Package 'tWLSA'

December 14, 2020

Type Package

Title Two way Kernel Weighted Least Squate Approach for Missing Value Imputation of Metabolomics Data

Version 1.0

Date 2020-12-14

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Description Missing value imputation technique by minimizing two-way kernel weighted square error loss function

License GPL (>= 2)

R topics documented:

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tWLSA-package	*Two way weighted least square approach for missing value imputation of metabolomics data Two way Kernel Weighted Least Squate Approach for Missing Value Imputation of Metabolomics Data*

Description

This package implements a Kernel weight based two way weighted least square approach for missing value imputation of metabolomics data

Package:	tWLSA
Type:	Package
Version:	1.0

Date:	2020-12-14
License:	GPL
Depends:	R (>=2.10)

Package tWLSA has the following functions:

chkMiss():	This function check the missing values in the dataset function.
chkOutliers():	This function Checks row wise outliers in a data matrix function.
chkOutMiss():	This function Checks both outliers and missing values data matrix function.
missChkOut():	This function clean the outliers function.
wlsMisImp():	This function impute the missing values using two way kernel weight based least square approach

Nishith Kumar
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package

| chkMiss | *Checking Missing cell in a data matrix* |

Description

This function will check whether the data matrix contains missing values or not.

Usage

```
chkMiss(x)
```

Arguments

x   Metabolomics Data Matrix, whose row contains metabolites and column contains subjects

Value

Provide message about the missing values in the data matrix

Author(s)

Nishith Kumar <nk.bru09@gmail.com>

Examples

```
data(dummyDataMiss)
chkMiss(dummyDataMiss)
```

---

chkOutliers   *Checking row wise outliers in a data matrix*

Description

This function check the row-wise outliers in the data matrix using IQR rule.

Usage

```
chkOutliers(x)
```

Arguments

x   Metabolomics data matrix

Details

Checking the row-wise outliers in the data matrix using IQR rule

Value

Provide the information whether the data matrix contain outliers or not.

Author(s)

Nishith Kumar <nk.bru09@gmail.com>

Examples

```
data(dummyDataFull)
chkOutliers(dummyDataFull)
```

---

chkOutMiss   *Checking outliers and missing values data matrix*

Description

Checking outliers and missing values data matrix

Usage

```
chkOutMiss(x)
```

Arguments

x   Metabolomics data matrix

Details

This function will Check both the outliers and missing values data matrix

Value

Provide the information whether the data matrix contain both the outliers and missing values or not.

Author(s)

Nishith Kumar <nk.bru09@gmail.com>

Examples

```
data(dummyDataMiss)
chkOutMiss(dummyDataMiss)
```

---

dummyDataFull   *Dummy Metabolomics Data matrix*

Description

Dummy Metabolomics Data matrix with no missing values

Usage

```
data("dummyDataFull")
```

Format

The format is: num [1:40, 1:45] 0.678 0.671 0.651 5.645 2.437 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:40] "Guanidoacetate" "O-Acetylcarnitine" "2-Aminobutyrate" "Formate" ... ..$: chr [1:45] "Cancer_1" "Cancer_2" "Cancer_3" "Cancer_4" ...

Details

Dummy Metabolomics Data matrix with no missing values

Source

Dummy Data

Examples

```
data(dummyDataFull)
## maybe str(dummyDataFull) ; plot(dummyDataFull) ...
```

---

dummyDataMiss   *Dummy Metabolomics Dataset with Missing values*

Description

Dummy Metabolomics Dataset with Missing values

Usage

```
data("dummyDataMiss")
```

Format

The format is: num [1:40, 1:45] 0.678 NA 0.651 5.645 NA ... - attr(*, "dimnames")=List of 2 ..$: chr [1:40] "Guanidoacetate" "O-Acetylcarnitine" "2-Aminobutyrate" "Formate" ... ..$: chr [1:45] "Cancer_1" "Cancer_2" "Cancer_3" "Cancer_4" ...

Details

Dummy Metabolomics Dataset with Missing values

Examples

```
data(dummyDataMiss)
## maybe str(dummyDataMiss) ; plot(dummyDataMiss) ...
```

---

missChkOut   *Outliers Cleaning*

Description

Checking Outliers using IQR rule and replaced it into the group median

Usage

```
missChkOut(x)
```

Arguments

x   Metabolomics Data Matrix

Value

Modified Metabolomics Data Matrix by cleaning Outliers

Author(s)

Nishith Kumar <nk.bru09@gmail.com>

Examples

```
data(dummyDataFull)
modiData<-missChkOut(dummyDataFull)
```

---

wlsMisImp   *Two way kernel weight based least square approach for missing value imputation*

Description

Two way kernel weight based least square approach for missing value imputation

Usage

```
wlsMisImp(x, lamda = 0.1, conRate = 99, group = 1, noGrpMem = c(ncol(x)), outlier = TRUE)
```

Arguments

x	Metabolomics Data Matrix
lamda	Tuning parameter. Default is 0.1
conRate	Percent of variation explained by the modiffied dataset. Default is 99.
group	Number of group in the dataset. Default is 1.
noGrpMem	Number of subject of each group.
outlier	Outlier condition TRUE/FALSE.

Value

Reconstructed data matrix after inputing missing values

Author(s)

Nishith Kumar<nk.bru09@gmail.com>

Examples

```
data(dummyDataMiss)
recData<-wlsMisImp(dummyDataMiss)
```

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