Package: DFP (via r-universe)

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Description This package provides a supervised technique able to identify differentially expressed genes, based on the construction of \emph{Fuzzy Patterns} (FPs). The Fuzzy Patterns are built by means of applying 3 Membership Functions to discretized gene expression values.

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`DFP-package` *DFP Package Overview*

Description

This package provides a supervised technique able to identify differentially expressed genes, based on the construction of *Fuzzy Patterns* (FPs). The *Fuzzy Patterns* are built by means of applying 3 *Membership Functions* to discretized gene expression values.

Details

Package:	DFP
Type:	Package
Version:	1.0
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License:	GPL-2

The main functionality of the package is provided by the `discriminantFuzzyPattern` function, which works in a 4-step process:

1. Calculates the *Membership Functions*. These functions are used in the next step to discretize gene expression data.
2. Discretizes the gene expression data (float values) into 'Low', 'Medium' or 'High' labels.
3. Calculates a *Fuzzy Pattern* for each category. To do this, a given percentage of the samples belonging to a category must have the same label ('Low', 'Medium' or 'High').
4. Calculates the *Discriminant Fuzzy Pattern* (DFP) that includes those genes present in two or more FPs with different assigned labels.

Additional data classes: `ExpressionSet`, `AnnotatedDataFrame`.

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References

F. Diaz; F. Fdez-Riverola; D. Glez-Pena; J.M. Corchado. Using Fuzzy Patterns for Gene Selection and Data Reduction on Microarray Data. 7th International Conference on Intelligent Data Engineering and Automated Learning: IDEAL 2006, (2006) pp. 1095-1102

Examples

```
########################################
############ Get sample data ############
########################################
library(DFP)
data(rmadataset)

########################################
# Filter the most representative genes  #
########################################
res <- discriminantFuzzyPattern(rmadataset)

########################################
###### Different result displays ########
########################################
plotMembershipFunctions(rmadataset, res$membership.functions, featureNames(rmadataset)[1:2])
showDiscreteValues(res$discrete.values, featureNames(rmadataset)[1:10], c("healthy", "AML-inv"))
showFuzzyPatterns(res$fuzzy.patterns, "healthy")[21:50]
plotDiscriminantFuzzyPattern(res$discriminant.fuzzy.pattern)
```

---

calculateDiscriminantFuzzyPattern

Calculates the Discriminant Fuzzy Pattern to select significative genes

---

Description

Calculates the *Discriminant Fuzzy Pattern* (DFP) that includes those genes present in two or more FPs with different assigned labels.

Usage

```
calculateDiscriminantFuzzyPattern(rmadataset, fps)
```

Arguments

rmadataset	ExpressionSet with numeric values containing gene expression values (rows) of samples belonging to different categories (columns). The ExpressionSet also contains an AnnotatedDataFrame with metadata regarding the classes to which each sample belongs.
fps	Genes belonging to each *Fuzzy Patterns*. There are one FP for each class. Includes an attribute *ifs* with the *Impact Factor* for each category.

Value

Genes belonging to the final DFP.
Includes an attribute *ifs* with the *Impact Factor* for each category.

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F. Diaz; F. Fdez-Riverola; D. Glez-Pena; J.M. Corchado. Using Fuzzy Patterns for Gene Selection and Data Reduction on Microarray Data. 7th International Conference on Intelligent Data Engineering and Automated Learning: IDEAL 2006, (2006) pp. 1095-1102

---

calculateFuzzyPatterns

Calculates a Fuzzy Pattern for each category of the samples

Description

Calculates a *Fuzzy Pattern* for each category. To do this, a given percentage of the samples belonging to a category must have the same label ('Low', 'Medium' or 'High').

Usage

```
calculateFuzzyPatterns(rmadataset, dvs, piVal = 0.9, overlapping = 2)
```

Arguments

rmadataset	ExpressionSet with numeric values containing gene expression values (rows) of samples belonging to different categories (columns). The ExpressionSet also contains an AnnotatedDataFrame with metadata regarding the classes to which each sample belongs.

`dvs` Matrix containing discrete values according to the overlapping parameter after discretizing the gene expression values.
Includes an attribute *types* which determines the category of each sample.

`piVal` Controls the degree of exigency for selecting a gene as a member of a *Fuzzy Pattern*.
`Default value = 0.9. Range[0,1].`

`overlapping` Modifies the number of membership functions used in the discretization process. Possible values:

1. 'Low', 'Medium', 'High'.
2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'.
3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'.

`Default value = 2.`

Value

Genes belonging to each *Fuzzy Patterns*. There are one FP for each class.
Includes an attribute *ifs* with the *Impact Factor* for each category.

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`calculateMembershipFunctions`

Calculates Membership Functions

Description

Calculates the *Membership Functions*. These functions are used in the next step (`discretizeExpressionValues`) to discretize gene expression data.

Usage

```
calculateMembershipFunctions(rmadataset, skipFactor = 3)
```

Arguments

rmadataset	ExpressionSet with numeric values containing gene expression values (rows) of samples belonging to different categories (columns). The ExpressionSet also contains an AnnotatedDataFrame with metadata regarding the classes to which each sample belongs.
skipFactor	Numeric value to omit odd values (a way of normalization). Higher values imply that less samples of a gene are considered as odd. If *skipFactor*=0 do **NOT** skip. Default value = 3. Range[0,).

Value

Membership functions to determine the discret value (linguistic label) corresponding to a given gene expression level.

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discretizeExpressionValues

Function to discretize gene expression data

Description

Discretizes the gene expression data (float values) into 'Low', 'Medium' or 'High' labels.

Usage

```
discretizeExpressionValues(rmadataset, mfs, zeta = 0.5, overlapping = 2)
```

Arguments

rmadataset	ExpressionSet with numeric values containing gene expression values (rows) of samples belonging to different categories (columns). The ExpressionSet also contains an AnnotatedDataFrame with metadata regarding the classes to which each sample belongs.
mfs	*Membership functions* to determine the discret value (linguistic label) corresponding to a given gene expression level.
zeta	Threshold value which controls the activation of a linguistic label ('Low', 'Medium' or 'High'). The lower, the less posibilities of having genes with more than one assigned linguistic label. Default value = 0.5. Range[0,1].
overlapping	Modifies the number of membership functions used in the discretization process. Possible values: 1. 'Low', 'Medium', 'High'. 2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'. 3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'. Default value = 2.

Value

Matrix containing discrete values according to the overlapping parameter after discretizing the gene expression values.
Includes an attribute *types* which determines the category of each sample.

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References

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`discriminantFuzzyPattern` *Discriminant Fuzzy Pattern to filter genes*

Description

discriminantFuzzyPattern discovers significant genes based on the construction of *Fuzzy Patterns* (FPs). The *Fuzzy Patterns* are built by means of applying 3 *Membership Functions* to the gene expression values in the matrix *rmadataset*.

Usage

```
discriminantFuzzyPattern(rmadataset, skipFactor = 3, zeta = 0.5, overlapping = 2, piVal = 0.9)
```

Arguments

`rmadataset`	`ExpressionSet` with numeric values containing gene expression values (rows) of samples belonging to different categories (columns). The `ExpressionSet` also contains an `AnnotatedDataFrame` with metadata regarding the classes to which each sample belongs.
`skipFactor`	Numeric value to omit odd values (a way of normalization). Higher values imply that less samples of a gene are considered as odd. If *skipFactor*=`0` do **NOT** skip. `Default value = 3. Range[0,)`.
`zeta`	Threshold value which controls the activation of a linguistic label ('Low', 'Medium' or 'High'). The lower, the less posibilities of having genes with more than one assigned linguistic label. `Default value = 0.5. Range[0,1]`.
`overlapping`	Modifies the number of membership functions used in the discretization process. Possible values: 1. 'Low', 'Medium', 'High'. 2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'. 3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'. `Default value = 2`.
`piVal`	Controls the degree of exigency for selecting a gene as a member of a *Fuzzy Pattern*. `Default value = 0.9. Range[0,1]`.

Details

The `discriminantFuzzyPattern` function works in a 4-step process:

1. Calculates the *Membership Functions*. These functions are used in the next step to discretize gene expression data.

2. Discretizes the gene expression data (float values) into 'Low', 'Medium' or 'High' labels.
3. Calculates a *Fuzzy Pattern* for each category. To do this, a given percentage of the samples belonging to a category must have the same label ('Low', 'Medium' or 'High').
4. Calculates the *Discriminant Fuzzy Pattern* (DFP) that includes those genes present in two or more FPs with different assigned labels.

Value

`membership.functions`
: *Membership functions* to determine the discret value corresponding to a given gene expression level.

`discrete.values`
: Discrete values according to the overlapping parameter after discretizing the gene expression values.
Includes an attribute *types* which determines the category of each sample.

`fuzzy.patterns`
: Genes belonging to each *Fuzzy Patterns*. There are one FP for each class.
Includes an attribute *ifs* with the *Impact Factor* for each category.

`discriminant.fuzzy.pattern`
: Genes belonging to the final DFP.
Includes an attribute *ifs* with the *Impact Factor* for each category.

`params`
: The parameters used to tune the algorithm (as arguments in the function).

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Examples

```
########################################
############ Get sample data ############
########################################
library(DFP)
data(rmadataset)

########################################
# Filters the most representative genes #
########################################
res <- discriminantFuzzyPattern(rmadataset)
summary(res)
```

`ExpressionLevel-class` *Class "ExpressionLevel"*

Description

A virtual class which represents a generic *Membership Function*.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

`center`**:** Object of class `"numeric"`. Represents the peak point in the function curve.

`width`**:** Object of class `"numeric"`. Represents the length of values lower than 1 and greater than 0 in the function curve.

Methods

show `signature(object = "ExpressionLevel")`: Prints the ExpressionLevel subclass of the object.

setValues `signature(object = "ExpressionLevel", values = "numeric")`: Generic function to be implemented in the subclasses.

computeMembership `signature(object = "ExpressionLevel", x = "numeric")`: Generic function to be implemented in the subclasses.

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Examples

```
showClass("ExpressionLevel")
```

HighExpressionLevel-class
Class "HighExpressionLevel"

Description

A class which represents a *Membership Function* to determine the membership of a numeric value to the 'High' discrete label. The result depends on the 'center' and 'width' values.

Objects from the Class

Objects can be created by calls of the form `new("HighExpressionLevel")`.

Slots

`center`**:** Object of class `"numeric"`. Represents the peak point in the function curve.

`width`**:** Object of class `"numeric"`. Represents the length of values lower than 1 and greater than 0 in the function curve.

Extends

Class `"ExpressionLevel"`, directly.

Methods

setValues `signature(object = "HighExpressionLevel", values = "numeric")`: Establishes the 'center' and 'width' slots of the object, given a vector of numeric values.

computeMembership `signature(object = "HighExpressionLevel", x = "numeric")`: Returns a value in the [0,1] interval, which represents the membership to the 'High' discrete label.

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References

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Examples

```
showClass("HighExpressionLevel")
```

LowExpressionLevel-class
Class "LowExpressionLevel"

Description

A class which represents a *Membership Function* to determine the membership of a numeric value to the 'Low' discrete label. The result depends on the 'center' and 'width' values.

Objects from the Class

Objects can be created by calls of the form `new("LowExpressionLevel")`.

Slots

`center`**:** Object of class `"numeric"`. Represents the peak point in the function curve.

`width`**:** Object of class `"numeric"`. Represents the length of values lower than 1 and greater than 0 in the function curve.

Extends

Class `"ExpressionLevel"`, directly.

Methods

setValues `signature(object = "LowExpressionLevel", values = "numeric")`: Establishes the 'center' and 'width' slots of the object, given a vector of numeric values.

computeMembership `signature(object = "LowExpressionLevel", x = "numeric")`: Returns a value in the [0,1] interval, which represents the membership to the 'Low' discrete label.

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References

F. Diaz; F. Fdez-Riverola; D. Glez-Pena; J.M. Corchado. Using Fuzzy Patterns for Gene Selection and Data Reduction on Microarray Data. 7th International Conference on Intelligent Data Engineering and Automated Learning: IDEAL 2006, (2006) pp. 1095-1102

Examples

```
showClass("LowExpressionLevel")
```

MediumExpressionLevel-class
Class "MediumExpressionLevel"

Description

A class which represents a *Membership Function* to determine the membership of a numeric value to the 'Medium' discrete label. The result depends on the 'center' and 'width' values.

Objects from the Class

Objects can be created by calls of the form `new("MediumExpressionLevel")`.

Slots

`center`: Object of class `"numeric"`. Represents the peak point in the function curve.

`width`: Object of class `"numeric"`. Represents the length of values lower than 1 and greater than 0 in the function curve.

Extends

Class `"ExpressionLevel"`, directly.

Methods

setValues `signature(object = "MediumExpressionLevel", values = "numeric")`: Establishes the 'center' and 'width' slots of the object, given a vector of numeric values.

computeMembership `signature(object = "MediumExpressionLevel", x = "numeric")`: Returns a value in the [0,1] interval, which represents the membership to the 'Medium' discrete label.

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References

F. Diaz; F. Fdez-Riverola; D. Glez-Pena; J.M. Corchado. Using Fuzzy Patterns for Gene Selection and Data Reduction on Microarray Data. 7th International Conference on Intelligent Data Engineering and Automated Learning: IDEAL 2006, (2006) pp. 1095-1102

Examples

```
showClass("MediumExpressionLevel")
```

`plotDiscriminantFuzzyPattern` *Plots the Discriminant Fuzzy Pattern of the relevant genes*

Description

This function plots the *Discriminant Fuzzy Pattern* of the relevant genes (in rows) for the sample classes (in columns), as well as the impact factor which determines if a gene belongs to a *Fuzzy Pattern* in a class (if its value is higher than the *piVal*).
The relevant genes are those which are present in almost two different *Fuzzy Patterns* with different linguistic labels.
The plotting is made in both graphical and text mode.

Usage

```
plotDiscriminantFuzzyPattern(dfp, overlapping = 2)
```

Arguments

`dfp`	A matrix with the fuzzy patterns and impact factors for the relevant genes.
`overlapping`	Modifies the number of membership functions used in the discretization process. Possible values: 1. 'Low', 'Medium', 'High'. 2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'. 3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'. `Default value = 2`.

Value

A matrix with the discriminant genes in rows, along with the *Fuzzy Pattern* for each class (in columns).
This object contains an attribute (`ifs`) which stores the *Impact Factors* used to determine if a gene belongs to a *Fuzzy Pattern* in a class (if the value is higher than the *piVal*).

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References

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`plotMembershipFunctions`

Plots the Membership Functions (Low, Medium, High) used to discretize gene expression values

---

Description

Each gene has 3 *Membership Functions* ('Low', 'Medium' and 'High') which can be plotted as curves in graphical mode.
In the text mode a membership function is represented with its *center* and *width*.
This function receives one or more gene names and plots the results in both graphical and text mode.
If a set of genes containing more than 36 elements is provided, only the text mode is available.

Usage

```
plotMembershipFunctions(rmadataset, mfs, genes)
```

Arguments

`rmadataset`	An `ExpressionSet` object with `AnnotatedDataFrame` metadata.
`mfs`	A list of 3 ExpressionLevel objects ('Low', 'Medium' and 'High') for each gene (a list of lists).
`genes`	The set of genes to plot (a vector).

Value

A dataframe with the values of the membership functions ('Low', 'Medium' and 'High') for each gene (in rows) received as a parameter.

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readCSV *Creates an ExpressionSet with an AnnotatedDataFrame from CSV files*

Description

This function creates an ExpressionSet with an AnnotatedDataFrame. To do this, it requires two CSV files in a predefined format:

1. 'exprsData' with the expression values of genes (in rows) of different samples (in columns).
2. 'pData' with the samples (in columns) and the metadata 'class' (the most important for the algorithm discriminantFuzzyPattern), 'age' and 'sex'.

Usage

```
readCSV(fileExprs, filePhenodata)
```

Arguments

fileExprs	The path to the exprsData file.
filePhenodata	The path to the pData file.

Value

An ExpressionSet object with an AnnotatedDataFrame storing 'class', 'age' and 'sex' information.

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References

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Examples

```
dataDir <- system.file("extdata", package="DFP"); dataDir
fileExprs <- file.path(dataDir, "exprsData.csv"); fileExprs
filePhenodata <- file.path(dataDir, "pData.csv"); filePhenodata
rmadataset <- readCSV(fileExprs, filePhenodata); rmadataset
pData(phenoData(rmadataset))
exprs(rmadataset)[1:10,1:5]
```

rmadataset *A sample ExpressionSet object*

Description

This ExpressionSet object includes an AnnotatedDataFrame with metadata about 'Disease type' (the most important for the algorithm), 'Patient age' and 'Patient gender'.
This data set gives the expression values of 500 genes in 35 samples.

Usage

```
data(rmadataset)
```

Format

ExpressionSet	`str(pData(phenoData(rmadataset)))`
AnnotatedDataFrame	`str(exprs(rmadataset))`

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Examples

```
data(rmadataset)
featureNames(rmadataset)[1:20]
sampleNames(rmadataset)
varLabels(rmadataset)
pData(phenoData(rmadataset))
exprs(rmadataset)[1:10,1:5]
```

---

show-methods *Prints the slots (attributes) of an ExpressionLevel object*

Description

Prints the slots (center and width) of an "ExpressionLevel" object.

Methods

object = "ExpressionLevel" See "ExpressionLevel".

---

showDiscreteValues *Prints the labels to which the algorithm converts the gene expression values*

Description

In an intermediate step, the algorithm discriminantFuzzyPattern converts the gene expression values into discrete labels (combining 'Low', 'Medium' and 'High', depending on the value of the param 'overlapping').
This function permits printing these labels, specifying a set of genes (a vector) and/or classes of samples.

Usage

```
showDiscreteValues(dvs, genes, classes)
```

Arguments

dvs	A matrix with discrete labels for a set of genes (in rows) of several samples (in columns).
genes	[optional] The set of genes to plot.
classes	[optional] A set of classes to which the samples belong. It must be one of the classes stored in the phenoData of the original ExpressionSet object.

Value

A subset of the matrix dvs determined by the restrictions (genes and/or classes).

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References

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`showFuzzyPatterns` *Plots the Fuzzy Patterns corresponding to a class*

Description

This functions prints (in text mode) the *Fuzzy Patterns* (discrete labels) calculated for a single class of samples.

Usage

```
showFuzzyPatterns(fps, class)
```

Arguments

`fps`	A matrix with the *Fuzzy Patterns* (discrete labels) for all the samples and genes.
`class`	A class to which the samples belong. It must be one of the classes stored in the phenoData of the original `ExpressionSet` *rmadataset* object.

Value

A vector of *Fuzzy Patterns* (discrete labels) for a single class of samples, with the genes associated.

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References

F. Diaz; F. Fdez-Riverola; D. Glez-Pena; J.M. Corchado. Using Fuzzy Patterns for Gene Selection and Data Reduction on Microarray Data. 7th International Conference on Intelligent Data Engineering and Automated Learning: IDEAL 2006, (2006) pp. 1095-1102

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