

Package ‘flowMap’

April 5, 2014

Title A probabilistic algorithm for matching and comparing multiple flow cytometry samples

Description This package provides an algorithm to compare and match cell populations across multiple flow cytometry samples. The method is based on the Friedman-Rafsky test, a nonparametric multivariate statistical test, where two cell distributions match if they occupy a similar feature space. The algorithm allows the users to specify a reference sample for comparison or to construct a reference sample from the available data. The output of the algorithm is a set of text files where the cell population labels are replaced by a metaset of population labels, generated from the matching process.

Version 1.0.0

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Depends R (>= 3.0.1), ade4(>= 1.5-2), doParallel(>= 1.0.3), abind(>= 1.4.0), reshape2(>= 1.2.2), ggplot2(>= 0.9.3.1), scales(>= 0.2.3), methods (>= 2.14),

biocViews MultipleComparisons, FlowCytometry

License GPL (>=2)

LazyData true

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flowMatch-package	<i>Flow cytometry data cross-sample comparison</i>
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Description

This package implements a method for matching cell populations across multiple flow cytometry samples.

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

crossMap-class	<i>Statistics of mapping the test samples and the reference sample (or the proxy reference)</i>
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Description

This class stores statistics of multiple-sample comparison.

Usage

```
## usage
## Accessors
getFRmapStats(object)
getFRmapPnorms(object)
getFRmapPnulls(object)
getCrossList(object)
```

Arguments

object Object of class `crossMap`

Accessors

In the following code object is a `crossMap` object.

`getFRmapStats`: list of matrices; each contains the observed FR statistics between a test sample and the reference

`getFRmapPnorm`: list of matrices; each contains the theoretical p-values between a test sample and the reference

`getFRmapPnulls`: list of matrices; each contains the empirical p-values between a test sample and the reference

`getCrossList`: matrix of test and reference sample population labels. A `data.frame` with columns

`SampleID`: an unique identifying number for the sample file

`testSample`: cell population label in the test sample

`refSample`: the match reference population label (NA if no match)

`newID`: the new population label in the proxy reference sample

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata",package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir,centroidDir=NULL)
refDataDir <- system.file("extdata/refData",package="flowMap")
crossMap <- makeCrossMap(stats=info,refDataDir,filtRes=NULL,
  draws=2,cutoff=10^(-5),sampleMethod="equalSize",sampleSize=10,
  nperms=100)
getFRmapStats(crossMap)
getFRmapPnorms(crossMap)
getFRmapPnulls(crossMap)
getCrossList(crossMap)
```

FRmapping

*Multiple sample comparison with a user-defined reference***Description**

Make a reference sample from a subset of the sample files. Map all sample files to the reference. Create an summary file of the sample file names, sample file IDs, reference sample IDs, original subpopulation IDs in each sample, and the corresponding new subpopulation IDs.

Usage

```
FRmapping(outputDir, sampleDir, centroidDir,
  refDataDir = NULL, refCentroidDir = NULL,
  makeRefSampleDir = NULL, makeRefCentroidDir = NULL,
  nPopFilt = 3, draws, cutoff = 0.01/30,
  sampleMethod = "equalSize", sampleSize = 100,
  nperms = 1000)
```

Arguments

outputDir	directory where the output files will be saved.
sampleDir	directory where all sample files are located. Note that samples need to be in txt format with the cell populations indexed by the last column in the data (which needs to be called id)
centroidDir	directory where all centroid files corresponding to the sample files are located. These also need to be in txt forma.
refDataDir	directory where the reference sample file is located.
refCentroidDir	directory where the centroid file for the reference sample is located.
makeRefSampleDir	directory of sample files to be used in making a reference file
makeRefCentroidDir	directory of centroids corresponding to the sample files in makeRefSampleDir
nPopFilt	to reduce running time, the users can choose to compute F-R statistic on some reference populations that are likely to be similar to the sample population (based on Euclidean distance between centroids). Default value: 3.
draws	number of random draws per population comparison. The F-R estimate is calculated as the median of the F-R statistics across random draws. Default value: 100.
cutoff	Cut-off for the pvalues in determining matched vs mismatched populations. Default value: 0.01/30.
sampleMethod	Downsampling method. Equal size sampling is the only available method at this point. The method takes an equal number of events from the two groups. For group sizes smaller than the default sample size, the group size is used in the computations. Default value: equalSize.

sampleSize	The number of events to be sampled from each group in the equalSize sampling method. Default value: 100.
nperms	Cell population labels within a single cross-sample comparisons are permuted to computed the empirical p-value for the F-R statistic. Results of 1000 permutations are similar to results of 10,000 permutations. Default value: 1000.

Value

refData	name of the reference sample file
testSet	sample files mapped
fileRes	list of prefiltering matrix
nNewPops	number of new populations discovered during mapping
pairList	mapping results for each sample file (including sample cell population IDs and reference sample IDs)
Pnulls	empirical p-values of FR statistics for each sample file
Pnorms	p-value of FR-statistics for each sample file
Wwobs	observed F-R statistic for each sample file
Wnulls	permuted distributions

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
## Not run: FRmapping(outputDir, sampleDir, centroidDir,
  refDataDir = NULL, refCentroidDir = NULL,
  makeRefSampleDir = NULL, makeRefCentroidDir = NULL,
  nPopFilt = 3, draws, cutoff = 0.01/30,
  sampleMethod = "equalSize", sampleSize = 100,
  nperms = 1000)

## End(Not run)
```

FRmappingSimple

Multiple sample comparisons

Description

Perform Friedman-Rafsky test on multiple flow cytometry samples. This function performs similar tasks as FRmapping, except that FRmappingSimple does not generate text files and takes in matrices or list of matrices as input arguments instead of text file directories.

Usage

```
FRmappingSimple(samples, centroids, refSample,
  refCentroid, nPopFilt = 3, draws = 100,
  cutoff = 0.01/30, sampleMethod = "equalSize",
  sampleSize = 100, nperms = 1000)
```

Arguments

<code>samples</code>	list of matrices or data.frames. Each matrix or data.frame is a flow cytometry sample where the last column indicates population id (variable id)
<code>centroids</code>	list of matrices or data.frames. Each matrix or data.frame consists of centroids for the corresponding flow cytometry sample specified under the argument <code>sample</code> .
<code>refSample</code>	a matrix or data.frame of reference sample. Each sample specified under the argument <code>sample</code> will be compared against this reference sample using F-R test.
<code>refCentroid</code>	a matrix or data.frame of the centroids of the sample populations specified in the <code>refSample</code> argument.
<code>nPopFilt</code>	to reduce running time, the users can choose to compute F-R statistic on some reference populations that are likely to be similar to the sample population (based on Euclidean distance between centroids). Default value: 3.
<code>draws</code>	number of random draws per population comparison. The F-R estimate is calculated as the median of the F-R statistics across random draws. Default value: 100.
<code>cutoff</code>	Cut-off for the p-values in determining matched vs mismatched populations. Default value: 0.01/30.
<code>sampleMethod</code>	Downsampling method. Equal size sampling is the only available method at this point. The method takes an equal number of events from the two groups. For group sizes smaller than the default sample size, the group size is used in the computations. Default value: <code>equalSize</code> .
<code>sampleSize</code>	The number of events to be sampled from each group in the <code>equalSize</code> sampling method. Default value: 100.
<code>nperms</code>	Cell population labels within a single cross-sample comparisons are permuted to compute the empirical p-value for the F-R statistic. Results of 1000 permutations are similar to results of 10,000 permutations. Default value: 1000.

Value

<code>fileRes</code>	list of prefiltering matrices
<code>nNewPops</code>	number of new populations discovered during mapping.
<code>pairList</code>	mapping results for each sample file (including sample cell population IDs and reference sample IDs)
<code>Pnulls</code>	empirical p-values of FR statistics for each sample file
<code>Pnorms</code>	p-value of FR-statistics for each sample file
<code>WWobs</code>	observed F-R statistic for each sample file
<code>Wnulls</code>	permuted distributions

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sam1 <- read.table(system.file("extdata/sample1.txt",
  package="flowMap"),header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt",
  package="flowMap"),header=TRUE)
res <- FRmappingSimple(samples=list(sam1),centroids=NULL,
  refSample=sam2,refCentroid=NULL,nPopFilt=NULL,
  draws=2,cutoff=10^(-5),sampleMethod="equalSize",
  sampleSize=10,nperm=100)
```

FRstats-class	<i>FR statistics and p-values generated from one single draw of the population pair comparison</i>
---------------	--

Description

This class stores the statistics required to compute median FR statistics across random draws.

Usage

```
## Accessors
getFRstats(object)
getPnorm(object)
```

Arguments

object Object of class [FRstats](#)

Accessors

In the following code object is a FRstats object.

getFRstats: matrix of median FR statistics across random draws

getPnorm: matrix of median theoretical null p-values across random draws

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap"),
  ,header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap"),
  ,header=TRUE)
xx1 <- sam1[sam1$id==1,]; xx1 <- xx1[sample(nrow(xx1),20),]
xx2 <- sam2[sam2$id==1,]; xx2 <- xx2[sample(nrow(xx2),20),]
res <- getFRest(XX1=sam1, XX2=sam2, iiTest=NULL, draws=1,
  sampleMethod="equalSize", sampleSize=10, estStat="median")
getFRstats(res)
getPnorm(res)
```

FRvalsPerm-class	<i>Statistics generated from the permuted distribution of the observed FR statistics</i>
------------------	--

Description

This class stores the statistics required to decide whether a population pair is matched or not.

Usage

```
## Accessors
getPnulls(object)
getWnulls(object)
```

Arguments

object Object of class [FRvalsPerm](#)

Accessors

In the following code object is a [FRvalsPerm](#) object.

getPnulls: matrix of empirical null p-values (test sample by reference sample)

getWnulls: matrix of the permuted FR statistics (used to calculate the empirical null p-values)

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

See Also

[FRstats](#) for the class of objects from which the observed FR statistics are calculated. [getMatched](#) is the method used to identify the matched pairs.

Examples

```

sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap"),
  header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap"),
  header=TRUE)
xx1 <- sam1[sam1$id==1,]; xx1 <- xx1[sample(nrow(xx1),20),]
xx2 <- sam2[sam2$id==1,]; xx2 <- xx2[sample(nrow(xx2),20),]
res <- getFRest(XX1=sam1, XX2=sam2, iiTest=NULL, draws=1,
  sampleMethod="equalSize", sampleSize=10, estStat="median")
permRes <- getFRvalsPerm(res, nperms=100, iiTest=NULL)
getPnulls(permRes)
getWnulls(permRes)

```

getFR

*F-R test for one population comparison***Description**

Compute a minimal spanning tree using package *ade4* (optimized MST computation in C). Following Friedman and Rafsky (1979), the number of runs is standardized by subtracting the expected number of runs and dividing the difference by the square root of estimated variance. Each FR statistic is dependent on the topology of the minimal spanning tree of the given population comparison.

Usage

```
getFR(xx1, xx2)
```

Arguments

xx1	matrix of events (rows) by features (columns)
xx2	matrix of events (rows) by features (columns)

Value

ww	FR statistic
runs	total number of within-group subtrees (or equivalently, total number of between-group edges plus 1)
mu	estimated mean of runs
sigma2	estimated variance of runs
pNorm	p-values of the F-R statistic assuming large sample asymptotic normal assumption

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```

sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap"),
  ,header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap"),
  ,header=TRUE)
xx1 <- sam1[sam1$id==1,]; xx1 <- xx1[sample(nrow(xx1),20),]
xx2 <- sam2[sam2$id==1,]; xx2 <- xx2[sample(nrow(xx2),20),]
FR0ne <- getFR(xx1,xx2)

```

getFRest

F-R statistic estimates across two samples

Description

Compute an estimate of F-R statistics based on random draws of each population pair comparison. The computation is optimized by incorporating the RParallel package. Users can specify the number of processing cores to be used during computation.

Usage

```

getFRest(XX1, XX2, iiTest, draws, sampleMethod,
  sampleSize, estStat)

```

Arguments

XX1	sample 1 txt file (cell populations are indexed by id)
XX2	sample 2 txt file (cell populations are indexed by id)
iiTest	an matrix of cell population pairs to be included in the cross-sample comparison.
draws	number of random draws
sampleMethod	methods of downsampling. The current default is equalSize, which samples an equal number of events from each group.
sampleSize	for the equalSize sampling method, specify the number of events to be sample from each group
estStat	statistic that used to estimate population F-R statistic (median is the default)

Value

a object of class FRstats

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap"),
  ,header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap"),
  ,header=TRUE)
xx1 <- sam1[sam1$id==1,]; xx1 <- xx1[sample(nrow(xx1),20),]
xx2 <- sam2[sam2$id==1,]; xx2 <- xx2[sample(nrow(xx2),20),]
res <- getFRest(XX1=sam1, XX2=sam2, iiTest=NULL, draws=1,
  sampleMethod="equalSize", sampleSize=10, estStat="median")
```

getFRmat

*F-R tests for two-sampbetween two samples***Description**

Compute the F-R statistics for all possible population comparisons between two samples. The function also provides an argument `iiTest` that selects a subset of population comparisons that are likely to produce a match. The computing time of this function grows with `sampleSize` and the number of population comparisons.

Usage

```
getFRmat(i, XX1, XX2, iiTest = NULL, sampleMethod,
  sampleSize)
```

Arguments

<code>i</code>	dummy variable to initialize parallel computing (package <code>Rparallel</code>)
<code>XX1</code>	matrix or data.frame of events by feature where the events are indexed by a variable <code>id</code> in the last column of the matrix or data.frame. This sample is consisted of the populations to be mapped.
<code>XX2</code>	matrix or data.frame of events by feature where the events are indexed by a variable <code>id</code> in the last column of the matrix or data.frame. This sample is the designated reference sample. <code>XX1</code> populations are mapped onto the <code>XX2</code> populations during cross-sample comparisons.
<code>iiTest</code>	matrix of 0/1, indexing the population pairs across the two samples that are likely to produce a match. Default is all pairs. The first column of <code>iiTest</code> indexes the population ID in <code>XX1</code> and the subsequent columns index the <code>XX2</code> populations to be compared with each <code>XX1</code> population.
<code>sampleMethod</code>	method of downsampling. Currently, the only available method is <code>equalSize</code> . This method randomly selects the same number of events from each group.
<code>sampleSize</code>	given the method <code>equalSize</code> , specify the number of events to sample in each group of a population comparison.

Value

wmat	FR statistics for each population comparison (XX1 populations by XX2 populations). The table entry is marked as N/A if F-R test is not performed per filtering table iiTest.
runsmat	the number of runs for each comparison (XX1 populations by XX2 populations)
mumat	the expected number of runs for each comparison (XX1 populations by XX2 populations)
sigma2mat	the estimated variance of runs for each comparison (XX1 populations by XX2 populations)
pNormat	the two-sided p-value associated with the F-R statistic under asymptotic normal assumption of the F-R statistic (XX1 populations by XX2 populations)

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap"),
,header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap"),
,header=TRUE)
res <- getFRmat(i=1, XX1=sam1, XX2=sam2, iiTest = NULL,
sampleMethod="equalSize", sampleSize=10)
```

getFRvalsPerm

Compute statistics for the empirical distribution

Description

This method permutes the observed FR statistics for each cross-sample comparison and creates an empirical null distribution of the FR statistics on which empirical values are decided.

Usage

```
getFRvalsPerm(stats, nperms, iiTest)
```

Arguments

stats	an object of class FRstats as produced by the getFRest function
nperms	number of permutations required to create the empirical distribution of the FR statistic
iiTest	prefiltering matrix indicating which populaiton pairs to perform testing on

Value

a object of class FRvalsPerms

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap"),
,header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap"),
,header=TRUE)
xx1 <- sam1[sam1$id==1,]; xx1 <- xx1[sample(nrow(xx1),20),]
xx2 <- sam2[sam2$id==1,]; xx2 <- xx2[sample(nrow(xx2),20),]
res <- getFRest(XX1=sam1, XX2=sam2, iiTest=NULL, draws=1,
sampleMethod="equalSize",sampleSize=10, estStat="median")
permRes <- getFRvalsPerm(res,nperms=100,iiTest=NULL)
```

getMatched

Identify matched population pairs

Description

This method applies a prespecified cutoff to the empirical p-values to identify the matched populations.

Usage

```
getMatched(stats,cutoff)
```

Arguments

stats	an object of FRvalsPerm class
cutoff	cutoff for identifying significant p-values, i.e., which population pairs matched/mismatched

Value

an object of class matchMat containing matched population pair labels

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```

sam1 <- read.table(system.file("extdata/sample1.txt",package="flowMap"),
  header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt",package="flowMap"),
  header=TRUE)
xx1 <- sam1[sam1$id==1,]; xx1 <- xx1[sample(nrow(xx1),20),]
xx2 <- sam2[sam2$id==1,]; xx2 <- xx2[sample(nrow(xx2),20),]
res <- getFRest(XX1=sam1, XX2=sam2, iiTest=NULL, draws=1,
  sampleMethod="equalSize",sampleSize=10, estStat="median")
permRes <- getFRvalsPerm(res,nperms=100,iiTest=NULL)
matchRes <- getMatched(permRes,cutoff=10^(-5))

```

getSomePops

Make prefiltering matrix for each test sample

Description

This method select the population pairs (within each test population) that are the most similar by centroid distance (Euclidean).

Usage

```
getSomePops(stats,refCentroidDir,nPopFilt)
```

Arguments

stats an object of [SampleInfo](#) class
refCentroidDir directory where the centroid file of the reference samples are located
nPopFilt number of reference populations to be compared for each test sample population

Value

an object of somePops class.

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```

sampleDir <- system.file("extdata",package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir,centroidDir=NULL)
## Not run:
  getSomePops(info,refCentroidDir,nPopFilt=3)

## End(Not run)

```

makeCrossMap	<i>Make mapping information for the meta set of populations</i>
--------------	---

Description

Make a reference sample from a subset of the sample files. Map all sample files to the reference. Create an summary file of the sample file names, sample file IDs, reference sample IDs, original subpopulation IDs in each sample, and the corresponding new subpopulation IDs.

Usage

```
makeCrossMap(stats, refDataDir, filtRes, draws, cutoff, sampleMethod,
             sampleSize, nperms)
```

Arguments

stats	an object of SampleInfo class
refDataDir	directory where the user-defined sample file is located
filtRes	list of matrices containing prefiltering population pairs for each cross-sample comparison
draws	number of random draws to compute estimated FR statistics for a population pair comparison
cutoff	p-value cutoff for identifying matched pairs
sampleMethod	sampling scheme for each population comparison
sampleSize	number of events to draw from each population in a population pair comparison
nperms	number of permutations required to make the empirical null distribution

Value

an object of crossMap class.

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata", package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir, centroidDir=NULL)
refDataDir <- system.file("extdata/refData", package="flowMap")
crossMap <- makeCrossMap(stats=info, refDataDir, filtRes=NULL,
                        draws=2, cutoff=10^(-5), sampleMethod="equalSize", sampleSize=10,
                        nperms=100)
```

`makeRefMap`*Make mapping information for the proxy reference sample*

Description

This function performs multiple sample comparison among a set of specified sample files and then creates mapping information for proxy reference sample accordingly.

Usage

```
makeRefMap(stats, draws, nPopFilt, cutoff, sampleMethod, sampleSize, nperms)
```

Arguments

<code>stats</code>	an object of <code>SampleInfo</code> class
<code>draws</code>	number of random draws to compute estimated FR statistics for a population pair comparison
<code>nPopFilt</code>	number of reference populations to be compared for a test population
<code>cutoff</code>	p-value cutoff for matched/mismatched population pairs
<code>sampleMethod</code>	sampling scheme for each population comparison
<code>sampleSize</code>	number of events to draw from each population in a population pair comparison
<code>nperms</code>	number of permutations required to make the empirical null distribution

Value

an object of `refMap` class

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata", package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir, centroidDir=NULL)
refMap <- makeRefMap(stats=info, draws=2, nPopFilt=3, cutoff=10^(-5)
, sampleMethod="equalSize", sampleSize=10, nperms=100)
```

makeRefSample	<i>Make a proxy reference sample</i>
---------------	--------------------------------------

Description

This function applies the refMap method and generates a proxy reference sample accordingly.

Usage

```
makeRefSample(stats, draws, nPopFilt, cutoff, sampleMethod, sampleSize, nperms)
```

Arguments

stats	an object of SampleInfo class
draws	number of random draws to compute estimated FR statistics for a population pair comparison
nPopFilt	number of reference populations to be compared for a test population
cutoff	p-value cutoff for matched/mismatched population pairs
sampleMethod	sampling scheme for each population comparison
sampleSize	number of events to draw from each population in a population pair comparison
nperms	number of permutations required to make the empirical null distribution

Value

an object of refSample class

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata", package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir, centroidDir=NULL)
refSam <- makeRefSample(stats=info, draws=2, nPopFilt=3, cutoff=10^(-5),
  sampleMethod="equalSize", sampleSize=10, nperms=100)
```

makeSampleInfo *Prepare background files to downstream data processing*

Description

Create a txt files of the location of sample directory, centroid directory, and output directory. Create a txt file of the sample file information, including the sample file names, identifying number for each sample file, and the number of subpopulations contained in each sample.

Usage

```
makeSampleInfo(sampleDir, centroidDir = NULL)
```

Arguments

sampleDir directory where sample files are located
centroidDir directory where centroid files are located

Value

an object of class SampleInfo

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata",package="flowMap")  
info <- makeSampleInfo(sampleDir=sampleDir,centroidDir=NULL)
```

matchMat-class *Matching information about a single cross-sample comparison*

Description

This class stores the information required to identify matched/mismatched cell population comparisons.

Usage

```
## Accessors  
getMatchPairs(object)  
getMatchMat(object)
```

Arguments

object Object of class `matchMat`

Accessors

In the following code object is a `matchMat` object.

`getMatchedPairs`: a matrix of matched population labels with columns

`testSample`: all population labels in the test sample

`refSample`: matched reference sample population label

`getMatchMat`: a matrix of 0 and 1 entries indexing matched/mismatched population pairs

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap"),
  ,header=TRUE)
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap"),
  ,header=TRUE)
xx1 <- sam1[sam1$id==1,]; xx1 <- xx1[sample(nrow(xx1),20),]
xx2 <- sam2[sam2$id==1,]; xx2 <- xx2[sample(nrow(xx2),20),]
res <- getFRest(XX1=sam1, XX2=sam2, iiTest=NULL, draws=1,
  sampleMethod="equalSize", sampleSize=10, estStat="median")
permRes <- getFRvalsPerm(res, nperms=100, iiTest=NULL)
matchRes <- getMatched(permRes, cutoff=10^(-5))
getMatchPairs(matchRes)
getMatchMat(matchRes)
```

permutePops

Permute cell population labels across two samples

Description

In order to compute the empirical p-value of the F-R statistics, we permute the labels of the cell populations across samples.

Usage

```
permutePops(XX1, XX2)
```

Arguments

XX1 sample 1 matrix of cell populations (indexed by the variable `id`, the last column of the matrix)

XX2 sample 2 matrix of cell populations (indexed by the variable `id`, the last column of the matrix)

Value

XX1 sample 1 matrix based on permuted data
XX2 sample 2 matrix based on permuted data

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sam1 <- read.table(system.file("extdata/sample1.txt", package="flowMap")  
  ,header=TRUE)  
sam2 <- read.table(system.file("extdata/sample2.txt", package="flowMap")  
  ,header=TRUE)  
permSam <- permutePops(sam1, sam2)
```

refMap-class

Information required to making a proxy reference sample

Description

This class stores the information used to generate a proxy reference sample.

Usage

```
## Accessors  
  
getPairList(object)
```

Arguments

object Object of class [refMap](#)

Accessors

In the following code object is a refMap object.

getPairList: a data.frame with columns

 SampleID: an unique identifying number for the sample file
 testSample: cell population label in the test sample
 refSample: the match reference population label (NA if no match)
 newID: the new population label in the proxy reference sample

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata",package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir,centroidDir=NULL)
refMap <- makeRefMap(stats=info,draws=2,nPopFilt=3,cutoff=10^(-5)
, sampleMethod="equalSize",sampleSize=10,nperms=100)
getPairList(refMap)
```

refSample-class

Data and summary information of the proxy reference sample

Description

This class stores the information used to generate a proxy reference sample as well as the resultant sample data.

Usage

```
## Accessors
getNewPops(object)
getRefData(object)
```

Arguments

object Object of class [refSample](#)

Accessors

In the following code object is a refSample object.

getNewPops: an integer, number of new populations added after the mapping process

getRefData: a data.frame of flow cytometry data combining samples used to create this proxy refernece sample; the rows are the events/cells, and the columns are the FCM features with the last column being the new population label

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata",package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir,centroidDir=NULL)
refSam <- makeRefSample(stats=info,draws=2,nPopFilt=3,cutoff=10^(-5),
, sampleMethod="equalSize",sampleSize=10,nperms=100)
getNewPops(refSam)
getRefData(refSam)
```

SampleInfo-class *List of directories and sample files*

Description

This class stores the information necessary to uniquely identify each test sample.

Usage

```
## Accessors  
  
getSampleInfo(object)
```

Arguments

object Object of class (or inheriting from) [SampleInfo](#)

Accessors

In the following code object is a SampleInfo object.

```
getSampleInfo: a data.frame with columns  
  sampleID: unique identifying number for the inputted sample files  
  sampleNames: names of the inputted sample files
```

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata",package="flowMap")  
info <- makeSampleInfo(sampleDir=sampleDir,centroidDir=NULL)  
getSampleInfo(info)
```

somePops-class *List of population pairs to be compared during multiple-sample comparisons*

Description

This class stores the population pairs selected after the prefiltering process.

Usage

```
## Accessors  
  
getPopFilt(object)
```

Arguments

object Object of class `somePops`

Accessors

In the following code object is a `somePops` object.

`getPopFilt`: a list with matrices as list elements. Each matrix contains labels of population pairs that are selected via prefiltering process.

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
sampleDir <- system.file("extdata",package="flowMap")
info <- makeSampleInfo(sampleDir=sampleDir,centroidDir=NULL)
# this example is not run;
# getSomePops(refCentroidDir,nPopFilt=3)
```

statCrossLists *summary statistic across elements of lists*

Description

Compute an estimate of F-R statistics across random draws of cell population comparison.

Usage

```
statCrossLists(obj, STAT)
```

Arguments

obj an object of one or more lists. List elements must be matrices of sample dimensions

STAT the statistic to be computed for each entry in the matrix across lists. Default value: median.

Value

est a matrix of the estimated statistic across random draws.

Author(s)

Chiaowen Joyce Hsiao <joyce.hsiao1@gmail.com>

Examples

```
xx <- list(x1=matrix(seq(1:10),nr=5,nc=2),  
          x2=matrix(seq(21:30),nr=5,nc=2))  
res <- statCrossLists(xx,"median")
```


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