# Package 'UPMASK'

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**Type** Package

**Title** Unsupervised Photometric Membership Assignment in Stellar Clusters

**Version** 1.2

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**Maintainer** Alberto Krone-Martins <algol@sim.ul.pt>

**Description** An implementation of the UPMASK method for performing membership assignment in stellar clusters in R. It is prepared to use photometry and spatial positions, but it can take into account other types of data. The method is able to take into account arbitrary error models, and it is unsupervised, data-driven, physical-model-free and relies on as few assumptions as possible. The approach followed for membership assessment is based on an iterative process, dimensionality reduction, a clustering algorithm and a kernel density estimation.

**Depends** R (>= 3.0)

**License** GPL (>= 3)

**Imports** parallel, MASS, RSQLite, DBI, dimRed, loe

**NeedsCompilation** no

**RoxygenNote** 6.0.1

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## R topics documented:

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`UPMASK-package` *Unsupervised Photometric Membership Assignment in Stellar Clusters*

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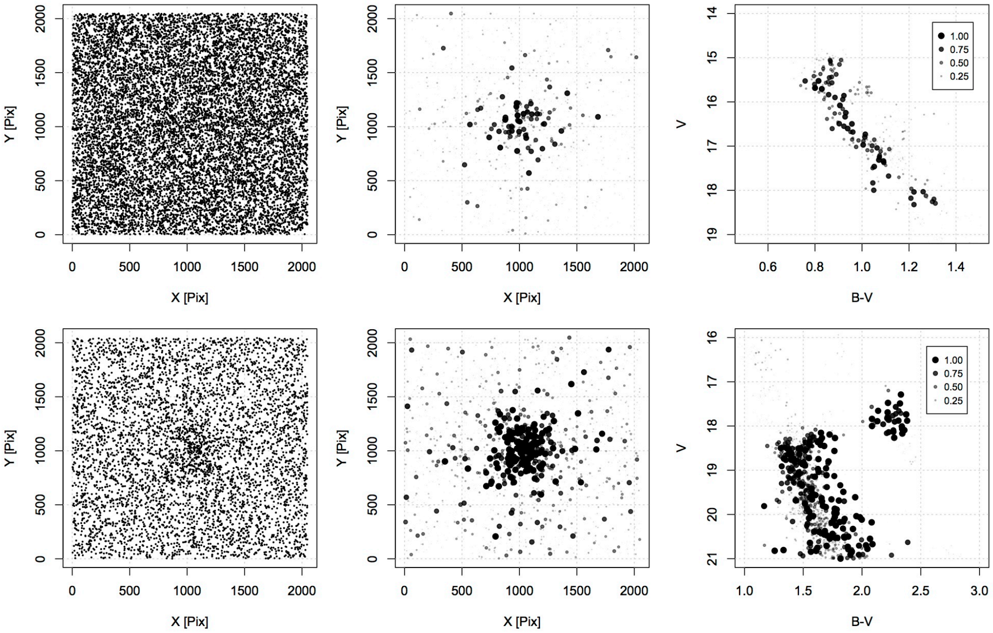
## Description

An implementation of the UPMASK method for performing membership assignment in stellar clusters in R. It is prepared to use photometry and spatial positions, but it can take into account other types of data. The method is able to take into account arbitrary error models, and it is unsupervised, data-driven, physical-model-free and relies on as few assumptions as possible. The approach followed for membership assessment is based on an iterative process, principal component analysis, a clustering algorithm and a kernel density estimation.

## Details

| | |
|---|---|
| Package: | UPMASK |
| Type: | Package |
| Version: | 1.2 |
| Date: | 2017-06-09 |
| License: | GPL (>= 3) |



The two main functions in the `UPMASK` package are `UPMASKfile` and `UPMASKdata`. The later will run the `UPMASK` method on data inside a data frame, while the former will perform the analysis on a file (the later deals with loading a file inside a data frame, calling the `UPMASKdata` function and writing the results to an output file).

The package includes data from two simulated fields comprising simulated data from cluster and field stars – to be used for demonstration. The analysis of these files using UPMASK lead to results presented in the figures above (from Krone-Martins&Moitinho, 2014), which show the spatial positions of the objects in the original datasets (in the left), the same objects but color coded by membership probability after the `UPMASK` analysis (in the center) and the color-magnitude diagram of all the stars also color coded by membership probability (in the right).

## Author(s)

Alberto Krone-Martins, Andre Moitinho

Maintainer: Alberto Krone-Martins <algol@sim.ul.pt>

## References

Krone-Martins, A. & Moitinho, A., Astronomy&Astrophysics, v.561, p.A57, 2014

## See Also

`UPMASKfile`, `UPMASKdata`

## Examples

```
## Not run:
```

```
#
# Example of how to run UPMASK using data from a file
# Note: serious analysis require larger nRuns, and see UPMASKfile documentation
# for the parametrization.
# Write a string with the filename of the input and output files
inputFileName <- system.file("extdata",
           "oc_12_500_1000_1.0_p019_0880_1_25km_120nR_withcolors.dat", package="UPMASK")
outputFileName <- file.path(tempdir(), "RESULTS.dat")
# Run UPMASK
UPMASKfile(inputFileName, outputFileName, nRuns=5, starsPerClust_kmeans=25,
          verbose=TRUE, fileWithHeader=TRUE)
# Done, the results are written to the file outputFileName

#
# Example of how to run UPMASK using data from a data frame
# Note: serious analysis require larger nRuns, and see UPMASKdata documentation
# for the parametrization.
# Load the data into a data frame
inputFileName <- system.file("extdata",
          "oc_12_5000_4000_4.0_p019_0900_1_15km_120nR_withcolors.dat", package="UPMASK")
ocData <- read.table(inputFileName, header=TRUE)
# Run UPMASK
upmaskRes <- UPMASKdata(ocData, nRuns=5, starsPerClust_kmeans=25, verbose=TRUE)
# Done, the results are in the data frame upmaskRes

# Clean the environment
rm(list=c("inputFileName","outputFileName","ocData","upmaskRes"))

## End(Not run)
```

## analyse_randomKde2d *Perform analysis of random 2d distributions*

### Description

analyse_randomKde2d will compute statistics from uniformly randomly created 2D fields based on Kernel Density Estimations (calling the code create_randomKde2d).

### Usage

```
analyse_randomKde2d(nfields=100, nstars, maxX, maxY, nKde=50,
showStats=FALSE, returnStats=TRUE)
```

### Arguments

nfields an integer with the number of individual field realisations

nstars an integer with the number of stars to consider

maxX the length of the field in X

maxY the length of the field in Y

| | |
|---|---|
| `nKde` | the number of samplings of the kernel in each direction |
| `showStats` | a boolean indicating if the user wants to see statistics |
| `returnStats` | a boolean indicating if the user wants statistics to be returned |

### Value

A data frame with the `mean` and `sd` fields containing the results of the random field analysis.

### Author(s)

Alberto Krone-Martins, Andre Moitinho

### Examples

```
# Runs the analysis on random fields
toyRes <- analyse_randomKde2d(100, 200, 100, 100, showStats=TRUE)

# Clean the environment
rm(toyRes)
```

## `analyse_randomKde2d_AutoCalibrated` *Perform analysis of random 2d distributions (auto calibrated)*

### Description

The experimental code `analyse_randomKde2d_AutoCalibrated` computes statistics from uniformly randomly created 2D fields based on kernel density estimations (using `create_randomKde2d`). It runs for as many interations as necessary for the statistical measuremnt stabilize (but it will abort after `maxIter` iterations is reached).

### Usage

```
analyse_randomKde2d_AutoCalibrated(nstars, maxX, maxY, nKde=50, maxIter=40,
                                              showStats=FALSE, returnStats=TRUE)
```

### Arguments

| | |
|---|---|
| `nstars` | an integer with the number of stars to consider |
| `maxX` | the length of the field in X |
| `maxY` | the length of the field in Y |
| `nKde` | the number of samplings of the kernel in each direction |
| `maxIter` | an integer with the maximum number of iterations |
| `showStats` | a boolean indicating if the user wants to see statistics |
| `returnStats` | a boolean indicating if the user wants statistics to be returned |

### Value

A data frame with the `mean` and `sd` fields containing the results of the random field analysis.

### Author(s)

Alberto Krone-Martins, Andre Moitinho

### Examples

```
# Runs the analysis on random fields
toyRes <- analyse_randomKde2d_AutoCalibrated(100, 100, 100, 100, showStats=TRUE)

# Clean the environment
rm(toyRes)
```

## analyse_randomKde2d_smart

*Perform analysis of random 2d distributions*

### Description

`analyse_randomKde2d_smart` will compute statistics from uniformly randomly created 2D fields based on Kernel Density Estimations (calling the code `analyse_randomKde2d`). However, if a random field using the same number of stars was already computed in this run of UPMASK, it will avoid computing it again and will return the value that is stored in a SQLite database table. If the random field was not yet analysed, it will run the analysis, store the result in the database table, and return the value.

### Usage

```
analyse_randomKde2d_smart(nfields=100, nstars, maxX, maxY, nKde=50,
showStats=FALSE, returnStats=TRUE, smartTableDB)
```

### Arguments

`nfields` an integer with the number of individual field realisations

`nstars` an integer with the number of stars to consider

`maxX` the length of the field in X

`maxY` the length of the field in Y

`nKde` the number of samplings of the kernel in each direction

`showStats` a boolean indicating if the user wants to see statistics

`returnStats` a boolean indicating if the user wants statistics to be returned

`smartTableDB` a database connection to the smart look-up table

### Value

A data frame with the `mean` and `sd` fields containing the results of the random field analysis.

### Author(s)

Alberto Krone-Martins, Andre Moitinho

### Examples

```
# Create the smart look-up table
library(RSQLite)
stcon <- create_smartTable()

# Runs the analysis on random fields
system.time(
toyRes1 <- analyse_randomKde2d_smart(300, 200, 100, 100, smartTableDB=stcon)) # slow
system.time(
toyRes2 <- analyse_randomKde2d_smart(300, 200, 100, 100, smartTableDB=stcon)) # quick

# Clean the environment
rm(list=c("toyRes1", "toyRes2"))
dbDisconnect(stcon)
```

## `create_randomKde2d` *Compute the density based distance quantity using a 2D Kernel Density Estimation*

### Description

`create_randomKde2d` will compute the 2D Kernel Density Estimation for a random sampling of the requested number of points and will return the quantiy `(max(d)-mean(d))/sd(d)`, if the option `returnDistance` is set to TRUE.

### Usage

```
create_randomKde2d(nstars, maxX, maxY, nKde=50, printPlots=FALSE,
showStats=FALSE, returnDistance=FALSE)
```

### Arguments

| | |
|---|---|
| `nstars` | an integer with the number of stars to consider |
| `maxX` | the length of the field in X |
| `maxY` | the length of the field in Y |
| `nKde` | the number of samplings of the kernel in each direction |
| `printPlots` | a boolean indicating if the user wants to see plots |
| `showStats` | a boolean indicating if the user wants to see statistics |
| `returnDistance` | a boolean indicating if the user wants statistics to be returned |

## Value

A double representing the density based distance quantity.

## Author(s)

Alberto Krone-Martins, Andre Moitinho

## References

Krone-Martins, A. & Moitinho, A., A&A, v.561, p.A57, 2014

## Examples

```
# Compute the density based distance quantity with random fields
distVar <- create_randomKde2d(100, 10, 10, showStats=FALSE,
                              printPlots=FALSE, returnDistance=TRUE)

# Clean the environment
rm(distVar)
```

---

# create_smartTable *Create a look up table*

---

## Description

create_smartTable will create a look up table for random field analysis inside an SQLite database. The table is automatically filled each time UPMASK calls the function analyse_randomKde2d_smart.

## Usage

```
create_smartTable()
```

## Value

A data base connection to the SQLite database containing the smartTable.

## Author(s)

Alberto Krone-Martins, Andre Moitinho

## Examples

```
# Create the table
library(RSQLite)
stcon <- create_smartTable()

# Clean the environment
dbDisconnect(stcon)
```

## getStarsAtHighestDensityRegion

*Perform cut in the membership list based on the 2D space distribution*

### Description

getStarsAtHighestDensityRegion will compute the 2D Kernel Density Estimation for the requested subset of data and will return only the stars in the most dense region.

### Usage

```
getStarsAtHighestDensityRegion(ocdata_out, threshold=2, posIdx=c(1,2),
plotAnalysis=FALSE, verbose=FALSE)
```

### Arguments

| | |
|---|---|
| ocdata_out | a data frame to use |
| threshold | a double with the thresholding level |
| posIdx | an array of integers indicating the columns of the data frame containing the spatial positions |
| plotAnalysis | a boolean indicating if the anaylsis should be plotted |
| verbose | a boolean indicating if the code should be verbose |

### Value

A data frame with the objects which were selected from ocdata_out

### Author(s)

Alberto Krone-Martins, Andre Moitinho

### Examples

```
# Create a simple data set
toyDataDF <- data.frame(x=runif(50, 0, 10), y=runif(50, 0, 10), resMclust.class=rep(1, 50))
toyDataDF <- rbind(toyDataDF, data.frame(x=rnorm(50, 2, 3),
                   y=rnorm(50, 4, 3), resMclust.class=rep(1, 50)))

# Perform the XY density based cut
toyRes <- getStarsAtHighestDensityRegion(toyDataDF)

# Clean the environment
rm(list=c("toyDataDF", "toyRes"))
```

## innerLoop *UPMASK inner loop*

### Description

innerLoop executes the UPMASK method's inner loop and returns the stars which were considered as cluster member stars.

The innerLoop perform the PCA, runs the clustering algorithm and check for overdensities in the spatial distribution for the clustered stars in the PC space using a 2d kernel density estimation.

### Usage

```
innerLoop(ocdata_full, ocdata, classAlgol="kmeans", autoThresholdLevel=3,
autoThreshold=TRUE, iiter=0, plotIter=FALSE, verbosity=1, starsPerClust_kmeans=50,
nstarts_kmeans=50, runId=0, autoCalibrated=FALSE, stopIfEmpty=FALSE,
positionDataIndexes=c(1,2), smartTableDB, nDimsToKeep=4, dimRed="PCA", scale=TRUE)
```

### Arguments

`ocdata_full` a data frame with the data to perform the analysis

`ocdata` a data frame with the data to consider in the PCA step

`classAlgol` a string indicating the type of clustering algorithm to consider. Only k-means is implemented at this moment (defaults to kmeans)

`autoThresholdLevel` an integer indicating the level for thresholding of the spatial distribution

`autoThreshold` a boolean indicating if autoThresolding should be adopted (defaults to TRUE)

`iiter` and integer indicating the number of the iteration (passed by the outerLoop)

`plotIter` a boolean indicating if the user wants to see iteration plots (defaults to FALSE)

`verbosity` a flag indicating the verbosity level: it can be 0 (no screen output at all), 1 (minimum), >=2 (all)

`starsPerClust_kmeans` an integer with the average number of stars per k-means cluster

`nstarts_kmeans` an integer the amount of random re-initializations of the k-means clustering method (usually it is not necessary to modify this)

`runId` an integer greater than zero indicating the run Id (passed by the outerLoop)

`autoCalibrated` a boolean indicating if the number of random field realizations for the clustering check in the position space should be autocalibrated (experimental code, defaults to FALSE).

`stopIfEmpty` a boolean indicating if the code should completely stop if no spatial clustering is detected (defaults to FALSE)

`positionDataIndexes` an array of integers indicating the columns of the data frame containing the spatial position measurements `smartTableDB` a database connection to the smart look-up table

`nDimsToKeep` an integer with the number of dimensions to consider (defaults to 4)

`dimRed` a string with the dimensionality reduction method to use (defaults to PCA. The only other options are LaplacianEigenmaps or None)

`scale` a boolean indicating if the data should be scaled and centered

## Value

A data frame with objects considered as members at this iteration.

## Author(s)

Alberto Krone-Martins, Andre Moitinho

## References

Krone-Martins, A. & Moitinho, A., A&A, v.561, p.A57, 2014

## Examples

```
## Not run:
# Perform a one run of the innerLoop using a simulated open cluster with
# spatial and photometric data
# Load the data into a data frame
fileName <- "oc_12_500_1000_1.0_p019_0880_1_25km_120nR_withcolors.dat"
inputFileName <- system.file("extdata", fileName, package="UPMASK")
ocData <- read.table(inputFileName, header=TRUE)
ocData <- data.frame(ocData, id=(1:length(ocData[,1]))) # create an id

# Prepare the data to run the inner loop
posIdx <- c(1,2)
photIdx <- c(3,5,7,9,11,19,21,23,25,27)

# Create the look up table
library(RSQLite)
stcon <- create_smartTable()

# Run the inner loop
innerLoopRes <- innerLoop(ocData, ocData[,photIdx], autoThresholdLevel=1, verbosity=2,
                          starsPerClust_kmeans=25, positionDataIndexes=posIdx,
                          smartTableDB=stcon)

# Clean the environment
rm(list=c("inputFileName", "ocData", "posIdx", "photIdx", "innerLoopRes",
   "fileName"))
dbDisconnect(stcon)

## End(Not run)
```

## kde2dForSubset — *Compute the density based distance quantity using a 2D Kernel Density Estimation*

### Description

`kde2dForSubset` will compute the 2D Kernel Density Estimation for the requested subset of data and will return the quantiy `(max(d)-mean(d))/sd(d)` if the option `returnDistance` is set to TRUE.

### Usage

```
kde2dForSubset(df, setw=1, n=50, showStats=TRUE, printPlots=TRUE,
returnDistance=FALSE, positionDataIndexes=c(1,2))
```

### Arguments

| | |
|---|---|
| `df` | a data frame to use |
| `setw` | an integer with the class of the stars to perform the analysis |
| `n` | the number of points in the regular grid of the density estimation |
| `showStats` | a boolean indicating if the user wants to see output statistics |
| `printPlots` | a boolean indicating if the user wants to see plots |
| `returnDistance` | a boolean indicating if the distance between the max and the mean in units of standard deviations should be returned |
| `positionDataIndexes` | an array of integers indicating the columns of the file containing the spatial position measurements |

### Value

A double representing the density based distance quantity.

### Author(s)

Alberto Krone-Martins, Andre Moitinho

### References

Krone-Martins, A. & Moitinho, A., A&A, v.561, p.A57, 2014

## Examples

```
# Create a simple data set with the values and errors
toyDataDF <- data.frame(x=runif(50, 0, 10), y=runif(50, 0, 10), resMclust.class=rep(1, 50))

# Run the KDE 2D analysis for the required subset
disV <- kde2dForSubset(toyDataDF, showStats=FALSE, printPlots=FALSE, returnDistance=TRUE)

# Clean the environment
rm(list=c("toyDataDF", "disV"))
```

# meanThreeSigRej *Perform cuts in the data*

## Description

meanThreeSigRej will perform an interative rejection using the mean and three sigma of the data. The function will compute the mean and standard deviation of the input vector, reject all entries lying farther than three-sigma, and iterate until the mean varies (fractionaly) by less than the tolerance value. The function will return a data frame with the mean, standard deviation value and the number of iterations until the convergence was reached.

## Usage

```
meanThreeSigRej(vec, maxI, tolerance)
```

## Arguments

| | |
|---|---|
| vec | a vector with the data to consider |
| maxI | an integer with the maximum amount of iterations allowed |
| tolerance | a double with the tolerance value (as (old-new)/old) |

## Value

A data frame with the fields mean, sd (the standard deviation) and convergenceAtIter (the iteration where the convergence was reached).

## Author(s)

Alberto Krone-Martins, Andre Moitinho

## Examples

```
# Create a simple data set with the values and errors
toyData <- c(rnorm(30, mean=0, sd=5), 10000, 1000)

# Call the function to perform cuts
toyDataItStat <- meanThreeSigRej(toyData)

cat(paste("True mean             = 0\n"))
cat(paste("Before rejection mean =",round(mean(toyData),2),"\n"))
cat(paste("After rejetion mean   =",round(toyDataItStat$mean,2),"\n"))

# Clean the environment
rm(list=c("toyData", "toyDataItStat"))
```

---

# outerLoop *UPMASK outer loop*

---

## Description

outerLoop executes the UPMASK method's outer loop on a data frame, and returns another data frame as output, with the id of the object and it's classification as a stellar cluster member or not.

The outerLoop perform cuts in the data if necessary (by calling performCuts), take errors in the data table into account if the user request (by calling innerLoop), runs the inner loop (by calling innerLoop) until convergence of the membership list or util the maximum number of iterations is reached.

## Usage

```
outerLoop(ocdata_full, positionDataIndexes=c(1,2),
photometricDataIndexes=c(3,5,7,9,11,19,21,23,25,27),
photometricErrorDataIndexes=c(4,6,8,10,12,20,22,24,26,28), threshold=1, maxIter=25,
plotIter=FALSE, verbose=FALSE, starsPerClust_kmeans=50, nstarts_kmeans=50,
finalXYCut=FALSE, autoCalibrated=FALSE, considerErrors=FALSE, run=0,
smartTableDB, nDimsToKeep=4, dimRed="PCA", scale=TRUE)
```

## Arguments

ocdata_full a data frame with the data to perform the analysis

positionDataIndexes
: an array of integers indicating the columns of the data frame containing the spatial position measurements

photometricDataIndexes
: an array of integers with the column numbers containing photometric measurements (or any other measurement to go into the PCA step)

`photometricErrorDataIndexes`
an array of integers with the column numbers containing the errors of the photometric measurements

`threshold` a double indicating the thresholding level for the random field analysis

`maxIter` an integer the maximum amount of iterations of the outer loop before giving up convergence (usually it is not necessary to modify this)

`plotIter` a boolean indicating if the user wants to see iteration plots

`verbose` a boolean indicating if the output to screen should be verbose

`starsPerClust_kmeans`
an integer with the average number of stars per k-means cluster

`nstarts_kmeans` an integer the amount of random re-initializations of the k-means clustering method (usually it is not necessary to modify this)

`finalXYCut` a boolean indicating if a final cut in the XY space should be performed (defaults to FALSE)

`autoCalibrated` a boolean indicating if the number of random field realizations for the clustering check in the position space should be autocalibrated (experimental code, defaults to FALSE).

`considerErrors` a boolean indicating if the errors should be taken into account

`run` an integer greater than zero indicating the run number

`smartTableDB` a database connection to the smart look-up table

`nDimsToKeep` an integer with the number of dimensions to consider (defaults to 4)

`dimRed` a string with the dimensionality reduction method to use (defaults to PCA. The only other options are LaplacianEigenmaps or None)

`scale` a boolean indicating if the data should be scaled and centered

## Value

A data frame with the id and class (member / not member) of each object at this run.

## Author(s)

Alberto Krone-Martins, Andre Moitinho

## References

Krone-Martins, A. & Moitinho, A., A&A, v.561, p.A57, 2014

## Examples

```
## Not run:
# Perform a one run of the outerLoop using a simulated open cluster with
# spatial and photometric data
# Load the data into a data frame
fileName <- "oc_12_500_1000_1.0_p019_0880_1_25km_120nR_withcolors.dat"
inputFileName <- system.file("extdata", fileName, package="UPMASK")
ocData <- read.table(inputFileName, header=TRUE)
```

```
# Create the look up table
library(RSQLite)
stcon <- create_smartTable()

# Run the outer loop
posIdx <- c(1,2)
photIdx <- c(3,5,7,9,11,19,21,23,25,27)
photErrIdx <- c(4,6,8,10,12,20,22,24,26,28)
outerLoopRes <- outerLoop(ocData, posIdx, photIdx, PhotErrIdx,
                          starsPerClust_kmeans=25, verbose=TRUE, smartTableDB=stcon)

# Clean the environment
rm(list=c("inputFileName", "ocData", "posIdx", "photIdx", "photErrIdx",
          "outerLoopRes", "fileName"))
dbDisconnect(stcon)

## End(Not run)
```

## performCuts *Perform cuts in the data*

### Description

performCuts will perform cuts in the data. This function is provided as a place holder, and it is empty, but it is called by UPMASK, so if the user needs to perform cuts in the data for the UPMASK analysis, this function should be tailored.

### Usage

```
performCuts(originalData)
```

### Arguments

| | |
|---|---|
| originalData | a data frame to use as the baseline |

### Value

A data frame.

### Author(s)

Alberto Krone-Martins, Andre Moitinho

### Examples

```
# Create a simple data set with the values and errors
toyDataDF <- data.frame(x=runif(10, 0, 10), dx=rep(0.2, 10), y=runif(10, 0, 10),
                        dy=rep(0.1, 10))

# Call the function to perform cuts
newToyDataDF <- performCuts(toyDataDF)

# Clean the environment
rm(list=c("toyDataDF", "newToyDataDF"))
```

## takeErrorsIntoAccount *Take Errors Into Account for UPMASK analysis*

### Description

Based on a data frame containing measurements and errors, the takeErrorsIntoAccount will produce another data frame where each measurement of the original data frame is replaced by another value taken from a random distribution. The implemented error model is gaussian, so each value of the output data frame will be a random sampling from a gaussian distribution where the mean is the value in the original data frame (indicated by the photometricDataIndexes column argument) and the standard deviation is the value from its corresponding error (indicated by the photometricErrorDataIndexes column argument). The newly constructed dataframe is returned by the function.

The user can adapt this function so it can take any error model into account during the UPMASK analysis.

### Usage

```
takeErrorsIntoAccount(originalData, dataIndexes, errorIndexes)
```

### Arguments

| | |
|---|---|
| originalData | a data frame to use as the baseline |
| dataIndexes | an array of integers indicating the columns corresponding to the measurements |
| errorIndexes | an array of integers indicating the columns corresponding to the errors |

### Value

A data frame with the new values sampled from the error distributions.

### Author(s)

Alberto Krone-Martins, Andre Moitinho

### References

Krone-Martins, A. & Moitinho, A., A&A, v.561, p.A57, 2014

### Examples

```
# Create a simple data set with the values and errors
toyDataDF <- data.frame(x=runif(10, 0, 10), dx=rep(0.2, 10), y=runif(10, 0, 10),
                        dy=rep(0.1, 10))

# Apply the error models to create another data frame
newToyDataDF <- takeErrorsIntoAccount(toyDataDF, c(1,3), c(2,4))

# Plot the results
plot(toyDataDF$x, toyDataDF$y)
points(newToyDataDF$x, newToyDataDF$y, pch=19, cex=0.8, col="red")

# Clean the environment
rm(list=c("toyDataDF", "newToyDataDF"))
```

---

## UPMASKdata *Run UPMASK in a data frame*

---

### Description

UPMASKdata executes the UPMASK method on a data frame, and returns another data frame as output, including the membership analysis result as additional columns.

UPMASKdata is a method for performing membership assignment in stellar clusters. The distributed code is prepared to use photometry and spatial positions, but it can take into account other types of data as well. The method is able to take into account arbitrary error models (the used must rewrite the takeErrorsIntoAccount function), and it is unsupervised, data-driven, physical-model-free and relies on as few assumptions as possible. The approach followed for membership assessment is based on an iterative process, dimensionality reduction, a clustering algorithm and a kernel density estimation.

### Usage

```
UPMASKdata(dataTable, positionDataIndexes=c(1,2),
photometricDataIndexes=c(3,5,7,9,11,19,21,23,25,27),
photometricErrorDataIndexes=c(4,6,8,10,12,20,22,24,26,28), threshold=1,
classAlgol="kmeans", maxIter=25, starsPerClust_kmeans=25, nstarts_kmeans=50,
nRuns=8, runInParallel=FALSE, paralelization="multicore", independent=TRUE,
verbose=FALSE, autoCalibrated=FALSE, considerErrors=FALSE,
finalXYCut=FALSE, nDimsToKeep=4, dimRed="PCA", scale=TRUE)
```

## Arguments

`dataTable` a data frame with the data to perform the analysis

`positionDataIndexes` an array of integers indicating the columns of the data frame containing the spatial position measurements

`photometricDataIndexes` an array of integers with the column numbers containing photometric measurements (or any other measurement to go into the PCA step)

`photometricErrorDataIndexes` an array of integers with the column numbers containing the errors of the photometric measurements

`threshold` a double indicating the thresholding level for the random field analysis

`classAlgol` a string indicating the type of clustering algorithm to consider. Only k-means is implemented at this moment (defaults to kmeans)

`maxIter` an integer the maximum amount of iterations of the outer loop before giving up convergence (usually it is not necessary to modify this)

`starsPerClust_kmeans` an integer with the average number of stars per k-means cluster

`nstarts_kmeans` an integer the amount of random re-initializations of the k-means clustering method (usually it is not necessary to modify this)

`nRuns` the total number of individual runs to execute the total number of outer loop runs to execute

`runInParallel` a boolean indicating if the code should run in parallel

`paralelization` a string with the type of paralilization to use. the paralelization can be: "multicore" or "MPIcluster". At this moment only "multicore" is implemented (defaults to multicore).

`independent` a boolean indicating if non-parallel runs should be completely independent

`verbose` a boolean indicating if the output to screen should be verbose

`autoCalibrated` a boolean indicating if the number of random field realizations for the clustering check in the position space should be autocalibrated (experimental code, defaults to FALSE).

`considerErrors` a boolean indicating if the errors should be taken into account

`finalXYCut` a boolean indicating if a final cut in the XY space should be performed (defaults to FALSE)

`nDimsToKeep` an integer with the number of dimensions to consider (defaults to 4)

`dimRed` a string with the dimensionality reduction method to use (defaults to PCA. The only other options are LaplacianEigenmaps or None)

`scale` a boolean indicating if the data should be scaled and centered

## Value

A data frame with the original data used to run the method and additional columns indicating the classification at each run, as well as a membership probability in the frequentist sense.

## Author(s)

Alberto Krone-Martins, Andre Moitinho

## References

Krone-Martins, A. & Moitinho, A., A&A, v.561, p.A57, 2014

## Examples

```
## Not run:
# Analyse a simulated open cluster using spatial and photometric data
# Load the data into a data frame
fileNameI <- "oc_12_500_1000_1.0_p019_0880_1_25km_120nR_withcolors.dat"
inputFileName <- system.file("extdata", fileNameI, package="UPMASK")
ocData <- read.table(inputFileName, header=TRUE)

# Example of how to run UPMASK using data from a data frame
# (serious analysis require at least larger nRuns)
posIdx <- c(1,2)
photIdx <- c(3,5,7,9,11,19,21,23,25,27)
photErrIdx <- c(4,6,8,10,12,20,22,24,26,28)

upmaskRes <- UPMASKdata(ocData, posIdx, photIdx, PhotErrIdx, nRuns=2,
                        starsPerClust_kmeans=25, verbose=TRUE)

# Create a simple raw plot to see the results
pCols <- upmaskRes[,length(upmaskRes)]/max(upmaskRes[,length(upmaskRes)])
plot(upmaskRes[,1], upmaskRes[,2], col=rgb(0,0,0,pCols), cex=0.5, pch=19)

# Clean the environment
rm(list=c("inputFileName", "ocData", "posIdx", "photIdx", "photErrIdx",
          "upmaskRes", "pCols"))

## End(Not run)
```

## `UPMASKfile` *Run UPMASK in a file*

## Description

`UPMASKfile` executes the UPMASK method using a file as an input and writes another file as an output. This is a wrapper function that only reads a file into an R data frame, calls the `UPMASKdata` function using this data frame and the parameters passed by the user and writes the output into another file.

## Usage

```
UPMASKfile(filenameWithPathInput, filenameWithPathOuput,
positionDataIndexes=c(1,2), photometricDataIndexes=c(3,5,7,9,11,19,21,23,25,27),
photometricErrorDataIndexes=c(4,6,8,10,12,20,22,24,26,28), threshold=1,
maxIter=20, starsPerClust_kmeans=50, nstarts_kmeans=50, nRuns=5,
runInParallel=FALSE, paralelization="multicore", independent=TRUE, verbose=FALSE,
autoCalibrated=FALSE, considerErrors=FALSE, finalXYCut=FALSE,
fileWithHeader=FALSE, nDimsToKeep=4, dimRed="PCA", scale=TRUE)
```

## Arguments

`filenameWithPathInput`
a string indicating the file containing the data to run UPMASK on (with full path)

`filenameWithPathOuput`
a string indicating the file where the output shall be written (with full path)

`positionDataIndexes`
an array of integers indicating the columns of the file containing the spatial position measurements

`photometricDataIndexes`
an array of integers with the column numbers containing photometric measurements (or any other measurement to go into the PCA step)

`photometricErrorDataIndexes`
an array of integers with the column numbers containing the errors of the photometric measurements

`threshold` a double indicating the thresholding level for the random field analysis

`maxIter` an integer the maximum amount of iterations of the outer loop before giving up convergence (usually it is not necessary to modify this)

`starsPerClust_kmeans`
an integer with the average number of stars per k-means cluster

`nstarts_kmeans` an integer the amount of random re-initializations of the k-means clustering method (usually it is not necessary to modify this)

`nRuns` the total number of individual runs to execute the total number of outer loop runs to execute

`runInParallel` a boolean indicating if the code should run in parallel

`paralelization` a string with the type of paralilization to use. the paralelization can be: "multicore" or "MPIcluster". At this moment only "multicore" is implemented (defaults to multicore).

`independent` a boolean indicating if non-parallel runs should be completely independent

`verbose` a boolean indicating if the output to screen should be verbose

`autoCalibrated` a boolean indicating if the number of random field realizations for the clustering check in the position space should be autocalibrated (experimental code, defaults to FALSE).

`considerErrors` a boolean indicating if the errors should be taken into account `finalXYCut` a boolean indicating if a final cut in the XY space should be performed (defaults to FALSE)

`fileWithHeader` a boolean indicating if the input file has a text header

`nDimsToKeep` an integer with the number of dimensions to consider (defaults to 4)

`dimRed` a string with the dimensionality reduction method to use (defaults to PCA. The only other options are LaplacianEigenmaps or None)

`scale` a boolean indicating if the data should be scaled and centered

## Author(s)

Alberto Krone-Martins, Andre Moitinho

## References

Krone-Martins, A. & Moitinho, A., A&A, v.561, p.A57, 2014

## Examples

```
## Not run:
# Analyse a simulated open cluster using spatial and photometric data
# Create strings with filenames
fileNameI <- "oc_12_500_1000_1.0_p019_0880_1_25km_120nR_withcolors.dat"
inputFileName <- system.file("extdata", fileNameI, package="UPMASK")
outputFileName <- file.path(tempdir(), "up-RESULTS.dat")

# Example of how to run UPMASK using data from a file
# (serious analysis require at least larger nRuns)
posIdx <- c(1,2)
photIdx <- c(3,5,7,9,11,19,21,23,25,27)
photErrIdx <- c(4,6,8,10,12,20,22,24,26,28)
UPMASKfile(inputFileName, outputFileName, posIdx, photIdx, photErrIdx, nRuns=5,
           starsPerClust_kmeans=25, verbose=TRUE, fileWithHeader=TRUE)

# Open the resulting file to inspect the results
tempResults <- read.table(outputFileName, header=TRUE)

# Create a simple raw plot to see the results
pCols <- tempResults[,length(tempResults)]/max(tempResults[,length(tempResults)])
plot(tempResults[,1], tempResults[,2], col=rgb(0,0,0,pCols), cex=0.5, pch=19)

# Clean the environment
rm(list=c("tempResults", "inputFileName", "outputFileName", "pCols", "fileNameI"))

## End(Not run)
```

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