Package ‘UNDO’

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biocViews Software
Description UNDO is an R package for unsupervised deconvolution of tumor and stromal mixed expression data. It detects marker genes and deconvolutes the mixing expression data without any prior knowledge.
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Implementation of UNDO (unsupervised deconvolution of tumor-stromal mixed expressions)

Description

This package contains main function "two_source_deconv" to implement the deconvolution of mixed tumor-stromal expressions in a completely unsupervised way. The prior knowledge of mixing matrix or pure expression is not needed. The package detects marker genes and calculate the mixing matrix and pure expressions automatically.

Details

Package: UNDO
Type: Package
Version: 1.7.3
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two_source_deconv(ExpressionData,lowper=0.4,highper=0.1,epsilon1=0.01,epsilon2=0.01,A=NULL,S1=NULL,S2=NULL,return=0)

Author(s)

Niya Wang <wangny@vt.edu>

Examples

data(NumericalMixMCF7HS27)
X <- NumericalMixMCF7HS27
deconvResult <- two_source_deconv(X, lowper = 0.4, highper = 0.1, epsilon1 = 0.01, epsilon2 = 0.01, A = NULL, S1 = NULL, S2 = NULL)
BiologicalMixMCF7HS27  MCF7 and HS27 biologically mixed

Description

Expression data from MCF7 and HS27 biologically mixing

Usage

data(BiologicalMixMCF7HS27)

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ...
@ experimentData: Formal class 'MIAME' [package "Biobase"] with 13 slots ...
@ samples: list() ...
@ hybridizations: list() ...
@ normControls: list() ...
@ preprocessing: list() ...
@ other: list() ...
@ __classVersion__: Formal class 'Versions' [package "Biobase"] with 1 slots ...
@ data.frame: 2 obs. of 0 variables ...
@ dimLabels: chr[1:2] "sampleNames" "sampleColumns"

Examples

data(BiologicalMixMCF7HS27)
str(BiologicalMixMCF7HS27)
calc_E1  
*function calculating the E1 measurement*

**Description**
A function used to calculate the E1 measurement when the real mixing matrix is provided.

**Usage**
calc_E1(A, Aest)

**Arguments**
- A: real mixing matrix
- Aest: estimated mixing matrix

**Value**
E1 measurement (numeric)

**Author(s)**
Niya Wang <wangny@vt.edu>

**Examples**
```
A <- matrix(runif(4),2,2)
Aest <- matrix(runif(4),2,2)
E1 <- calc_E1(A,Aest)  # to calculate the similarity of two random 2x2 matrix
```

---

dimension_reduction  
*Dimension reduction function*

**Description**
When the number of input samples is larger than 2, this function is called to reduce the dimension to 2 by using PCA.

**Usage**
dimension_reduction(X)

**Arguments**
- X: gene expression data matrix
**gene_expression_input**

**Value**
- `X`

**dimenMatrix**
the dimension reduction matrix used to recover the mixing matrix for all the samples

**Author(s)**
Niya Wang (wangny@vt.edu)

**Examples**

```r
X <- matrix(runif(5000),1000,5)
dimenResult <- dimension_reduction(X)
```

---

**gene_expression_input**  *Detect whether the input gene expression data are valid*

**Description**
Check the input gene expression data to see whether they are nonempty, nonnegative, etc.

**Usage**
```
gene_expression_input(X)
```

**Arguments**
- `X` gene expression data matrix with row representing genes/probe sets, and column representing samples.

**Value**
If the input is valid, the output will be the same as the input; otherwise, if the input contains NA, the corresponding rows will be deleted. if the input contains negative value, the algorithm will stop and give error information.

**Author(s)**
Niya Wang (wangny@vt.edu)

**Examples**
```
gene_expression <- matrix(runif(2000),1000,2)
valid_gene_expression <- gene_expression_input(gene_expression)
```
marker_gene_selection  \hspace{1em} Select marker genes in two sources

**Description**

Select the marker genes in tumor and stroma in an unsupervised way

**Usage**

marker_gene_selection(X, lowper, highper, epsilon1, epsilon2)

**Arguments**

- **X** \hspace{1em} gene expression data
- **lowper** \hspace{1em} The percentage of genes the user wants to remove with lowest norm. The range should be between 0 and 1.
- **highper** \hspace{1em} The percentage of genes the user wants to remove with highest norm. The range should be between 0 and 1.
- **epsilon1** \hspace{1em} Influence the number of marker genes. With increasing of epsilon1, the number marker genes in source 1 will increase. The value should be positive.
- **epsilon2** \hspace{1em} Influence the number of marker genes. With increasing of epsilon1, the number marker genes in source 2 will increase. The value should be positive.

**Value**

- **a1** \hspace{1em} The slope of marker genes in source 1
- **a2** \hspace{1em} The slope of marker genes in source 2
- **MG1** \hspace{1em} The gene list of marker genes in source 1
- **MG2** \hspace{1em} The gene list of marker genes in source 2
- **dimenMatrix** \hspace{1em} dimension reduction matrix

**Author(s)**

Niya Wang (wangny@vt.edu)

**Examples**

X <- matrix(runif(20000), 10000, 2)
MG_set <- marker_gene_selection(X, 0.4, 0.1, 0.1, 0.1)
mixing_matrix_computation

Calculate and scale the mixing matrix

Description

Calculate the mixing matrix based on the output from marker_gene_selection(), and scale the mixing matrix to make the sum of proportions from tumor and stroma equal to 1. The pure expression levels of tumor and stroma are also computed.

Usage

mixing_matrix_computation(X, a1, a2, dimenMatrix)

Arguments

X Gene expression data matrix
a1 The slope of marker genes in source 1
a2 The slope of marker genes in source 2
dimenMatrix The dimention reduction matrix used to recover mixing matrix for all the samples

Value

Aest estimated mixing matrix
Sest estimated pure gene expression of two sources

Author(s)

Niya Wang (wangny@vt.edu)

Examples

a1<- matrix(runif(2),2,1)
a2<- matrix(runif(2),2,1)
X <- 1000*matrix(runif(20000),10000,2)
dimenMatrix <- NULL
Deconv <- mixing_matrix_computation(X, a1, a2, dimenMatrix)
NumericalMixMCF7HS27

Description

real mixing matrix of data NumericalMixMCF7HS27

Usage

data(NumericalMixMCF7HS27)

Format

The format is: num [1:2, 1:2] 0.775 0.15 0.225 0.85 - attr(*, "dimnames")=List of 2 ..$ : NULL ..$ : chr [1:2] "V1" "V2"

Examples

data(NumericalMixMCF7HS27)
str(NumericalMixMCF7HS27)

NumericalMixMCF7HS27  MCF7 and HS27 numerically mixed

Description

Expression data from MCF7 and HS27 numerically mixing

Usage

data(NumericalMixMCF7HS27)

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots ..@ name : chr "" ..@ lab : chr "" ..@ title : chr "" ..@ abstract : chr "" ..@ url : chr "" ..@ pubMedIds : chr "" ..@ samples : list() ..@ hybridizations : list() ..@ normControls : list() ..@ preprocessing : list() ..@ other : list() ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots ..@ assayData :<environment: 0x000000000e86a5d0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots ..@ varMetadata :'data.frame': 0 obs. of 1 variable: ..@ data :'data.frame': 2 obs. of 0 variables ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots ..@ .Data:List of 1 ..@ .featureData :Formal class 'AnnotatedDataFrame'
Examples

data(NumericalMixMCF7HS27)
str(NumericalMixMCF7HS27)

Description

pure MCF7 and HS27 expression data

Usage

data(PureMCF7HS27)

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots
@ experimentData:Formal class 'MIAME' [package "Biobase"] with 13 slots
@ name: chr "" ...
@ lab: chr "" ...
@ contact: chr "" ...
@ title: chr "" ...
@ abstract: chr "" ...
@ url: chr "" ...
@ pubMedIds: chr "" ...
@ samples: list() ...
@ hybridizations: list() ...
@ normControls: list() ...
@ preprocessing: list() ...
@ other: list() ...
@ __classVersion__: Formal class 'Versions' [package "Biobase"] with 1 slots
@ .Data:List of 2
@ assayData: <environment: 0x000000000e979d20>
@ phenoData: Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
@ varMetadata: formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
@ .Data:List of 1
@ featureData: Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
@ .Data:List of 1
@ .Data:List of 1

Examples

data(NumericalMixMCF7HS27)
str(NumericalMixMCF7HS27)
two_source_deconv


Examples

data(PureMCF7HS27)
str(PureMCF7HS27)

two_source_deconv Main function to call other subfunction to deconvolute the mixed expression data.

Description

This is the main function that is to call all the other subfunctions and realize the deconvolution of mixed expression data. When the real mixing matrix exist, it will also compare the estimated mixing matrix and real mixing matrix and give the E1 measurement.

Usage

two_source_deconv(ExpressionData, lowper = 0.4, highper = 0.1, epsilon1 = 0.01, epsilon2 = 0.01, A = NULL, S1 = NULL, S2 = NULL, return = 0)

Arguments

ExpressionData gene expression data matrix/ExpressionSet object
lowper The percentage of genes the user wants to remove with lowest norm. The range should be between 0 and 1.
highper The percentage of genes the user wants to remove with highest norm. The range should be between 0 and 1.
epsilon1 Influence the number of marker genes. With increasing of epsilon1, the number marker genes in source 1 will increase. The value should be positive.
epsilon2 Influence the number of marker genes. With increasing of epsilon1, the number marker genes in source 2 will increase. The value should be positive.
A real mixing matrix if existing
S1 Pure expression profile of first source if existing
S2 Pure expression profile of second source if existing
return if it is equal to 0, do not return estimated S; otherwise, return the estimated S.
two_source_deconv

Value

Aest     estimated mixing matrix
E1       E1 measurement between real and estimated mixing matrix

Author(s)

Niya Wang (wangny@vt.edu)

Examples

data(NumericalMixMCF7HS27)
X <- NumericalMixMCF7HS27
decovResult <- two_source_deconv(X, lowper = 0.4, highper = 0.1, epsilon1 = 0.1, epsilon2 = 0.1, A = NULL, S1=NULL, S2=NULL, return = 0)
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