Package 'kml3d'

August 8, 2017

Type Package

Title K-Means for Joint Longitudinal Data

Version 2.4.2

Date 2017-08-01

Description An implementation of k-means specifically design
to cluster joint trajectories (longitudinal data on
several variable-trajectories).
Like 'kml', it provides facilities to deal with missing
value, compute several quality criterion (Calinski and Harabatz,
Ray and Turie, Davies and Bouldin, BIC,...) and propose a graphical
interface for choosing the 'best' number of clusters. In addition, the 3D graph
representing the mean joint-trajectories of each cluster can be exported through
LaTeX in a 3D dynamic rotating PDF graph.

License GPL (>= 2)

LazyData yes

URL http:www.r-project.org

Collate global.r distance3d.r clusterLongData3d.r kml3d.r

Depends methods,clv,rgl,misc3d,longitudinalData(>= 2.4.1), kml(>=
2.4.1)

Encoding latin1

NeedsCompilation no

Author Christophe Genolini [cre, aut],
Bruno Falissard [ctb],
Jean-Baptiste Pingault [ctb]

Maintainer Christophe Genolini <christophe.genolini@u-paris10.fr>

Repository CRAN

Date/Publication 2017-08-08 07:31:57 UTC

R topics documented:

`kml3d-package` *~ Overview: KmL3D, K-means for joint Longitudinal data ~*

Description

`KmL3D` is a new implementation of k-means for longitudinal data (or trajectories). Here is an overview of the package.

Details

Package:	KmL3D
Type:	Package
Version:	2.4.2
Date:	2017-08-01
License:	GPL (>= 2)
LazyData:	yes
Depends:	methods,graphics,rgl,misc3d,longitudinalData(>=2.2),KmL(>=2.2)
URL:	http://www.r-project.org
URL:	http://christophe.genolini.free.fr/kml

Overview

To cluster data, `KmL3D` go through three steps, each of which is associated to some functions:

1. Data preparation

2. Building "optimal" clusterization.
3. Exporting results
4. Visualizing and exporting 3D object

1. Data preparation

kml3d works on object of class ClusterLongData3d. Data preparation therefore simply consists in transforming data into an object ClusterLongData3d. This can be done via function clusterLongData3d (cld3d in short) that converts a data.frame or an array into a ClusterLongData3d.

Working on several variables mesured on different scales can give to much weight to one of the dimension. So the function scale normalizes data.

Instead of working on real data, one can also work on artificial data. Such data can be created with generateArtificialLongData3d (gald3d in short).

2. Building "optimal" clustering

Once an object of class ClusterLongData3d has been created, the algorithm kml3d can be run.

Starting with a ClusterLongData3d, kml3d built several Partition. A object of class Partition is a partition of trajectories into subgroups. It also contains some information like the percentage of trajectories contained in each group or some quality critetion (like the Calinski & Harabasz).

k-means is a "hill-climbing" algorithm. The specificity of this kind of algorithm is that it always converges towards a maximum, but one cannot know whether it is a local or a global maximum. It offers no guarantee of optimality.

To maximize one's chances of getting a quality Partition, it is better to execute the hill climbing algorithm several times, then to choose the best solution. By default, kml3d executes the hill climbing algorithm 20 times.

To date, it is not possible to know the optimum number of clusters even if the calculatous of some qualities criterion can gives some clues. kml3d computes various of them.

In the end, kml3d tests by default 2, 3, 4, 5 et 6 clusters, 20 times each.

3. Exporting results

When kml3d has constructed some Partition, the user can examine them one by one and choose to export some. This can be done via function choice. choice opens a graphic windows showing various information including the trajectories cluterized by a specific Partition.

When some Partition has been selected (the user can select more than 1), it is possible to save them. The clusters are therefore exported towards the file name-cluster.csv. Criteria are exported towards name-criteres.csv. The graphs are exported according to their extension.

4. Visualizing and exporting 3D object

KmL3D also propose tools to visualize the trajectories in 3D. plot3d using the library rgl to plot two variables according to time (either the all set of joint-trajectories, or just the mean joint-trajectories). Then the user can make the graphical representation turn using the mouse. plot3dPdf build an Triangles object. These kind of object can be include in a pdf file using saveTrianglesAsASY

and the software asymptote. Once again, it is possible to make the image in the pdf file move using the mouse -so the reader gets real 3D-.

How to get help?

For those who are not familiar with S4 programming: In S4 programming, each function can be adapted for some specific arguments.

- To get help on a function (for example plot), use: ?(plot).
- To get help on a function adapted to its argument (for example plot on argument ClusterLongData), used: ?"plot,ClusterLongData".

Examples

```
### 1. Data Preparation
data(pregnandiol)
names(pregnandiol)
cld3dPregTemp <- cld3d(pregnandiol,timeInData=list(temp=1:30*2,preg=1:30*2+1))

### 2. Building "optimal" clusteration (with only 2 redrawings)
###    Real analysis needs at least 20 redrawings
kml3d(cld3dPregTemp,3:5,nbRedrawing=2,toPlot="both")

### 3. Exporting results
try(choice(cld3dPregTemp))

### 4. Visualizing in 3D
plotMeans3d(cld3dPregTemp,4)
```

---

affectIndiv3d *~ Function: affectIndiv3d ~*

Description

Given some longitudinal data (trajectories) and k clusters centers, affectIndiv3d affects each individual to the cluster whose center is the closest.

Usage

```
affectIndiv3d(traj, clustersCenter, distance = dist3d)
```

Arguments

traj	[array(numeric)]: longitudinal data. Each line is an individual, each column is a time measurement, each plan of the third dimension is for one variable.
clustersCenter	[array(numeric)]: cluster center. Each line is a cluster centers, each column is a time measurement, each plan of the third dimension is for one variable. .

distance [numeric <- function(joint-trajectory,joint-trajectory)]: distance between an individual and a clusters centre.

Details

Given an array of clusters center clustersCenter (each plan of the first dimension is a cluster center, that is clusterCenter[2,,] is the second cluster center), the function affectIndiv3d affect each individual of the array traj to the closest clusters, according to distance.

affectIndiv3d used with calculTrajMean3d simulates one k-means 3D step.

Value

Object of classPartition.

Examples

```
######################
### affectIndiv

### Some trajectories
traj <- gald3d()["traj"]

### 4 clusters centers
center <- traj[runif(4,1,nrow(traj)),,]

### Affectation of each individual
part <- affectIndiv3d(traj,center)


#################
### K-means simulation (3 steps)
plot(clusterLongData3d(traj),parTraj=parTRAJ(col=part+1))
for (i in 1:3){
    center <- calculTrajMean3d(traj,part)
    part <- affectIndiv3d(traj,center)
    plot(clusterLongData3d(traj),parTraj=parTRAJ(col=part+1))
}
```

---

calculTrajMean3d ~ *Function: calculTrajMean3d* ~

Description

Given some joint longitudinal data and a cluster affectation, calculTrajMean3d computes the mean joint-trajectories of each cluster.

Usage

```
calculTrajMean3d(traj, clust,centerMethod=function(x){mean(x,na.rm=TRUE)})
```

Arguments

traj	[array(numeric)]: joint longitudinal data. Each line is an individual, each column is a time measurement, the third dimension is for variables.
clust	[vector(numeric)]: affectation of each individual.
centerMethod	[joint-trajectory <- function(array(numeric))]: function used to compute the clusters' centers.

Details

Given a vector of affectation to a cluster, the function calculTrajMean3d compute the "central" trajectory of each clusters. The "center" can be define using the argument centerMethod.

affectIndiv3d used with calculTrajMean3d simulates one k-means step.

Value

An array of dimension (k,t,v) with k number of groups, t number of time mesurement and v number of variables.

Examples

```
#######################
### calculTrajMean3d

### Some LongitudinalData3d
traj <- gald3d()["traj"]

### A partition
part <- floor(runif(150,1,5))
plot(clusterLongData3d(traj),parTraj=parTRAJ(col=part+1))

### Clusters center
(center <- calculTrajMean3d(traj,part))


#################
### K-means simulation (4 steps)
plot(clusterLongData3d(traj),parTraj=parTRAJ(col=part+1))
for (i in 1:4){
    part <- affectIndiv3d(traj,center)
    center <- calculTrajMean3d(traj,part)
    plot(clusterLongData3d(traj),parTraj=parTRAJ(col=part+1))
}
```

clusterLongData3d ~ *Function: clusterLongData3d (or cld3d)* ~

Description

clusterLongData3d (or cld3d in short) is the constructor for ClusterLongData3d object.

Usage

```
clusterLongData3d(traj, idAll, time, timeInData, varNames, maxNA)
cld3d(traj, idAll, time, timeInData, varNames, maxNA)
```

Arguments

traj	[array(numeric)] or [data.frame]: structure containning the joint-trajectories. Each line (traj[i,,]) is a joint-trajectory of an individual ; columns (traj[,j,]) refer to the time during which measures were made ; the third dimensions (traj[,,1]) are for variables.
idAll	[vector(character)]: single identifier for each trajectory (ie each individual). Note that the identifiers are of type character (that allow to deal identifiers like XUK32-612, identifiers that our favorite epidemiologists are so good at providing). If idAll are numeric, they are converted into characters.
time	[vector(numeric)]: time at which measures were made.
timeInData	[list(vector(numeric))]: precise the column containing the trajectories. The list labels are the names of the variables (like list(A=c(2,3,4),B=c(5,7,9))).
varNames	[character]: name of the variable being measured.
maxNA	[numeric] or [vector(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. Note the maxNA can take diffents values for each variable-trajectories. The default value is length(time)-2.

Details

clusterLongData3d construct a object of class ClusterLongData. Two cases can be distinguised:

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 mesearment are in column 2,3 and 4. The second variable-trajectory is 'W', its measurment 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 ClusterLongData3d.

Examples

```
###############
### Building an array
tr1n <- array(c(1,2,NA, 1,4,NA, 6,1,8, 10,NA,2, 3,NA,NA,
                4,NA,5,  6,3,4, 3,4,4, 4,NA,NA, 5,5,4),
           dim=c(3,5,2))


###############
### clusterLongData

### With maxNA=3
clusterLongData3d(traj=tr1n,
    idAll=as.character(c(100,102,104)),
    time=c(1,2,4,8,16),
    varNames=c("P","A"),
    maxNA=3
)

### With maxNA=2
### Individual 104 is exclude
clusterLongData3d(traj=tr1n,
    idAll=as.character(c(100,102,104)),
    time=c(1,2,4,8,16),
    varNames=c("P","A"),
    maxNA=2
)
```

ClusterLongData3d-class

~ Class: ClusterLongData3d ~

Description

ClusterLongData3d is an object containing joint-trajectories and associated Partition.

Objects from the Class

kml3d is an algorithm that builds a set of Partition from joint longitudinal data. ClusterLongData3d is the object containing the original joint longitudinal data and all the Partition that kml3d finds.

When created, an ClusterLongData3d object simply contains initial data (the joint-trajectories). After the execution of kml3d, it contains the original data and the Partition which has just been find by kml3d.

Note that if kml3d is executed several times, every new Partition are added to the original ones, no pre-existing Partition is erased.

Slots

idAll [vector(character)]: Single identifier for each of the joint-trajectory (each individual). Usefull for exporting clusters.

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

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

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

traj [array(numeric)]: Contains the joint longitudianl data. Each horizontal plan (first dimension) corresponds to the 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 c(length(idFewNA),length(time),length(varNames))).

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

reverse [matrix(numeric)]: contain the mean (first line) and the standard deviation (second line) used to normalize the data. Usefull to restaure the original data after a scaling operation.

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

initializationMethod [vector(chararcter)]: 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 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.

...

c26 [list(Partition)]: list of Partition with 26 clusters.

Extends

Class LongData3d, directly. Class ListPartition, directly.

Methods

object['xxx'] Get the value of the field xxx. Inherit from LongData3d and ListPartition.

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

plot Display the ClusterLongData3d, one graph for each variable, according to a Partition.

plot3d Display two variables of the ClusterLongData3d in 3D according to a Partition.

plot3dPdf Export the AZY code for displaying two variables of the ClusterLongData3d in a 3D pdf graph.

Special thanks

Special thanks to Boris Hejblum for debugging the '[' and '[<-' operators (the previous version was not compatible with the matrix package, which is used by lme4).

Examples

```
### Building longData
traj <- array(c(1,2,3,1,4, 3,6,1,8,10, 1,2,1,3,2, 4,2,5,6,3, 4,3,4,4,4, 7,6,5,5,4),
            dim=c(3,5,2))

myCld <- clusterLongData3d(
    traj=traj,
    idAll=as.character(c(100,102,103)),
    time=c(1,2,4,8,15),
    varNames=c("P","A"),
    maxNA=3
)

### Show
myCld

### Get
myCld['varNames']

### Set
myCld['criterionActif']<-"Davies.Bouldin"

### Plot
plot(myCld)
```

`dist3d` *~ Function: dist3d ~*

Description

Compute the distante between two joint trajectories.

Usage

```
dist3d(x, y, method = "euclidian", power = 2)
```

Arguments

`x`	`[matrix(numeric)]`: first trajectory. The colomn are time, the line are variables.
`y`	`[matrix(numeric)]`: second trajectory. The colomn are time, the line are variables.

method	[character]: method used. Should be one of the method used by the function dist.
power	[numeric]: if method="minkowski", poweris the power used.

Details

Compute the distante between two joint trajectories, using one of the distance define by dist.

Value

A numeric

Examples

```
### Generate artificial data
myCld <- gald3d()

### Distance between individual 1 and 3 (there are in the same group)
dist3d(myCld['traj'][1,,],myCld['traj'][3,,])

### Distance between individual 1 and 51 (there are in two different groups)
dist3d(myCld['traj'][1,,],myCld['traj'][51,,])
```

---

generateArtificialLongData3d

~ Function: generateArtificialLongData3d (or gald3d) ~

Description

This function builp up an artificial longitudinal data set (joint trajectories) an turn them into an object of class ClusterLongData.

Usage

```
gald3d(nbEachClusters=50,time=0:10,varNames=c("V","T"),
    meanTrajectories=list(function(t){c(0,0)},
       function(t){c(10,10)},function(t){c(10-t,10-t)}),
    personalVariation=function(t){c(rnorm(1,0,2),rnorm(1,0,2))},
    residualVariation=function(t){c(rnorm(1,0,2),rnorm(1,0,2))},
    decimal=2,percentOfMissing=0)

generateArtificialLongData3d(nbEachClusters=50,time=0:10,varNames=c("V","T"),
    meanTrajectories=list(function(t){c(0,0)},
       function(t){c(10,10)},function(t){c(10-t,10-t)}),
    personalVariation=function(t){c(rnorm(1,0,2),rnorm(1,0,2))},
    residualVariation=function(t){c(rnorm(1,0,2),rnorm(1,0,2))},
    decimal=2,percentOfMissing=0)
```

Arguments

nbEachClusters	[vector(numeric)]: number of trajectories that each cluster must contain. If a single number is given, it is duplicated for all groups.
time	[vector(numeric)]: time at which measures are made.
varNames	[vector(character)]: names of the variables.
meanTrajectories	[list(function)]: lists the functions that define the average trajectories of each cluster. Each functions shall return a vector containing one value for each variable of varNames.
personalVariation	[function] or [list(function)]: lists the functions defining the personnal variation between an individual and the mean trajectories of its cluster. Note that these function should be constant function (the personal variation can not evolve with time). If a single function is given, it is duplicated for all groups (see detail).
residualVariation	[function] or [list(function)]: lists the functions generating the noise of each trajectory within its own cluster. Each functions shall return a vector containing one value for each variable of varNames. If a single function is given, it is duplicated for all groups.
decimal	[numeric]: number of decimals used to round up values.
percentOfMissing	[numeric]: percentage (between 0 and 1) of missing data generated in each cluster. If a single value is given, it is duplicated for all groups. The missing values are Missing Completly At Random (MCAR).

Details

generateArtificialLongData3d (gald3d in short) is a function that contruct a set of artificial joint longitudinal data. Each individual is considered as belonging to a group. This group follows a theoretical trajectory, function of time. These functions (one per group) are given via the argument meanTrajectories.

Within a group, the individual undergoes individal variations. Individual variations are given via the argument residualVariation.

The number of individuals in each group is given by nbEachClusters.

Finally, it is possible to add missing values randomly (MCAR) striking the data thanks to percentOfMissing.

Value

Object of class ClusterLongData.

Author

Christophe Genolini
1. UMR U1027, INSERM, Université Paul Sabatier / Toulouse III / France
2. CeRSME, EA 2931, UFR STAPS, Université de Paris Ouest-Nanterre-La Défense / Nanterre / France

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

ClusterLongData3d, clusterLongData3d, generateArtificialLongData

Examples

```
#####################
### Default example

ex1 <- generateArtificialLongData3d()
plot3d(ex1,parTraj=parTRAJ(col=rep(2:4,each=50)))


#####################
### 4 lines with unbalanced groups

ex2 <- generateArtificialLongData3d(
  nbEachClusters=c(5,10,20,40),
  meanTrajectories=list(
     function(t)c(t,t^3/100),
     function(t)c(0,t),
     function(t)c(t,t),
     function(t)c(0,t^3/100)
  ),
  residualVariation = function(t){c(rnorm(1,0,1),rnorm(1,0,1))}
)

plot3d(ex2,parTraj=parTRAJ(col=rep(1:4,time=c(5,10,20,40))))
```

---

kml3d *~ Algorithm kml3d: K-means for Joint Longitidinal data ~*

Description

kml3d is a new implementation of k-means for joint longitudinal data (or joint trajectories). This algorithm is able to deal with missing value and provides an easy way to re roll the algorithm several times, varying the starting conditions and/or the number of clusters looked for.

Here is the description of the algorithm. For an overview of the package, see kml3d-package.

Usage

```
kml3d(object, nbClusters = 2:6, nbRedrawing = 20, toPlot = "none",
    parAlgo = parKml3d())
```

Arguments

object	[ClusterLongData3d]: contains trajectories to clusterize and some Partition.
nbClusters	[vector(numeric)]: Vector containing the number of clusters with which kml3d must work. By default, nbClusters is 2:6 which indicates that kml3d must search partitions with respectively 2, then 3, ... up to 6 clusters. Maximum number of cluster is 26.
nbRedrawing	[numeric]: Sets the number of time that k-means must be re-run (with different starting conditions) for each number of clusters.
toPlot	[character]: during computation, kml3d can display some graphes. If toPlot="traj", then the trajectories are plot (like with function plot,ClusterLongData). If toPlot="criterion", the quality criterions are plot (like with function plotCriterion). If toPlot="both", the graphic windows is split in two and both graphs are displayed. If "none", there is no graphical display.
parAlgo	[ParKml]: set the option used by kml3d (like the starting condition, the imputation methods, the save frequency, the maximum number of iteration, , the distance used...) See ParKml for details. The default values are describe in parKml3d.

Details

kml3d works on object of class ClusterLongData. For each number i included in nbClusters, kml3d computes a Partition then stores it in the field cX of the object ClusterLongData according to its number of clusters 'X'. The algorithm starts over as many times as it is told in nbRedrawing. By default, it is executed for 2, 3, 4, 5 and 6 clusters 20 times each, namely 100 times.

When a Partition has been found, it is added to the slot c1, c2, c3, ... or c26. cX stores the all Partition with X clusters. Inside a sublist, the Partition are sorted from the biggest quality criterion to the smallest (the best are stored first, using ordered,ListPartition), or not.

Note that Partition are saved throughout the algorithm. If the user interrupts the execution of kml3d, the result is not lost. If the user run kml3d on an object, then running kml3d again on the same object will add some new Partition to the one already found.

The possible starting conditions are defined in initializePartition.

Value

A ClusterLongData3d object, after having added some Partition to it.

Optimisation

Behind kml3d, there are two different procedures :

1. Fast: when the parameter distance is set to "euclidean3d" and toPlot is set to 'none' or 'criterion', kml3d call a C compiled (optimized) procedure.

2. Slow: when the user defines its own distance or if he wants to see the construction of the clusters by setting `toPlot` to 'traj' or 'both', `kml3d` uses a R non compiled programmes.

The C prodecure is 25 times faster than the R one.

So we advice to use the R procedure 1/ for trying some new method (like using a new distance) or 2/ to "see" the very first clusters construction, in order to check that every thing goes right. Then it is better to switch to the C procedure (like we do in `Example` section).

If for a specific use, you need a different distance, feel free to contact the author.

See Also

Overview: `kml3d-package`
Classes : `ClusterLongData3d`, `Partition`
Methods : `clusterLongData3d`, `choice`

Examples

```
### Generation of some data
cld1 <- generateArtificialLongData3d(15)

### We suspect 2, 3, 4 or 5 clusters, we want 3 redrawing.
###   We want to "see" what happen (so toPlot="both")
kml3d(cld1,2:5,3,toPlot="both")

### 3 seems to be the best.
###   We don't want to see again, we want to get the result as fast as possible.
###   Just, to check the overall process, we plot the criterion evolution
kml3d(cld1,3,10,toPlot="criterion")
```

`parKml3d` *~ Function: parKml3d ~*

Description

`parKml3d` is a constructor of object `ParKml` that provide adequate default value for the use of function `kml3d`.

Usage

```
parKml3d(saveFreq = 100, maxIt = 200, imputationMethod = "copyMean",
    distanceName = "euclidean3d", power = 2, distance = function() {
   }, centerMethod = meanNA, startingCond = "nearlyAll", nbCriterion =100,scale=TRUE)
```

Arguments

saveFreq	[numeric]: Long computations can take several days. So it is possible to save the object ClusterLongData3d on which works kml3d once in a while. saveFreq defines the frequency of the saving process. The ClusterLongData3d is saved every saveFreq clustering calculations. The object is saved in the file objectName.Rdata in the curent folder.
maxIt	[numeric]: Set a limit to the number of iteration if convergence is not reached.
imputationMethod	[character]: the calculation of quality criterion can not be done if some value are missing. imputationMethod define the method use to impute the missing value. See imputation for detail.
distanceName	[character]: name of the distance used by k-means. If the distanceName is "euclidean3d", a compiled optimized version specificaly design for joint-trajectories version is used. Otherwise, the function define in the slot distance is used.
power	[numeric]: If distanceName="minkowski", this define the power that will be used.
distance	[numeric <- function(trajA,trajB)]: function that computes the distance between two trajectories. If no function is specified, the Euclidian distance with Gower adjustment (to deal with missing value) is used.
centerMethod	[numeric <- function(vector(numeric))]: k-means algorithm computes the centers of each cluster. It is possible to personalize the definition of "center" by defining a function "centerMethod". This function should take a vector of numeric as argument and return a single numeric -the center of the vector-.
startingCond	[character]: specifies the starting condition. Should be one of "randomAll", "randomK", "maxDist", "kmeans++", "kmeans+", "kmeans-" or "kmeans–" (see initializePartition for details). It also could take two specifics values: "all" stands for c("maxDist","kmeans-") then an alternance of "kmeans–" and "randomK" while "nearlyAll" stands for "kmeans-" then an alternance of "kmeans–" and "randomK".
nbCriterion	[numeric]: set the maximum number of quality criterion that are display on the graph (since displaying a high criterion number an slow down the overall process, the default value is 100).
scale	[logical]: if TRUE, then the data will be automaticaly scaled (using the function scale with default values) before the execution of k-means on joint trajectories. Then the data will be restore (using the function restoreRealData) just before the end of the function kml3d. This option has no effect on kml.

Details

parKml3d is a constructor of object ParKml that provide adequate default value for the use of function kml3d.

Value

An object ParKml.

Examples

```
### Generation of some data
cld1 <- generateArtificialLongData3d(c(15,15,15))

### Setting two different set of option :
(option1 <- parKml3d())
(option2 <- parKml3d(centerMethod=function(x)median(x,na.rm=TRUE)))

### Running kml. Formaly, the second exemple is 'k-median'
kml3d(cld1,4,1,toPlot="both",parAlgo=option1)
kml3d(cld1,4,1,toPlot="both",parAlgo=option2)
```

---

plot,ClusterLongData3d

~ Function: plot for ClusterLongData3d ~

Description

plot the trajectories of an object ClusterLongData3d relativly to a Partition. One graphe for each variable is displayed.

Usage

```
## S4 method for signature 'ClusterLongData3d,ANY'
plot(x,y=NA,parTraj=parTRAJ(),parMean=parMEAN(),
   addLegend=TRUE,adjustLegend=-0.05,toPlot="both",nbCriterion=1000,...)
```

Arguments

x	[ClusterLongData3d]: Object containing the joint-trajectories to plot.
y	[numeric] or [vector2(numeric)]: Give the Partition to represent. If y is missing, the Partition with the highest quality criterion (the actif one) is selected. If y is a number, the first Partition of the sublist c-y is selected. If y is a couple of numeric, the y[2]th Partition of the sublist c-y[1] is selected.
parTraj	[ParLongData]: Specification of the plotting parameters of the individual trajectories. Fields that can be changes are 'type','col','pch','xlab' and 'ylab'. In addition to the standard possible values, the option col="clusters" can be use to color the individual trajectories according to their clusters (exemple: parTraj=parTRAJ(type="o",col="clusters")). See ParLongData for details.
parMean	[ParLongData]: Specification of the plotting parameters of the mean trajectories (only when y is non missing). Fields that can be changes are 'type','col','pch','pchPeriod' and 'cex'. See ParLongData for details.
toPlot	[character]: either 'traj' for plotting trajectories alone, 'criterion' for plotting criterion alone, 'both' for plotting both or 'none' for not display anything.

nbCriterion	[numeric]: if a single criterion is given to criterion (and thus is displayed for 'all' the Partition), this slot alows to fix a limit on the number of points that will be display.
addLegend	[logical]: should the legend be displayed?
adjustLegend	[numeric]: fix the hight of the legend
...	Some other parameters can be passed to the method (like "xlab" or "ylab".

Details

plot the trajectories of an object ClusterLongData3d relativly to the 'best' Partition, or 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.

See Also

Overview: kml3d-package
Classes : ClusterLongData3d
Plot : plotTraj, plotCriterion

Examples

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

myCld <- gald3d()

### Basic plotting
plot(myCld)

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

### No letters on the mean trajectories
kml3d(myCld,2:7,2)
plot(myCld,2,parMean=parMEAN(type="l"))

### Only one letter on the mean trajectories
plot(myCld,3,parMean=parMEAN(pchPeriod=Inf))

### Color individual according to its clusters (col="clusters")
plot(myCld,4,parTraj=parTRAJ(col="clusters"))

### Mean without individual
plot(myCld,5,parTraj=parTRAJ(type="n"))


### No mean trajectories (type="n")
```

```
### Color individual according to its clusters (col="clusters")
plot(myCld,6,parTraj=parTRAJ(col="clusters"),parMean=parMEAN(type="n"))

### Only few trajectories
plot(myCld,7,nbSample=10,parTraj=parTRAJ(col='clusters'),parMean=parMEAN(type="n"))
```

---

plot3d,ClusterLongData3d

~ Function: plot3d for ClusterLongData3d ~

Description

Plot two variables of a ClusterLongData3d object in 3D, optionnaly relatively to a Partition.

Usage

```
## S4 method for signature 'ClusterLongData3d,numeric'
plot3d(x,y,varY=1,varZ=2,
   parTraj=parTRAJ(),parMean=parMEAN(),...)
```

Arguments

x	[ClusterLongData3d]: Object containing the trajectories to plot.
y	[numeric] or [vector2(numeric)]: Define the Partition P that will be use to plot the object. P is a Partition hold in the field c2, c3, ... c26. If y=c(a,b), then P is the Partition number b with a clusters. If y=a, then P is the partition number 1 with a clusters. If y is missing, P is the Partition with the best criterion.
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 ClusterLongData3d. See ParLongData for details.
parMean	[ParLongData]: Set the graphical parameters used to plot the mean trajectories of each clusters ClusterLongData3d (only when y is non missing). See ParLongData for details.
...	Arguments to be passed to methods, such as graphical parameters.

Details

Plot two variables of a ClusterLongData3d object in 3D. It use the rgl library. The user can make the graphical representation turn using its mouse.

See Also

ClusterLongData3d

Examples

```
##################
### Real example on array

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)
myCld <- clusterLongData3d(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)))

### Basic plot
plot(myCld,parTraj=parTRAJ(col=rep(1:6,20)))

### plot3d, variable 1 and 2
plot3d(myCld,parTraj=parTRAJ(col=rep(1:6,20)))

### plot3d, variable 1 and 3
plot3d(myCld,parTraj=parTRAJ(col=rep(1:6,20)),varZ=3)
plot3d(myCld,parTraj=parTRAJ(col="red"))
```

---

plot3dPdf *~ Function: plot3dPdf for ClusterLongData3d ~*

Description

Given a ClusterLongData3d and a Partition, this function create Triangle objects representing the 3D plot of two variables of the main trajectories.

Usage

```
## S4 method for signature 'ClusterLongData3d,missing'
plot3dPdf(x,y,varY=1,varZ=2)
## S4 method for signature 'ClusterLongData3d,numeric'
plot3dPdf(x,y,varY=1,varZ=2)
```

Arguments

x	[ClusterLongData]: Object containing the trajectories to plot.
y	[numeric]: Define Partition P that will be use to plot the object. P is a Partition hold in the field c2, c3, ... c26. If y=c(a,b), then P is the Partition number b with a clusters. If y=a, then P is the partition number 1 with a clusters. If y is missing, P is the Partition with the best criterion.

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 ClusterLongData.

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. '.azy' can not be include in LaTeX file. LaTeX can read only '.pre' file. So the next step is to use asymptote to convert '.asy' tp '.pre'. This is done by the command `asy -inlineimage -tex pdflatex scene.azy`.
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.

Author(s)

Christophe Genolini
INSERM U669 / PSIGIAM: Paris Sud Innovation Group in Adolescent Mental Health
Modal'X / Universite Paris Ouest-Nanterre- La Defense

Contact author : <genolini@u-paris10.fr>

References

Article "KmL: K-means for Longitudinal Data", in Computational Statistics, Volume 25, Issue 2 (2010), Page 317.
Web site: http://christophe.genolini.free.fr/kml

See Also

makeTriangles

Examples

```
### Generating the data
myCld3d <- gald3d(c(5,5,5))
kml3d(myCld3d,3:4,1)

### Creation of the scene
scene <- plot3dPdf(myCld3d,3)
drawScene.rgl(scene)

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

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

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

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

`plotMeans3d,ClusterLongData3d`
~ Function: plotMeans3d for ClusterLongData3d ~

Description

Plot the means of two variables of a `ClusterLongData3d` object in 3D relatively to a `Partition`.

Usage

```
## S4 method for signature 'ClusterLongData3d,numeric'
plotMeans3d(x,y,varY=1,varZ=2,
   parTraj=parTRAJ(type="n"),parMean=parMEAN(),...)
```

Arguments

x	[ClusterLongData3d]: Object containing the trajectories to plot.
y	[numeric] or [vector2(numeric)]: Define the Partition P that will be use to plot the object. P is a Partition hold in the field c2, c3, ... c26. If y=c(a,b), then P is the Partition number b with a clusters. If y=a, then P is the partition number 1 with a clusters.
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 ClusterLongData3d. See ParLongData for details.
parMean	[ParLongData]: Set the graphical parameters used to plot the mean trajectories of each clusters ClusterLongData3d (only when y is non missing). See ParLongData for details.
...	Arguments to be passed to methods, such as graphical parameters.

Details

Plot two variables of a ClusterLongData3d object in 3D. It use the rgl library. The user can make the graphical representation turn using its mouse.

See Also

ClusterLongData3d

Examples

```
##################
### Real example on array

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)
myCld <- clusterLongData3d(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)))
kml3d(myCld,3:4,2)

### Basic plot
plotMeans3d(myCld,3)

### plotMeans3d, variable 1 and 3
plotMeans3d(myCld,4,varZ=3)
plotMeans3d(myCld,3,parTraj=parTRAJ(col="red"))
```

---

plotTraj3d,ClusterLongData3d

~ Function: plotTraj3d for ClusterLongData3d ~

Description

Plot the trajectories of two variables of a ClusterLongData3d object in 3D relatively to a Partition.

Usage

```
## S4 method for signature 'ClusterLongData3d,numeric'
plotTraj3d(x,y,varY=1,varZ=2,
   parTraj=parTRAJ(col="clusters"),parMean=parMEAN(type="n"),...)
```

Arguments

x	[ClusterLongData3d]: Object containing the trajectories to plot.
y	[numeric] or [vector2(numeric)]: Define the Partition P that will be use to plot the object. P is a Partition hold in the field c2, c3, ... c26. If y=c(a,b), then P is the Partition number b with a clusters. If y=a, then P is the partition number 1 with a clusters.
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 ClusterLongData3d. See ParLongData for details.
parMean	[ParLongData]: Set the graphical parameters used to plot the mean trajectories of each clusters ClusterLongData3d (only when y is non missing). See ParLongData for details.
...	Arguments to be passed to methods, such as graphical parameters.

Details

Plot the means trajectories of two variables of a ClusterLongData3d object in 3D. It use the rgl library. The user can make the graphical representation turn using its mouse.

See Also

ClusterLongData3d

Examples

```
##################
### Real example on array

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)
myCld <- clusterLongData3d(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)))
kml3d(myCld,3:4,2)
```

```
### Basic plot
plotMeans3d(myCld,3)

### plotTraj3d, variable 1 and 3
plotMeans3d(myCld,4,varZ=3)
plotMeans3d(myCld,3,parMean=parMEAN(col="red"))
```

`pregnandiol` *~ Pregnandiol measure (from QUIDEL database, René Écochard) ~*

Description

These longitudinal data are extract form the QUIDEL database whose aims is to studies hormone profiles among women who have no fertility problem.

Usage

```
data(pregnandiol)
```

Format

Some longitudinal data in wide format. It includes 107 women who have been followed during up to 49 days. Each column correspond to a specific time meseaurement. The outcome is the hormone "pregnandiol".

`id` unique idenfier for each patient.

`day1` Measurement of pregnandiol at day 1.

`day2` Measurement of pregnandiol at day 2.

`day3` Measurement of pregnandiol at day 3.

`...` ...

`day 49` Measurement of pregnandiol at day 49.

Details

The QUIDEL database aims to gain better knowledge of hormone profiles among women who have no fertility problem. This database has been described as the largest existing database on hormone profiles in the normal human menstrual cycle, involving ultrasound scan of the day of ovulation [eco06]. It involves 107 women and 283 cycles in all, with identification of the day of ovulation and daily titration of the levels of the four main hormones in the ovulation cycle. The database belongs to the laboratory in charge of the analysis of hormone trajectories (CNRS 5558, René Ecochard). It has already been the subject of numerous publications, including [eco00, eco01].

Source

QUIDEL cohort

References

[eco00] Ecochard R, Gougeon A. Side of ovulation and cycle characteristics in normally fertile women. Human reproduction (Oxford, England). 2000;15(4):752-755.

[eco01] Ecochard R et al. Chronological aspects of ultrasonic, hormonal, and other indirect indices of ovulation. BJOG : an international journal of obstetrics and gynaecology. 2001;108(8):822-829.

Index