

# Package ‘tscR’

January 11, 2023

**Type** Package

**Title** A time series clustering package combining slope and Frechet distances

**Version** 1.11.0

**Description** Clustering for time series data using slope distance and/or shape distance.

**License** Artistic-2.0

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combineCluster	<i>Combine clusters function</i>
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## Description

Combine clusters from two different clustering

## Usage

```
combineCluster(x, y)
```

## Arguments

x	Object of class pam. Output of getClusters.
y	Object of class pam. Output of getClusters.

## Details

This function combines the clusters obtained in getClusters with 'slope' distance and the ones obtained with Frechet distance, resulting in a new clustering combining both distances.

## Value

Object of class 'pam'. See [pam.object](#) for details

## Author(s)

Fernando Pérez-Sanz (<fernando.perez8@um.es>)  
 Miriam Riquelme-Pérez (<miriam.riquelmep@gmail.com>)

## See Also

[getClusters](#), [plotCluster](#)

**Examples**

```
data(tscR)
data <- tscR
time <- c(1,2,3)
dist_slope <- slopeDist(data, time)
dist_frechet <- frechetDistC(data, time)
slope.cluster <- getClusters(dist_slope, 3)
frechet.cluster <- getClusters(dist_frechet, 4)
comb.cluster <- combineCluster(slope.cluster, frechet.cluster)
```

---

frechetDist

*Pairwise Frechet distance*

---

**Description**

Compute pair-wise Frechet distance in a matrix of trajectories

**Usage**

```
frechetDist(x, time, ...)
```

**Arguments**

x	Numeric matrix or data.frame with trajectory values. Rows are trajectories, columns are time or similar. SummarizedExperiment object can be provided for compatibility with bioconductor container (for more information see vignette).
time	Numeric vector with time data (time intervals), with equal length to columns number in x.
...	Other arguments to pass to importFromSE if <code>_x_</code> is SummarizedExperiment-class.

**Details**

This function is a wrapper of the `distFrechet` code from `kmlShape` package for use with a matrix or a data.frame so that the user can compute pairwise distances between all trajectories.

**Value**

A dist class object of size  $N \times N$ , where  $N$  is rows number in the input data

**Author(s)**

Fernando Pérez-Sanz (<fernando.perez8@um.es>)

Miriam Riquelme-Pérez (<miriam.riquelmep@gmail.com>)

**See Also**

[distFrechet](#) (package `kmlShape`), [slopeDist](#), [frechetDistC](#) (C and faster version than `frechetDist`), [importFromSE](#).

**Examples**

```
data(tscR)
data <- tscR
time <- c(1,2,3)
dist_tscR <- frechetDist(data, time)
```

---

frechetDistC	<i>Pairwise Frechet distance (C version)</i>
--------------	--

---

**Description**

Compute pairwise Frechet distance in a matrix of trajectories. This function is a C implementation and a lot faster version than `frechetDist`

**Usage**

```
frechetDistC(x, time, ...)
```

**Arguments**

<code>x</code>	Numeric matrix or <code>data.frame</code> with trajectory values. Rows are trajectories, columns are time or similar. <code>SummarizedExperiment</code> object can be provided for compatibility with <code>bioconductor</code> container (for more information see vignette).
<code>time</code>	Numeric vector with time data (time intervals), with equal length to columns number in <code>x</code> .
<code>...</code>	Other arguments to pass to <code>importFromSE</code> if <code>_x_</code> is <code>SummarizedExperiment</code> -class.

**Details**

This function is a C adaptation of the `distFrechet` code from `kmlShape` package for use with a matrix or a `dataframe` so that the user can compute pairwise distances between all trajectories.

It is highly recommended to use this function over `frechetDist` because it is a lot faster.

**Value**

A `dist` class object of size  $N \times N$ , where  $N$  is rows number in the input data

**Author(s)**

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Miriam Riquelme-Pérez (<miriam.riquelmep@gmail.com>)

**See Also**

[distFrechet](#) (package kmlShape), [slopeDist](#), [frechetDist](#) (R and slower versión than [frechetDistC](#)), [importFromSE](#).

**Examples**

```
data(tscR)
data <- tscR
time <- c(1,2,3)
dist_tscR <- frechetDistC(data, time)
```

---

getClusters

*Generic clustering function*

---

**Description**

Compute clustering with pam function and a distance class object.

**Usage**

```
getClusters(x, k)
```

**Arguments**

x	Numeric distance object obtained with dimension n x n.
k	Numeric. Number of clusters

**Details**

This function is a wrapper of `pam` (`cluster`). `x` must be a `dist` object obtained from `frechetdist`, `slopedist` or any other distance metric on condition that it be an object of the `dist` class and has dimensions `nxn`, where `n` is equal to the number of trajectories.

**Value**

Object of class 'pam'. See [pam.object](#) for details

**Author(s)**

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Miriam Riquelme-Pérez (<miriam.riquelmep@gmail.com>)

**See Also**

[pam](#), [plotCluster](#).

**Examples**

```
data(tscR)
data <- tscR
time <- c(1,2,3)
dist_tscR <- slopeDist(data, time)
res.cluster <- getClusters(dist_tscR, 3)
```

---

importFromSE

*Convenient import from a SummarizedExperiment object*


---

**Description**

Import a summarizedExperiment object containing expression data at different times.

**Usage**

```
importFromSE(se, sample, SE_byTime = FALSE)
```

**Arguments**

se	SummarizedExperiment. Where assays slot can be organized either by samples or by times.
sample	Numeric or character. Sample identifier. See details and vignette
SE_byTime	Logical. Default FALSE. Indicates whether the data is organized by sample or by time.

**Details**

This function enables the integration of an object of the summarizedExpmeriment class and is integrated into all other functions, so there is no need to run it in an isolated way. There are two possible organization options in the slot assays. A) each row is a gene each column, is a sample and each matrix is a time. In this case SE\_byTime=FALSE. B) each row is a gene , each column is a time and each matrix is a sample. In this case SE\_byTime= TRUE. This concept is illustrated in package vignette.

**Value**

Sample data frame where rows are genes and columns are times.,

**Author(s)**

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**Examples**

```
# Each matrix one time / each column one sample (SE_byTime=FALSE)
# Code to create dummy data

nrows <- 200
ncols <- 6
time1 <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
time2 <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GenomicRanges::GRanges(rep(c("chr1", "chr2"), c(50, 150)),
                                     IRanges::IRanges(floor(runif(200, 1e5, 1e6)), width=100),
                                     strand=sample(c("+", "-"), 200, TRUE),
                                     feature_id=sprintf("ID%03d", 1:200))
colData <- S4Vectors::DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                               Samples = LETTERS[1:6],
                               row.names=LETTERS[1:6])
se <- SummarizedExperiment::SummarizedExperiment(assays=list(time1=time1, time2=time2),
                                                rowRanges=rowRanges, colData=colData)

# Get sample "A" with all times

importFromSE(se, sample="A", SE_byTime = FALSE)

# or sample = 1 because is first columns in each matrix (each time)

# Each matrix one sample / each column one time (SE_byTime=TRUE)
# Code to create dummy data

nrows <- 200
ncols <- 6
sampleA <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
sampleB <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GenomicRanges::GRanges(rep(c("chr1", "chr2"), c(50, 150)),
                                     IRanges::IRanges(floor(runif(200, 1e5, 1e6)), width=100),
                                     strand=sample(c("+", "-"), 200, TRUE),
                                     feature_id=sprintf("ID%03d", 1:200))
colData <- S4Vectors::DataFrame(Time=paste("time",seq(1:6), sep=""),
                               sampleA = rep("A",6),
                               sampleB = rep("B", 6),
                               row.names = paste("time",seq(1:6), sep=""))
se <- SummarizedExperiment::SummarizedExperiment(assays=list(sampleA=sampleA, sampleB=sampleB),
                                                rowRanges=rowRanges, colData=colData)
# Get sample "sampleA" with all times

importFromSE(se, sample=1, SE_byTime = TRUE)

# or sample = 1 because is the first matrix in assays structure.
```

---

imputeSenator-class    *Class 'imputeSenator' This class represents the result imputeSenators function*

---

### Description

Class 'imputeSenator' This class represents the result imputeSenators function

### Slots

data    Dataframe with original data  
 senators    Senators data value  
 endCluster    Final cluster assignment

### Author(s)

Fernando Pérez Sanz (<fernando.perez8@um.es>)  
 Miriam Riquelme Pérez (<miriam.riquelmep@gmail.com>)

### See Also

[imputeSenators](#)

---

imputeSenators    *Preclustering function for large data*

---

### Description

Compute clustering with clara function to obtain a number of 'senators'

### Usage

```
imputeSenators(x, k = 100, ...)
```

### Arguments

x	Numeric matrix or data.frame with trajectory values. Rows are trajectories, columns are time or similar. SummarizedExperiment object can be provided for compatibility with bioconductor container (for more information see vignette).
k	Numeric. Number of senators
...	Other arguments to pass to importFromSE if <code>_x_</code> is SummarizedExperiment-class.



## Details

Calculates a series of senators representing a large set of trajectories that would otherwise be computationally very expensive. For it, by means of the [clara](#) function of the cluster package a clustering is made obtaining the centroids as senators. These centroids can then be clustered based on the slope distance or Frechet or both. Finally, the data set will be assigned to the same cluster your senator is assigned to.

## Value

List with three slots:

**data** Dataframe with original data.

**senatorData** Matrix with senator trajectories.

**senatorCluster** Vector with senator clusters.

## Author(s)

Fernando Pérez-Sanz (<fernando.perez8@um.es>)

Miriam Riquelme-Pérez (<miriam.riquelmep@gmail.com>)

## See Also

[plotClusterSenator](#), [imputeSenatorToData](#), [importFromSE](#).

## Examples

```
data( tscR )
data <- tscR
time <- c( 1, 2, 3 )
senators <- imputeSenators( data, k = 100 )
senatorDist <- slopeDist( senators$senatorData, time )
sClust <- getClusters( senatorDist, k = 5 )
plotCluster( senators$senatorData, sClust, 2 )
```

---

`imputeSenatorToData` *Impute clusters from senators to data*

---

## Description

Assign trajetories from the original data to senator clusters.

## Usage

```
imputeSenatorToData(senators, clusters)
```

**Arguments**

senators        List object obtained from imputeSenator function  
clusters        Pam object obtained from [getClusters](#) or [combineCluster](#).

**Details**

When it's computed a clustering over senators, it's necessary to assign those cluster to original data. To do this, it's known which senator each original trajectory belong to, therefore the final cluster of each senator is identified and the trajectories of that senator are assigned to its definitive cluster.

**Value**

Object of [imputeSenator-class](#).

**Author(s)**

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**See Also**

[plotClusterSenator](#), [imputeSenators](#), [getClusters](#), [imputeSenator-class](#).

**Examples**

```
data( tscR )  
data <- tscR  
time <- c( 1, 2, 3 )  
senators <- imputeSenators( data, k = 100 )  
senatorDist <- slopeDist( senators$senatorData, time )  
sClust <- getClusters( senatorDist, k = 5 )  
plotCluster( senators$senatorData, sClust, 2 )  
endCluster <- imputeSenatorToData( senators, sClust )
```

---

plotCluster

*Plot trajectories based on clustering*

---

**Description**

Draw trajectories and are colored based on their clusters

**Usage**

```
plotCluster(data, clust, ncluster, ...)
```

**Arguments**

data	Numeric data frame or matrix with de original data. SummarizedExperiment object can be provided for compatibility with bioconductor container (for more information see vignette).
clust	Object of class pam or partition obtained from getClusters output.
ncluster	When nclust = 'all', plots all trajectories and cluster together in a single plot. If it's an integer, it draws only trajectories that belong to that cluster. Finally, if it is a numeric vector, it draws trajectories corresponding to each cluster within a subplot.
...	Other arguments to pass to importFromSE if <code>_x_</code> is SummarizedExperiment-class.

**Details**

It draws trajectories where x axis is time data and y axis trayectory values.

**Value**

Plot clustered trayectories

**Author(s)**

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**See Also**

[matplot](#), [plotClusterSenator](#), [importFromSE](#).

**Examples**

```
data(tscR)
data <- tscR
time <- c(1,2,3)
fdist <- frechetDistC(data, time)
fclust <- getClusters(fdist, 3)
plotCluster(data, fclust, 'all')
```

---

plotClusterSenator      *Plot trajectories based on clustering*

---

## Description

Draw trajectories and are colored based on their clusters with imputesenator object

## Usage

```
plotClusterSenator(x, ncluster)
```

## Arguments

x	imputesenator class object from <a href="#">imputeSenatorToData</a> function.
ncluster	When nclust = 'all', plots all trajectories and cluster together in a single plot. If it's an integer, it draws only trajectories that belong to that cluster. Finally, if it is a numeric vector, it draws trajectories corresponding to each cluster within a subplot.

## Details

It draws trajectories where x axis is time data and y axis trajectory values.

## Value

Plot clustered trayectories

## Examples

```
data( tscR )
data <- tscR
time <- c( 1, 2, 3 )
senators <- imputeSenators( data, k = 100 )
senatorDist <- slopeDist( senators$senatorData, time )
sClust <- getClusters( senatorDist, k = 5 )
endCluster <- imputeSenatorToData( senators, sClust )
plotClusterSenator( endCluster, 'all' )
```

---

slopeDist	<i>Pairwise slope distance</i>
-----------	--------------------------------

---

### Description

Compute pairwise distance based on slopes in a matrix of trajectories

### Usage

```
slopeDist(x, time, ...)
```

### Arguments

x	Numeric matrix or data.frame with trajectory values. Rows are trajectories, columns are time or similar. SummarizedExperiment object can be provided for compatibility with bioconductor container (for more information see vignette).
time	Numeric vector with time data (time intervals), with equal length to columns number in x.
...	Other arguments to pass to importFromSE if <code>_x_</code> is SummarizedExperiment-class.

### Value

A dist class object of size NxN, where N is rows number in the input data

### Author(s)

Fernando Pérez-Sanz (<fernando.perez8@um.es>)

Miriam Riquelme Pérez (<miriam.riquelmep@gmail.com>)

### See Also

[frechetDistC](#) and [frechetDist](#) (R and slower versión than [frechetDistC.](#)), [importFromSE](#).

### Examples

```
data(tscR)
data <- tscR
time <- c(1,2,3)
dist_tscR <- slopeDist(data, time)
```

---

tscR

*Dummy trajectories data*

---

### Description

A dataset containing 300 trajectories and 3 time points

### Usage

```
tscR
```

### Format

A data frame 300 rows and 3 columns:

**T1** time interval

**T2** time interval

**T3** time interval

### Details

This dataset has been created specifically to be able to illustrate the operation of the package with different distance metrics. Thus, from 3-4 hand-created trajectories (ascending, descending, quasi-horizontal) we have generated 300 trajectories with random variations from the original ones. The code used was similar to the one attached here:

### Source

Simulated data

### Examples

```
df <- data.frame(T1 = c(4,3.9,4.1,4),
                 T2=c(5.5, 4.3, 3.7, 2.5),
                 T3 = c(7, 3.9,4.1, 1))
df1 <- matrix(NA, nrow=100, ncol=3)
df2 <- matrix(NA, nrow=100, ncol=3)
df3 <- matrix(NA, nrow=100, ncol=3)
df4 <- matrix(NA, nrow=100, ncol=3)
for(i in seq(1,75)){
  df1[i,] <- jitter(as.numeric(df[1,]), factor = 2.5)
  df2[i,] <- jitter(as.numeric(df[2,]), factor = 7.5)
  df3[i,] <- jitter(as.numeric(df[3,]), factor = 7.5)
  df4[i,] <- jitter(as.numeric(df[4,]), factor = 2.5)
}
df <- as.data.frame(rbind(df1,df2,df3, df4))
names(df) <- c("T1","T2","T3")
```

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