Package ‘moduleColor’

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moduleColor-package  Basic Module Functions

Description

Methods for color labeling, calculation of eigengenes, merging of closely related modules.

Details

Package: moduleColor
Version: 1.08-3
Date: 2014-11-25
Depends: R, stats, impute, grDevices, dynamicTreeCut
ZipData: no
License: GPL version 2 or newer
URL: http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/BranchCutting/

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checkSets

    multiSetMEs      Calculate module eigengenes.
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    orderMEs        Put close eigenvectors next to each other.
    plotHclustColors Plot color bars corresponding to modules.
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    standardColors  Colors this library uses for labeling modules.

Author(s)

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Maintainer: Peter Langfelder <Peter.Langfelder@gmail.com>

checkSets

    Check structure and retrieve sizes of a group of datasets.

Description

Checks whether given sets have the correct format and retrieves dimensions.

Usage

    checkSets(data, checkStructure = FALSE, useSets = NULL)

Arguments

    data       A vector of lists; in each list there must be a component named data whose
                content is a matrix or dataframe or array of dimension 2.
    checkStructure If FALSE, incorrect structure of data will trigger an error. If TRUE, an appropriate
                    flag (see output) will be set to indicate whether data has correct structure.
    useSets    Optional specification of entries of the vector data that are to be checked. De-
               faults to all components. This may be useful when data only contains informa-
                tion for some of the sets.

Details

For multiset calculations, many quantities (such as expression data, traits, module eigengenes etc)
are presented by a common structure, a vector of lists (one list for each set) where each list has a
component data that contains the actual (expression, trait, eigengene) data for the corresponding
set in the form of a dataframe. This function checks whether data conforms to this convention and
retrieves some basic dimension information (see output).
Value

A list with components

nSets Number of sets (length of the vector data).

nGenes Number of columns in the data components in the lists. This number must be the same for all sets.

nSamples A vector of length nSets giving the number of rows in the data components.

structureOK Only set if the argument checkStructure equals TRUE. The value is TRUE if the parameter data passes a few tests of its structure, and FALSE otherwise. The tests are not exhaustive and are meant to catch obvious user errors rather than be bulletproof.

Author(s)

Peter Langfelder, <peter.Langfelder@gmail.com>

collectGarbage

Iterative garbage collection.

Description

Performs garbage collection until free memory indicators show no change.

Usage

collectGarbage()

Value

None.

Author(s)

Steve Horvath
Consensus dissimilarity of module eigengenes.

Description

Calculates consensus dissimilarity (1-cor) of given module eigengenes related in several sets.

Usage

\texttt{consensusMEDissimilarity(MEs, useAbs = FALSE, useSets = NULL, method = \"consensus\")}

Arguments

- \texttt{MEs} Module eigengenes of the same modules in several sets.
- \texttt{useAbs} Controls whether absolute value of correlation should be used instead of correlation in the calculation of dissimilarity.
- \texttt{useSets} If the consensus is to include only a selection of the given sets, this vector (or scalar in the case of a single set) can be used to specify the selection. If \texttt{NULL}, all sets will be used.
- \texttt{method} A character string giving the method to use. Allowed values are (abbreviations of) \texttt{\"consensus\"} and \texttt{\"majority\"}. The consensus dissimilarity is calculated as the minimum of given set dissimilarities for \texttt{\"consensus\"} and as the average for \texttt{\"majority\"}.

Details

This function calculates the individual set dissimilarities of the given eigengenes in each set, then takes the (parallel) maximum or average over all sets. For details on the structure of input data, see \texttt{checkSets}.

Value

A dataframe containing the matrix of dissimilarities, with names and row names set appropriately.

Author(s)

Peter Langfelder, <Peter.Langfelder@gmail.com>

See Also

\texttt{checkSets}
consensusOrderMEs

Put close eigenvectors next to each other in several sets.

Description

Reorder given (eigen-)vectors such that similar ones (as measured by correlation) are next to each other. This is a multi-set version of orderMEs: the dissimilarity used can be of consensus type (for each pair of eigenvectors the consensus dissimilarity is the maximum of individual set dissimilarities over all sets) or of majority type (for each pair of eigenvectors the consensus dissimilarity is the average of individual set dissimilarities over all sets).

Usage

consensusOrderMEs(MEs, useAbs = FALSE, useSets = NULL, greyLast = TRUE, greyName = paste(moduleColor.getMEprefix(), "grey", sep=""), method = "consensus")

Arguments

MEs      Module eigengenes of several sets in a multi-set format (see checkSets). A vector of lists, with each list corresponding to one dataset and the module eigengenes in the component data, that is MES[[set]]$data[sample, module] is the expression of the eigengene of module module in sample sample in dataset set. The number of samples can be different between the sets, but the modules must be the same.

useAbs   Controls whether vector similarity should be given by absolute value of correlation or plain correlation.

useSets  Allows the user to specify for which sets the eigengene ordering is to be performed.

greyLast Normally the color grey is reserved for unassigned genes; hence the grey module is not a proper module and it is conventional to put it last. If this is not desired, set the parameter to FALSE.

greyName Name of the grey module eigengene.

method   A character string giving the method to be used calculating the consensus dissimilarity. Allowed values are (abbreviations of) "consensus" and "majority". The consensus dissimilarity is calculated as the maximum of given set dissimilarities for "consensus" and as the average for "majority".

Details

Ordering module eigengenes is useful for plotting purposes. This function calculates the consensus or majority dissimilarity of given eigengenes over the sets specified by useSets (defaults to all sets). A hierarchical dendrogram is calculated using the dissimilarity and the order given by the dendrogram is used for the eigengenes in all other sets.
Value

A vector of lists of the same type as MEs containing the re-ordered eigengenes.

Author(s)

Peter Langfelder, <peter.Langfelder@gmail.com>

See Also

moduleEigengenes, multiSetMEs, orderMEs

Description

Encapsulates single-set data in a wrapper that makes the data suitable for functions working on multiset data collections.

Usage

fixDataStructure(data, verbose = 0, indent = 0)

Arguments

data A dataframe, matrix or array with two dimensions to be encapsulated.
verbose Controls verbosity. 0 is silent.
indent Controls indentation of printed progress messages. 0 means no indentation, every unit adds two spaces.

Details

For multiset calculations, many quantities (such as expression data, traits, module eigengenes etc) are presented by a common structure, a vector of lists (one list for each set) where each list has a component data that contains the actual (expression, trait, eigengene) data for the corresponding set in the form of a dataframe. This function creates a vector of lists of length 1 and fills the component data with the content of parameter data.

Value

As described above, input data in a format suitable for functions operating on multiset data collections.

Author(s)

Peter Langfelder, <peter.Langfelder@gmail.com>
See Also

checkSets

Examples

```r
singleSetData = matrix(rnorm(100), 10, 10);
encapsData = fixDataStructure(singleSetData);
length(encapsData)
names(encapsData[[1]])
dim(encapsData[[1]]$data)
all.equal(encapsData[[1]]$data, singleSetData);
```

**labels2colors**

*Convert numerical labels to colors.*

Description

Converts a vector or array of numerical labels into a corresponding vector or array of colors corresponding to the labels.

Usage

`labels2colors(labels, zeroIsGrey = TRUE, colorSeq = NULL)`

Arguments

- `labels` Vector of non-negative integer labels.
- `zeroIsGrey` If TRUE, labels 0 will be assigned color grey. Otherwise, labels below 1 will trigger an error.
- `colorSeq` Color sequence corresponding to labels. If not given, a standard sequence will be used.

Details

The standard sequence start with well-distinguishable colors, and after about 40 turns into a quasi-random sampling of all colors available in R with the exception of all shades of grey (and gray).

If the input `labels` have a dimension attribute, it is copied into the output, meaning the dimensions of the returned value are the same as those of the input `labels`.

Value

A vector or array of character strings of the same length or dimensions as `labels`.

Author(s)

Peter Langfelder, <Peter.Langfelder@gmail.com>
mergeCloseModules

Examples

```r
labels = c(0:20);
labels2colors(labels);
```

mergeCloseModules  Merge close modules of gene expression data.

Description

Merges modules in gene expression networks that are too close as measured by the correlation of their eigengenes.

Usage

```r
mergeCloseModules(exprData, colors,
cutHeight = 0.2,
MEs = NULL,
impute = TRUE,
useAbs = FALSE,
itrate = TRUE,
relabel = FALSE,
colorSeq = NULL,
getNewMEs = TRUE,
getNewUnassdME = TRUE,
useSets = NULL,
checkDataFormat = TRUE,
unassdColor = ifelse(is.numeric(colors), 0, "grey"),
trapErrors = FALSE,
verbose = 1, indent = 0)
```

Arguments

- **.exprData**  Expression data, either a single data frame with rows corresponding to samples and columns to genes, or in a multi-set format (see `checkSets`). See `checkDataStructure` below.
- **colors**  A vector (numeric, character or a factor) giving module colors for genes. The method only makes sense when genes have the same color label in all sets, hence a single vector.
- **cutHeight**  Maximum dissimilarity (i.e., 1-correlation) that qualifies modules for merging.
- **MEs**  If module eigengenes have been calculated before, the user can save some computational time by inputting them. `MEs` should have the same format as `exprData`. If they are not given, they will be calculated.
- **impute**  Should missing values be imputed in eigengene calculation? If imputation is disabled, the presence of NA entries will cause the eigengene calculation to fail and eigengenes will be replaced by their hubgene approximation. See `moduleEigengenes` for more details.
mergeCloseModules

useAbs  Specifies whether absolute value of correlation or plain correlation (of module eigengenes) should be used in calculating module dissimilarity.

iterate Controls whether the merging procedure should be repeated until there is no change. If FALSE, only one iteration will be executed.

relabel Controls whether, after merging, color labels should be ordered by module size.

colorSeq Color labels to be used for relabeling. Defaults to the standard color order used in this package if colors are not numeric, and to integers starting from 1 if colors is numeric.

getNewMEs Controls whether module eigengenes of merged modules should be calculated and returned.

getNewUnassdME When doing module eigengene manipulations, the function does not normally calculate the eigengene of the 'module' of unassigned ('grey') genes. Setting this option to TRUE will force the calculation of the unassigned eigengene in the returned newMEs, but not in the returned oldMEs.

useSets A vector of scalar allowing the user to specify which sets will be used to calculate the consensus dissimilarity of module eigengenes. Defaults to all given sets.

checkDataFormat If TRUE, the function will check exprData and MEs for correct multi-set structure. If single set data is given, it will be converted into a format usable for the function. If FALSE, incorrect structure of input data will trigger an error.

unassdColor Specifies the string that labels unassigned genes. Module of this color will not enter the module eigengene clustering and will not be merged with other modules.

trapErrors Controls whether computational errors in calculating module eigengenes, their dissimilarity, and merging trees should be trapped. If TRUE, errors will be trapped and the function will return the input colors. If FALSE, errors will cause the function to stop.

verbose Controls verbosity of printed progress messages. 0 means silent, up to (about) 5 the verbosity gradually increases.

indent A single non-negative integer controlling indentation of printed messages. 0 means no indentation, each unit above that adds two spaces.

Details

This function returns the color labels for modules that are obtained from the input modules by merging ones that are closely related. The relationships are quantified by correlations of module eigengenes; a "consensus" measure is defined as the minimum over the corresponding relationship in each set. Once the (dis-)similarity is calculated, average linkage hierarchical clustering of the module eigengenes is performed, the dendrogram is cut at the height cutHeight and modules on each branch are merged. The process is (optionally) repeated until no more modules are merged.

If, for a particular module, the module eigengene calculation fails, a hubgene approximation will be used.

The user should be aware that if a computational error occurs and trapErrors==TRUE, the returned list (see below) will not contain all of the components returned upon normal execution.
moduleColor.getMEprefix

**Value**

If no errors occurred, a list with components

- **colors**: Color labels for the genes corresponding to merged modules. The function attempts to mimic the mode of the input `colors`: if the input `colors` is numeric, character and factor, respectively, so is the output. Note, however, that if the function performs relabeling, a standard sequence of labels will be used: integers starting at 1 if the input `colors` is numeric, and a sequence of color labels otherwise (see `colorseq` above).

- **dendro**: Hierarchical clustering dendrogram (average linkage) of the eigengenes of the most recently computed tree. If `iterate` was set TRUE, this will be the dendrogram of the merged modules, otherwise it will be the dendrogram of the original modules.

- **oldDendro**: Hierarchical clustering dendrogram (average linkage) of the eigengenes of the original modules.

- **cutHeight**: The input `cutHeight`.

- **oldMEs**: Module eigengenes of the original modules in the sets given by `useSets`.

- **newMEs**: Module eigengenes of the merged modules in the sets given by `useSets`.

- **allok**: A boolean set to TRUE.

If an error occurred and `trapErrors==TRUE`, the list only contains these components:

- **colors**: A copy of the input `colors`.

- **allok**: A boolean set to FALSE.

**Author(s)**

Peter Langfelder, <Peter.Langfelder@gmail.com>

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moduleColor.getMEprefix

*Get the prefix used to label module eigengenes.*

**Description**

Returns the currently used prefix used to label module eigengenes. When returning module eigengenes in a dataframe, names of the corresponding columns will start with the given prefix.

**Usage**

moduleColor.getMEprefix()
moduleColor.revisionDate

**Details**

Returns the prefix used to label module eigengenes. When returning module eigengenes in a dataframe, names of the corresponding columns will consist of the corresponding color label preceded by the given prefix. For example, if the prefix is "PC" and the module is turquoise, the corresponding module eigengene will be labeled "PCTurquoise". Most of old code assumes "PC", but "ME" is more instructive and used in some newer analyses.

**Value**

A character string.

**Author(s)**

Peter Langfelder, <Peter.Langfelder@gmail.com>

**See Also**

moduleColor.setMEprefix, moduleEigengenes

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moduleColor.revisionDate

*Get the last revision date of the package.*

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**Description**

Returns the last revision date of the package.

**Usage**

moduleColor.revisionDate()

**Value**

A character string.

**Author(s)**

Peter Langfelder, <Peter.Langfelder@gmail.com>
moduleColor.setMEprefix

Set the prefix used to label module eigengenes.

Description

Sets the prefix used to label module eigengenes. When returning module eigengenes in a dataframe, names of the corresponding columns will start with the given prefix.

Usage

moduleColor.setMEprefix(prefix)

Arguments

prefix A character string of length 2. Recommended values are "PC" (the default start-up value) and "ME".

Details

Sets the prefix used to label module eigengenes. When returning module eigengenes in a dataframe, names of the corresponding columns will consist of the corresponding color label preceded by the given prefix. For example, if the prefix is "PC" and the module is turquoise, the corresponding module eigengene will be labeled "PCturquoise". Most of old code assumes "PC", but "ME" is more instructive and used in some newer analyses.

Value

None.

Author(s)

Peter Langfelder, <Peter.Langfelder@gmail.com>

See Also

moduleColor.getMEprefix, moduleEigengenes
moduleColor.version  Get the version number of the package.

Description
Returns the version number of the package.

Usage
moduleColor.version()

Value
A character string.

Author(s)
Peter Langfelder, <Peter.Langfelder@gmail.com>

moduleEigengenes  Calculate module eigengenes.

Description
Calculates module eigengenes (1st principal component) of modules in a given single dataset.

Usage
moduleEigengenes(expr, colors, impute = TRUE, nPC = 1, align = "along average", excludeGrey = FALSE, grey = ifelse(is.numeric(colors), 0, "grey"), subHubs = TRUE, trapErrors = FALSE, returnValidOnly = trapErrors, softPower = 6, verbose = 0, indent = 0)
Arguments

**expr**
Expression data for a single set in the form of a data frame where rows are samples and columns are genes (probes).

**colors**
A vector of the same length as the number of probes in `expr`, giving module color for all probes (genes). Color "grey" is reserved for unassigned genes.

**impute**
If TRUE, expression data will be checked for the presence of NA entries and if the latter are present, numerical data will be imputed, using function `impute.knn` and probes from the same module as the missing datum. The function `impute.knn` uses a fixed random seed giving repeatable results.

**nPC**
Number of principal components and variance explained entries to be calculated. Note that only the first principal component is returned; the rest are used only for the calculation of proportion of variance explained. The number of returned variance explained entries is currently \( \min(nPC, 10) \). If given `nPC` is greater than 10, a warning is issued.

**align**
Controls whether eigengenes, whose orientation is undetermined, should be aligned with average expression (align = "along average", the default) or left as they are (align = ""). Any other value will trigger an error.

**excludeGrey**
Should the improper module consisting of 'grey' genes be excluded from the eigengenes?

**grey**
Value of `colors` designating the improper module. Note that if `colors` is a factor of numbers, the default value will be incorrect.

**subHubs**
Controls whether hub genes should be substituted for missing eigengenes. If TRUE, each missing eigengene (i.e., eigengene whose calculation failed and the error was trapped) will be replaced by a weighted average of the most connected hub genes in the corresponding module. If this calculation fails, or if `subHubs==FALSE`, the value of `trapErrors` will determine whether the offending module will be removed or whether the function will issue an error and stop.

**trapErrors**
Controls handling of errors from that may arise when there are too many NA entries in expression data. If TRUE, errors from calling these functions will be trapped without abnormal exit. If FALSE, errors will cause the function to stop. Note, however, that `subHubs` takes precedence in the sense that if `subHubs==TRUE` and `trapErrors==FALSE`, an error will be issued only if both the principal component and the hubgene calculations have failed.

**returnValidOnly**
Boolean. Controls whether the returned data frame of module eigengenes contains columns corresponding only to modules whose eigengenes or hub genes could be calculated correctly (TRUE), or whether the data frame should have columns for each of the input color labels (FALSE).

**softPower**
The power used in soft-thresholding the adjacency matrix. Only used when the hubgene approximation is necessary because the principal component calculation failed. It must be non-negative. The default value should only be changed if there is a clear indication that it leads to incorrect results.

**verbose**
Controls verbosity of printed progress messages. 0 means silent, up to (about) 5 the verbosity gradually increases.

**indent**
A single non-negative integer controlling indentation of printed messages. 0 means no indentation, each unit above that adds two spaces.
Details

Module eigengene is defined as the first principal component of the expression matrix of the corresponding module. The calculation may fail if the expression data has too many missing entries. Handling of such errors is controlled by the arguments subHubs and trapErrors. If subHubs==TRUE, errors in principal component calculation will be trapped and a substitute calculation of hubgenes will be attempted. If this fails as well, behaviour depends on trapErrors: if TRUE, the offending module will be ignored and the return value will allow the user to remove the module from further analysis; if FALSE, the function will stop.

From the user's point of view, setting trapErrors=FALSE ensures that if the function returns normally, there will be a valid eigengene (principal component or hubgene) for each of the input colors. If the user sets trapErrors=TRUE, all calculational (but not input) errors will be trapped, but the user should check the output (see below) to make sure all modules have a valid returned eigengene.

While the principal component calculation can fail even on relatively sound data (it does not take all that many "well-placed" NA to torpedo the calculation), it takes many more irregularities in the data for the hubgene calculation to fail. In fact such a failure signals there likely is something seriously wrong with the data.

Value

A list with the following components:

- **eigengenes**: Module eigengenes in a dataframe, with each column corresponding to one eigengene. The columns are named by the corresponding color with an "ME" prepended, e.g., METurquoise etc. If returnValidOnly==FALSE, module eigengenes whose calculation failed have all components set to NA.

- **averageExpr**: If align == "along average", a dataframe containing average normalized expression in each module. The columns are named by the corresponding color with an "AE" prepended, e.g., AETurquoise etc.

- **varExplained**: A dataframe in which each column corresponds to a module, with the component varExplained[PC, module] giving the variance of module module explained by the principal component no. PC. The calculation is exact irrespective of the number of computed principal components. At most 10 variance explained values are recorded in this dataframe.

- **nPC**: A copy of the input nPC.

- **validMEs**: A boolean vector. Each component (corresponding to the columns in data) is TRUE if the corresponding eigengene is valid, and FALSE if it is invalid. Valid eigengenes include both principal components and their hubgene approximations. When returnValidOnly==FALSE, by definition all returned eigengenes are valid and the entries of validMEs are all TRUE.

- **validColors**: A copy of the input colors with entries corresponding to invalid modules set to grey if given, otherwise 0 if colors is numeric and "grey" otherwise.

- **allOK**: Boolean flag signalling whether all eigengenes have been calculated correctly, either as principal components or as the hubgene average approximation.

- **allPC**: Boolean flag signalling whether all returned eigengenes are principal components.
isPC Boolean vector. Each component (corresponding to the columns in eigengenes) is \texttt{TRUE} if the corresponding eigengene is the first principal component and \texttt{FALSE} if it is the hubgene approximation or is invalid.

ishub Boolean vector. Each component (corresponding to the columns in eigengenes) is \texttt{TRUE} if the corresponding eigengene is the hubgene approximation and \texttt{FALSE} if it is the first principal component or is invalid.

validAEs Boolean vector. Each component (corresponding to the columns in eigengenes) is \texttt{TRUE} if the corresponding module average expression is valid.

allAEOK Boolean flag signalling whether all returned module average expressions contain valid data. Note that \texttt{returnValidOnly==TRUE} does not imply \texttt{allAEOK==TRUE}: some invalid average expressions may be returned if their corresponding eigengenes have been calculated correctly.

Author(s)

Steve Horvath <SHorvath@mednet.ucla.edu>, Peter Langfelder <Peter.Langfelder@gmail.com>

References


See Also

\texttt{svd}, \texttt{impute.knn}

---

moduleNumber Fixed-height cut of a dendrogram.

Description

Detects branches of on the input dendrogram by performing a fixed-height cut.

Usage

\texttt{moduleNumber(dendro, cutHeight = 0.9, minSize = 50)}

Arguments

dendro a hierarchical clustering dendrogram such as one returned by \texttt{hclust}.
cutHeight Maximum joining heights that will be considered.
minSize Minimum cluster size.
multiSetMEs

Details
All contiguous branches below the height cutHeight that contain at least minSize objects are assigned unique positive numerical labels; all unassigned objects are assigned label 0.

Value
A vector of numerical labels giving the assignment of each object.

Note
The numerical labels may not be sequential. See normalizeLabels for a way to put the labels into a standard order.

Author(s)
Peter Langfelder, <Peter.Langfelder@gmail.com>

See Also
hclust, cutree, normalizeLabels

Description
Calculates module eigengenes for several sets.

Usage
multiSetMEs(exprData, 
colors, 
universalColors = NULL, 
useSets = NULL, 
useGenes = NULL, 
impute = TRUE, 
nPC = 1, 
align = "along average", 
excludeGrey = FALSE, 
grey = ifelse(is.null(universalColors), ifelse(is.numeric(colors), 0, "grey"), 
ifelse(is.numeric(universalColors), 0, "grey")), 
subHubs = TRUE, 
trapErrors = FALSE, 
returnValidOnly = trapErrors, 
softPower = 6, 
verbose = 1, indent = 0)
Arguments

exprData  Expression data in a multi-set format (see checkSets). A vector of lists, with each list corresponding to one microarray dataset and expression data in the component data, i.e., that is expr[[[set]]][data][sample, probe] is the expression of probe probe in sample sample in dataset set. The number of samples can be different between the sets, but the probes must be the same.

colors  A matrix of dimensions (number of probes, number of sets) giving the module assignment of each gene in each set. The color "grey" is interpreted as unassigned.

universalColors  Alternative specification of module assignment. A single vector of length (number of probes) giving the module assignment of each gene in all sets (that is the modules are common to all sets). If given, takes precedence over color.

useSets  If calculations are requested in (a) selected set(s) only, the set(s) can be specified here. Defaults to all sets.

useGenes  Can be used to restrict calculation to a subset of genes (the same subset in all sets). If given, validColors in the returned list will only contain colors for the genes specified in useGenes.

impute  Logical. If TRUE, expression data will be checked for the presence of NA entries and if the latter are present, numerical data will be imputed, using function impute.knn and probes from the same module as the missing datum. The function impute.knn uses a fixed random seed giving repeatable results.

nPC  Number of principal components to be calculated. If only eigengenes are needed, it is best to set it to 1 (default). If variance explained is needed as well, use value NULL. This will cause all principal components to be computed, which is slower.

align  Controls whether eigengenes, whose orientation is undetermined, should be aligned with average expression (align = "along average", the default) or left as they are (align = ""). Any other value will trigger an error.

excludeGrey  Should the improper module consisting of ‘grey’ genes be excluded from the eigengenes?

grey  Value of colors or universalColors (whichever applies) designating the improper module. Note that if the appropriate colors argument is a factor of numbers, the default value will be incorrect.

subHubs  Controls whether hub genes should be substituted for missing eigengenes. If TRUE, each missing eigengene (i.e., eigengene whose calculation failed and the error was trapped) will be replaced by a weighted average of the most connected hub genes in the corresponding module. If this calculation fails, or if subHubs=='FALSE, the value of trapErrors will determine whether the offending module will be removed or whether the function will issue an error and stop.

trapErrors  Controls handling of errors from that may arise when there are too many NA entries in expression data. If TRUE, errors from calling these functions will be trapped without abnormal exit. If FALSE, errors will cause the function to stop. Note, however, that subHubs takes precedence in the sense that if subHubs==TRUE and trapErrors==FALSE, an error will be issued only if both the principal component and the hubgene calculations have failed.
returnValidOnly

Boolean. Controls whether the returned data frames of module eigengenes contain columns corresponding only to modules whose eigengenes or hub genes could be calculated correctly in every set (TRUE), or whether the data frame should have columns for each of the input color labels (FALSE).

softPower

The power used in soft-thresholding the adjacency matrix. Only used when the hubgene approximation is necessary because the principal component calculation failed. It must be non-negative. The default value should only be changed if there is a clear indication that it leads to incorrect results.

verbose

Controls verbosity of printed progress messages. 0 means silent, up to (about) 5 the verbosity gradually increases.

indent

A single non-negative integer controlling indentation of printed messages. 0 means no indentation, each unit above that adds two spaces.

Details

This function calls `moduleEigengenes` for each set in `exprData`.

Module eigengene is defined as the first principal component of the expression matrix of the corresponding module. The calculation may fail if the expression data has too many missing entries. Handling of such errors is controlled by the arguments `subHubs` and `trapErrors`. If `subHubs`=TRUE, errors in principal component calculation will be trapped and a substitute calculation of hubgenes will be attempted. If this fails as well, behaviour depends on `trapErrors`: if TRUE, the offending module will be ignored and the return value will allow the user to remove the module from further analysis; if FALSE, the function will stop. If `universalColors` is given, any offending module will be removed from all sets (see `validMEs` in return value below).

From the user's point of view, setting `trapErrors`=FALSE ensures that if the function returns normally, there will be a valid eigengene (principal component or hubgene) for each of the input colors. If the user sets `trapErrors`=TRUE, all calculational (but not input) errors will be trapped, but the user should check the output (see below) to make sure all modules have a valid returned eigengene.

While the principal component calculation can fail even on relatively sound data (it does not take all that many "well-placed" NA to torpedo the calculation), it takes many more irregularities in the data for the hubgene calculation to fail. In fact such a failure signals there likely is something seriously wrong with the data.

Value

A vector of lists similar in spirit to the input `exprData`. For each set there is a list with the following components:

`data`

Module eigengenes in a data frame, with each column corresponding to one eigengene. The columns are named by the corresponding color with an "ME" prepended, e.g., MEturquoise etc. Note that, when `trapErrors` == TRUE and `returnValidOnly`=FALSE, this data frame also contains entries corresponding to removed modules, if any. (`validMEs` below indicates which eigengenes are valid and `allOK` whether all module eigengens were successfully calculated.)

`averageExpr`

If `align` == "along average", a dataframe containing average normalized expression in each module. The columns are named by the corresponding color with an "AE" prepended, e.g., AEturquoise etc.
varExplained A dataframe in which each column corresponds to a module, with the component varExplained[PC, module] giving the variance of module module explained by the principal component no. PC. This is only accurate if all principal components have been computed (input npc = NULL). At most 5 principal components are recorded in this dataframe.

npc A copy of the input npc.

validMEs A boolean vector. Each component (corresponding to the columns in data) is TRUE if the corresponding eigengene is valid, and FALSE if it is invalid. Valid eigengenes include both principal components and their hubgene approximations. When returnValidOnly==FALSE, by definition all returned eigengenes are valid and the entries of validMEs are all TRUE.

validColors A copy of the input colors (universalColors if set, otherwise colors[, set]) with entries corresponding to invalid modules set to grey if given, otherwise 0 if the appropriate input colors are numeric and "grey" otherwise.

allOK Boolean flag signalling whether all eigengenes have been calculated correctly, either as principal components or as the hubgene approximation. If universalColors is set, this flag signals whether all eigengenes are valid in all sets.

allPC Boolean flag signalling whether all returned eigengenes are principal components. This flag (as well as the subsequent ones) is set independently for each set.

isPC Boolean vector. Each component (corresponding to the columns in eigengenes) is TRUE if the corresponding eigengene is the first principal component and FALSE if it is the hubgene approximation or is invalid.

isHub Boolean vector. Each component (corresponding to the columns in eigengenes) is TRUE if the corresponding eigengene is the hubgene approximation and FALSE if it is the first principal component or is invalid.

validAEs Boolean vector. Each component (corresponding to the columns in eigengenes) is TRUE if the corresponding module average expression is valid.

allAEOK Boolean flag signalling whether all returned module average expressions contain valid data. Note that returnValidOnly==TRUE does not imply allAEOK==TRUE: some invalid average expressions may be returned if their corresponding eigengenes have been calculated correctly.

Author(s)

Peter Langfelder, <Peter.Langfelder@gmail.com>

See Also

moduleEigengenes
normalizeLabels  
Transform numerical labels into normal order.

Description
Transforms numerical labels into normal order, that is the largest group will be labeled 1, next largest 2 etc. Label 0 is optionally preserved.

Usage
normalizeLabels(labels, keepZero = TRUE)

Arguments
- labels: Numerical labels.
- keepZero: If TRUE (the default), labels 0 are preserved.

Value
A vector of the same length as input, containing the normalized labels.

Author(s)
Peter Langfelder, <peter.Langfelder@gmail.com>

orderMEs  
Put close eigenvectors next to each other

Description
Reorder given (eigen-)vectors such that similar ones (as measured by correlation) are next to each other.

Usage
orderMEs(MEs, greyLast = TRUE,
   greyName = paste(moduleColor.getMEprefix(), "grey", sep=""),
   orderBy = 1, order = NULL,
   useSets = NULL, verbose = 0, indent = 0)
Arguments

MEs
Module eigengenes in a multi-set format (see `checkSets`). A vector of lists, with each list corresponding to one dataset and the module eigengenes in the component data, that is `MEs[[set]]$data[sample, module]` is the expression of the eigengene of module module in sample sample in dataset set. The number of samples can be different between the sets, but the modules must be the same.

greyLast
Normally the color grey is reserved for unassigned genes; hence the grey module is not a proper module and it is conventional to put it last. If this is not desired, set the parameter to FALSE.

greyName
Name of the grey module eigengene.

orderBy
Specifies the set by which the eigengenes are to be ordered (in all other sets as well). Defaults to the first set in `useSets` (or the first set, if `useSets` is not given).

order
Allows the user to specify a custom ordering.

useSets
Allows the user to specify for which sets the eigengene ordering is to be performed.

verbose
Controls verbosity of printed progress messages. 0 means silent, nonzero verbose.

indent
A single non-negative integer controlling indentation of printed messages. 0 means no indentation, each unit above zero adds two spaces.

Details

Ordering module eigengenes is useful for plotting purposes. For this function the order can be specified explicitly, or a set can be given in which the correlations of the eigengenes will determine the order. For the latter, a hierarchical dendrogram is calculated and the order given by the dendrogram is used for the eigengenes in all other sets.

Value

A vector of lists of the same type as `MEs` containing the re-ordered eigengenes.

Author(s)

Peter Langfelder, <Peter.Langfelder@gmail.com>

See Also

`moduleEigengenes, multiSetMEs, consensusOrderMEs`
plotHclustColors

Plot color rows corresponding to modules

Description
Plot color bars corresponding to modules, usually beneath a dendrogram.

Usage
plotHclustColors(dendro, colors, rowLabels = NULL, cex.rowLabels = 0.9, ...)

Arguments
dendro     A dendrogram such as returned by `hclust`.
colors     Coloring of objects on the dendrogram. Either a vector (one color per object) or a matrix (can also be an array or a data frame) with each column giving one color per object. Each column will be plotted as a horizontal row of colors under the dendrogram.
rowLabels  Labels for the colorings given in `colors`. The labels will be printed to the left of the color rows in the plot. If the argument is given, it must be a vector of length equal to the number of columns in `colors`. If not given, `names(colors)` will be used if available. If not, sequential numbers starting from 1 will be used.
cex.rowLabels  Font size scale factor for the row labels. See `par`.
...          Other parameters to be passed on to the plotting method (such as `main` for the main title etc).

Details
It is often useful to plot module assignment (by color) that was obtained by cutting a hierarchical dendrogram, to visually check whether the obtained modules are meaningful, or which one of several possible module assignments looks best. One way to do it is to section the screen into two parts, plot the dendrogram (via `plot(hclust)`) in the upper section and use this function to plot colors in the order corresponding to the dendrogram in the lower section.

Value
None.

Author(s)
Steve Horvath <shorvath@mednet.ucla.edu> and Peter Langfelder <peter.langfelder@gmail.com>

See Also
`cutreeDynamic` for module detection in a dendrogram.
removeGreyME

Removes the grey eigengene from a given collection of eigengenes.

Description
Given module eigengenes either in a single data frame or in a multi-set format, removes the grey eigengenes from each set. If the grey eigengenes are not found, a warning is issued.

Usage
```
removeGreyME(MEs, greyMEName = paste(moduleColor.getMEprefix(), "grey", sep=""))
```

Arguments
- `MEs`: Module eigengenes, either in a single data frame (typically for a single set), or in a multi-set format. See `checkSets` for a description of the multi-set format.
- `greyMEName`: Name of the module eigengene (in each corresponding data frame) that corresponds to the grey color. This will typically be "PCgrey" or "MEgrey". If the module eigengenes were calculated using standard functions in this library, the default should work.

Value
Module eigengenes in the same format as input (either a single data frame or a vector of lists) with the grey eigengene removed.

Author(s)
Peter Langfelder, <Peter.Langfelder@gmail.com>

standardColors

Colors this library uses for labeling modules.

Description
Returns the vector of color names in the order they are assigned by other functions in this library.

Usage
```
standardColors(n = NULL)
```

Arguments
- `n`: Number of colors requested. If `NULL`, all (approx. 450) colors will be returned. Any other invalid argument such as less than one or more than maximum `(length(standardColors()))` will trigger an error.
Value

A vector of character color names of the requested length.

Author(s)

Peter Langfelder, <Peter.Langfelder@gmail.com>

Examples

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