

DFP

October 5, 2010

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`.

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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(rmadata)

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

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

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.

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

References

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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.

Author(s)

Rodrigo Alvarez-Gonzalez
 Daniel Glez-Pena
 Fernando Diaz
 Florentino Fdez-Riverola
 Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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.

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

References

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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.

Author(s)

Rodrigo Alvarez-Gonzalez
 Daniel Glez-Pena
 Fernando Diaz
 Florentino Fdez-Riverola
 Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

References

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Examples

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

```
calculateDiscriminantFuzzyPattern
```

Calculates the Discriminant Fuzzy Pattern to select significant 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 meta-data regarding the classes to which each sample belongs.
fps	Genes belonging to each <i>Fuzzy Patterns</i> . There are one FP for each class. Includes an attribute <i>ifs</i> with the <i>Impact Factor</i> for each category.

Value

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

Author(s)

Rodrigo Alvarez-Gonzalez
 Daniel Glez-Pena
 Fernando Diaz
 Florentino Fdez-Riverola
 Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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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 meta-data 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 <i>types</i> which determines the category of each sample.
piVal	Controls the degree of exigency for selecting a gene as a member of a <i>Fuzzy Pattern</i> . Default value = 0.9. Range[0,1].
overlapping	Modifies the number of membership functions used in the discretization process. Possible values: <ol style="list-style-type: none"> 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.

Author(s)

Rodrigo Alvarez-Gonzalez
 Daniel Glez-Pena
 Fernando Diaz
 Florentino Fdez-Riverola
 Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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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

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

Value

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

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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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

- | | |
|--------------------------|---|
| <code>rmadataSet</code> | <code>ExpressionSet</code> with numeric values containing gene expression values (rows) of samples belonging to different categories (columns).
The <code>ExpressionSet</code> also contains an <code>AnnotatedDataFrame</code> with meta-data regarding the classes to which each sample belongs. |
| <code>mfs</code> | <i>Membership functions</i> to determine the discret value (linguistic label) corresponding to a given gene expression level. |
| <code>zeta</code> | Threshold value which controls the activation of a linguistic label ('Low', 'Medium' or 'High').
The lower, the less possibilities of having genes with more than one assigned linguistic label.
Default value = 0.5. Range[0,1]. |
| <code>overlapping</code> | Modifies the number of membership functions used in the discretization process.
Possible values: <ol style="list-style-type: none">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.

Author(s)

Rodrigo Alvarez-Gonzalez

Daniel Glez-Pena

Fernando Diaz

Florentino Fdez-Riverola

Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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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)
```

Arguments

- | | |
|--------------------------|--|
| <code>rmadataset</code> | <code>ExpressionSet</code> with numeric values containing gene expression values (rows) of samples belonging to different categories (columns).
The <code>ExpressionSet</code> also contains an <code>AnnotatedDataFrame</code> with meta-data regarding the classes to which each sample belongs. |
| <code>skipFactor</code> | Numeric value to omit odd values (a way of normalization).
Higher values imply that less samples of a gene are considered as odd. If <i>skipFactor</i> =0 do NOT skip.
Default value = 3. Range[0,). |
| <code>zeta</code> | Threshold value which controls the activation of a linguistic label ('Low', 'Medium' or 'High').
The lower, the less possibilities of having genes with more than one assigned linguistic label.
Default value = 0.5. Range[0, 1]. |
| <code>overlapping</code> | Modifies the number of membership functions used in the discretization process.
Possible values: <ol style="list-style-type: none"> 'Low', 'Medium', 'High'. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'. Default value = 2. |
| <code>piVal</code> | Controls the degree of exigency for selecting a gene as a member of a <i>Fuzzy Pattern</i> .
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

<code>membership.functions</code>	<i>Membership functions</i> to determine the discret value corresponding to a given gene expression level.
<code>discrete.values</code>	Discrete values according to the overlapping parameter after discretizing the gene expression values. Includes an attribute <i>types</i> which determines the category of each sample.
<code>fuzzy.patterns</code>	Genes belonging to each <i>Fuzzy Patterns</i> . There are one FP for each class. Includes an attribute <i>ifs</i> with the <i>Impact Factor</i> for each category.
<code>discriminant.fuzzy.pattern</code>	Genes belonging to the final DFP. Includes an attribute <i>ifs</i> with the <i>Impact Factor</i> for each category.
<code>params</code>	The parameters used to tune the algorithm (as arguments in the function).

Author(s)

Rodrigo Alvarez-Gonzalez
 Daniel Glez-Pena
 Fernando Diaz
 Florentino Fdez-Riverola
 Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

References

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Examples

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

#####
# Filters the most representative genes #
```

```
#####
res <- discriminantFuzzyPattern(rmadataset)
summary(res)
```

```
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: <ol style="list-style-type: none"> 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*).

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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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

<code>rmadataset</code>	An ExpressionSet object with AnnotatedDataFrame metadata.
<code>mfs</code>	A list of 3 ExpressionLevel objects ('Low', 'Medium' and 'High') for each gene (a list of lists).
<code>genes</code>	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.

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

References

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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.

Author(s)

```
Rodrigo Alvarez-Gonzalez  
Daniel Glez-Pena  
Fernando Diaz  
Florentino Fdez-Riverola  
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>
```

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

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

rmadatASET	<i>A sample ExpressionSet object</i>
------------	--------------------------------------

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(rmdatASET)
```

Format

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

Author(s)

Rodrigo Alvarez-Gonzalez
 Daniel Glez-Pena
 Fernando Diaz
 Florentino Fdez-Riverola
 Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

References

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Examples

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

show-methods	<i>Prints the slots (attributes) of an ExpressionLevel object</i>
--------------	---

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`).

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

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 <i>Fuzzy Patterns</i> (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 <i>rmadataset</i> object.

Value

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

Author(s)

Rodrigo Alvarez-Gonzalez
Daniel Glez-Pena
Fernando Diaz
Florentino Fdez-Riverola
Maintainer: Rodrigo Alvarez-Gonzalez <<rodrigo.djv@uvigo.es>>

References

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