `bubblePlot` to indicate the size of the circle. If `sizeTable=NULL`, then it is assumed that the object argument is the table of counts and both the `propTable` and `sizeTable` are set to the same value (hence turning off the coloring of the circle/bubbles). This is equivalent effect to the `margin=NA` option of `plotClustersTable` applied to the `ClusterExperiment` class.

Note that the cluster labels in `plotClustersTable` and `tableClusters` are converted to "proper" R names via `make.names`. This is because `tableClusters` calls the R function `table`, which makes this conversion.

For `plotClustersTable`, whichClusters should define 2 clusters, while for `tableClusters` it can indicate arbitrary number.

`bubblePlot` is mainly used internally by `plotClustersTable` but is made public for users who want more control and to allow documentation of the arguments. `bubblePlot` plots a circle for each intersection of two clusters, where the color of the circle is based on the value in `propTable` and the size of the circle is based on the value in `sizeTable`. If `propTable` is equal to `sizeTable`, then the `propTable` is ignored and the coloring of the circles is not performed, only the adjusting of the size of the circles based on the total size. The size is determined by setting the `cex` value of the point as $\sqrt{sizeTable[i,j]}/\sqrt{\text{max}(sizeTable)}*\text{cexFactor}$.

**Value**

- `tableClusters` returns an object of class `table` (see `table`).
- `plotClustersTables` returns invisibly the plotted proportion table. In particular, this is the result of applying `prop.table` to the results of `tableClusters` (after removing unclustered samples if `ignoreUnassigned=TRUE`).

**Author(s)**

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**See Also**

- `plotHeatmap`
- `table`
- `prop.table`

**Examples**

```r
# clustering using pam: try using different dimensions of pca and different k
data(simData)
cl <- clusterMany(simData, nReducedDims=c(5, 10, 50), reducedDim="PCA",
                 clusterFunction="pam", ks=2:4, findBestK=c(TRUE,FALSE),
```
removeSil=c(TRUE, FALSE), makeMissingDiss=TRUE)
# give arbitrary names to clusters for demonstration
cl<-renameClusters(cl, value=letters[1:nClusters(cl)[1]], whichCluster=1)
tableClusters(cl, whichClusters=1:2)
# show options of margin in heatmap format:
par(mfrow=c(2,3))
plotClustersTable(cl, whichClusters=1:2, margin=NA, legend=FALSE, ignoreUnassigned=TRUE)
plotClustersTable(cl, whichClusters=1:2, margin=0, legend=FALSE, ignoreUnassigned=TRUE)
plotClustersTable(cl, whichClusters=1:2, margin=1, legend=FALSE, ignoreUnassigned=TRUE)
plotClustersTable(cl, whichClusters=1:2, margin=2, legend=FALSE, ignoreUnassigned=TRUE)
plotClustersTable(cl, whichClusters=1:2, margin=NULL, legend=FALSE, ignoreUnassigned=TRUE)
# show options of margin in bubble format:
par(mfrow=c(2,3))
plotClustersTable(cl, whichClusters=1:2, margin=NA, ignoreUnassigned=TRUE, plotType="bubble")
plotClustersTable(cl, whichClusters=1:2, margin=0, ignoreUnassigned=TRUE, plotType="bubble")
plotClustersTable(cl, whichClusters=1:2, margin=1, ignoreUnassigned=TRUE, plotType="bubble")
plotClustersTable(cl, whichClusters=1:2, margin=2, ignoreUnassigned=TRUE, plotType="bubble")
plotClustersTable(cl, whichClusters=1:2, margin=NULL, ignoreUnassigned=TRUE, plotType="bubble")

plotClustersWorkflow, ClusterExperiment-method

A plot of clusterings specific for clusterMany and workflow visualization

Description

A realization of plotClusters call specific to separating out the results of clusterMany and other clustering results.

Usage

## S4 method for signature 'ClusterExperiment'
plotClustersWorkflow(
  object, 
  whichClusters = c("mergeClusters", "makeConsensus"), 
  whichClusterMany = NULL, 
  nBlankLines = ceiling(nClusterings(object) * 0.05), 
  existingColors = c("ignore", "all", "highlightOnly"),
plotClustersWorkflow, ClusterExperiment-method

nSizeResult = ceiling(nClusterings(object) * 0.02),
clusterLabels = TRUE,
clusterManyLabels = TRUE,
sortBy = c("highlighted", "clusterMany"),
highlightOnTop = TRUE,
...
)

Arguments

object A ClusterExperiment object on which clusterMany has been run
whichClusters which clusterings to "highlight", i.e. draw separately from the bulk of the plot, see argument whichClusters of getClusterIndex for description of format allowed.
whichClusterMany indicate which clusterings to plot in the bulk of the plot, see argument whichClusters of getClusterIndex for description of format allowed.
nBlankLines the number of blank (i.e. white) rows to add between the clusterMany clusterings and the highlighted clusterings.
existingColors one of "ignore","all","highlightOnly". Whether the plot should use the stored colors in the ClusterExperiment object given. "highlightOnly" means only the highlighted clusters will use the stored colors, not the clusterMany clusterings.
nSizeResult the number of rows each highlighted clustering should take up. Increasing the number increases the thickness of the rectangles representing the highlighted clusterings.
clusterLabels either logical, indicating whether to plot the labels for the clusterings identified to be highlighted in the whichClusters argument, or a character vector of labels to use.
clusterManyLabels either logical, indicating whether to plot the labels for the clusterings from clusterMany identified in the whichClusterMany, or a character vector of labels to use.
sortBy how to align the clusters. If "highlighted" then the highlighted clusters indicated in the argument whichClusters are first in the alignment done by plotClusters. If "clusterMany", then the clusterMany results are first in the alignment. (Note this does not determine where they will be plotted, but how they are ordered in the aligning step done by plotClusters)
highlightOnTop logical. Whether the highlighted clusters should be plotted on the top of clusterMany results or underneath.
...
arguments passed to the matrix version of plotClusters

Details

This plot is solely intended to make it easier to use the plotClusters visualization when there are a large number of clusterings from a call to clusterMany. This plot separates out the clusterMany results from a designated clustering of interest, as indicated by the whichClusters argument (by default clusterings from a call to makeConsensus or mergeClusters). In addition the highlighted clusters are made bigger so that they can be easily seen.
Value

A plot is produced, nothing is returned.

See Also

plotClusters, clusterMany

Examples

# clustering using pam: try using different dimensions of pca and different k
## Not run:
data(simData)

cl <- clusterMany(simData, nReducedDims=c(5, 10, 50), reduceMethod="PCA",
clusterFunction="pam", ks=2:4, findBestK=c(TRUE, FALSE),
removeSil=c(TRUE, FALSE), makeMissingDiss=TRUE)
cl <- makeConsensus(cl, proportion=0.7)
plotClustersWorkflow(cl)

## End(Not run)
whichCluster if not NULL, indicates cluster used in making the significance table. Used to match to colors in clusterLegend(object) (relevant for one-vs-all contrast so that color aligns). See description of argument in getClusterIndex for further details.

contrastColors vector of colors to be given to contrasts. Should match the name of the contrasts in the 'Contrast' column of signifTable or 'ContrastName', if given. If missing, default colors given by match to the cluster names of whichCluster (see above), or otherwise given a default assignment.

... Arguments passed to plotHeatmap

Details

If the column 'ContrastName' is given in signifTable, these names will be used to describe the contrast in the legend.

Within each contrast, the genes are sorted by log fold-change if the column "logFC" is in the signifTable data.frame

Note that if whichCluster is NOT given (the default) then there is no automatic match of colors with contrasts based on the information in object.

Value

A heatmap is created. The output of plotHeatmap is returned.

See Also

plotHeatmap, makeBlankData, getBestFeatures

Examples

data(simData)

cl <- clusterSingle(simData, subsample=FALSE, sequential=FALSE, mainClusterArgs=list(clusterFunction="pam", clusterArgs=list(k=8)))

#Do all pairwise, only return significant, try different adjustments:
pairsPerC <- getBestFeatures(cl, contrastType="Pairs", number=5, p.value=0.05, DEMethod="limma")
plotContrastHeatmap(cl,pairsPerC)
Usage

```r
## S4 method for signature 'ClusterExperiment'
plotDendrogram(
  x,
  whichClusters = "dendro",
  leafType = c("samples", "clusters"),
  plotType = c("colorblock", "name", "ids"),
  mergeInfo = "none",
  main,
  sub,
  clusterLabelAngle = 45,
  removeOutbranch = TRUE,
  legend = c("side", "below", "none"),
  nodeColors = NULL,
  colData = NULL,
  clusterLegend = NULL,
  ...
)
```

Arguments

- `x` a `ClusterExperiment` object.
- `whichClusters` argument that can be either numeric or character vector indicating the clusterings to be used. See details of `getClusterIndex`.
- `leafType` if "samples" the dendrogram has one leaf per sample, otherwise it has one per cluster.
- `plotType` one of 'name', 'colorblock' or 'id'. If 'Name' then dendrogram will be plotted, and name of cluster or sample (depending on type of value for `leafType`) will be plotted next to the leaf of the dendrogram. If 'colorblock', rectangular blocks, corresponding to the color of the cluster will be plotted, along with cluster name legend. If 'id' the internal clusterIds value will be plotted (only appropriate if `leafType="clusters"`).
- `mergeInfo` What kind of information about merge to plot on dendrogram. If not equal to "none", will replicate the kind of plot that `mergeClusters` creates, and the input to `mergeInfo` corresponds to that of `plotInfo` in `mergeClusters`.
- `main` passed to the `plot.phylo` function to set main title.
- `sub` passed to the `plot.phylo` function to set subtitle.
- `clusterLabelAngle` angle at which label of cluster will be drawn. Only applicable if `plotType="colorblock"`.
- `removeOutbranch` logical, only applicable if there are missing samples (i.e. equal to -1 or -2), `leafType="samples"` and the dendrogram for the samples was made by putting missing samples in an outbranch. In which case, if this parameter is TRUE, the outbranch will not be plotted, and if FALSE it will be plotted.
- `legend` character, only applicable if `plotType="colorblock"`. Passed to `phydataplot` in `ape` package that is used to draw the color values of the clusters/samples next
to the dendrogram. Options are 'none', 'below', or 'side'. (Note 'none' is only available for 'ape' package >= 4.1-0.6).

nodeColors named vector of colors to be plotted on a node in the dendrogram (calls nodelabels). Names should match the internal name of the node (the "NodeId" value, see clusterDendrogram).

colData index (by integer or name) the sample data stored as a DataFrame in colData slot of the object. Only discrete valued ("character" or "factor" variables) will be plotted; indexing of continous variables will be ignored. Whether that data is continuous or not will be determined by the properties of colData (no user input is needed). This argument is only relevant if plotType="colorblock" and leafType="samples"

clusterLegend Assignment of colors to the clusters or sample data (as designated by colData argument) plotted with the dendrogram. If NULL or a particular variable/cluster are not assigned a color, colors will be assigned internally for sample data and pull from the clusterLegend slot of the x for the clusters.

... arguments passed to the plot.phylo function of ape that plots the dendrogram.

Details

If leafType="clusters", the plotting function will work best if the clusters in the dendrogram correspond to the primary cluster. This is because the function colors the cluster labels based on the colors of the clusterIds of the primaryCluster

Value

A dendrogram is plotted. Returns ( invisibly) a list with elements

- plottedObject the phylo object that is plotted.
- originalObject the phylo object before adjusting the node/tip labels.

See Also

mergeClusters,plot.phylo,nodelabels,tiplabels

Examples

data(simData)

# create a clustering, for 8 clusters (truth was 3)
cl <- clusterSingle(simData, subsample=FALSE, sequential=FALSE, mainClusterArgs=list(clusterFunction="pam", clusterArgs=list(k=8)))

# create dendrogram of clusters and then
# merge clusters based on dendrogram:
cl <- makeDendrogram(cl)
cl <- mergeClusters(cl,mergeMethod="adjP",DEMethod="limma",
cutoff=0.1,plot=FALSE)
plotDendrogram(cl)
plotFeatureBoxplot

Plot boxplot of feature values by cluster

Description
Plot a boxplot of the (transformed) values for a particular gene, separated by cluster

Usage
## S4 method for signature 'ClusterExperiment,character'
plotFeatureBoxplot(object, feature, whichCluster = "primary", ...)

## S4 method for signature 'ClusterExperiment,numeric'
plotFeatureBoxplot(
onject, feature, whichCluster = "primary", plotUnassigned = FALSE, unassignedColor = NULL, missingColor = NULL, main = NULL, whichAssay = 1, ...
)

Arguments
- object: a ClusterExperiment object
- feature: identification of feature to plot, either row name or index
- whichCluster: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of getClusterIndex.
- plotUnassigned: whether to plot the unassigned samples as a cluster (either -1 or -2)
- unassignedColor: If not NULL, should be character value giving the color for unassigned (-2) samples (overrides clusterLegend) default.
- missingColor: If not NULL, should be character value giving the color for missing (-2) samples (overrides clusterLegend) default.
- main: title of plot. If NULL, given default title.
- whichAssay: numeric or character specifying which assay to use. See assay for details.
Plot scatter plot of feature values colored by cluster

Description

Plot a scatter plot of the (transformed) values for a set of gene expression values, colored by cluster

Usage

```r
## S4 method for signature 'ClusterExperiment,character'
plotFeatureScatter(object, features, ...)

## S4 method for signature 'ClusterExperiment,numeric'
plotFeatureScatter(
  object,
  features,
  whichCluster = "primary",
  plotUnassigned = TRUE,
  unassignedColor = "grey",
  missingColor = "white",
  whichAssay = 1,
  legendLocation = NA,
  jitterFactor = NA,
  ...
)
```

Examples

```r
data(simData)
#Create a ClusterExperiment object
c1 <- clusterMany(simData, nReducedDims=c(5, 10, 50), reducedDim="PCA",
  clusterFunction="pam", ks=2:4, findBestK=c(TRUE,FALSE),
  removeSil=c(TRUE,FALSE), makeMissingDiss=TRUE)
#give names to the clusters
cl<-renameClusters(cl, whichCluster=1,
  value=letters[1:nClusters(cl)[1]])
plotFeatureBoxplot(cl,feature=1)
```
Arguments

- **object**: a ClusterExperiment object
- **features**: the indices of the features (either numeric or character matching rownames of object) to be plotted.
- **...**: arguments passed to boxplot
- **whichCluster**: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.
- **plotUnassigned**: whether to plot the unassigned samples as a cluster (either -1 or -2)
- **unassignedColor**: If not NULL, should be character value giving the color for unassigned (-2) samples (overrides clusterLegend) default.
- **missingColor**: If not NULL, should be character value giving the color for missing (-2) samples (overrides clusterLegend) default.
- **whichAssay**: numeric or character specifying which assay to use. See `assay` for details.
- **legendLocation**: character value passed to location argument of plotClusterLegend indicating where to put the legend. If NA, legend will not be plotted.
- **jitterFactor**: numeric. If NA, no jittering is done. Otherwise, passed to factor of function `jitter` (useful for low counts)

Value

returns invisibly the results of `pairs` or `plot` command.

Examples

```r
data(simData)
#Create a ClusterExperiment object
c1 <- clusterMany(simData, nReducedDims=c(5, 10, 50), reducedDim="PCA",
   clusterFunction="pam", ks=2:4, findBestK=c(TRUE,FALSE),
   removeSil=c(TRUE,FALSE), makeMissingDiss=TRUE)
#give names to the clusters
c1<-renameClusters(c1, whichCluster=1,
   value=letters[1:nClusters(c1)[1]])
plotFeatureScatter(c1,feature=1:2,pch=19,legendLocation="topright")
```

Description

Make heatmap with color scale from one matrix and hierarchical clustering of samples/features from another. Also built in functionality for showing the clusterings with the heatmap. Builds on `aheatmap` function of NMF package.
plotHeatmap

Usage

## S4 method for signature 'SingleCellExperiment'
plotHeatmap(data, isCount = FALSE, transFun = NULL, ...)

## S4 method for signature 'SummarizedExperiment'
plotHeatmap(data, isCount = FALSE, transFun = NULL, ...)

## S4 method for signature 'table'
plotHeatmap(data, ...)

## S4 method for signature 'ClusterExperiment'
plotHeatmap(
  data,
  clusterSamplesData = c("dendrogramValue", "hclust", "orderSamplesValue", "primaryCluster"),
  clusterFeaturesData = "var",
  nFeatures = NA,
  visualizeData = c("transformed", "centeredAndScaled", "original"),
  whichClusters = c("primary", "workflow", "all", "none"),
  colData = NULL,
  clusterFeatures = TRUE,
  nBlankLines = 2,
  colorScale,
  whichAssay = 1,
  ...
)

## S4 method for signature 'data.frame'
plotHeatmap(data, ...)

## S4 method for signature 'ExpressionSet'
plotHeatmap(data, ...)

## S4 method for signature 'matrixOrHDF5'
plotHeatmap(
  data,
  colData = NULL,
  clusterSamplesData = NULL,
  clusterFeaturesData = NULL,
  whColDataCont = NULL,
  clusterSamples = TRUE,
  showSampleNames = FALSE,
  clusterFeatures = TRUE,
  showFeatureNames = FALSE,
  colorScale = seqPal5,
  clusterLegend = NULL,
  alignColData = FALSE,
  unassignedColor = "white",
  ...)
missingColor = "grey",
breaks = NA,
symmetricBreaks = FALSE,
capBreaksLegend = FALSE,
isSymmetric = FALSE,
overRideClusterLimit = FALSE,
plot = TRUE,
labelTracks = TRUE,
...
)

## S4 method for signature 'ClusterExperiment'
plotCoClustering(data, invert, saveDistance = FALSE, ...)

Arguments

data data to use to determine the heatmap. Can be a matrix, ClusterExperiment, SingleCellExperiment or SummarizedExperiment object. The interpretation of parameters depends on the type of the input to data.

isCount if transFun=NULL, then isCount=TRUE will determine the transformation as defined by function(x){log2(x+1)}, and isCount=FALSE will give a transformation function function(x){x}. Ignored if transFun=NULL. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

transFun a transformation function to be applied to the data. If the transformation applied to the data creates an error or NA values, then the function will throw an error. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

... for signature matrix, arguments passed to aheatmap. For the other signatures, passed to the method for signature matrix. Not all arguments can be passed to aheatmap effectively, see details.

clusterSamplesData

If data is a matrix, clusterSamplesData is either a matrix that will be used by hclust to define the hierarchical clustering of samples (e.g. normalized data) or a pre-existing dendrogram (of class dendrogram) that clusters the samples. If data is a ClusterExperiment object, clusterSamplesData should be either character or integers or logical which indicates how (and whether) the samples should be clustered (or gives indices of the order for the samples). See details.

clusterFeaturesData

If data is a matrix, either a matrix that will be used in hclust to define the hierarchical clustering of features (e.g. normalized data) or a pre-existing dendrogram that clusters the features. If data is a ClusterExperiment object, the input should be either character or integers indicating which features should be used (see details).

nFeatures integer indicating how many features should be used (if clusterFeaturesData is 'var' or 'PCA').
either a character string, indicating what form of the data should be used for visualizing the data (i.e. for making the color-scale), or a data.frame/matrix with same number of samples as assay(data). If a new data.frame/matrix, any character arguments to clusterFeaturesData will be ignored.

whichClusters argument that can be either numeric or character vector indicating the clusterings to be used. See details of getClusterIndex.

colData If input to data is either a ClusterExperiment or SummarizedExperiment object or SingleCellExperiment, then colData must index the colData stored as a DataFrame in colData slot of the object. Whether that data is continuous or not will be determined by the properties of colData (no user input is needed). If input to data is matrix, colData is a matrix of additional data on the samples to show above heatmap. In this case, unless indicated by whColDataCont, colData will be converted into factors, even if numeric. “-1” indicates the sample was not assigned to a cluster and gets color ‘unassignedColor’ and “-2” gets the color ‘missingColor’.

colData columns will be assigned colors internally. See details for more.

Logical as to whether should align the colors of the colData (only if clusterLegend not given and colData is not NULL).

alignColData Logical as to whether to do hierarchical clustering of features (if FALSE, any input to clusterFeaturesData is ignored).

clusterFeatures

Logical as to whether to do hierarchical clustering of cells (if FALSE, any input to clusterSamplesData is ignored).

clusterSamples

Logical as to whether show sample names.

showSampleNames

Logical as to whether show feature names.

showFeatureNames

Assignment of colors to the clusters. If NULL, colData columns will be assigned colors internally. See details for more.

clusterLegend

color assigned to cluster values of ’-1’ (“unassigned”).

unassignedColor

color assigned to cluster values of ’-2’ (“missing”).

missingColor

Either a vector of breaks (should be equal to length 52), or a number between 0 and 1, indicating that the breaks should be equally spaced (based on the range in the data) up to the ‘breaks’ quantile, see setBreaks.

breaks

logical as to whether the breaks created for the color scale should be symmetrical around 0.

symmetricBreaks
capBreaksLegend

logical as to whether the legend for the breaks should be capped. Only relevant if breaks is a value < 1, in which case if capBreaksLegend=TRUE, only the values between the quantiles requested will show in the color scale legend.

isSymmetric

logical. If TRUE indicates that the input matrix is symmetric. Useful when plotting a co-clustering matrix or other sample by sample matrices (e.g., correlation).

overRideClusterLimit

logical. Whether to override the internal limit that only allows 10 clusterings/annotations. If overridden, may result in incomprehensible errors from aheatmap. Only override this if you have a very large plotting device and want to see if aheatmap can render it.

plot

logical indicating whether to plot the heatmap. Mainly useful for package maintenance to avoid calls to aheatmap on unit tests that take a long time.

labelTracks

logical, whether to put labels next to the color tracks corresponding to the colData.

invert

logical determining whether the coClustering matrix should be inverted to be 1-coClustering for plotting. By default, if the diagonal elements are all zero, invert=TRUE, and otherwise invert=FALSE. If coClustering matrix is not a 0-1 matrix (e.g. if equal to a distance matrix output from clusterSingle, then the user should manually set this parameter to FALSE.)

saveDistance

logical. When the coClustering slot contains indices of the clusterings or a NxB set of clusterings, the hamming distance will be calculated before running the plot. This argument determines whether the ClusterExperiment object with that distance in coClustering slot should be returned (so as to avoid recalculating it in the future) or not.

Details

The plotHeatmap function calls aheatmap to draw the heatmap. The main points of plotHeatmap are to 1) allow for different matrix inputs, separating out the color scale visualization and the clustering of the samples/features. 2) to visualize the clusters and meta data with the heatmap. The intended use case is to allow the user to visualize the original count scale of the data (on the log-scale), but create the hierarchical clustering on another, more appropriate dataset for clustering, such as normalized data. Similarly, some of the palettes in the package were developed assuming that the visualization might be on unscaled/uncentered data, rather than the residual from the mean of the gene, and thus palettes need to take on a greater range of relevant values so as to show meaningful comparisons with genes on very different scales.

If data is a ClusterExperiment object, visualizeData indicates what kind of transformation should be done to assay(data) for calculating the color scale. The features will be clustered based on these data as well. A different data.frame or matrix can be given for the visualization. For example, if the ClusterExperiment object contains normalized data, but the user wishes that the color scale be based on the log-counts for easier interpretation, visualizeData could be set to be the log2(counts + 1).

If data is a ClusterExperiment object, clusterSamplesData can be used to indicate the type of clustering for the samples. If equal to ‘dendrogramValue’ the dendrogram stored in data will be
used if dendrogram is missing, a new one will be created based on the primaryCluster of data using `makeDendrogram`, assuming no errors are created (if errors are created, then `clusterSamplesData` will be set to "primaryCluster"). If `clusterSamplesData` is equal to "hclust", then standard hierarchical clustering of the transformed data will be used. If `clusterSamplesData` is equal to 'orderSamplesValue' no clustering of the samples will be done, and instead the samples will be ordered as in the slot `orderSamples` of data. If `clusterSamplesData` is equal to 'primaryCluster', again no clustering will be done, and instead the samples will be ordered based on grouping the samples to match the primaryCluster of data; however, if the primaryCluster of data is only one cluster or consists solely of -1/-2 values, `clusterSamplesData` will be set to "hclust". If `clusterSamplesData` is not a character value, `clusterSamplesData` can be an integer valued vector giving the order of the samples.

If `data` is a matrix, then `colData` is a data.frame of annotation data to be plotted above the heatmap and `whColDataCont` gives the index of the column(s) of this dataset that should be considered continuous. Otherwise the annotation data for `colData` will be forced into a factor (which will be nonsensical for continuous data). If `data` is a ClusterExperiment object, `colData` should refer to a index or column name of the `colData` slot of data. In this case `colData` will be added to any choices of clusterings chosen by the `whichClusters` argument (if any). If both clusterings and sample data are chosen, the clusterings will be shown closest to data (i.e. on bottom).

If `data` is a ClusterExperiment object, `clusterFeaturesData` is not a dataset, but instead indicates which features should be shown in the heatmap. In this case `clusterFeaturesData` can be one of the following:

- "all" All rows/genes will be shown
- character giving dimensionality reduction Should match one of values saved in `reducedDims` slot or a builtin function in `listBuiltInReducedDims()`. `nFeatures` then gives the number of dimensions to show. The heatmap will then be of the dimension reduction vectors
- character giving filtering Should match one of values saved in `filterStats` slot or a builtin function in `listBuiltInFilterStats()`. `nFeatures` gives the number of genes to keep after filtering.
- character giving gene/row names
- vector of integers giving row indices
- a list of indices or rownames This is used to indicate that the features should be grouped according to the elements of the list, with blank (white) space between them (see `makeBlankData` for more details). In this case, no clustering is done of the features.

If `breaks` is a numeric value between 0 and 1, then `breaks` is assumed to indicate the upper quantile (on the log scale) at which the heatmap color scale should stop. For example, if `breaks=0.9`, then the breaks will evenly spaced up until the 0.9 upper quantile of data, and then all values after the 0.9 quantile will be absorbed by the upper-most color bin. This can help to reduce the visual impact of a few highly expressed genes (features).

Note that `plotHeatmap` calls `aheatmap` under the hood. This allows you to plot multiple heatmaps via `par(mfrow=c(2,2))`, etc. However, the dendrograms do not resize if you change the size of your plot window in an interactive session of R (this might be a problem for RStudio if you want to pop it out into a large window...). Also, plotting to a pdf adds a blank page; see help pages of `aheatmap` for how to turn this off.

`clusterLegend` takes the place of argument `annColors` from `aheatmap` for giving colors to the annotation on the heatmap. `clusterLegend` should be list of length equal to `ncol(colData)` with
names equal to the colnames of colData. Each element of the list should be a either the format requested by `aheatmap` (a vector of colors with names corresponding to the levels of the column of colData), or should be format of the clusterLegend slot in a ClusterExperiment object. Color assignments to the rows/genes should also be passed via clusterLegend (assuming annRow is an argument passed to ...). If clusterFeaturesData is a named list describing groupings of genes then the colors for those groups can be given in clusterLegend under the name "Gene Group".

If you have a factor with many levels, it is important to note that `aheatmap` does not recycle colors across factors in the colData, and in fact runs out of colors and the remaining levels get the color white. Thus if you have many factors or many levels in those factors, you should set their colors via clusterLegend.

Many arguments can be passed on to `aheatmap`, however, some are set internally by `plotHeatmap`. In particular, setting the values of Rowv or Colv will cause errors. color in `aheatmap` is replaced by colorScale in `plotHeatmap`. The annCol to give annotation to the samples is replaced by the colData; moreover, the annColors option in `aheatmap` will also be set internally to give more vibrant colors than the default in `aheatmap` (for ClusterExperiment objects, these values can also be set in the clusterLegend slot). Other options should be passed on to `aheatmap`, though they have not been all tested. Useful options include treeheight=0 to suppress plotting of the dendrograms, annLegend=FALSE to suppress the legend of factors shown beside columns/rows, and cexRow=0 or cexCol=0 to suppress plotting of row/column labels.

`plotCoClustering` is a convenience function to plot the heatmap of the co-clustering distance matrix from the coClustering slot of a ClusterExperiment object (either by calculating the hamming distance of the clusterings stored in the coClustering slot, or the distance stored in the coClustering slot if it has already been calculated).

**Value**

Returns (invisibly) a list with elements

- aheatmapOut The output from the final call of `aheatmap`.
- colData the annotation data.frame given to the argument annCol in `aheatmap`.
- clusterLegend the annotation colors given to the argument annColors `aheatmap`.
- breaks The breaks used for `aheatmap`, after adjusting for quantile.

**Author(s)**

Elizabeth Purdom

**See Also**

`aheatmap, makeBlankData, showHeatmapPalettes, makeDendrogram, dendrogram`

**Examples**

```r
## Not run:
data(simData)
c1 <- rep(1:3,each=100)
c12 <- c1
```
changeAssign <- sample(1:length(cl), 80)
c12[changeAssign] <- sample(cl[changeAssign])
ce <- ClusterExperiment(simCount, c12, transformation=function(x){log2(x+1)})

#simple, minimal, example. Show counts, but cluster on underlying means
plotHeatmap(ce)

#assign cluster colors
colors <- bigPalette[20:23]
names(colors) <- 1:3
plotHeatmap(data=simCount, clusterSamplesData=simData,
colData=data.frame(cl), clusterLegend=list(colors))

#show two different clusters
anno <- data.frame(cluster1=cl, cluster2=c12)
out <- plotHeatmap(simData, colData=anno)

#return the values to see format for giving colors to the annotations
out$clusterLegend

#assign colors to the clusters based on plotClusters algorithm
plotHeatmap(simData, colData=anno, alignColData=TRUE)

#assign colors manually
annoColors <- list(cluster1=c("black", "red", "green"),
cluster2=c("blue","purple","yellow"))
plotHeatmap(simData, colData=anno, clusterLegend=annoColors)

#give a continuous valued -- need to indicate columns
anno2 <- cbind(anno, Cont=c(rnorm(100, 0), rnorm(100, 2), rnorm(100, 3)))
plotHeatmap(simData, colData=anno2, whColDataCont=3)

#compare changing breaks quantile on visual effect
par(mfrow=c(2,2))
plotHeatmap(simData, colorScale=seqPal1, breaks=1, main="Full length")
plotHeatmap(simData,colorScale=seqPal1, breaks=.99, main="0.99 Quantile Upper Limit")
plotHeatmap(simData,colorScale=seqPal1, breaks=.95, main="0.95 Quantile Upper Limit")
plotHeatmap(simData, colorScale=seqPal1, breaks=.90, main="0.90 Quantile Upper Limit")

## End(Not run)

---

**plotReducedDims**

*Plot 2-dimensional representation with clusters*

**Description**

Plot a 2-dimensional representation of the data, color-code by a clustering.
Usage

```r
## S4 method for signature 'ClusterExperiment'
plotReducedDims(
  object,
  whichCluster = "primary",
  reducedDim = "PCA",
  whichDims = c(1, 2),
  plotUnassigned = TRUE,
  legend = TRUE,
  legendTitle = "",
  nColLegend = 6,
  clusterLegend = NULL,
  unassignedColor = NULL,
  missingColor = NULL,
  pch = 19,
  xlab = NULL,
  ylab = NULL,
  ...
)
```

Arguments

- **object**: a ClusterExperiment object
- **whichCluster**: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.
- **reducedDim**: What dimensionality reduction method to use. Should match either a value in `reducedDimNames(object)` or one of the built-in functions of `listBuiltInReducedDims()`.
- **whichDims**: vector of length 2 giving the indices of which dimensions to show. The first value goes on the x-axis and the second on the y-axis.
- **plotUnassigned**: logical as to whether unassigned (either -1 or -2 cluster values) should be plotted.
- **legend**: either logical, indicating whether to plot legend, or character giving the location of the legend (passed to `legend`).
- **legendTitle**: character value giving title for the legend. If NULL, uses the clusterLabels value for clustering.
- **nColLegend**: The number of columns in legend. If missing, picks number of columns internally.
- **clusterLegend**: matrix with three columns and colnames 'clusterIds', 'name', and 'color' that give the color and name of the clusters in whichCluster. If NULL, pulls the information from object.
- **unassignedColor**: If not NULL, should be character value giving the color for unassigned (-1) samples (overrides `clusterLegend`) default.
- **missingColor**: If not NULL, should be character value giving the color for missing (-2) samples (overrides `clusterLegend`) default.
plottingFunctions

pch  the point type, passed to plot.default
xlab  Label for x axis
ylab  Label for y axis
...  arguments passed to plot.default

Details

If plotUnassigned=TRUE, and the color for -1 or -2 is set to "white", will be coerced to "lightgrey" regardless of user input to missingColor and unassignedColor. If plotUnassigned=FALSE, the samples with -1/-2 will not be plotted, nor will the category show up in the legend.

If the requested reducedDim method has not been created yet, the function will call makeReducedDims on the FIRST assay of x. The results of this method will be saved as part of the object and returned INVISIBLY (meaning if you don’t save the output of the plotting command, the results will vanish). To pick another assay, you should call ‘makeReducedDims’ directly and specify the assay.

Value

A plot is created. Nothing is returned.

See Also

plot.default, makeReducedDims, listBuiltInReducedDims()

Examples

#clustering using pam: try using different dimensions of pca and different k
data(simData)

c1 <- clusterMany(simData, nReducedDims=c(5, 10, 50), reducedDim="PCA",
clusterFunction="pam", ks=2:4, findBestK=c(TRUE, FALSE),
removeSil=c(TRUE, FALSE), makeMissingDiss=TRUE)

plotReducedDims(c1, legend="bottomright")

plottingFunctions  Convert clusterLegend into useful formats

Description

Function for converting the information stored in the clusterLegend slot into other useful formats. Most of these functions are called internally by plotting functions, but are exported in case the user finds them useful.
Usage

makeBlankData(
  data,
  groupsOfFeatures = NULL,
  groupsOfSamples = NULL,
  nBlankFeatures = 1,
  nBlankSamples = 1
)

## S4 method for signature 'ClusterExperiment'
convertClusterLegend(
  object,
  output = c("plotAndLegend", "aheatmapFormat", "matrixNames", "matrixColors"),
  whichClusters = ifelse(output == "plotAndLegend", "primary", "all")
)

showPalette(colPalette = bigPalette, which = NULL, cex = 1)

bigPalette

massivePalette

setBreaks(data, breaks = NA, makeSymmetric = FALSE, returnBreaks = TRUE)

showHeatmapPalettes()

seqPal5

seqPal2

seqPal3

seqPal4

seqPal1

## S4 method for signature 'ClusterExperiment'
plotClusterLegend(
  object,
  whichCluster = "primary",
  clusterNames,
  title,
  add = FALSE,
  location = if (add) "topright" else "center",
  ...
)
Arguments

data
  matrix with samples on columns and features on rows.
groupsOfFeatures
  list, with each element of the list containing a vector of numeric indices of features (rows).
groupsOfSamples
  list, with each element of the list containing a vector of numeric indices of samples (columns).
nBlankFeatures
  the number of blank lines to add in the data matrix to separate the groups of feature indices (will govern the amount of white space if data is then fed to heatmap.)
nBlankSamples
  the number of blank lines to add in the data matrix to separate the groups of sample indices (will govern the amount of white space if data is then fed to heatmap.)
object
  a ClusterExperiment object.
output
  character value, indicating desired type of conversion.
whichClusters
  argument that can be either numeric or character vector indicating the clusterings to be used. See details of getClusterIndex.
colPalette
  a vector of character colors. By default, the palette bigPalette is used
which
  numeric. Which colors to plot. Must be a numeric vector with values between 1 and length of colPalette. If missing, all colors plotted.
cex
  numeric value giving the cex for the text of the plot.
b breaks
  either vector of breaks, or number of breaks (integer) or a number between 0 and 1 indicating a quantile, between which evenly spaced breaks should be calculated. If missing or NA, will determine evenly spaced breaks in the range of the data.
makeSymmetric
  whether to make the range of the breaks symmetric around zero (only used if not all of the data is non-positive and not all of the data is non-negative)
returnBreaks
  logical as to whether to return the vector of breaks. See details.
whichCluster
  argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of getClusterIndex.
clusterNames
  vector of names for the clusters; vector should have names that correspond to the clusterIds in the ClusterExperiment object. If this argument is missing, will use the names in the "name" column of the clusterLegend slot of the object.
title
  title for the clusterLegend plot
add
  logical. Whether legend should be added to the existing plot.
location
  character passed to x argument of legend indicating where to place legend.
...
  arguments passed to legend
Format

An object of class character of length 56.
An object of class character of length 484.
An object of class character of length 16.
An object of class character of length 14.
An object of class character of length 11.
An object of class character of length 11.

Details

makeBlankData pulls the data corresponding to the row indices in groupsOfFeatures adds lines of NA values into data between these groups. When given to heatmap, will create white space between these groups of features.

convertClusterLegend pulls out information stored in the clusterLegend slot of the object and returns it in useful format.

bigPalette is a long palette of colors (length 58) used by plotClusters and accompanying functions. showPalette creates plot that gives index of each color in a vector of colors. massivePalette is a combination of bigPalette and the non-grey colors of colors() (length 487). massivePalette is mainly useful for when doing plotClusters of a very large number of clusterings, each with many clusters, so that the code doesn’t run out of colors. However, many of the colors will be very similar to each other.

showPalette will plot the colPalette colors with their labels and index.

if returnBreaks if FALSE, instead of returning the vector of breaks, the function will just return the second smallest and second largest value of the breaks. This is useful for alternatively just setting values of the data matrix larger than these values to this value if breaks was a percentile. This argument is only used if breaks<1, indicating truncating the breaks for large values of data.

setBreaks gives a set of breaks (of length 52) equally spaced between the boundaries of the data. If breaks is between 0 and 1, then the evenly spaced breaks are between these quantiles of the data.

seqPal1-seqPal4 are palettes for the heatmap. showHeatmapPalettes will show you these palettes.

Value

makeBlankData returns a list with items

- "dataWBlanks" The data with the rows of NAs separating the given indices.
- "rowNamesWBlanks" A vector of characters giving the rownames for the data, including blanks for the NA rows. These are not given as rownames to the returned data because they are not necessarily unique. However, they can be given to the labRow argument of heatmap or plotHeatmap.
- "colNamesWBlanks" A vector of characters giving the colnames for the data, including blanks for the NA rows. They can be given to the labCol argument of heatmap or plotHeatmap.
• "featureGroupNamesWBlanks" A vector of characters of the same length as the number of rows of the new data (i.e. with blanks) giving the group name for the data, indicating which group (i.e. which element of groupsOfFeatures list) the feature came from. If groupsOfFeatures has unique names, these names will be used, otherwise "Feature Group1", "Feature Group2", etc. The NA rows are given NA values.

• "sampleGroupNamesWBlanks" A vector of characters of the same length as the number of columns of the new data (i.e. with blanks) giving the group name for the data, indicating which group (i.e. which element of groupsOfFeatures list) the feature came from. If groupsOfFeatures has unique names, these names will be used, otherwise "SampleGroup1", "Group2", etc. The NA rows are given NA values.

If output="plotAndLegend", "convertClusterLegend" will return a list that provides the necessary information to color samples according to cluster and create a legend for it:

• "colorVector" A vector the same length as the number of samples, assigning a color to each cluster of the primaryCluster of the object.

• "legendNames" A vector the length of the number of clusters of primaryCluster of the object giving the name of the cluster.

• "legendColors" A vector the length of the number of clusters of primaryCluster of the object giving the color of the cluster.

If output="aheatmap" a conversion of the clusterLegend to be in the format requested by aheatmap. The column 'name' is used for the names and the column 'color' for the color of the clusters.

If output="matrixNames" or "matrixColors" a matrix the same dimension of clusterMatrix(object), but with the cluster color or cluster name instead of the clusterIds, respectively.

See Also
plotHeatmap

Examples

data(simData)

x <- makeBlankData(simData[,1:10], groupsOfFeatures=list(c(5, 2, 3), c(20, 34, 25)))

plotHeatmap(x$dataWBlanks, clusterFeatures=FALSE)

showPalette()

showPalette(massivePalette,cex=0.6)

setBreaks(data=simData,breaks=.9)

#show the palette colors

showHeatmapPalettes()

#compare the palettes on heatmap

c1 <- clusterSingle(simData, subsample=FALSE, sequential=FALSE, mainClusterArgs=list(clusterFunction="pam", clusterArgs=list(k=8)))

## Not run:
renameClusters  

Change assigned names or colors of clusters

Description

Change the assigned names or colors of the clusters in a clustering stored in the clusterLegend slot of the object.

Usage

```r
## S4 method for signature 'ClusterExperiment,character'
renameClusters(
  object,
  value,
  whichCluster = "primary",
  matchTo = c("name", "clusterIds")
)
```

```r
## S4 method for signature 'ClusterExperiment,character'
recolorClusters(
  object,
  value,
  whichCluster = "primary",
  matchTo = c("name", "clusterIds")
)
```

Arguments

- `value`: The value to be substituted in the corresponding slot. See the slot descriptions in `ClusterExperiment` for details on what objects may be passed to these functions.
- `whichCluster`: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.
- `matchTo`: whether to match to the cluster name ("name") or internal cluster id ("clusterIds")
Value

renameClusters changes the names assigned to clusters within a clustering
recolorClusters changes the colors assigned to clusters within a clustering

Examples

# create CE object
data(simData)
c11 <- clusterSingle(simData, subsample=FALSE,
  sequential=FALSE, mainClusterArgs=list(clusterArgs=list(k=3),
  clusterFunction="pam"))
# Give names to the clusters
clusterLegend(c11)
c11<-renameClusters(c11, c("1"="A","2"="B","3"="C"), matchTo="clusterIds")
clusterLegend(c11)
# Change name of single one
cl1<-renameClusters(cl11, c("1"="D"), matchTo="clusterIds")
clusterLegend(cl1)
# Match to existing name, rather than clusterId
cl1<-renameClusters(cl11, c("B"="N"), matchTo="name")
clusterLegend(cl1)
# Change colors in similar way
cl1<-recolorClusters(cl11, c("N"="red"),matchTo=c("name"))
clusterLegend(cl1)

Description

Implementation of the RSEC algorithm (Resampling-based Sequential Ensemble Clustering) for single cell sequencing data. This is a wrapper function around the existing ClusterExperiment workflow that results in the output of RSEC.

Usage

---

# S4 method for signature 'SummarizedExperiment'
RSEC(x, ...)

# S4 method for signature 'data.frame'
RSEC(x, ...)

# S4 method for signature 'ClusterExperiment'
RSEC(x, eraseOld = FALSE, rerunClusterMany = FALSE, ...)

# S4 method for signature 'matrixOrHDF5'
RSEC(x, ...)
## S4 method for signature 'SingleCellExperiment'

RSEC(
  x,
  isCount = FALSE,
  transFun = NULL,
  reduceMethod = "PCA",
  nFilterDims = defaultNDims(x, reduceMethod, type = "filterStats"),
  nReducedDims = defaultNDims(x, reduceMethod, type = "reducedDims"),
  k0s = 4:15,
  subsample = TRUE,
  sequential = TRUE,
  clusterFunction = "hierarchical01",
  alphas = c(0.1, 0.2, 0.3),
  betas = 0.9,
  minSizes = 1,
  makeMissingDiss = if (ncol(x) < 1000) TRUE else FALSE,
  consensusProportion = 0.7,
  consensusMinSize,
  dendroReduce,
  dendroNDims,
  mergeMethod = "adjP",
  mergeCutoff,
  mergeLogFCcutoff,
  mergeDEMethod = if (isCount) "limma-voom" else "limma",
  verbose = FALSE,
  parameterWarnings = FALSE,
  mainClusterArgs = NULL,
  subsampleArgs = NULL,
  seqArgs = NULL,
  consensusArgs = NULL,
  whichAssay = 1,
  ncores = 1,
  random.seed = NULL,
  stopOnErrors = FALSE,
  run = TRUE
)

**Arguments**

- **x**: the data matrix on which to run the clustering. Can be object of the following classes: matrix (with genes in rows), **SummarizedExperiment**, **SingleCellExperiment** or **ClusterExperiment**.

- **...**: For signature matrix, arguments to be passed on to mclapply (if ncores>1). For all the other signatures, arguments to be passed to the method for signature matrix.

- **eraseOld**: logical. Only relevant if input `x` is of class `ClusterExperiment`. If TRUE, will erase existing workflow results (clusterMany as well as mergeClusters and makeConsensus). If FALSE, existing workflow results will have ".i" added.
to the clusterTypes value, where i is one more than the largest such existing workflow clusterTypes.

rerunClusterMany
logical. If the object is a ClusterExperiment object, determines whether to rerun the clusterMany step. Useful if want to try different parameters for combining clusters after the clusterMany step, without the computational costs of the clusterMany step.

isCount
if transFun=NULL, then isCount=TRUE will determine the transformation as defined by function(x){log2(x+1)}, and isCount=FALSE will give a transformation function function(x){x}. Ignored if transFun=NULL. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

transFun
a transformation function to be applied to the data. If the transformation applied to the data creates an error or NA values, then the function will throw an error. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.

reduceMethod
character A character identifying what type of dimensionality reduction to perform before clustering. Options are 1) "none", 2) one of listBuiltInReducedDims() or listBuiltInFilterStats OR 3) stored filtering or reducedDim values in the object.

nFilterDims
vector of the number of the most variable features to keep (when "var", "abscv", or "mad" is identified in reduceMethod).

nReducedDims
vector of the number of dimensions to use (when reduceMethod gives a dimensionality reduction method).

k0s
the k0 parameter for sequential clustering (see seqCluster)

subsample
logical as to whether to subsample via subsampleClustering. If TRUE, clustering in mainClustering step is done on the co-occurrence between clusterings in the subsampled clustering results. If FALSE, the mainClustering step will be run directly on x/diss

sequential
logical whether to use the sequential strategy (see details of seqCluster). Can be used in combination with subsample=TRUE or FALSE.

clusterFunction
function used for the clustering. This must be either 1) a character vector of built-in clustering techniques, or 2) a named list of ClusterFunction objects. Current functions can be found by typing listBuiltInFunctions() into the command-line.

alphas
values of alpha to be tried. Only used for clusterFunctions of type '01'. Determines tightness required in creating clusters from the dissimilarity matrix. Takes on values in [0,1]. See documentation of ClusterFunction.

betas
values of beta to be tried in sequential steps. Only used for sequential=TRUE. Determines the similarity between two clusters required in order to deem the cluster stable. Takes on values in [0,1]. See documentation of seqCluster.

minSizes
the minimum size required for a cluster (in the mainClustering step). Clusters smaller than this are not kept and samples are left unassigned.
**makeMissingDiss**
logical. Whether to calculate necessary distance matrices needed when input is not "diss". If TRUE, then when a clustering function calls for an inputType "diss", but the given matrix is of type "X", the function will calculate a distance function. A dissimilarity matrix will also be calculated if a post-processing argument like `findBestK` or `removeSil` is chosen, since these rely on calculating silhouette widths from distances.

**consensusProportion**
passed to proportion in `makeConsensus`

**consensusMinSize**
passed to `minSize` in `makeConsensus`

**dendroReduce**
passed to `reduceMethod` in `makeDendrogram`

**dendroNDims**
passed to `nDims` in `makeDendrogram`

**mergeMethod**
passed to `mergeMethod` in `mergeClusters`

**mergeCutoff**
passed to `cutoff` in `mergeClusters`

**mergeLogFCcutoff**
passed to `logFCcutoff` in `mergeClusters`

**mergeDEMethod**
passed to `DEMethod` argument in `mergeClusters`. By default, unless otherwise chosen by the user, if `isCount=TRUE`, then `mergeDEMethod="limma-voom"`, otherwise `mergeDEMethod="limma"`. These choices are for speed considerations and the user may want to try `mergeDEMethod="edgeR"` on smaller datasets of counts.

**verbose**
logical. If TRUE it will print informative messages.

**parameterWarnings**
logical, as to whether warnings and comments from checking the validity of the parameter combinations should be printed.

**mainClusterArgs**
list of arguments to be passed for the mainClustering step, see help pages of `mainClustering`.

**subsampleArgs**
list of arguments to be passed to the subsampling step (if `subsample=TRUE`), see help pages of `subsampleClustering`.

**seqArgs**
list of arguments to be passed to `seqCluster`.

**consensusArgs**
list of additional arguments to be passed to `makeConsensus`

**whichAssay**
numeric or character specifying which assay to use. See `assay` for details.

**ncores**
the number of threads

**random.seed**
a value to set seed before each run of `clusterSingle` (so that all of the runs are run on the same subsample of the data). Note, if `random.seed` is set, argument 'ncores' should NOT be passed via `subsampleArgs`; instead set the argument 'ncores' of `clusterMany` directly (which is preferred for improving speed anyway).

**stopOnErrors**
logical. If FALSE, if RSEC hits an error after the `clusterMany` step, it will return the results up to that point, rather than generating a stop error. The text of error will be printed as a NOTE. This allows the user to get the results to that point, so as to not have to rerun the computationally heavy earlier steps. The TRUE option is only provided for debugging purposes.
logical. If FALSE, doesn’t run clustering, but just returns matrix of parameters that will be run, for the purpose of inspection by user (with rownames equal to the names of the resulting column names of clMat object that would be returned if run=TRUE). Even if run=FALSE, however, the function will create the dimensionality reductions of the data indicated by the user input.

Details
Note that the argument isCount is mainly used when the input is a matrix or SingleCellExperiment Class and passed to clusterMany to set the transformation function of the data. However, if RSEC is being re-called on an existing ClusterExperiment object, it does not reset the transformation; in this case the only impact it will have is in setting the default value for DEMethod for mergeClusters step, but ONLY if mergeClusters hasn’t already been calculated. To set arguments that allow you to recalculate the non-null probabilities of the hierarchy see mergeClusters.

Value
A ClusterExperiment object is returned containing all of the clusterings from the steps of RSEC

rsecFluidigm
documentation of rsecFluidigm object

description
Documentation of the creation of rsecFluidigm, result of RSEC run on fluidigm data for vignette

Usage
makeRsecFluidigmObject(object)

Arguments
object object given to functions

Format
rsecFluidigm is a ClusterExperiment object, the result of running RSEC on fluidigm data described in vignette and available in the scRNAseq package.

Details
The functions makeRsecFluidigmObject and checkRsecFluidigmObject are helper functions whose sole purpose is to create rsecFluidigm and check that the results are the same as expected. makeRsecFluidigmObject also serves as documentation of the specific RSEC call that was made to create the rsecFluidigm object, as well as filtering and normalization of the fluidigm data. The purpose of making them functions is internal, to help more easily maintain and check if changes to the package have affected the results.
Author(s)

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See Also

fluidigm.

Examples

# see code used create rsecFluidigm
# (print out the function)
makeRsecFluidigmObject
#code actualy run to create rsecFluidigm:
## Not run:
library(clusterExperiment)
data(fluidigmData)
data(fluidigmColData)
se<-SummarizedExperiment(assays=fluidigmData, colData=fluidigmColData)
RNGversion("3.5.0")
rsecFluidigm<-makeRsecFluidigmObject(se)
# Internal function for checking got correct results...
clusterExperiment:::checkRsecFluidigmObject(rsecFluidigm)
usethis::use_data(rsecFluidigm,overwrite=FALSE)

## End(Not run)

search_pairs

Search pairs of samples that co-cluster across subsamples

Description

Assume that our input is a matrix, with N columns and B rows (the number of subsamples), storing integers – the cluster labels.

Usage

search_pairs(clusterings)

Arguments

clusterings         a matrix with the cluster labels

Value

A matrix with the co-clusters, but only the lower triangle is populated.
seqCluster

Program for sequentially clustering, removing cluster, and starting again.

Description

Given a data matrix, this function will call clustering routines, and sequentially remove best clusters, and iterate to find clusters.

Usage

seqCluster(
  inputMatrix,
  inputType,
  k0,
  subsample = TRUE,
  beta,
  top.can = 0.01,
  remain.n = 30,
  k.min = 3,
  k.max = k0 + 10,
  verbose = TRUE,
  subsampleArgs = NULL,
  mainClusterArgs = NULL,
  warnings = FALSE
)

Arguments

inputMatrix  numerical matrix on which to run the clustering or a SummarizedExperiment, SingleCellExperiment, or ClusterExperiment object.

inputType  a character vector defining what type of input is given in the inputMatrix argument. Must consist of values "diss","X", or "cat" (see details). "X" and "cat" should be indicate matrices with features in the row and samples in the column; "cat" corresponds to the features being numerical integers corresponding to categories, while "X" are continuous valued features. "diss" corresponds to an inputMatrix that is a NxN dissimilarity matrix. "cat" is largely used internally for clustering of sets of clusterings.

k0  the value of K at the first iteration of sequential algorithm, see details below or vignette.

subsample  logical as to whether to subsample via subsampleClustering to get the distance matrix at each iteration; otherwise the distance matrix is set by arguments to mainClustering.

beta  value between 0 and 1 to decide how stable clustership membership has to be before 'finding' and removing the cluster.
seqCluster

`top.can` only the top.can clusters from `mainClustering` (ranked by 'orderBy' argument given to `mainClustering`) will be compared pairwise for stability. Can be either an integer value, identifying the absolute number of clusters, or a value between 0 and 1, meaning to keep all clusters with at least this proportion of the remaining samples in the cluster. Making this either a very big integer or equal to 0 will effectively remove this parameter and all pairwise comparisons of all clusters found will be considered; this might result in smaller clusters being found. If top.can is between 0 and 1, then there is still a hard threshold of at least 5 samples in a cluster to be considered as a cluster.

`remain.n` when only this number of samples are left (i.e. not yet clustered) then algorithm will stop.

`k.min` each iteration of sequential detection of clustering will decrease the beginning K of subsampling, but not lower than k.min.

`k.max` algorithm will stop if K in iteration is increased beyond this point.

`verbose` whether the algorithm should print out information as to its progress.

`subsampleArgs` list of arguments to be passed to `subsampleClustering`.

`mainClusterArgs` list of arguments to be passed to `mainClustering`.

`warnings` logical. Whether to print out the many possible warnings and messages regarding checking the internal consistency of the parameters.

Details

seqCluster is not meant to be called by the user. It is only an exported function so as to be able to clearly document the arguments for seqCluster which can be passed via the argument `seqArgs` in functions like `clusterSingle` and `clusterMany`.

This code is adapted from the sequential portion of the code of the tightClust package of Tseng and Wong. At each iteration of the algorithm it finds a set of samples that constitute a homogeneous cluster and remove them, and iterate again to find the next set of samples that form a cluster.

In each iteration, to determine the next set of homogeneous set of samples, the algorithm will iteratively cluster the current set of samples for a series of increasing values of the parameter $K$, starting at a value `kinit` and increasing by 1 at each iteration, until a sufficiently homogeneous set of clusters is found. For the first set of homogeneous samples, `kinit` is set to the argument `k0`, and for iteration, `kinit` is increased internally.

Depending on the value of `subsample` how the value of $K$s is used differs. If `subsample=TRUE`, $K$s is the $k$ sent to the cluster function `clusterFunction` sent to `subsampleClustering` via `subsampleArgs`; then `mainClustering` is run on the result of the co-occurrence matrix from `subsampleClustering` with the `ClusterFunction` object defined in the argument `clusterFunction` set via `mainClusterArgs`. The number of clusters actually resulting from this run of `mainClustering` may not be equal to the $K$s sent to the clustering done in `subsampleClustering`. If `subsample=FALSE`, `mainClustering` is called directly on the data to determine the clusters and $K$s set by seqCluster for this iteration determines the parameter of the clustering done by `mainClustering`. Specifically, the argument `clusterFunction` defines the clustering of the `mainClustering` step and $k$ is sent to that `ClusterFunction` object. This means that if `subsample=FALSE`, the `clusterFunction` must be of `algorithmType"K"`. 
In either setting of subsample, the resulting clusters from `mainClustering` for a particular $K$ will be compared to clusters found in the previous iteration of $K-1$. For computational (and other?) convenience, only the first `top.can` clusters of each iteration will be compared to the first `top.can` clusters of previous iteration for similarity (where `top.can` currently refers to ordering by size, so first `top.can` largest clusters.

If there is no cluster of the first `top.can` in the current iteration $K$ that has overlap similarity > $\beta$ to any in the previous iteration, then the algorithm will move to the next iteration, increasing to $K+1$.

If, however, of these clusters there is a cluster in the current iteration $K$ that has overlap similarity > $\beta$ to a cluster in the previous iteration $K-1$, then the cluster with the largest such similarity will be identified as a homogenous set of samples and the samples in it will be removed and designated as such. The algorithm will then start again to determine the next set of homogenous samples, but without these samples. Furthermore, in this case (i.e. a cluster was found and removed), the value of `kinit` will be be reset to `kinit-1`; i.e. the range of increasing $K$s that will be iterated over to find a set of homogenous samples will start off one value less than was the case for the previous set of homogeneous samples. If `kinit-1<k.min`, then `kinit` will be set to `k.min`.

If there are less than `remain.n` samples left after finding a cluster and removing its samples, the algorithm will stop, as subsampling is deemed to no longer be appropriate. If the $K$ has to be increased beyond $k.max$ without finding any pair of clusters with overlap > $\beta$, then the algorithm will stop. Any samples not found as part of a homogenous set of clusters at that point will be classified as unclustered (given a value of `-1`)

Certain combinations of inputs to `mainClusterArgs` and `subsampleArgs` are not allowed. See `clusterSingle` for these explanations.

**Value**

A list with values

- `clustering` a vector of length equal to `nrows(x)` giving the integer-valued cluster ids for each sample. The integer values are assigned in the order that the clusters were found. "-1" indicates the sample was not clustered.
- `clusterInfo` if clusters were successfully found, a matrix of information regarding the algorithm behavior for each cluster (the starting and stopping $K$ for each cluster, and the number of iterations for each cluster).
- `whyStop` a character string explaining what triggered the algorithm to stop.

**References**

Tseng and Wong (2005), "Tight Clustering: A Resampling-Based Approach for Identifying Stable and Tight Patterns in Data", Biometrics, 61:10-16.

**See Also**

tight.clust, `clusterSingle`, `mainClustering`, `subsampleClustering`
## Not run:
data(simData)

set.seed(12908)
clustSeqHier <- seqCluster(simData, inputType="X", k0=5, subsample=TRUE,
                         beta=0.8, subsampleArgs=list(resamp.n=100,
                         samp.p=0.7, clusterFunction="kmeans", clusterArgs=list(nstart=10)),
                         mainClusterArgs=list(minSize=5,clusterFunction="hierarchical01",
                         clusterArgs=list(alpha=0.1)))

## End(Not run)

---

**simData**

*Simulated data for running examples*

---

### Description

Simulated data for running examples

### Format

Three objects are loaded, two data frame(s) of simulated data each with 300 samples/columns and 153 variables/rows, and a vector of length 300 with the true cluster assignments.

### Details

**simData** is simulated normal data of 300 observations with 51 relevant variables and the rest of the variables being noise, with observations being in one of 3 groups. **simCount** is simulated count data of the same dimensions. **trueCluster** gives the true cluster identifications of the samples. The true clusters are each of size 100 and are in order in the columns of the data.frames.

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### Examples

```r
#code used to create data:
## Not run:
nvar<-51  #multiple of 3
n<-100
x<-cbind(matrix(rnorm(n*nvar,mean=5),nrow=nvar),
          matrix(rnorm(n*nvar,mean=-5),nrow=nvar),
          matrix(rnorm(n*nvar,mean=0),nrow=nvar))
#make some of them flipped effects (better for testing if both sig under/over
#expressed variables)
geneGroup<-sample(rep(1:3,each=floor(nvar/3)))
gpIndex<-list(1:n,(n+1):(n*2),(2*n+1):(n*3))
```
x[ geneGroup==1, ] <- x[ geneGroup==1, unlist( gpIndex[ c(3, 1, 2) ] ) ]
x[ geneGroup==2, ] <- x[ geneGroup==2, unlist( gpIndex[ c(2, 3, 1) ] ) ]

# add in differences in variable means
smp <- sample( 1:nrow( x ), 10 )
x[ smp, ] <- x[ smp, ] + 10

# make different signal y
y <- cbind( matrix( rnorm( n*nvar, mean=1 ), nrow=nvar ),
            matrix( rnorm( n*nvar, mean=-1 ), nrow=nvar ),
            matrix( rnorm( n*nvar, mean=0 ), nrow=nvar ) )
y <- y[, sample( 1:ncol( y ) ) ] * matrix( rnorm( 3*n*nvar, sd=3 ), nrow=nvar )

# add together the two signals
simData <- x + y

# add pure noise variables
simData <- rbind( simData, matrix( rnorm( 3*n*nvar, mean=10 ), nrow=nvar ),
                  matrix( rnorm( 3*n*nvar, mean=5 ), nrow=nvar ) )

# make count data
countMean <- exp( simData / 2 )
simCount <- matrix( rpois( n=length( as.vector( countMean ) ), lambda = as.vector( countMean ) + 1 ), nrow=nrow( countMean ), ncol=ncol( countMean ) )

# labels for the truth
trueCluster <- rep( c( 1:3 ), each=n )
save( list=c( "simCount", "simData", "trueCluster" ), file="data/simData.rda" )

## End(Not run)

---

subsampleClustering  

Cluster subsamples of the data

Description

Given input data, this function will subsample the samples, cluster the subsamples, and return a \( n \times n \) matrix with the probability of co-occurrence.

Usage

```
## S4 method for signature 'character'
subsampleClustering( clusterFunction, ... )

## S4 method for signature 'ClusterFunction'
subsampleClustering(
  clusterFunction,
  inputMatrix,    
  inputType,
  clusterArgs = NULL,
  classifyMethod = c("All", "InSample", "OutOfSample"),
) ```
resamp.num = 100,
samp.p = 0.7,
ncores = 1,
warnings = TRUE,
...
)

Arguments

clusterFunction

A ClusterFunction object that defines the clustering routine. See ClusterFunction for required format of user-defined clustering routines. User can also give a character value to the argument clusterFunction to indicate the use of clustering routines provided in package. Type listBuiltInFunctions at command prompt to see the built-in clustering routines. If clusterFunction is missing, the default is set to "pam".

... arguments passed to mclapply (if ncores>1).

inputMatrix

A numerical matrix on which to run the clustering or a SummarizedExperiment, SingleCellExperiment, or ClusterExperiment object.

inputType

A character vector defining what type of input is given in the inputMatrix argument. Must consist of values "diss", "X", or "cat" (see details). "X" and "cat" should be indicate matrices with features in the row and samples in the column; "cat" corresponds to the features being numerical integers corresponding to categories, while "X" are continuous valued features. "diss" corresponds to an inputMatrix that is a NxN dissimilarity matrix. "cat" is largely used internally for clustering of sets of clusterings.

clusterArgs

A list of parameter arguments to be passed to the function defined in the clusterFunction slot of the ClusterFunction object. For any given ClusterFunction object, use function requiredArgs to get a list of required arguments for the object.

classifyMethod

Method for determining which samples should be used in computing the co-occurrence matrix. "All" = all samples, "OutOfSample" = those not subsampled, and "InSample" = those in the subsample. See details for explanation.

resamp.num

The number of subsamples to draw.

samp.p

The proportion of samples to sample for each subsample.

ncores

Integer giving the number of cores. If ncores>1, mclapply will be called.

warnings

Logical as to whether should give warning if arguments given that don’t match clustering choices given. Otherwise, inapplicable arguments will be ignored without warning.

Details

subsampleClustering is not usually called directly by the user. It is only an exported function so as to be able to clearly document the arguments for subsampleClustering which can be passed via the argument subsampleArgs in functions like clusterSingle and clusterMany.

requiredArgs: The choice of "All" or "OutOfSample" for requiredArgs require the classification of arbitrary samples not originally in the clustering to clusters; this is done via the classifyFUN
provided in the `ClusterFunction` object. If the `ClusterFunction` object does not have such a function to define how to classify into a cluster samples not in the subsample that created the clustering then `classifyMethod` must be "InSample". Note that if "All" is chosen, all samples will be classified into clusters via the `classifyFUN`, not just those that are out-of-sample; this could result in different assignments to clusters for the in-sample samples than their original assignment by the clustering depending on the classification function. If you do not choose 'All', it is possible to get NAs in resulting S matrix (particularly if when not enough subsamples are taken) which can cause errors if you then pass the resulting D=1-S matrix to `mainClustering`. For this reason the default is "All".

**Value**

A n x n matrix of co-occurrences, i.e. a symmetric matrix with [i,j] entries equal to the percentage of subsamples where the ith and jth sample were clustered into the same cluster. The percentage is only out of those subsamples where the ith and jth samples were both assigned to a clustering. If `classifyMethod`="All", this is all subsamples for all i,j pairs. But if `classifyMethod`="InSample" or `classifyMethod`="OutOfSample", then the percentage is only taken on those subsamples where the ith and jth sample were both in or out of sample, respectively, relative to the subsample.

**Examples**

```r
## Not run:
# takes a bit of time, not run on checks:
data(simData)
coOccur <- subsampleClustering( inputMatrix=simData, inputType="X",
clusterFunction="kmeans",
clusterArgs=list(k=3,nstart=10), resamp.n=100, samp.p=0.7)

# visualize the resulting co-occurrence matrix
plotHeatmap(coOccur)
## End(Not run)
```

---

**subset**

*Functions to subset ClusterExperiment Objects*

**Description**

These functions are used to subset ClusterExperiment objects, either by removing samples, genes, or clusterings.

**Usage**

```r
## S4 method for signature 'ClusterExperiment'
removeClusterings(x, whichClusters)

## S4 method for signature 'ClusterExperiment'
```
removeClusters(
  x,
  whichCluster,
  clustersToRemove,
  makePrimary = FALSE,
  clusterLabels = NULL
)

## S4 method for signature 'ClusterExperiment,ANY,character,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'ClusterExperiment,ANY,logical,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'ClusterExperiment,ANY,numeric,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'ClusterExperiment'
subsetByCluster(
  x,
  clusterValue,
  whichCluster = "primary",
  matchTo = c("name", "clusterIds")
)

Arguments

x a ClusterExperiment object.

whichClusters argument that can be either numeric or character vector indicating the clusterings to be used. See details of getClusterIndex.

whichCluster argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of getClusterIndex.

clustersToRemove numeric vector identifying the clusters to remove (whose samples will be re-assigned to -1 value).

makePrimary whether to make the added cluster the primary cluster (only relevant if y is a vector)

clusterLabels label(s) for the clusters being added. If y a matrix, the column names of that matrix will be used by default, if clusterLabels is not given.

i, j A vector of logical or integer subscripts, indicating the rows and columns to be subsetted for i and j, respectively.

... The arguments transformation, clusterTypes and clusterInfo to be passed to the constructor for signature SingleCellExperiment, matrix.

drop A logical scalar that is ignored.

clusterValue values of the cluster to match to for subsetting

matchTo whether to match to the cluster name ("name") or internal cluster id ("clusterIds")
Details

removeClusterings removes the clusters given by whichClusters. If the primaryCluster is one of the clusters removed, the primaryClusterIndex is set to 1 and the dendrogram and co-clustering matrix are discarded and orderSamples is set to 1:NCOL(x).

removeClusters creates a new cluster that unassigns samples in cluster clustersToRemove (in the clustering defined by whichClusters) and assigns them to -1 (unassigned).

Note that when subsetting the data, the dendrogram information and the co-clustering matrix are lost.

Value

A ClusterExperiment object.

removeClusterings returns a ClusterExperiment object, unless all clusters are removed, in which case it returns a SingleCellExperiment object.

subsetByCluster subsets the object by clusters in a clustering and returns a ClusterExperiment object with only those samples.

Examples

# load CE object
data(rsecFluidigm)
# remove the mergeClusters step from the object
clusterLabels(rsecFluidigm)
test<-removeClusterings(rsecFluidigm,whichClusters="mergeClusters")
clusterLabels(test)
tableClusters(rsecFluidigm)
test<-removeClusters(rsecFluidigm,whichCluster="mergeClusters",clustersToRemove=c("m01","m04"))
tableClusters(test,whichCluster="mergeClusters")

transformData  Transform the original data in a ClusterExperiment object

Description

Provides the transformed data.

Usage

## S4 method for signature 'matrixOrHDF5'
transformData(object, transFun = NULL, isCount = FALSE)

## S4 method for signature 'ClusterExperiment'
transformData(object, whichAssay = 1, ...)

## S4 method for signature 'SingleCellExperiment'
transformData(object, whichAssay = 1, ...)
## S4 method for signature 'SummarizedExperiment'
transformData(object, ...)

### Arguments
- **object**: a matrix, SummarizedExperiment, SingleCellExperiment or ClusterExperiment object.
- **transFun**: a transformation function to be applied to the data. If the transformation applied to the data creates an error or NA values, then the function will throw an error. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.
- **isCount**: if transFun=NULL, then isCount=TRUE will determine the transformation as defined by function(x){log2(x+1)}, and isCount=FALSE will give a transformation function function(x){x}. Ignored if transFun=NULL. If object is of class ClusterExperiment, the stored transformation will be used and giving this parameter will result in an error.
- **whichAssay**: numeric or character specifying which assay to use. See `assay` for details.
- **...**: Values passed on the the 'matrix' method.

### Details
The data matrix defined by `assay(x)` is transformed based on the transformation function either defined in x (in the case of a ClusterExperiment object) or by user given values for other classes.

### Value
A DataFrame defined by `assay(x)` suitably transformed

### Examples
```r
code snippet
```

---

`updateObject`  
*Update old ClusterExperiment object to current class definition*

### Description
This function updates ClusterExperiment objects from previous versions of package into the current definition
updateObject

Usage

## S4 method for signature 'ClusterExperiment'
updateObject(object, checkTransformAndAssay = FALSE, ..., verbose = FALSE)

Arguments

object a ClusterExperiment (or clusterExperiment from older versions). Must have at a minimum a slot clusterMatrix.
checkTransformAndAssay logical. Whether to check the content of the assay and given transformation function for whether they are valid.
... Additional arguments, for use in specific updateObject methods.
verbose TRUE or FALSE, indicating whether information about the update should be reported. Use message to report this information.

Details

The function creates a valid ClusterExperiment object by adding the default values of missing slots. It does so by calling the ClusterExperiment function, which imputes default (empty) values for missing slots.

The object is required to have minimal components to be updated. Specifically, it must have all the required elements of a Summarized Experiment as well as the basic slots of a ClusterExperiment object which have not changed over time. These are: clusterMatrix, primaryIndex, clusterInfo, transformation, clusterTypes, clusterLegend, orderSamples.

If any of the dendrogram-related slots are missing, ALL of the dendrogram and merge related slots will be cleared to default values. Similarly, if any of the merge-related slots are missing, ALL of the merge-related slots will be cleared to the default values.

Cluster and Sample dendrograms of the class dendrogram will be updated to the phylo4d class now used in ClusterExperiment objects; the merge information on these nodes will be updated to have the correct format (i.e. match to the internal node id names in the new dendrogram). The previous identification of nodes that was previously created internally by plotDendrogram and the merging (labels in the form of 'Node1','Node2'), will be kept as nodeLabels in the new dendrogram class.

The function currently only works for object of ClusterExperiment, not the older name clusterExperiment.

Value

A valid ClusterExperiment object based on the current definition of ClusterExperiment.

See Also

ClusterExperiment
Description

The main workflow of the package is made of `clusterMany`, `makeConsensus`, and `mergeClusters`. The clusterings from these functions (and not those obtained in a different way) can be obtained with the functions documented here.

Usage

```r
## S4 method for signature 'ClusterExperiment'
workflowClusters(x, iteration = 0)
## S4 method for signature 'ClusterExperiment'
workflowClusterDetails(x)
## S4 method for signature 'ClusterExperiment'
workflowClusterTable(x)
## S4 method for signature 'ClusterExperiment'
setToCurrent(x, whichCluster, eraseOld = FALSE)
## S4 method for signature 'ClusterExperiment'
setToFinal(x, whichCluster, clusterLabel)
```

Arguments

- **x**: a `ClusterExperiment` object.
- **iteration**: numeric. Which iteration of the workflow should be used.
- **whichCluster**: argument that can be a single numeric or character value indicating the single clustering to be used. Giving values that result in more than one clustering will result in an error. See details of `getClusterIndex`.
- **eraseOld**: logical. Only relevant if input `x` is of class `ClusterExperiment`. If TRUE, will erase existing workflow results (clusterMany as well as mergeClusters and makeConsensus). If FALSE, existing workflow results will have "_i" added to the clusterTypes value, where `i` is one more than the largest such existing workflow clusterTypes.
- **clusterLabel**: optional string value to give to cluster set to be "final"

Value

`workflowClusters` returns a matrix consisting of the appropriate columns of the `clusterMatrix` slot.

`workflowClusterDetails` returns a `data.frame` with some details on the clusterings, such as the type (e.g., 'clusterMany', 'makeConsensus') and iteration.
workflowClusterTable returns a table of how many of the clusterings belong to each of the following possible values: 'final', 'mergeClusters', 'makeConsensus' and 'clusterMany'.

setToCurrent returns a ClusterExperiment object where the indicated cluster of whichCluster has been set to the most current iteration in the workflow. Pre-existing clusters are appropriately updated.

setToFinal returns a ClusterExperiment object where the indicated cluster of whichCluster has clusterType set to "final". The primaryClusterIndex is also set to this cluster, and the clusterLabel, if given.

Examples

```r
## Not run:
data(simData)

cl <- clusterMany(simData, nReducedDims=c(5,10,50), reduceMethod="PCA", clusterFunction="pam", ks=2:4, findBestK=c(FALSE), removeSil=TRUE, subsample=FALSE, makeMissingDiss=TRUE)

clCommon <- makeConsensus(cl, whichClusters="workflow", proportion=0.7, minSize=10)

clCommon <- makeDendrogram(clCommon)

clMerged <- mergeClusters(clCommon, mergeMethod="adjP", DEMethod="limma")

head(workflowClusters(clMerged))
workflowClusterDetails(clMerged)
workflowClusterTable(clMerged)

## End(Not run)
```
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