

Package ‘longitudinalData’

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Type Package

Title Longitudinal Data

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Description Tools for longitudinal data and joint longitudinal data (used by packages kml and kml3d).

License GPL (>= 2)

LazyData yes

Depends methods,clv,class,rgl,utils,misc3d

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longitudinalData-package

~ Package overview: longitudinalData ~

Description

longitudinalData package provide some tools to deal with the clusterization of longitudinal data.

Details

Package:	longitudinalData
Type:	Package
Version:	2.4.1
Date:	2016-02-02

License: GPL (≥ 2)
LazyData: yes
Depends: methods,clv,rgl,misc3d
URL: <http://www.r-project.org>

Overview

longitudinalData provide some tools to deal with the clustering of longitudinal data, mainly:

1. [plotTrajMeans](#)
2. [imputation](#)
3. [qualityCriterion](#)

Author

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References

[1] Christophe M. Genolini and Bruno Falissard
"KmL: k-means for longitudinal data"
Computational Statistics, vol 25(2), pp 317-328, 2010

[2] Christophe M. Genolini and Bruno Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

Classes: [LongData](#), [Partition](#)
Methods: [longData](#), [partition](#), [ordered](#)
Plot: [plotTrajMeans](#), [plotTrajMeans3d](#)
Imputation: [imputation](#)
Criterion: [qualityCriterion](#)

Examples

```
### Generation of artificial longData
data(artificialJointLongData)
myData <- longData3d(artificialJointLongData,timeInData=list(var1=2:12,var2=13:23,var3=24:34))

part <- partition(rep(1:3,each=50))
```

```
plotTrajMeans3d(myData,part)

### Quality criterion
qualityCriterion(myData,part)
```

```
artificialJointLongData
~ Data: artificialJointLongData ~
```

Description

Some artificial joint longitudinal data.

Usage

```
data(artificialJointLongData)
```

Format

Some joint longitudinal data in wide format. It includes 90 trajectories divided in 3 groups.

```
id unique idenfier for each patient.
v0 Measurement of variable 'V' at time t0
v1 Measurement of variable 'V' at time t1
... ..
v10 Measurement of variable 'V' at time t0
w0 Measurement of variable 'W' at time t0
w1 Measurement of variable 'W' at time t1
... ..
w10 Measurement of variable 'W' at time t0
x0 Measurement of variable 'X' at time t0
x1 Measurement of variable 'X' at time t1
... ..
x10 Measurement of variable 'X' at time t0
```

Details

Some joint longitudinal data in wide format. It includes 90 trajectories divided in 3 groups.

Author(s)

Christophe Genolini

Examples

```
data(artificialJointLongData)
str(artificialJointLongData)
```

artificialLongData ~ Data: artificialLongData ~

Description

Some artificial longitudinal data.

Usage

```
data(artificialLongData)
```

Format

Some longitudinal data in wide format. It includes 120 trajectories divided in 4 groups.

id unique identifier for each patient.

t0 Measurement at time t0

t1 Measurement at time t1

... ..

t10 Measurement at time t10

Details

Some artificial longitudinal data in wide format. It includes 120 trajectories divided in 4 groups.

Author(s)

Christophe Genolini

Examples

```
data(artificialLongData)
str(artificialLongData)
```

Constants ~ Constants ~

Description

Constants define in the package ~

Usage

```

MAX_CLUSTERS
CLUSTERS_NAMES
CRITERION_MIN_OR_MAX
CRITERION_NAMES
DISTANCE_METHODS
CHOICE_STYLE

```

Value

```

MAX_CLUSTERS = 26
CLUSTER_NAMES = paste("c",2:MAX_CLUSTERS,sep="")
CRITERION_NAMES <- c(
  "Calinski.Harabatz","Kryszczuk.Calinski","Genolini.Calinski","Ray.Turi","Davies.Bouldin",
  "BIC","BIC2","AIC","AICc","AICc2","postProbaGlobal","random"
)
DISTANCE_METHODS = c("manhattan", "euclidean", "minkowski", "maximum", "canberra",
"binary")
CHOICE_STYLE = list(
  typeTraj=c("l","l","n"),
  colTraj=c("clusters","black","black"),
  typeMean=c("b","b","b","b","l","l","n"),
  colMean=c("clusters","black","clusters","black","clusters","black","black"),
  pchMean=c("letters","letters","symbols","symbols","letters","letters","letters")
)

```

Examples

```

### Maximum number of clusters that kml can deal with
MAX_CLUSTERS

### Names of the field that save clusters in object 'ClusterLongData'
cat(CLUSTER_NAMES,"\n")

### List of the available criterion
CRITERION_NAMES

### Distance available
DISTANCE_METHODS[2]

### Define the style use by choice
CHOICE_STYLE[['typeTraj']][2]

```

distFrechet ~ Function: Frechet distance ~

Description

Compute Frechet distance between two trajectories.

Usage

```
distFrechet(Px,Py,Qx, Qy, timeScale=0.1, FrechetSumOrMax = "max")
```

Arguments

Px	[vector(numeric)] Times (abscisse) of the first trajectories.
Py	[vector(numeric)] Values of the first trajectories.
Qx	[vector(numeric)] Times of the second trajectories.
Qy	[vector(numeric)] Values of the second trajectories.
timeScale	[numeric]: allow to modify the time scale, increasing or decreasing the cost of the horizontal shift. If timeScale is very big, then the Frechet's distance is equal to the euclidienne distance. If timeScale is very small, then it is equal to the Dynamic Time Warping.
FrechetSumOrMax	[character]: The Frechet's distance can be define using the 'sum' function or the 'max' function. This option let the user to chose one or the other.

Details

Given two curve P and Q, Frechet distance between P and Q is define as $\inf_{a,b} \max_{t} d(P(a(t)), Q(b(t)))$. It's computation is a NP-complex problem. When P and Q are trajectories (discrete curve), the problem is polynomial.

The Frechet distance can also be define using a sum instead of a max: $\inf_{a,b} \sum_{t} d(P(a(t)), Q(b(t)))$

The function distFrechet is C compiled, the function distFrechetR is in R, the function distFrechetRec is in recursive (the slowest) in R.

Value

A numeric value.

Author

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References

- [1] Thomas Eiter & Heikki Mannila:
"Computing Discrete Fréchet Distance"
- [2] C. Genolini and B. Falissard
"KmL: k-means for longitudinal data"
Computational Statistics, vol 25(2), pp 317-328, 2010
- [3] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

distTraj

Examples

```
Px <- 1:20
Py <- dnorm(1:20, 12, 2)
Qx <- 1:20
Qy <- dnorm(1:20, 8, 2)

distFrechet(Px, Py, Qx, Qy)

### Frechet using sum instead of max.
distFrechet(Px, Py, Qx, Qy, FrechetSumOrMax="sum")
```

expandParLongData ~ *Function: expandParLongData* ~

Description

Prepare the values of an object [ParLongData](#) to make them being usable by a plotting function.

Usage

```
expandParLongData(xParLongData, y)
```

Arguments

xParLongData [ParLongData]: The object to expand.
y [Partition] or [numeric]: see detail.

Details

`ParLongData` object can hold values that are easy to specify (like `col="clusters"` or `pch="symbol"`) but that can not be directly used by graphical functions `plotTrajMeans` and `plotTrajMeans3d`. This function modify these values to make them fit with `plotTrajMeans` and `plotTrajMeans3d` expectations.

The field `col` and `pch` are the ones concern by this function.

If `y` is a `Partition`, `col` and `pch` are extended to fit with the number of individual. If `y` is a number of clusters, `col` and `pch` are extended to fit with the number of clusters.

If `col='clusters'`, a color is affected to each clusters. Then the field `col` receive a vector of color such that each individual (if `y` is a `Partition`) or each clusters (if `y` is a number of clusters) get its corresponding color.

If `pch='letters'`, a letters is affected to each clusters. Then the field `pch` receive a vector of letters such that each individual (if `y` is a `Partition`) or each clusters (if `y` is a number of clusters) get its corresponding letters.

Same if `pch='symbols'`.

Value

An object of class `ParLongData`

Author

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[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

Examples

```
#####
### Some parameters for trajectories
(paramTraj <- parTRAJ(col="clusters"))

### Expand to a small partition with 3 clusters
part <- partition(LETTERS[rep(1:3,4)])
expandParLongData(paramTraj,part)
```

```
#####
### Some parameters for the mean trajectories
paramMean <- parMEAN()

### If there is 3 clusters :
expandParLongData(paramMean,3)

### If there is 5 clusters :
expandParLongData(paramMean,5)
```

imputation

~ Function: imputation ~

Description

imputation is a function that offer different methods to impute missing value of a [LongData](#) (or a matrix).

Usage

```
imputation(traj,method="copyMean",lowerBound="globalMin",upperBound="globalMax")
```

Arguments

traj	[LongData] or [matrix]: trajectories to impute.
method	[character]: Name of the imputation method (see detail)
lowerBound	[character] or [numeric]: fixes the smallest value that an imputed value can take. If a single value is given, it is duplicate for all the column. The special value 'min' means that the lower bound will be the smallest value of the column. The special value 'globalMin' means that the lower bound will be the overall smallest value (of each variable if there is several variable-trajectories). The special value 'NA' can be used to impute without using a lower bound.
upperBound	[character] or [numeric]: fixes the biggest value that an imputed value can take. If a single value is given, it is duplicate for all the column. The special value 'max' means that the upper bound will be the biggest value of the column. The special value 'globalMax' means that the upper bound will be the overall biggest value (of each variable if there is several variable-trajectories). The special value 'NA' can be used to impute without using an upper bound.

Details

imputation is a function that impute missing value of a [LongData](#) or a matrix. Several imputation methods are available. A brief description follows. For a fully detailed description, see [3]. Illustrating examples showing strengths and weakness of methods are presented section "examples".

For each method, the imputation has to deal with monotone missing value (at start and at end of the trajectories) and intermitant (in the middle). Here is a brief description of each methods.

- 'linearInterpol.locf' (linear interpolation, locf)
 - Intermitant: values imediatly surrounding the missing are join by a line.
 - Monotone: imputed by 'locf' or 'nocb'.
- 'linearInterpol.global' (linear interpolation, global slope)
 - Intermitant: values imediatly surrounding the missing are join by a line.
 - Monotone: the line joining the first and last non-missing value is considered (this line is the everage progression of the actual individual trajectoire). Missing-value at start and at end are chosen on this line.
- 'linearInterpol.local' (linear interpolation, global slope)
 - Intermitant: values imediatly surrounding the missing are join by a line.
 - Monotone at start: the line joining the first and second non-missing value is considered. Missing-value at start are chose on this line.
 - Monotone at end: the line joining the last and penultimate non-missing value is considered. Missing-value at end are chosen on this line.
- 'linearInterpol.bisector' (linear interpolation, bisector)
 - Intermitant: values imediatly surrounding the missing are join by a line.
 - Monotone: linearInterpol.global is not sensitive to local variation, linearInterpol.local might be too much sensitive to abnormal value. linearInterpol.bisector offer a medium solution by considering the bissectrice of Global and Local solution. Point are chosen on the bissectrices.
- 'copyMean.locf' (copy mean, locf) this method impute in two stages. First, it use 'linearInterpol.locf'. Then it add to each imputed value a variation that make the imputed value follow the shape of the average trajectory. For more details, see [3] and examples' section.
- 'copyMean.global' (copy mean, global slope) this method impute in two stages. First, it use 'linearInterpol.global'. Then it add to each imputed value a variation that make the imputed value follow the shape of the average trajectory. For more details, see [3] and examples' section.
- 'copyMean.local' (copy mean, local slope) this method impute in two stages. First, it use 'linearInterpol.local'. Then it add to each imputed value a variation that make the imputed value follow the shape of the average trajectory. For more details, see [3] and examples' section.
- 'copyMean.bisector' (copy mean, bisector) this method impute in two stages. First, it use 'linearInterpol.bisector'. Then it add to each imputed value a variation that make the imputed value follow the shape of the average trajectory. For more details, see [3] and examples' section.
- locf (Last Occurence Carried Forward) THIS METHOD HAS BEEN PROUVEN TO NOT BE EFFICIENT SEVERAL TIME BY VARIOUS AUTHOR, we strongly recommand to not use it !
 - Intermitant and monotone at end: the previous non-missing value is duplicated forward.
 - Monotone at start: the first non-missing value is duplicated backward (nocb).
- nocb (Next Occurence Carried Backward) THIS METHOD HAS BEEN PROUVEN TO NOT BE EFFICIENT SEVERAL TIME BY VARIOUS AUTHOR, we strongly recommand to not use it !

- Intermitant and monotone at start: the next non-missing value is duplicated backward.
- Monotone at end: the last non-missing value is duplicated forward (locf).
- trajMean missing are imputed by the mean of the trajectory.
- trajMedian missing are imputed by the median of the trajectory.
- trajHotDeck each missing is imputed by one non-missing (randomly chosen) value of the trajectory.
- crossMean missing value at time t are imputed by the mean of all value present at time t.
- crossMedian missing value at time t are imputed by the median of all value present at time t.
- crossHotDeck each missing value at time t is imputed by one non-missing (randomly chosen) value present at time t.

Value

A [LongData](#) or a matrix with no missing values.

Author

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References

[1] C. Genolini and B. Falissard
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Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

[3] Christophe Genolini, René Écochard and H  l  ne Jacqmin-Gadda
"Copy Mean: A New Method to Impute Intermittent Missing Values in Longitudinal Studies"
Open Journal of Statistics, vol 3(26),2013

See Also

[LongData](#), [Partition](#), [qualityCriterion](#)

Examples

```
#####
### Preparation of the data
par(ask=TRUE)
timeV <- 1:14
```

```

matMissing <- matrix(
  c(NA ,NA ,NA ,18 ,22 ,NA ,NA ,NA ,NA , 24 , 22 , NA , NA , NA,
    24 ,21 ,24 ,26 ,27 ,32 ,30 ,22 ,26 , 26 , 28 , 24 , 23 , 21,
    14 ,13 , 10 , 8 , 7 ,18 ,16 , 8 ,12 , 6 , 10 , 10 , 9 , 7,
    3 ,1 , 1 , 1 , 3,9 , 7 , -1 , 3 , 2 , 4 , 1 , 0 , -2
  ),4,byrow=TRUE
)

```

```

matplot(t(matMissing),col=c(2,1,1,1),lty=1,type="l",lwd=c(3,1,1,1),pch=16,
  xlab="Black=trajectories; Green=mean trajectory\nRed=trajectory to impute",
  ylab="",main="Four trajectories")
moy <- apply(matMissing,2,mean,na.rm=TRUE)
lines(moy,col=3,lwd=3)

```

```

#####
# Illustration of the different imputing method #
#           The best are at end !!!           #
#####

```

```

#####
### Methods using cross sectionnal information (cross-methods)

```

```

par(mfrow=c(1,3))
mat2 <- matrix(c(
  NA, 9, 8, 8, 7, 6,NA,
  7, 6,NA,NA,NA, 4,5,
  3, 4, 3,NA,NA, 2,3,
  NA,NA, 1,NA,NA, 1,1),4,7,byrow=TRUE)

```

```

### crossMean
matplot(t(imputation(mat2,"crossMean")),type="l",ylim=c(0,10),
  lty=1,col=1,main="crossMean")
matlines(t(mat2),type="o",col=2,lwd=3,pch=16,lty=1)

```

```

### crossMedian
matplot(t(imputation(mat2,"crossMedian")),type="l",ylim=c(0,10),
  lty=1,col=1,main="crossMedian")
matlines(t(mat2),type="o",col=2,lwd=3,pch=16,lty=1)

```

```

### crossHotDeck
matplot(t(imputation(mat2,"crossHotDeck")),type="l",ylim=c(0,10),
  lty=1,col=1,main="crossHotDeck")
matlines(t(mat2),type="o",col=2,lwd=3,pch=16,lty=1)

```

```

#####
### Methods using trajectory information (traj-methods)

```

```

par(mfrow=c(2,3))
mat1 <- matrix(c(NA,NA,3,8,NA,NA,2,2,1,NA,NA),1,11)

### locf
matplot(t(imputation(mat1,"locf")),type="l",ylim=c(0,10),
        main="locf\n DO NOT USE, BAD METHOD !!!")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16)

### nocb
matplot(t(imputation(mat1,"nocb")),type="l",ylim=c(0,10),
        main="nocb\n DO NOT USE, BAD METHOD !!!")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16)

### trajMean
matplot(t(imputation(mat1,"trajMean")),type="l",ylim=c(0,10),
        main="trajMean")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16)

### trajMedian
matplot(t(imputation(mat1,"trajMedian")),type="l",ylim=c(0,10),
        main="trajMedian")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16)

### trajHotDeck
matplot(t(imputation(mat1,"trajHotDeck")),type="l",ylim=c(0,10),
        main="trajHotDeck 1")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16)

### spline
matplot(t(imputation(mat1,"spline",lowerBound=NA,upperBound=NA)),
        type="l",ylim=c(-10,10),main="spline")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16)

#####
### Different linear interpolation

par(mfrow=c(2,2))

### linearInterpol.locf
matplot(t(imputation(mat1,"linearInterpol.locf",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="linearInterpol.locf")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16,lty=1)

### linearInterpol.global
matplot(t(imputation(mat1,"linearInterpol.global",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="linearInterpol.global")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16,lty=1)

### linearInterpol.local

```

```

matplot(t(imputation(mat1,"linearInterpol.local",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="linearInterpol.local")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16,lty=1)

### linearInterpol.bisector
matplot(t(imputation(mat1,"linearInterpol.bisector",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="linearInterpol.bisector")
matlines(t(mat1),type="o",col=2,lwd=3,pch=16,lty=1)

#####
### Copy mean

mat3 <- matrix(c(
  NA, 9, 8, 8, 7, 6,NA,
  7, 6,NA,NA,NA, 4,5,
  3, 4, 3,NA,NA, 2,3,
  NA,NA, 1,NA,NA, 1,1),4,7,byrow=TRUE)

par(mfrow=c(2,2))

### copyMean.locf
matplot(t(imputation(mat2,"copyMean.locf",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="copyMean.locf")
matlines(t(mat2),type="o",col=2,lwd=3,pch=16,lty=1)

### copyMean.global
matplot(t(imputation(mat2,"copyMean.global",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="copyMean.global")
matlines(t(mat2),type="o",col=2,lwd=3,pch=16,lty=1)

### copyMean.local
matplot(t(imputation(mat2,"copyMean.local",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="copyMean.local")
matlines(t(mat2),type="o",col=2,lwd=3,pch=16,lty=1)

### copyMean.bisector
matplot(t(imputation(mat2,"copyMean.bisector",NA,NA)),type="l",
        ylim=c(-5,10),lty=1,col=1,main="copyMean.bisector")
matlines(t(mat2),type="o",col=2,lwd=3,pch=16,lty=1)

### crossMean
matImp <- imputation(matMissing,method="crossMean")
matplot(t(matImp),col=c(2,1,1,1),lty=c(2,1,1,1),type="l",lwd=c(2,1,1,1),pch=16,
        xlab="Dotted red=imputed trajectory\nFull red=trajectory to impute",
        ylab="",main="Method 'crossMean'")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

```

```

### crossMedian
matImp <- imputation(matMissing,method="crossMedian")
matplot(t(matImp),col=c(2,1,1,1),lty=c(2,1,1,1),type="l",lwd=c(2,1,1,1),pch=16,
        xlab="Dotted red=imputed trajectory\nFull red=trajectory to impute",ylab="",
        main="Method 'crossMedian'")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### crossHotDeck
matImp <- imputation(matMissing,method="crossHotDeck")
matplot(t(matImp),col=c(2,1,1,1),lty=c(2,1,1,1),type="l",lwd=c(2,1,1,1),pch=16,
        xlab="Dotted red=imputed trajectory\nFull red=trajectory to impute",ylab="",
        main="Method 'crossHotDeck'")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

#####
### Method using trajectory

par(mfrow=c(2,3))
### trajMean
matImp <- imputation(matMissing,method="trajMean")
plot(timeV,matImp[1,],type="l",lwd=2,ylim=c(10,30),ylab="",xlab="nocb")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### trajMedian
matImp <- imputation(matMissing,method="trajMedian")
plot(timeV,matImp[1,],type="l",lwd=2,ylim=c(10,30),ylab="",xlab="nocb")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### trajHotDeck
matImp <- imputation(matMissing,method="trajHotDeck")
plot(timeV,matImp[1,],type="l",lwd=2,ylim=c(10,30),ylab="",xlab="nocb")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### locf
matImp <- imputation(matMissing,method="locf")
plot(timeV,matImp[1,],type="l",lwd=2,ylim=c(10,30),ylab="",xlab="locf")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### nocb
matImp <- imputation(matMissing,method="nocb")
plot(timeV,matImp[1,],type="l",lwd=2,ylim=c(10,30),ylab="",xlab="nocb")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

par(mfrow=c(2,2))

### linearInterpol.locf
matImp <- imputation(matMissing,method="linearInterpol.locf")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### linearInterpol.local

```



```

matImp <- imputation(matMissing,method="linearInterpol.local")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### linearInterpol.global
matImp <- imputation(matMissing,method="linearInterpol.global")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

### linearInterpol.bisector
matImp <- imputation(matMissing,method="linearInterpol.bisector")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)

par(mfrow=c(2,2))

### copyMean.locf
matImp <- imputation(matMissing,method="copyMean.locf")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)
lines(timeV,moy,col=3,type="o",lwd=3)

### copyMean.local
matImp <- imputation(matMissing,method="copyMean.local")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)
lines(timeV,moy,col=3,type="o",lwd=3)

### copyMean.global
matImp <- imputation(matMissing,method="copyMean.global")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)
lines(timeV,moy,col=3,type="o",lwd=3)

### copyMean.bisector
matImp <- imputation(matMissing,method="copyMean.bisector")
plot(timeV,matImp[1,],type="o",ylim=c(0,30),ylab="",xlab="LI-Global")
lines(timeV,matMissing[1,],col=2,type="o",lwd=3)
lines(timeV,moy,col=3,type="o",lwd=3)

par(ask=FALSE)

```

initializePartition ~ *Function: initializePartition* ~

Description

This function provide different way of setting the initial partition for an EM algorithm.

Usage

```
initializePartition(nbClusters, lengthPart, method = "kmeans++", data)
```

Arguments

nbClusters	[numeric]: number of clusters of that the initial partition should have.
lengthPart	[numeric]: number of individual in the partition.
method	[character]: one off "randomAll", "randomK", "maxDist", "kmeans++", "kmeans+", "kmeans-" or "kmeans-".
data	[matrix]: data is the matrix of the individuals (usefull for the methods that need to compute distance between individual). If data is an array, the distance is computed using "maxDist" is used, the function needs to know the matrix of the distance between each individual.

Details

Before alternating the phase Esperance and Maximisation, the EM algorithm needs to initialize a starting configuration. This initial partition has been proven to have an important impact on the final result and the convergence time.

This function provides different ways of setting the initial partition.

- randomAll: all the individual are randomly assigned to a cluster with at least one individual in each clusters.
- randomK: K individuals are randomly assigned to a cluster, all the other are not assigned (each cluster has only one individual).
- maxDist: K individuals are chosen. The two formers are the individual separated by the highest distance. The latter are added one by one, they are the "farthest" individual among those that are already been selected. "farthest" is the individual with the highest distance (min) to the selected individuals (if "t" are the individual already selected, the next selected individual is "i" such that $\max_i(\min_t(\text{dist}(\text{IND}_i, \text{IND}_t)))$). This method is efficient but time consuming.
- kmeans++: see [3]
- kmeans+, kmeans-, kmeans-: experimental methods derived from [3].

Value

vecteur of numeric.

Author

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References

- [1] C. Genolini and B. Falissard
 "KmL: k-means for longitudinal data"
 Computational Statistics, vol 25(2), pp 317-328, 2010
- [2] C. Genolini and B. Falissard
 "KmL: A package to cluster longitudinal data"
 Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011
- [3] D. Arthur and S. Vassilvitskii
 "k-means++: the advantages of careful seeding"
 Proceedings of the eighteenth annual ACM-SIAM symposium on Discrete algorithms. pp. 1027-1035, 2007.

Examples

```

par(ask=TRUE)
#####
### Construction of some longitudinal data
data(artificialLongData)
dn <- longData(artificialLongData)
plotTrajMeans(dn)

#####
### partition using randomAll
pa1a <- initializePartition(3,lengthPart=200,method="randomAll")
plotTrajMeans(dn,partition(pa1a),parMean=parMEAN(type="n"),parTraj=parTRAJ(col="clusters"))
pa1b <- initializePartition(3,lengthPart=200,method="randomAll")
plotTrajMeans(dn,partition(pa1b),parMean=parMEAN(type="n"),parTraj=parTRAJ(col="clusters"))

#####
### partition using randomK
pa2a <- initializePartition(3,lengthPart=200,method="randomK")
plotTrajMeans(dn,partition(pa2a),parMean=parMEAN(type="n"),parTraj=parTRAJ(col="clusters"))
pa2b <- initializePartition(3,lengthPart=200,method="randomK")
plotTrajMeans(dn,partition(pa2b),parMean=parMEAN(type="n"),parTraj=parTRAJ(col="clusters"))

#####
### partition using maxDist
pa3 <- initializePartition(3,lengthPart=200,method="maxDist",data=dn["traj"])
plotTrajMeans(dn,partition(pa3),parMean=parMEAN(type="n"),parTraj=parTRAJ(col="clusters"))
### maxDist is deterministic, so no need for a second example

#####
### Example to illustrate "maxDist" method on classical clusters
point <- matrix(c(0,0, 0,1, -1,0, 0,-1, 1,0),5,byrow=TRUE)
points <- rbind(point,t(t(point)+c(10,0)),t(t(point)+c(5,6)))
points <- rbind(points,t(t(points)+c(30,0)),t(t(points)+c(15,20)),t(-t(point)+c(20,10)))
plot(points,main="Some points")

```

```

paInit <- initializePartition(2,nrow(points),method="maxDist",points)
plot(points,main="Two farest points")
lines(points[!is.na(paInit),],col=2,type="p",pch=16)

paInit <- initializePartition(3,nrow(points),method="maxDist",points)
plot(points,main="Three farest points")
lines(points[!is.na(paInit),],col=2,type="p",pch=16)

paInit <- initializePartition(4,nrow(points),method="maxDist",points)
plot(points, main="Four farest points")
lines(points[!is.na(paInit),],col=2,type="p",pch=16)

par(ask=FALSE)

```

ListPartition-class ~ Class: ListPartition ~

Description

An object of class ListPartition contain several liste of Partition sorted by cluster numbers.

Objects from the Class

Objects are mainly design to store the numerous Partition found by kml or kml3d.

Slots

`criterionActif` [character]: Store the criterion name that will be used by fonctions that need a single criterion (like [plotCriterion](#) or [ordered](#)).

`initializationMethod` [vector(character)]: list all the initialization method that has allready been used to find some Partition (usefull to not run several time a deterministic method).

`sorted` [logical]: are the Partition curently hold in the object sorted in decreasing (or increasing, according to `criterionActif`) order ?

`c1` [list(Partition)]: list of Partition with 1 clusters.

`c2` [list(Partition)]: list of Partition with 2 clusters.

`c3` [list(Partition)]: list of Partition with 3 clusters.

`c4` [list(Partition)]: list of Partition with 4 clusters.

`c5` [list(Partition)]: list of Partition with 5 clusters.

`c6` [list(Partition)]: list of Partition with 6 clusters.

`c7` [list(Partition)]: list of Partition with 7 clusters.

`c8` [list(Partition)]: list of Partition with 8 clusters.

`c9` [list(Partition)]: list of Partition with 9 clusters.

`c10` [list(Partition)]: list of Partition with 10 clusters.

c11 [list(Partition)]: list of Partition with 11 clusters.
 c12 [list(Partition)]: list of Partition with 12 clusters.
 c13 [list(Partition)]: list of Partition with 13 clusters.
 c14 [list(Partition)]: list of Partition with 14 clusters.
 c15 [list(Partition)]: list of Partition with 15 clusters.
 c16 [list(Partition)]: list of Partition with 16 clusters.
 c17 [list(Partition)]: list of Partition with 17 clusters.
 c18 [list(Partition)]: list of Partition with 18 clusters.
 c19 [list(Partition)]: list of Partition with 19 clusters.
 c20 [list(Partition)]: list of Partition with 20 clusters.
 c21 [list(Partition)]: list of Partition with 21 clusters.
 c22 [list(Partition)]: list of Partition with 22 clusters.
 c23 [list(Partition)]: list of Partition with 23 clusters.
 c24 [list(Partition)]: list of Partition with 24 clusters.
 c25 [list(Partition)]: list of Partition with 25 clusters.
 c26 [list(Partition)]: list of Partition with 26 clusters.

Construction

Class ListPartition objects are mainly constructed by `km1`. Nevertheless, it is also possible to construct them from scratch using the fonction `listPartition` that does create an empty object.

Methods

`object['xxx']` If 'xxx' is 'cX', 'initializationMethod', 'sorted' or 'criterionActif', get the value of the field xxx.

`object['criterionValues', j]` Give the values of the criterion 'j' for all the Partitions. The result is return as a list. If 'j' is missing, the criterion actif is used.

`object['criterionValuesAsMatrix', j]` Give the values of the criterion 'j' for all the Partitions. The result is return as a matrix. If 'j' is missing, the criterion actif is used.

`object['xxx']` If 'xxx' is a criterion, this is equivalent to `object['criterionValuesAsMatrix', 'xxx']`

`object['initializationMethod']<-value` Set the field to value

`object['criterionActif']<-value` If 'value' is one of CRITERION_NAMES, it sets the field to the criterion 'value'.

`object['add']<-value` If 'value' is an object of class 'Partition', then value is added to the Partition already hold in the field 'cX'. Note that a Partition with 'X' clusters is automatiquement added to the correct list 'cX' according to its number of clusters.

`object['clear']<-cX` Clear the list 'cX'.

`listPartition` Constructor. Build an empty object.

`ordered` Order the Partition according to the criterion actif.

`regroup` Order then merge identical Partition (usefull to reduce the size of the ListPartition)

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References

[1] Christophe M. Genolini and Bruno Falissard
"KmL: k-means for longitudinal data"
Computational Statistics, vol 25(2), pp 317-328, 2010

[2] Christophe M. Genolini and Bruno Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

Classes: [LongData](#)

Methods: [Partition](#)

Examples

```
#####
### Preparing data
data(artificialLongData)
traj <- as.matrix(artificialLongData[,-1])

### Some clustering
part2 <- partition(rep(c("A","B"),time=100),traj)
part3 <- partition(rep(c("A","B","C","A"),time=50),traj)
part3b <- partition(rep(c("A","B","C","B","C"),time=40),traj)
part4 <- partition(rep(c("A","B","A","C","D"),time=40),traj)

#####
### ListPartition
listPart <- listPartition()
plotCriterion(listPart)

listPart["add"] <- part2
listPart["add"] <- part3
listPart["add"] <- part3b
listPart["add"] <- part4
listPart["add"] <- part4
listPart["add"] <- part3
listPart["add"] <- part3b

plotCriterion(listPart)
```

```

ordered(listPart)
plotCriterion(listPart)
regroup(listPart)
plotCriterion(listPart)
plotAllCriterion(listPart)

```

longData ~ Function: longData ~

Description

longData is a constructor for the class [LongData](#). It create object [LongData](#) containing a single variable-trajectory. For creating joint variable-trajectories, see [longData3d](#).

Usage

```
longData(traj, idAll, time, timeInData,varNames,maxNA)
```

Arguments

traj	[matrix(numeric)], [array(numeric)] or [data.frame]: structure containing the trajectories.
idAll	[vector(character)]: single identifier for each trajectory (ie each individual).
time	[vector(numeric)]: time at which measures were made.
timeInData	[list(vector(numeric))]: precise the column containing the trajectories.
varNames	[character]: name of the variable-trajectory being measured.
maxNA	[numeric]: maximum number of NA that are tolerates on a trajectory. If a trajectory has more missing than maxNA, then it is remove from the analysis.

Details

longData construct a object of class [LongData](#). Two cases can be distinguished:

traj is an array: lines are individual. Column are time of measurment.

If idAll is missing, the individuals are labelled i1, i2, i3,...

If timeInData is missing, all the column are used (timeInData=1:ncol(traj)).

If traj is a data.frame: lines are individual. Column are time of measurement.

If idAll is missing, then the first column of the data.frame is used for idAll

If timeInData is missing and idAll is missing, then all the columns but the first are used for timeInData (the first is omitted since it is already used for idAll): idAll=traj[, 1], timeInData=2:ncol(traj).

If timeInData is missing but idAll is not missing, then all the column including the first are used for timeInData: timeInData=1:ncol(traj).

Value

An object of class [LongData](#).

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References

[1] C. Genolini and B. Falissard
"KmL: k-means for longitudinal data"
Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[LongData](#)

Examples

```
#####
### From matrix

### Small data
mat <- matrix(c(1,NA,3,2,3,6,1,8,10),3,3,dimnames=list(c(101,102,104),c("T2","T4","T8")))
longData(mat)
(ld1 <- longData(traj=mat,idAll=as.character(c(101,102,104)),time=c(2,4,8),varNames="V"))
plotTrajMeans(ld1)

### Big data
mat <- matrix(runif(1051*325),1051,325)
(ld2 <- longData(traj=mat,idAll=paste("I-",1:1051,sep=""),time=(1:325)+0.5,varNames="Random"))

#####
### From data.frame

dn <- data.frame(id=1:3,v1=c(NA,2,1),v2=c(NA,1,0),v3=c(3,2,2),v4=c(4,2,NA))

### Basic
longData(dn)

### Selecting some times
(ld3 <- longData(dn,timeInData=c(1,2,4),varNames=c("Hyp")))

### Excluding trajectories with more than 1 NA
(ld3 <- longData(dn,maxNA=1))
```

LongData-class ~ Class: LongData ~

Description

LongData is an objet containing the longitudinal data (the individual trajectories) and some associate value (like time, individual identifiant,...). It can be used either for a single variable-trajectory or for joint variable-trajectories.

Objects from the Class

Object LongData for single variable-trajectory can be created using the fonction [longData](#) on a `data.frame` or on a `matrix`.

LongData for joint trajectories can be created by calling the fonction [longData3d](#) on a `data.frame` or on an array.

Slots

`idAll` [`vector(character)`]: Single identifier for each of the longData (each individual). Usefull to export clusters.

`idFewNA` [`vector(character)`]: Restriction of `idAll` to the trajectories that does not have 'too many' missing value. See `maxNA` for 'too many' definition.

`time` [`numeric`]: Time at which measures are made.

`varNames` [`character`]: Name of the variable measured.

`traj` [`matrix(numeric)`]: Contains the longitudianl data. Each lines is the trajectories of an individual. Each column is the time at which measures are made.

`dimTraj` [`vector3(numeric)`]: size of the matrix `traj` (ie `dimTraj=c(length(idFewNA),length(time))`).

`maxNA` [`numeric`] or [`vector(numeric)`]: Individual whose trajectories contain 'too many' missing value are exclude from `traj` and will no be use in the analysis. Their identifier is preserved in `idAll` but not in `idFewNA`. 'too many' is define by `maxNA`: a trajectory with more missing than `maxNA` is exclude.

`reverse` [`matrix(numeric)`]: if the trajectories are scale using the fonction [scale](#), the 'scaling parameters' (probably mean and standard deviation) are saved in `reverse`. This is usefull to restore the original data after a scaling operation.

Construction

Object LongData for single variable-trajectory can be created by calling the fonction [longData](#) on a `data.frame` or on a `matrix`.

LongData for joint trajectories can be created by calling the fonction [longData3d](#) on a `data.frame` or on an array.

Get [

Object["idAll"] [vecteur(character)]: Gets the full list of individual identifiant (the value of the slot idAll)

Object["idFewNA"] [vecteur(character)]: Gets the list of individual identifiant with not too many missing values (the value of the slot idFewNA)

Object["varNames"] [character]: Gets the name(s) of the variable (the value of the slot varNames)

Object["time"] [vecteur(numeric)]: Gets the times (the value of the slot time)

Object["traj"] [array(numeric)]: Gets all the longData' values (the value of the slot traj)

Object["dimTraj"] [vector3(numeric)]: Gets the dimension of traj.

Object["nbIdFewNA"] [numeric]: Gets the first dimension of traj (ie the number of individual include in the analysis).

Object["nbTime"] [numeric]: Gets the second dimension of traj (ie the number of time measurement).

Object["nbVar"] [numeric]: Gets the third dimension of traj (ie the number of variables).

Object["maxNA"] [vecteur(numeric)]: Gets maxNA.

Object["reverse"] [matrix(numeric)]: Gets the matrix of the scaling parameters.

Methods

scale scale the trajectories. Usefull to normalize variable trajectories measured with different units.

restoreRealData restore original data that have been modified after a scaling operation.

longDataFrom3d Extract a variable trajectory form a dataset of joint trajectories.

plotTrajMeans plot all the variables of the LongData, optionnaly according to a [Partition](#).

plotTrajMeans3d plot two variables of the LongData in 3 dimensions, optionnaly according to a [Partition](#).

plot3dPdf create 'Triangle objects' representing in 3D the cluster's center according to a [Partition](#). 'Triangle object' can latter be include in a LaTeX file to get a dynamique (rotationg) pdf figure.

imputation Impute the missing values of the trajectories.

qualityCriterion Compute some quality criterion that can be use to compare the quality of differents [Partition](#).

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"KmL: k-means for longitudinal data"
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- [2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

Overview: [longitudinalData-package](#)
Methods: [longData](#), [longData3d](#), [imputation](#), [qualityCriterion](#)
Plot: [plotTrajMeans](#), [plotTrajMeans3d](#), [plot3dPdf](#)

Examples

```
#####  
### building trajectory (longData)  
mat <- matrix(c(NA,2,3,4,1,6,2,5,1,3,8,10),4)  
ld <- longData(mat,idAll=c("I1","I2","I3","I4"),time=c(2,4,8),varNames="Age")  
  
### '[' and '[<-'  
ld["idAll"]  
ld["idFewNA"]  
ld["varNames"]  
ld["traj"]  
(ld)  
  
### Plot  
plotTrajMeans(ld,parMean=parMEAN(type="n"))
```

longData3d

~ Function: longData3d ~

Description

longData3d is a constructor of the class [LongData](#). It create object [LongData](#) containing several joint trajectory (two or more variable-trajectories). For creating a single variable-trajectory, see [longData](#).

Usage

```
longData3d(traj, idAll, time, timeInData,varNames,maxNA)
```

Arguments

traj	[array(numeric)] or data.frame: structure containing the variable-trajectories.
idAll	[vector(character)]: single identifier for each trajectory (ie each individual).
time	[vector(numeric)]: time at which measures were made.
timeInData	[list(vector(numeric))]: Precise the column containing the trajectories. If traj is a data.frame, it could be a list.
varNames	[character]: name of the variable-trajectories being measured.
maxNA	[vector(numeric)]: maximum number of NA that are tolerates on a trajectory (one for each variable). If a trajectory has more missing than maxNA, then it is remove from the analysis.

Details

longData3d construct a object of class [LongData](#). Two cases can be distinguished:

traj is an array: the first dimension (line) are individual. The second dimension (column) are time at which the measurement are made. The third dimension are the differents variable-trajectories. For example, `traj[, , 2]` is the second variable-trajectory.

If `idAll` is missing, the individuals are labelled `i1, i2, i3,...`

If `timeInData` is missing, all the column are used (`1:ncol(traj)`).

If traj is a data.frame: lines are individual. Time of measurement and variables should be provide through `timeInData`. `timeInData` is a list. The label of the list are the variable-trajectories names. Elements of the list are the column containning the trajectories. For example, if `timeInData=list(V=c(2,3,4),W=c(6,8,12))`, then the first variable-trajectory is 'V', its measurement are in column 2,3 and 4. The second variable-trajectory is 'W', its measurement are in column 6,8 and 12.

If `idAll` is missing, the first column of the data.frame is used.

Value

An object of class [LongData](#).

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References

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Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"

Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[LongData](#)

Examples

```
#####
### From array

mat <- array(c(1,NA,3,2,3,6,1,8,10,1,NA,1,2,NA,3,2,3,2),dim=c(3,3,2))
longData3d(mat)
(ld1 <- longData3d(mat,varNames=c("Hyp","Col"),idAll=c("i101","i104","i105")))
plotTrajMeans3d(ld1)

#####
### From data.frame

dn <- data.frame(id=1:3,v1=c(2,2,1),t1=c(20,21,22),v1=c(3,2,2),t2=c(23,20,28),t3=c(25,24,29))
longData3d(dn,timeInData=list(c(2,4),c(3,5)),varNames=c("V","T"))
(ld3 <- longData3d(dn,timeInData=list(V=c(2,4,NA),T=c(3,5,6))))
plotTrajMeans3d(ld3)
```

LongData3d-class ~ Class: LongData3d ~

Description

LongData3d is an objet containing joint longitudinal data and some associate value (like time, individual identifiant,...).

Objects from the Class

Object LongData3d can be created using the fonction [longData3d](#) on a data.frame or on an array.

Slots

`idAll` [vector(character)]: Single identifier for each of the longData3d (each individual). Useful to export clusters.

`idFewNA` [vector(character)]: Restriction of `idAll` to the trajectories that does not have 'too many' missing value. See `maxNA` for 'too many' definition.

`time` [numeric]: Time at which measures are made.

`varNames` [vector(character)]: Names of the variable measured.

`traj` [array(numeric)]: Contains the joint variable-trajectories. Each horizontal plan (first dimension) corresponds to the joint-trajectories of an individual. Vertical plans (second dimension) refer to the time at which measures are made. Transversal plans (the third dimension) are for variables.

`dimTraj` [vector3(numeric)]: size of the array `traj` (ie `dimTraj=c(length(idFewNA),length(time),length(varNames))`)

`maxNA` [numeric] or [vector(numeric)]: Individual whose trajectories contain 'too many' missing value are exclude from `traj` and will no be use in the analysis. Their identifier is preserved in `idAll` but not in `idFewNA`. 'too many' is define by `maxNA`: a trajectory with more missing than `maxNA` is exclude. When `maxNA` is a single number, it is recycled for all the variables.

`reverse` [matrix(numeric)]: if the trajectories are scale using the function [scale](#), the 'scaling parameters' (probably mean and standard deviation) are saved in `reverse`. This is usefull to restore the original data after a scaling operation.

Construction

`LongData3d` can be created by calling the fonction [longData3d](#) on a `data.frame` or on an array.

Get [

Object["idAll"] [vecteur(character)]: Gets the full list of individual identifiant (the value of the slot `idAll`)

Object["idFewNA"] [vecteur(character)]: Gets the list of individual identifiant with not too many missing values (the value of the slot `idFewNA`)

Object["varNames"] [character]: Gets the name(s) of the variable (the value of the slot `varNames`)

Object["time"] [vecteur(numeric)]: Gets the times (the value of the slot `time`)

Object["traj"] [array(numeric)]: Gets all the joint trajectories (the value of the slot `traj`)

Object["dimTraj"] [vector3(numeric)]: Gets the dimension of `traj`.

Object["nbIdFewNA"] [numeric]: Gets the first dimension of `traj` (ie the number of individual include in the analysis).

Object["nbTime"] [numeric]: Gets the second dimension of `traj` (ie the number of time measurement).

Object["nbVar"] [numeric]: Gets the third dimension of `traj` (ie the number of variables).

Object["maxNA"] [vecteur(numeric)]: Gets `maxNA`.

Object["reverse"] [matrix(numeric)]: Gets the matrix of the scaling parameters.

Methods

[scale](#) scale the trajectories. Usefull to normalize variable trajectories measured with different units.

[restoreRealData](#) restore original data that have been modified after a scaling operation.

[longDataFrom3d](#) Create a [LongData](#) by extracting a single variable trajectory form a dataset of joint variable-trajectories.

`plotTrajMeans` plot all the variable of the `LongData3d`, optionnaly according to a [Partition](#).

`plotTrajMeans3d` plot two variables of the `LongData3d` in a 3 dimensions graph, optionnaly according to a [Partition](#).

`plot3dPdf` create 'Triangle objects' representing in 3D the cluster's center according to a [Partition](#). 'Triangle object' can latter be include in a LaTeX file to get a dynamique (rotationg) pdf figure.

`imputation` Impute the missing values of the trajectories.

`qualityCriterion` Compute some quality criterion that can be use to compare the quality of differents [Partition](#).

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References

[1] C. Genolini and B. Falissard
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Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

Overview: [longitudinalData-package](#)

Methods: [LongData](#), [longData3d](#), [imputation](#), [qualityCriterion](#)

Plot: [plotTrajMeans](#), [plotTrajMeans3d](#), [plot3dPdf](#)

Examples

```
#####  
### building joint trajectories  
  
dn <- data.frame(id=1:3,v1=c(11,14,16),t1=c(1,5,7),v2=c(12,10,13),t2=c(2,5,0),t3=c(3,6,8))  
(ld <- longData3d(dn,timeInData=list(Vir=c(2,4,NA),Tes=c(3,5,6))))  
  
### Scaling  
scale(ld)  
(ld)  
  
### Plotting  
plotTrajMeans3d(ld)  
restoreRealData(ld)
```

longDataFrom3d

~ Function: longDataFrom3d ~

Description

Extract a single variable-trajectory from an object [LongData](#) that contain some joint-trajectories.

Usage

```
longDataFrom3d(xLongData3d,variable)
```

Arguments

xLongData3d [LongData3d]: structure containing some joint-trajectories.
 variable [character]: either the name of one of the variable of xLongData3d, or its number.

Details

Extract a single variable-trajectory from an object [LongData3d](#) that contain some join-trajectories.

Value

An object of class [LongData](#).

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 Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[LongData](#)

Examples

```
### Creation of joint-trajectories
mat <- array(c(1,NA,3,2,3,6,1,8,10,1,NA,1,2,NA,3,2,3,2),dim=c(3,3,2))
(ldJoint <- longData3d(mat,varNames=c("Hyp","Som")))

### Extraction of the first variable-trajectory
(ldHyp <- longDataFrom3d(ldJoint,variable="Hyp"))

### Extraction of the second variable-trajectory
(ldSom <- longDataFrom3d(ldJoint,variable="Som"))

### Extraction of the second variable-trajectory, using number
(ldSom <- longDataFrom3d(ldJoint,variable=2))
```

longDataTo3d ~ Function: longDataTo3d ~

Description

Build a object [LongData3d](#) from an object [LongData](#). The resulting object has a single variable-trajectory stored in a array.

Usage

```
longDataTo3d(xLongData)
```

Arguments

xLongData [[LongData](#)]: structure containing a variable-trajectory.

Details

Build a object [LongData3d](#) from an object [LongData](#). The resulting object has a single variable-trajectory stored in a array.

Value

An object of class [LongData3d](#).

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[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[LongData](#)

Examples

```
### Creation of single variable-trajectory
mat <- matrix(c(1,NA,3,2,3,6,1,8,10,1,NA,1,2,NA,3,2,3,2),6,3)
(ldSingle <- longData(mat))

### Extension to joint trajectories
(ldHyp <- longDataTo3d(ldSingle))
```

makeLatexFile *~ Function: makeLatexFile ~*

Description

Create a LaTeX document that include 3D objects into PDF documents.

Usage

```
makeLatexFile(filename = "main.tex", asyToInclude = "scene+0.prc")
```

Arguments

filename	Name of the LaTeX file
asyToInclude	Name of the file holding the 3D graph to include.

Details

Create a LaTeX document that include 3D objects into PDF documents with PDF-1.5/1.6 compatibility.

Value

A LaTeX file, in the current directory.

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References

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See Also

[makeTriangles](#), [plot3dPdf](#), [saveTrianglesAsASY](#).

Examples

```
### Generating the data
data(artificialJointLongData)
myLd <- longData3d(artificialJointLongData,timeInData=list(var1=2:12,var2=13:23))
part <- partition(rep(1:3,each=50))
plotTrajMeans3d(myLd,part)

### Creation of the scene
scene <- plot3dPdf(myLd,part)
drawScene.rgl(scene)

### Export in '.asy' file
saveTrianglesAsASY(scene)

### Creation of a '.prc' file
# Open a console, then run:
# 'asy -inlineimage -tex pdflatex scene.asy'

### Creation of the LaTeX main document
makeLatexFile()

### Creation of the '.pdf'
# Open a console window, then run
# pdfLatex main.tex
```

ordered(ListPartition)

~ Function: ordered(ListPartition) ~

Description

Sort the [Partition](#) of a [ListPartition](#) according to a quality criterion.

Usage

```
ordered(x,...)
```

Arguments

x	[ListPartition]: Object whose Partition should be sort.
...	Note used, for S4 compatibility only.

Details

Sort the Partition of a ListPartition for each list (sort the 'c2' list, the 'c3' list,...) according to a quality criterion. The criterion used to sort is the one in the field `criterionActif`.

Value

This function change internally the order of the fields `c2`, `c3`, ... `c26` of an object. In addition, it return the permutation matrix (the matrix use to re-ordered the `ci`).

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Examples

```
#####
### Preparing data
data(artificialLongData)
traj <- as.matrix(artificialLongData[,-1])

### Some clustering
part2 <- partition(rep(c("A","B"),time=100),traj)
part3 <- partition(rep(c("A","B","C","A"),time=50),traj)
part3b <- partition(rep(c("A","B","C","B"),time=50),traj)
part4 <- partition(rep(c("A","B","C","D"),time=50),traj)

#####
### ListPartition
listPart <- listPartition()
listPart['criterionActif'] <- "Davies.Bouldin"
plotCriterion(listPart)

listPart["add"] <- part2
listPart["add"] <- part3
listPart["add"] <- part3b
listPart["add"] <- part4
```

```

listPart["add"] <- part4
listPart["add"] <- part3
listPart["add"] <- part3b

plotCriterion(listPart)
ordered(listPart)
plotCriterion(listPart)

listPart['criterionActif'] <- "Calinski.Harabatz"
plotCriterion(listPart)
ordered(listPart)
plotCriterion(listPart)

```

parLongData ~ Function: parLongData, parTraj and parMean~

Description

parLongData, parTraj and parMean are constructors for the class [ParLongData](#).

Usage

```

parLongData(type, col, pch, pchPeriod, cex, xlab, ylab)
parTRAJ(type = "l", col = "black", pch = "1",
        pchPeriod = 0, cex = 1, xlab = "Time", ylab = "")
parMEAN(type = "b", col = "clusters", pch = "letters",
        pchPeriod = 1, cex = 1.2, xlab = "Time", ylab = "")

```

Arguments

type	[character]: Set type of the plot should be drawn ('p' for point, 'l' for line, 'b' for both, 'c' line appart, 'o' for overplot, 'h' for histogram, 's' and 'S' for steps, 'n' for no plotting)
col	[character]: Set the plotting color. Vector of values are accepted. The special value 'clusters' can be use to color each trajectories according to its clusters (see details).
pch	[numeric] or [character]: Either an integer specifying a symbol or special values 'letters' or 'symbol' (see details).
pchPeriod	[numeric]: Fix the number of point that should be plot. Usefull to plot points on trajectories with a lot of mesurement (see examples in plotTrajMeans for LongData for details).
cex	[numeric]: Set the amount by which plotting text and symbols should be magnified relative to the default.
xlab	[character]: Title for the x axis.
ylab	[character]: Title for the y axis.

Details

parLongData is the basic constructor of the class [ParLongData](#).

parTRAJ create an object with default values for plotting individual trajectories ;

parMEAN create an object with default values for plotting mean trajectories.

If col='clusters', pch='letters' or pch='symbol', the object can not be use directly, it should first be prepared using the function [expandParLongData](#).

Value

An object of class [ParLongData](#)

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English translation

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Examples

```
#####
### Construction of LongData

time=c(1,2,3,4,8,12,16,20)
id2=1:120
f <- function(id,t)((id-1)%3-1) * t
g <- function(id,t)(id%2+1)*t
ld2 <- longData3d(
  array(cbind(outer(id2,time,f),outer(id2,time,g))+rnorm(120*8*2,0,3),
    dim=c(120,8,2)))

### Example with default value
plotTrajMeans3d(ld2)
plotTrajMeans3d(ld2,parTraj=parTRAJ())

### Example with default value except for the color
plotTrajMeans3d(ld2,parTraj=parTRAJ(col="blue"))
```

ParLongData-class ~ Class: ParLongData ~

Description

ParLongData is an objet containing some graphical parameter used to plot [LongData](#) object and / or mean trajectories. They work as define in par.

Slots

type [character]: Type of the plot that should be drawn ('p' for point, 'l' for line, 'b' for both, 'c' line appart, 'o' for overplot, 'h' for histogram, 's' and 'S' for steps, 'n' for no plotting)

col [character]: A specification for the default plotting color. Can be either a single value or a vector.

pch [numeric] or [character]: Either an integer specifying a symbol or a single character to be used as the default in plotting points. See example in [points](#) for possible values and their interpretation.

pchPeriod [numeric]: Fix the number of point that should be plot. Usefull to plot points on trajectories with a lot of mesurement (see examples in [plotTrajMeans](#) for LongData for details).

cex [numeric]: A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default.

xlab [character]: A title for the x axis.

ylab [character]: A title for the y axis.

Construction

Object ParLongData can be created by three functions:

1. parLongData create an object from scratch ;
2. parTraj create an object containing default value to plot individutal trajectories;
3. parMean create an object containing default value to plot mean trajectories.

Methods

object['xxx'] Get the value of the field xxx.
object['xxx']<-value Set the field xxx to value.

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Examples

```
### Building ParLongData
parMyData <- parLongData(type="n",col=3,pch="1",pchPeriod=20,cex=1,xlab="Time",ylab="Size")

### Get
parMyData['col']

### Set
parMyData['cex'] <- 3
(parMyData)
```

partition ~ *Function: partition* ~

Description

partition is the constructor of the class [Partition](#). It can be build either alone or relatively to a object LongData.

Usage

```
partition(clusters, traj, details=character())
```

Arguments

clusters	[vector(factor)]: cluters to which each individual belongs. Each clusters is represented by an upper letters.
traj	[matrix] or [array]: if an object LongData is provide, it will be used to compute the quality criterion of the clustering. array are simply turn into matrix by "sticking" all the variables one behind the other.
details	[vector(character)]: the slot details is used to store various informations. If the Partition has been find using an algorithm, it can store the name of the algorithm, the time before convergence, the number of iteration and any other informations. The syntaxe is details=c(algorithm="kmeans", convergenceTime="6", otherInfo="Wha

Details

partition construct a object of class [Partition](#). It does not provide any default values. yLongData and details are optional.

Value

An object of class [Partition](#).

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[2] Christophe M. Genolini and Bruno Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[Partition,ordered](#)

Examples

```
### Empty partition
partition()

### Small partition
partition(clusters=c("A","B","A","C","C"))

### Random partition
partition(clusters=LETTERS[floor(runif(100,1,5))])

### Partition that clusters correctly some data
### Quality criterion are high
data(artificialLongData)
traj <- as.matrix(artificialLongData[,-1])
partition(clusters=rep(1:4,each=50),traj)

### Partition that does not cluster correctly the data
### Quality criterion are low
partition(clusters=rep(1:4,50),traj)
```

Partition-class ~ Class: Partition ~

Description

An object of class `Partition` is a partition of a population into subgroups. The object also contains some information like the percentage of trajectories in each group or some qualities criterion.

Objects from the Class

Objects are mainly intend to be created by some clustering methods (like k-means, fuzzy k-means, mixture modeling, latent class analysis,...)

Slots

`nbClusters` [numeric]: number of groups, between 1 and 26

`clusters` [vector(factor)]: vector containing the groups of each individual. Groups are in upper-case letters.

`percentEachCluster` [vector(numeric)]: percentage of trajectories contained in each group.

`postProba` [matrix(numeric)]: assuming that in each clusters C and for each time T , variable follow a normal law (mean and standard deviation of the variable at time T restricted to clusters C), then it is possible to compute the posterior probabilities of each individual (that is the probabilities that an individual has to belong to each clusters). These probabilities are hold in `postProba`.

`postProbaEachCluster` [vector(numeric)]: for each clusters C , mean of the post probabilities to belong to C of the individual that effectively belong to C . A high percent means that the individual that are in this cluter realy meant to be here.

`criterionValues` [vector(numeric)]: Value of the quality criterions used to evaluate the quality of the Clustering. See [qualityCriterion](#) for details.

`details` [vector(character)]: hold different optionnal informations like the algorithm (if any) used to find the partition, the convergence time, the imputation methods, the starting condition. Examples: `details=c(algorithm="kmeans",convergenceTime="3")`.

validation rules

A class `Partition` object must follow some rules to be valid:

- Slots should be either all empty, or all non empty.
- `nbClusters` has to be lower or equal to 26.
- `clusters` is a factor in `LETTERS[1:nbCluster]`.

Construction

Class `Partition` objects are mainly constructed by some clustering methods (like k-means, fuzzy k-means, mixture modeling, latent class analysis,...). Nevertheless, it is also possible to construct them from scratch using the fonction [partition](#).

Get [

- Object["nbClusters"]** [numeric]: Gets the number of clusters (the value of the slot nbClusters)
- Object["clusters"]** [vector(factor)]: Gets the cluster of each individual (the value of the slot clusters)
- Object["clustersAsInteger"]** [vector(integer)]: Gets the cluster of each individual and turn them into integer
- Object["percentEachClusters"]** [vector(numeric)]: Get the percent of individual in each clusters (the value of the slot nbClusters)
- Object["postProbaEachClusters"]** [vector(numeric)]: Get the post probabilities for each clusters.
- Object["postProba"]** [matrix(numeric)]: Get the post probabilities for each individual and each clusters.
- Object["criterionValues"]** [vector(numeric)]: gives the values of all the criterion values (the value of the slot criterionValues)
- Object["details"]** [vector(character)]: Get the values of the slot details.
- Object["XcriterionX"]** [numeric]: Get the value of the criterion XcriterionX. It can be one of Calinski.Harabatz, Krzysztof.Calinski, Genolini.Calinski, Ray.Turi, Davies.Bouldin, BIC, AIC, AICc or random.
- Object["XspecialX"]** [character]: Get the value named XspecialX in the slot details (probably one of multiplicity, convergenceTime, imputationMethod or algorithm.)

Setteur [<-

- Object["multiplicity" <-value]** [numeric]: In the slot details, sets the values names multiplicity to value.
- Object["convergenceTime" <-value]** [numeric]: In the slot details, sets the values names convergenceTime to value.

The others slot can not be change after the object creation.

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 Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

Overview: [longitudinalData-package](#)

Classes: [LongData](#)

Methods: [partition](#)

Examples

```
#####
### Building Partition

### number
part <- partition(rep(c(1,2,1,3),time=3))

### LETTERS
part <- partition(rep(c("A","B","D"),time=4),details=c(convergenceTime="3",multiplicity="1"))

### Others don't work
try(partition(rep(c("A","Bb","C"),time=3)))

#####
### Setteur and Getteur

### '['
part["clusters"]
part["clustersAsInteger"]
part["nbClusters"]

### '['<-
part["multiplicity"] <- 2
(part)
```

parWindows

~ Function: *parWindows* ~

Description

parWindows is the constructor of object [ParWindows](#).

Usage

```
parWindows(nbRow, nbCol, addLegend,closeScreen)
```

Arguments

nbRow	[numeric]: Number of row of the screen matrix.
nbCol	[numeric]: Number of column of the screen matrix.
addLegend	[logical]: Shall a legend be added on the graph?

`closeScreen` [logical]: Some function need to add details on a graph. This option let them call a plot function that will not call a `close.screen` on exit, so the graph will be modifiable.

Details

`parWindows` is the constructor of object `ParWindows`. Given a number of rows and colonnes, it computes the `screenMatrix` that is use by `split.screen` for plot object `LongData`. If `addLegend` is true, an extra space is added on the top of the graphes to print the legend.

Value

An object of class `ParWindows`.

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Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

Examples

```
### Building ParWindows
(paramWin <- parWindows(3,2,FALSE,TRUE))

### Get
figsScreen <- paramWin['screenMatrix']

### Usage
listScreen <- split.screen(figsScreen)
screen(listScreen[1])
plot(-5:5/10,2.5-(-5:5)^2/20,ylim=c(0,6),axes=FALSE,xlab="",ylab="",type="l",lwd=3)
lines(-5:5/10,(-5:5)^2/20,ylim=c(0,6),type="l",lwd=3)

screen(listScreen[3])
plot(-5:5/10,2.5-(-5:5)^2/20,ylim=c(0,6),axes=FALSE,xlab="",ylab="",type="l",lwd=3)
lines(-5:5/10,(-5:5)^2/20,ylim=c(0,6),type="l",lwd=3)

screen(listScreen[5])
```

```

plot(-5:5/10, (-5:5)^2/10, ylim=c(0,6), axes=FALSE, xlab="", ylab="", type="l", lwd=3)
lines(-5:5/10, (-5:5)^2/20+1.25, ylim=c(0,6), type="l", lwd=3)
close.screen(all.screens=TRUE)

### :-)

```

ParWindows-class ~ Class: ParWindows ~

Description

ParWindows is an objet containing graphical parameter used to set the screen display.

Slots

nbCol [numeric]: Number of column of the screen matrix.

nbRow [numeric]: Number of row of the screen matrix.

addLegend [logical]: Shall a legend be added on the graph?

closeScreen [logical]: On exit, high level plot function can either close the screen that they open and return nothing ; or not close it and return the list of the screen number.

screenMatrix [matrix(numeric)]: Matrix with 4 column defining the screen region, like the figs argument of the function [screen](#). The screenMatrix can be specified by the user (bad idea) or can be compute automatically according to nbCol, nbRow and addLegend. For that, use [windowsCut](#).

Construction

Object ParWindows can be created by the constructor [parWindows](#) or by the function [windowsCut](#).

Methods

object['xxx'] Get the value of the field xxx.

object['xxx']<-value Set the field xxx to value.

Author

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References

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- [2] C. Genolini and B. Falissard
 "KmL: A package to cluster longitudinal data"
 Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

Examples

```
### Building ParWindows
(paramWin <- parWindows(3,2,FALSE,TRUE))

### Get
figsScreen <- paramWin['screenMatrix']

### Usage
listScreen <- split.screen(figsScreen)
screen(listScreen[1])
plot(-5:5/10, 2.5-(-5:5)^2/20, ylim=c(0,6), axes=FALSE, xlab="", ylab="", type="l", lwd=3)
lines(-5:5/10, (-5:5)^2/20, ylim=c(0,6), type="l", lwd=3)

screen(listScreen[3])
plot(-5:5/10, 2.5-(-5:5)^2/20, ylim=c(0,6), axes=FALSE, xlab="", ylab="", type="l", lwd=3)
lines(-5:5/10, (-5:5)^2/20, ylim=c(0,6), type="l", lwd=3)

screen(listScreen[5])
plot(-5:5/10, (-5:5)^2/10, ylim=c(0,6), axes=FALSE, xlab="", ylab="", type="l", lwd=3)
lines(-5:5/10, (-5:5)^2/20+1.25, ylim=c(0,6), type="l", lwd=3)
close.screen(all.screens=TRUE)

### Sorry for that...
```

plot3dPdf

~ Function: plot3dPdf for LongData ~

Description

Given a [LongData](#) and a [Partition](#), this function create 'Triangle objects' representing the 3D plot the clusters centers. Triangle object can latter be used to include dynamic rotating graph in a pdf file.

Usage

```
## S4 method for signature 'LongData3d,missing'
plot3dPdf(x,y,varY=1,varZ=2)
```

```
## S4 method for signature 'LongData3d,numeric'
plot3dPdf(x,y,varY=1,varZ=2)
```

Arguments

x	[LongData]: Object containing the trajectories to plot.
y	[numeric]: Partition that will be use to plot the object.
varY	[numeric] or [character]: either the number or the name of the first variable to display. 1 by default.
varZ	[numeric] or [character]: either the number or the name of the second variable to display. 2 by default.

Details

Create Triangle objects representing the 3D plot of the main trajectories of a [LongData](#).

The three functions [plot3dPdf](#), [saveTrianglesAsASY](#) and [makeLatexFile](#) are design to export a 3D graph to a Pdf file. The process is the following:

1. [plot3dPdf](#): Create a scene, that is a collection of Triangle object that represent a 3D images.
2. [saveTrianglesAsASY](#): Export the scene in an '.asy' file.
3. '.asy' can not be include in LaTeX file. LaTeX can read only '.pre' file. So the next step is to use the software asymptote to convert '.asy' to '.pre'. This is done by the command `asy -inlineimage -tex pdfLatex scene.asy` (not in R, in a console).
4. The previous step did produce a file `scene+0.prc` that can be include in a LaTeX file. [makeLatexFile](#) create a LaTeX file that is directly compilable (using `pdfLatex`). It produce a pdf file that contain the 3D object.

Value

A Triangle object.

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References

[1] C. Genolini and B. Falissard
 "KmL: k-means for longitudinal data"
 Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
 "KmL: A package to cluster longitudinal data"
 Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[saveTrianglesAsASY](#), [makeLatexFile](#), [makeTriangles](#)

Examples

```
### Generating the data
data(artificialJointLongData)
myLd <- longData3d(artificialJointLongData,timeInData=list(var1=2:12,var2=13:23))
part <- partition(rep(1:3,each=50))
plotTrajMeans3d(myLd,part)

### Creation of the scene
scene <- plot3dPdf(myLd,part)
drawScene.rgl(scene)

### Export in '.asy' file
saveTrianglesAsASY(scene)

### Creation of a '.prc' file
# Open a console, then run:
# 'asy -inlineimage -tex pdflatex scene.asy'

### Creation of the LaTeX main document
makeLatexFile()

### Creation of the '.pdf'
# Open a console window, then run
# pdfLatex main.tex
```

plotAllCriterion ~ *Function: plotAllCriterion* ~

Description

This function graphically displays the quality criterion of all the [Partition](#) of a [ListPartition](#) object.

Usage

```
plotAllCriterion(x, criterion=CRITERION_NAMES[1:5],standardized = TRUE)
```

Arguments

x	[ClusterLongData]: object whose quality criterion should be displayed.
criterion	[character]: name of the criterion(s) to plot. It can either display all the value for a single specific criterion or display several criterion, only the best value for each clusters number and for each criterion.
standardized	[logical]: If standardized=TRUE, all the criterion will be mapped into [0,1]. This makes them more easily comparable.

Details

This function display graphically several quality criterion, probably to decide the best clusters' number.

Value

No value are return. A graph is printed.

Examples

```
#####
### Data generation
data(artificialLongData)
traj <- as.matrix(artificialLongData[,-1])

### Some clustering
listPart <- listPartition()
listPart["add"] <- partition(rep(c("A","B"),time=100),traj)
listPart["add"] <- partition(rep(c("A","B","B","B"),time=50),traj)
listPart["add"] <- partition(rep(c("A","B","C","A"),time=50),traj)
listPart["add"] <- partition(rep(c("A","B","C","D"),time=50),traj)
ordered(listPart)

#####
### graphical display
plotAllCriterion(listPart)
plotAllCriterion(listPart,criterion=CRITERION_NAMES[1:5],TRUE)
```

plotCriterion ~ Function: plotCriterion ~

Description

This function graphically displays the quality criterion of all the [Partition](#) of a [ListPartition](#) object.

Usage

```
plotCriterion(x, criterion=x["criterionActif"],nbCriterion=100)
```

Arguments

x	[ClusterLongData]: object whose quality criterion should be displayed.
criterion	[character]: name of the criterion(s) to plot. It can either display all the value for a single specific criterion or display several criterion, only the best value for each clusters number and for each criterion.
nbCriterion	[numeric]: if there is a big number of Partition , the graphical display of all of them can be slow. nbCriterion lets the user limit the number of criteria that will be taken in account.

Details

This function display graphically the quality criterion (probably to decide the best clusters' number). It can either display all the criterion ; this is useful to see the consistency of the result : is the best clusterization obtain several time or only one ? It can also display only the best result for each clusters number : this helps to find the local maximum, which is classically used to chose the "correct" clusters' number.

Value

No value are return. A graph is printed.

Examples

```
#####
### Data generation
data(artificialLongData)
traj <- as.matrix(artificialLongData[,-1])

### Some clustering
listPart <- listPartition()
listPart["add"] <- partition(rep(c("A","B"),time=100),traj)
listPart["add"] <- partition(rep(c("A","B","B","B"),time=50),traj)
listPart["add"] <- partition(rep(c("A","B","C","A"),time=50),traj)
listPart["add"] <- partition(rep(c("A","B","C","D"),time=50),traj)
ordered(listPart)

#####
### graphical display
plotCriterion(listPart)
plotAllCriterion(listPart,criterion=CRITERION_NAMES[1:5],TRUE)
```

plotTrajMeans,LongData

~ Function: plotTrajMeans for LongData ~

Description

Plot the [LongData](#) or [LongData3d](#) optionnaly relatively to a [Partition](#). For joint trajectories, one graphe for each variable trajectory is displayed.

Usage

```
plotTrajMeans(x, y, parTraj=parTRAJ(), parMean=parMEAN(),...)
```

Arguments

x	[LongData] or [LongData3d]: Object containing the trajectories to plot.
y	[numeric]: Partition that will be use to plot the object. If y is missing, a Partition with a single cluster is considered.
parTraj	[ParLongData]: Set the graphical parameters used to plot the trajectories. See ParLongData and examples for details.
parMean	[ParLongData]: Set the graphical parameters used to plot the mean trajectories of each clusters (only when y is non missing). See ParLongData and examples for details.
...	Arguments to be passed to methods, such as graphical parameters.

Details

Plot either a [LongData](#), or each variable of a [LongData3d](#) optionnaly according to the Partition define by y.

Graphical option concerning the individual trajectory (col, type, pch and xlab) can be change using parTraj. Graphical option concerning the cluster mean trajectory (col, type, pch, pchPeriod and cex) can be change using parMean. For more detail on parTraj and parMean, see object of class [ParLongData](#).

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[1] C. Genolini and B. Falissard
"KmL: k-means for longitudinal data"
Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[LongData](#), [LongData3d](#), [plotTrajMeans3d](#).

Examples

```
#####  
### Construction of the data  
data(artificialLongData)
```

```

ld <- longData(artificialJointLongData)
part <- partition(rep(1:3,each=50))

### Basic plotting
plotTrajMeans(ld)
plotTrajMeans(ld,part,xlab="Time")

#####
### Changing graphical parameters 'par'

### No letters on the mean trajectories
plotTrajMeans(ld,part,parMean=parMEAN(type="l"))

### Only one letter on the mean trajectories
plotTrajMeans(ld,part,parMean=parMEAN(pchPeriod=Inf))

### Color individual according to its clusters (col="clusters")
plotTrajMeans(ld,part,parTraj=parTRAJ(col="clusters"))

### Mean without individual
plotTrajMeans(ld,part,parTraj=parTRAJ(type="n"))

### No mean trajectories (type="n")
### Color individual according to its clusters (col="clusters")
plotTrajMeans(ld,part,parTraj=parTRAJ(col="clusters"),parMean=parMEAN(type="n"))

### Only few trajectories
plotTrajMeans(ld,part,nbSample=10,parTraj=parTRAJ(col='clusters'),parMean=parMEAN(type="n"))

#####
### single variable trajectory

data(artificialLongData)
ld2 <- longData(artificialLongData)
part2 <- partition(rep(1:4,each=50))
plotTrajMeans(ld2)
plotTrajMeans(ld2,part2)

```

plotTrajMeans3d,LongData

~ Function: plotTrajMeans3d for LongData3d ~

Description

Plot two variables of a [LongData3d](#) object in 3D, optionnaly relatively to a [Partition](#).

Usage

```
plotTrajMeans3d(x, y, varY=1, varZ=2,  
  parTraj=parTRAJ(), parMean=parMEAN(type="n"), ...)
```

Arguments

x	[LongData3d]: Object containing the trajectories to plot.
y	[Partition]: Partition that will be use to plot the object. If y is missing, a Partition with a single clusters is considered.
varY	[numeric] or [character]: either the number or the name of the first variable to display. 1 by default.
varZ	[numeric] or [character]: either the number or the name of the second variable to display. 2 by default.
parTraj	[parLongData]: Set the graphical parameters used to plot the trajectories of the LongData3d. See ParLongData and examples for details.
parMean	[parLongData]: Set the graphical parameters used to plot the mean trajectories of each clusters LongData3d (only when y is non missing). See ParLongData and examples for details.
...	Arguments to be passed to methods, such as graphical parameters.

Details

Plot two variables of a [LongData3d](#) object in 3D. It use the [rgl](#) library. The user can make the graphical representation turn using the mouse.

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- [1] C. Genolini and B. Falissard
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"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[LongData3d](#)

Examples

```
#####
### Construction of the data

time=c(1,2,3,4,8,12,16,20)
id2=1:120
f <- function(id,t)((id-1)%%3-1) * t
g <- function(id,t)(id%2+1)*t
h <- function(id,t)(id%4-0.5)*(20-t)
ld <- longData3d(array(cbind(outer(id2,time,f),outer(id2,time,g),outer(id2,time,h))+
  rnorm(120*8*3,0,3),dim=c(120,8,3)))
part <- partition(rep(1:6,20))

### Basic plotting
plotTrajMeans3d(ld)
plotTrajMeans3d(ld,part)

### Variable 1 and 3, then 2 and 3
plotTrajMeans3d(ld,part)
plotTrajMeans3d(ld,part,varY=3,varZ=2)
plotTrajMeans3d(ld,part,varY=1,varZ=3)

#####
### Changing graphical parameters 'par'

### Color individual according to its clusters (col="clusters")
plotTrajMeans3d(ld,part,parTraj=parTRAJ(col="clusters"))
plotTrajMeans3d(ld,part,parTraj=parTRAJ(col="clusters"),varY=1,varZ=3)

### No mean trajectories (type="n"), only few trajectories
### Color individual according to its clusters (col="clusters")
plotTrajMeans3d(ld,part,parTraj=parTRAJ(col="clusters"),parMean=parMEAN(type="n"),nbSample=10)
```

qualityCriterion ~ Function: qualityCriterion ~

Description

Given a [LongData](#) and a [Partition](#), the fonction qualityCriterion calculate some qualities criterion.

Usage

```
qualityCriterion(traj,clusters,imputationMethod="copyMean")
```

Arguments

traj	[LongData] or [matrix]: object containing the trajectories on which the criterion is calculate.
clusters	[Partition] or [vector(integer)]: clusters to which individual belongs.
imputationMethod	[character]: if some value are missing in the LongData, it is necessary to impute them. Then the function qualityCriterion call the function <code>imputation</code> using the method method.

Details

Given a `LongData` and a `Partition` (or a matrix and a vector of integer), the fonction `qualityCriterion` calculate several quality criterion and return then as a list (see 'value' below).

If some individual have no clusters (ie if `Partition` has some missing values), the corresponding trajectories are exclude from the calculation.

Note that if there is an empty cluster or an empty trajectory, most of the criterions are unavailable.

Basicly, 6 non-parametrics criterions are computed. In addition, ASSUMING THAT in each clusters C and for each time T , the variable follow a NORMAL LAW (mean and standard deviation of the variable at time T restricted to clusters C), it is possible to compute the the posterior probabilities of the individual trajectories and the likelihood. From there, we can also compute the BIC, the AIC and the global posterior probability. The function `qualityCriterion` also compute these criterion. But the user should alway keep in mind that these criterion are valid ONLY under the hypothesis of normality. If this hypothesis is not respected, algorithm like k-means will converge but the BIC and AIC will have no meaning.

IMPORTANT NOTE: Some criterion should be maximized, some other should be minimized. This might be confusing for the non expert. In order to simplify the comparison of the criterion, `qualityCriterion` compute the OPPOSITE of the criterion that should be minimized (Ray & Bouldin, Davies & Turi, BIC and AIC). Thus, all the criterion computed by this function should be maximized.

Value

A list with three fields: the first is the list of the criterions. the second is the clusters post probabilities; the third is the matrix of the individual post probabilities.

Non-parametric criterion

Notations: k =number of clusters; n =number of individual; B =Between variance ; W =Within variance The criterion are:

- `Calinski.Harabatz[numeric]`: Calinski and Harabatz criterion: $c(k)=\text{Trace}(B)/\text{Trace}(W)*(n-k)/(k-1)$.
- `Calinski.Harabatz2[numeric]`: Calinski and Harabatz criterion modified by Krysczuk: $c(k)=\text{Trace}(B)/\text{Trace}(W)*(n-k)$.
- `Calinski.Harabatz3[numeric]`: Calinski and Harabatz criterion modified by Genolini: $g(k)=\text{Trace}(B)/\text{Trace}(W)*(n-k)$.
- `Ray.Turi[numeric]`: Ray and Turi criterion: $r(k)=-\text{Vintra}/\text{Vinter}$ with $\text{Vintra}=\text{Sum}(\text{dist}(x, \text{center}(x)))$ and $\text{Vinter}=\min(\text{dist}(\text{center}_i, \text{center}_j)^2)$. (The "true" index of Ray and Turi is $\text{Vintra}/\text{Vinter}$ and should me minimized. See IMPORTANT NOTE above.)

- Davies.Bouldin[numeric]: Davies and Bouldin criterion: $d(k) = -\text{mean}(\text{Proximate}(\text{cluster}_i, \text{cluster}_j))$ with $\text{Proximate}(i, j) = (\text{DistInterne}(i) + \text{DistInterne}(j)) / (\text{DistExterne}(i, j))$. (The "true" index of Davies and Bouldin is $\text{mean}(\text{Proximate}())$ and should be minimized. See IMPORTANT NOTE above.)
- random[numeric]: random value following the normal law $N(0,1)$.

Parametric criterion

All the parametric indices should be minimized. So the function qualityCriterion compute their opposite (see IMPORTANT NOTE above.)

Notation: L=likelihood; h=number of parameters; n=number of trajectories; t=number of time measurement; N=total number of measurement ($N=t.n$).

SECOND IMPORTANT NOTE: the formula of parametrics criterion often include the size of the population. In the specific case on longitudinal data, the definition of the "size of the population" is not obvious. It can be either the number of individual n, or the number of measurement $N=n.t$. So, the function qualityCriterion gives two version of all the non parametrics criterion, the first using n, the second using N.

- BIC[numeric]: Bayesian Information Criterion: $\text{BIC} = 2 * \log(L) - h * \log(n)$. See IMPORTANT NOTE above.
- BIC2[numeric]: Bayesian Information Criterion: $\text{BIC} = 2 * \log(L) - h * \log(N)$. See IMPORTANT NOTE above.
- AIC[numeric]: Akaike Information Criterion, bis: $\text{AIC} = 2 * \log(L) - 2 * h$. See IMPORTANT NOTE above.
- AICc[numeric]: Akaike Information Criterion with correction: $\text{AIC} = \text{AIC} + (2h(h+1)) / (n-h-1)$. See IMPORTANT NOTE above.
- AICc2[numeric]: Akaike Information Criterion with correction, bis: $\text{AIC} = \text{AIC} + (2h(h+1)) / (n-h-1)$. See IMPORTANT NOTE above.

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Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[LongData](#), [Partition](#), [imputation](#).

Examples

```
#####
### Preparation of some artificial data
par(ask=TRUE)
data(artificialLongData)
ld <- longData(artificialLongData)

### Correct partition
part1 <- partition(rep(1:4,each=50))
plotTrajMeans(ld,part1)
(cr1 <- qualityCriterion(ld,part1))

### Random partition
part2 <- partition(floor(runif(200,1,5)))
plotTrajMeans(ld,part2)
(cr2 <- qualityCriterion(ld,part2))

### Partition with 3 clusters instead of 4
part3 <- partition(rep(c(1,2,3,3),each=50))
plotTrajMeans(ld,part3)
(cr3 <- qualityCriterion(ld,part3))

### Comparisons of the Partition
plot(c(cr1[[1]],cr2[[1]],cr3[[1]]),main="The highest give the best partition
(according to Calinski & Harabatz criterion)")
par(ask=FALSE)
```

regroup

~ *Function: regroup* ~

Description

Remove duplicate [Partition](#) present in a [ListPartition](#) (or, by inheritance, in [ClusterLongData](#) and [ClusterLongData3d](#) objects).

Usage

```
regroup(object)
```

Arguments

object [\[ListPartition\]](#): object that should be simplified.

Details

A clustering algorithm can find a `Partition` several time. It is store several time in object `ListPartition`(or in `ClusterLongData` or in `ClusterLongData3d`), enconbering the memory. `regroup` remove the duplicate `Partition`. Note that if the `ListPartition` is not ordered, then `regroup` sort it unless `toOrder=FALSE`.

Value

None (this function change internaly the field of an object, it does not return any values.)

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References

[1] Christophe M. Genolini and Bruno Falissard
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[2] Christophe M. Genolini and Bruno Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

Examples

```
### Some data
data(artificialLongData)
myLd <- as.matrix(artificialLongData[,-1])
### Some clustering
part2 <- partition(rep(c("A", "B", "A", "C"), time=50), myLd)
part3 <- partition(rep(c("A", "B", "C", "D"), time=50), myLd)

#####
### ListPartition
listPart <- listPartition()

listPart["add"] <- part2
listPart["add"] <- part3
listPart["add"] <- part2
listPart["add"] <- part3

### Some clustering has been found several time
### regroup will suppress the duplicate one
regroup(listPart)
plotCriterion(listPart)
```

reshapeLongToWide ~ Function: longToWide (or reshapeWide) ~

Description

This function reshapes a data frame in 'long' format (repeated measurements in the same column) into a data frame in 'wide' format (repeated measurements in separate columns). It also corrects a bug of reshape.

Usage

```
longToWide(trajLong)
reshapeLongToWide(trajLong)
```

Arguments

trajLong [data.frame]: data.frame that hold the trajectories in long format. The data.frame has to be (no choice!) in the following format: the first column should be the individual identifier. The second should be the times at which the measurement are made and should be numeric. The third one should be the measurement.

Details

This function reshapes a data frame in 'long' format (repeated measurements in the same column) into a data frame in 'wide' format (repeated measurements in separate columns).

Value

A data frame in 'wide' format (repeated measurements in separate columns).

Note

longToWide is just a 'friendly overlay' of the function [reshape](#). It also corrects a reshape bug (modification of the order of some trajectories value when some times are missing).

Author(s)

Christophe Genolini

See Also

[wideToLong](#), [reshape](#).

Examples

```
summary(Indometh)
longToWide(Indometh)

df2 <- data.frame(id = rep(LETTERS[1:4], rep(2,4)),
                  visit = I(rep(c("3","6"), 4)),
                  x = rnorm(4), y = runif(4),
                  sex=rep(c("H","F","H"),time=c(4,2,2)))[1:7,]
longToWide(df2[,1:3])
longToWide(df2[,c(1,2,4)])
```

reshapeWideToLong ~ *Function: wideToLong (or reshapeWideToLong) ~*

Description

This function reshapes a data frame in 'wide' format (repeated measurements in separate column) into a data frame in 'long' format (repeated measurements in the same columns).

Usage

```
wideToLong(trajWide, times=1:(ncol(trajWide)-1))
reshapeWideToLong(trajWide, times=1:(ncol(trajWide)-1))
```

Arguments

trajWide	[data.frame]: a data frame in 'wide' format (repeated measurements in separate column). The first column has to be the individual indentier. All the other column should be the trajectories.
times	[vector(numeric)]: specification of the times at wich the longitudinal data have been measured (like ages, year, month). If times is missing, it takes the value 1:(ncol(trajWide)-1).

Details

This function reshapes a data frame in 'wide' format (repeated measurements in separe column) into a data frame in 'long' format (repeated measurements in the same columns). The first column has to be the individual indentier. All the other column should be the trajectories. The missing values are removed in long format.

Value

A data frame in 'long' format.

Author(s)

Christophe Genolini

See Also

[longToWide](#), [reshape](#).

Examples

```
df3 <- data.frame(id = LETTERS[rep(1:4)], sex=c("H","F","H","F"),
  v1=rnorm(4),v2=rnorm(4),w1=rnorm(4),w2=rnorm(4))

wideToLong(df3[,c(1,3,4)])
wideToLong(df3[,c(1,5,6)])
wideToLong(df3[,c(1,3:6)])
wideToLong(df3[,c(1,3:6)],times=c(1,2,4,8))
```

restoreRealData ~ *Function: restoreRealData* ~

Description

This function revert the effect of [scale](#) by restauring the initial values of trajectories.

Usage

```
restoreRealData(object)
```

Arguments

object [LongData]: Object containnig trajectories to restore.

Details

This function revert the effect of [scale](#) by restauring the initial values of trajectories.

Value

None: this function change internaly the field of an object, it does not return any values.)

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- [2] C. Genolini and B. Falissard
 "KmL: A package to cluster longitudinal data"
 Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[scale](#)

Examples

```
#####
### Building LongData

time=c(1,2,3,4,8,12,16,20)
id2=1:12
f <- function(id,t)((id-1)%3-1) * t
g <- function(id,t)(id%2+1)*t
ld1 <- longData3d(array(cbind(outer(id2,time,f),outer(id2,time,g))+rnorm(12*8*2,0,1),dim=c(12,8,2)))
plotTrajMeans3d(ld1)

#####
### Scaling by 'mean' and 'standard deviation'
scale(ld1,scale=c(-1,-1))
plotTrajMeans3d(ld1)

#####
### Back to the first version of the data
restoreRealData(ld1)
plotTrajMeans3d(ld1)
```

saveTrianglesAsASY ~ *Function: saveTrianglesAsASY* ~

Description

Export a Triangle object to an '.asy' file.

Usage

```
saveTrianglesAsASY(scene, filename = "scene.asy")
```

Arguments

scene [Triangle]: Object representing the graph to plot, probably produce by [plot3dPdf](#).
filename [character]: Name of exported file.

Details

Export a Triangle object to an '.asy' file. See [plot3dPdf](#) for a summary of the overall procedure.

Value

An '.asy' file, in the current directory.

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References

<http://www.stat.uiowa.edu/~luke/R/misc3d/misc3d-pdf/>

See Also

[plot3dPdf](#), [makeLatexFile](#), [makeTriangles](#)

Examples

```
### Generating the data
data(artificialJointLongData)
myLd <- longData3d(artificialJointLongData, timeInData=list(var1=2:12, var2=13:23))
part <- partition(rep(1:3, each=50))
plotTrajMeans3d(myLd, part)

### Creation of the scene
scene <- plot3dPdf(myLd, part)
drawScene.rgl(scene)

### Export in '.asy' file
saveTrianglesAsASY(scene)

### Creation of a '.prc' file
# Open a console, then run:
# 'asy -inlineimage -tex pdflatex scene.asy'

### Creation of the LaTeX main document
makeLatexFile()

### Creation of the '.pdf'
```



```
# Open a console window, then run
# pdfLatex main.tex
```

scale *~ Function: scale for LongData ~*

Description

scale the trajectories of the different variable of a [LongData](#) object.

Usage

```
scale(x, center = TRUE, scale = TRUE)
```

Arguments

x	[LongData]: Object containning trajectories to be scale.
center	[logical] or [vector(numeric)]: Value that will be subtract from each measurement of a variable. If center=TRUE, the mean of each variable-trajectory is used. Otherwise, center should have a value for each variables.
scale	[logical] or [vector(numeric)]: Value that will divided, after the subtraction, each measurement of a variable. If scale=TRUE, the standard deviation of each variable-trajectory is used. Otherwise, scale should have a value for each variables.

Details

When variable with different unit are used jointly, it might be necessary to change their scale them in order to change their individual influence. This is what scale do.

More precisely, all the value $x[i,j,k]$ of the variable k will be scale according to the classic formula $(x[i,j,k] - m_k) / s_k$ where m_k and s_k are respectively the k -ieme value of the argument center and scale.

Note that center=TRUE is a special value that set $m_k = \text{mean}(x[, , k], na.rm=TRUE)$. Similarly, scale=TRUE is a special value that set $s_k = \text{sd}(x[, , k], na.rm=TRUE)$.

Value

scale directly modify the internal value of the LongData. No value is return.

Author

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References

- [1] C. Genolini and B. Falissard
 "KmL: k-means for longitudinal data"
 Computational Statistics, vol 25(2), pp 317-328, 2010
- [2] C. Genolini and B. Falissard
 "KmL: A package to cluster longitudinal data"
 Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

See Also

[restoreRealData](#)

Examples

```
#####
### Building LongData

time=c(1,2,3,4,8,12,16,20)
id2=1:12
f <- function(id,t)((id-1)%3-1) * t
g <- function(id,t)(id%2+1)*t
ld1 <- longData3d(array(cbind(outer(id2,time,f),outer(id2,time,g))+rnorm(12*8*2,0,1),dim=c(12,8,2)))
plotTrajMeans3d(ld1)

#####
### Scaling by 'mean' and 'standard deviation'
plotTrajMeans3d(ld1)
scale(ld1)
plotTrajMeans3d(ld1)

### Scaling by some parameters
scale(ld1,center=c(10,100),scale=c(3,-1))
plotTrajMeans3d(ld1)

#####
### To restore the data
restoreRealData(ld1)
```

windowsCut

~ Function: windowsCut ~

Description

windowsCut prepare an object [ParWindows](#) according to its arguments.

Usage

```
windowsCut(x, addLegend = TRUE,closeScreen=TRUE)
```

Arguments

x	[numeric] or [couple(numeric)]: x is used to calculate the fields nbCol and nbRow of the object ParWindows. If x is a couple, then x[1] is nbRow and x[2] is nbCol. If x is a single number (the number of plot that should be display), nbCol and nbRow parameters are calculate consequently (see detail).
addLegend	[logical]: If addLegendis true, an extra space is reserved on the top of the screen to print the legend.
closeScreen	[logical]: Some function need to add details on a graph. This option let them call a plot function that will not call a close . screen on exit, so the graph will be modifiable.

Details

If x is a number of variable, the column and row number are estimate according to the formula $nbCol \leftarrow \text{ceiling}(\sqrt{x})$ and $nbRow \leftarrow \text{ceiling}(x/nbCol)$.

Value

An object of class `ParWindows`.

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[1] C. Genolini and B. Falissard
"KmL: k-means for longitudinal data"
Computational Statistics, vol 25(2), pp 317-328, 2010

[2] C. Genolini and B. Falissard
"KmL: A package to cluster longitudinal data"
Computer Methods and Programs in Biomedicine, 104, pp e112-121, 2011

Examples

```
### Simple cut with no space for legent  
windowsCut(3,FALSE)  
windowsCut(4,FALSE)  
windowsCut(5,FALSE)
```

```
### Simple cut with legend  
windowsCut(5)
```

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