

# Package ‘DFP’

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**Title** Gene Selection

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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.

**License** GPL-2

**biocViews** Microarray, DifferentialExpression

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| DFP-package | <i>DFP Package Overview</i> |
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## 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  
 Date: 2008-07-03  
 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)

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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 | <a href="#">ExpressionSet</a> with numeric values containing gene expression values (rows) of samples belonging to different categories (columns).<br>The <a href="#">ExpressionSet</a> also contains an <a href="#">AnnotatedDataFrame</a> with metadata regarding the classes to which each sample belongs. |
| fps        | Genes belonging to each <i>Fuzzy Patterns</i> . There are one FP for each class.<br>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.

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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

---

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  | <a href="#">ExpressionSet</a> with numeric values containing gene expression values (rows) of samples belonging to different categories (columns).<br>The <a href="#">ExpressionSet</a> also contains an <a href="#">AnnotatedDataFrame</a> 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.<br>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> .<br>Default value = 0.9. Range[0,1].                                                                                                                                                                                                                               |
| overlapping | Modifies the number of membership functions used in the discretization process.<br>Possible values:<br><ol style="list-style-type: none"> <li>1. 'Low', 'Medium', 'High'.</li> <li>2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'.</li> <li>3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'.</li> </ol> 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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**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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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 | <a href="#">ExpressionSet</a> with numeric values containing gene expression values (rows) of samples belonging to different categories (columns).<br>The <a href="#">ExpressionSet</a> also contains an <a href="#">AnnotatedDataFrame</a> with metadata regarding the classes to which each sample belongs. |
| skipFactor | Numeric value to omit odd values (a way of normalization).<br>Higher values imply that less samples of a gene are considered as odd. If <i>skipFactor</i> =0 do <b>NOT</b> skip.<br>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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## 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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|              |                             |
|--------------|-----------------------------|
| DFP-internal | <i>Internal DFP objects</i> |
|--------------|-----------------------------|

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## Description

Internal DFP objects.

## Details

These are not to be called by the user.

---

|                            |                                                    |
|----------------------------|----------------------------------------------------|
| discretizeExpressionValues | <i>Function to discretize gene expression data</i> |
|----------------------------|----------------------------------------------------|

---

## Description

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

## Usage

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

## Arguments

|             |                                                                                                                                                                                                                                                                                                                                                                |
|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| rmadatastet | <a href="#">ExpressionSet</a> with numeric values containing gene expression values (rows) of samples belonging to different categories (columns).<br>The <a href="#">ExpressionSet</a> also contains an <a href="#">AnnotatedDataFrame</a> with metadata regarding the classes to which each sample belongs.                                                  |
| mfs         | <i>Membership functions</i> 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').<br>The lower, the less possibilities of having genes with more than one assigned linguistic label.<br>Default value = 0.5. Range[0,1].                                                                                                                        |
| overlapping | Modifies the number of membership functions used in the discretization process.<br>Possible values:<br><ol style="list-style-type: none"> <li>1. 'Low', 'Medium', 'High'.</li> <li>2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'.</li> <li>3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'.</li> </ol> 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**

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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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  | <a href="#">ExpressionSet</a> with numeric values containing gene expression values (rows) of samples belonging to different categories (columns).<br>The <a href="#">ExpressionSet</a> also contains an <a href="#">AnnotatedDataFrame</a> with metadata regarding the classes to which each sample belongs. |
| skipFactor  | Numeric value to omit odd values (a way of normalization).<br>Higher values imply that less samples of a gene are considered as odd. If <i>skipFactor</i> =0 do <b>NOT</b> skip.<br>Default value = 3. Range[0, ).                                                                                            |
| zeta        | Threshold value which controls the activation of a linguistic label ('Low', 'Medium' or 'High').<br>The lower, the less possibilities of having genes with more than one assigned linguistic label.<br>Default value = 0.5. Range[0, 1].                                                                      |
| overlapping | Modifies the number of membership functions used in the discretization process.<br>Possible values:                                                                                                                                                                                                           |

|       |                                                                                                                                                                                                                                      |
|-------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|       | <ol style="list-style-type: none"> <li>1. 'Low', 'Medium', 'High'.</li> <li>2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'.</li> <li>3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'.</li> </ol> |
|       | Default value = 2.                                                                                                                                                                                                                   |
| piVal | Controls the degree of exigency for selecting a gene as a member of a <i>Fuzzy Pattern</i> .<br>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       | <i>Membership functions</i> 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.<br>Includes an attribute <i>types</i> which determines the category of each sample. |
| fuzzy.patterns             | Genes belonging to each <i>Fuzzy Patterns</i> . There are one FP for each class.<br>Includes an attribute <i>ifs</i> with the <i>Impact Factor</i> for each category.                     |
| discriminant.fuzzy.pattern | Genes belonging to the final DFP.<br>Includes an attribute <i>ifs</i> with the <i>Impact Factor</i> for each category.                                                                    |
| params                     | The parameters used to tune the algorithm (as arguments in the function).                                                                                                                 |

## Author(s)

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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)

#####
# 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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**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("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**

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("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)

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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.

### Author(s)

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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.<br>Possible values:<br><ol style="list-style-type: none"> <li>1. 'Low', 'Medium', 'High'.</li> <li>2. 'Low', 'Low-Medium', 'Medium', 'Medium-High', 'High'.</li> <li>3. 'Low', 'Low-Medium', 'Low-Medium-High', 'Medium', 'Medium-High', 'High'.</li> </ol> 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)

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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

---

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 <a href="#">ExpressionSet</a> object with <a href="#">AnnotatedDataFrame</a> 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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## 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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|         |                                                                           |
|---------|---------------------------------------------------------------------------|
| readCSV | <i>Creates an ExpressionSet with an AnnotatedDataFrame from CSV files</i> |
|---------|---------------------------------------------------------------------------|

---

## 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)

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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  
rmdatASET <- readCSV(fileExprs, filePhenodata); rmdatASET  
pData(phenoData(rmdatASET))  
exprs(rmdatASET)[1:10,1:5]
```

---

`rmdatASET`*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(rmdatASET)
```

## Format

|                                 |                                               |
|---------------------------------|-----------------------------------------------|
| <code>ExpressionSet</code>      | <code>str(pData(phenoData(rmdatASET)))</code> |
| <code>AnnotatedDataFrame</code> | <code>str(exprs(rmdatASET))</code>            |

## Author(s)

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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

```
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 | <i>Prints the labels to which the algorithm converts the gene expression values</i> |
|--------------------|-------------------------------------------------------------------------------------|

---

### 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 <a href="#">ExpressionSet</a> object. |

### Value

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

### Author(s)

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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

---

|                   |                                                          |
|-------------------|----------------------------------------------------------|
| showFuzzyPatterns | <i>Plots the Fuzzy Patterns corresponding to a class</i> |
|-------------------|----------------------------------------------------------|

---

## 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 <a href="#">ExpressionSet</a> <i>rmadataset</i> object. |

## Value

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

## Author(s)

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 Daniel Glez-Pena  
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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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