

Package ‘flowMerge’

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Type Package

Title Cluster Merging for Flow Cytometry Data

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Description Merging of mixture components for model-based automated
gating of flow cytometry data using the flowClust framework.
Note: users should have a working copy of flowClust 2.0
installed.

License Artistic-2.0

LazyLoad yes

Collate SetClasses.R SetMethods.R flowMerge.R

Depends graph,feature,flowClust,Rgraphviz,foreach,snow

Enhances doMC, multicore

Imports rrcov,flowCore, graphics, methods, stats, utils

biocViews ImmunoOncology, Clustering, FlowCytometry

Suggests knitr, rmarkdown

VignetteBuilder knitr

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flowMerge-package	<i>Merging of mixture components for automated gating of flow cytometry data.</i>
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Description

Merges mixture components from the **flowClust** framework based on the entropy of clustering and provides a simple representation of complicated, non-convex cell populations.

Details

Package:	flowMerge
Type:	Package
Version:	0.4.1
Date:	2009-09-07
License:	Artistic-2.0

```
LazyLoad: yes
Depends: methods
```

High density, non-convex cell populations in flow cytometry data often require multiple mixture components for a good model fit. The components are often overlapping, resulting in a complicated representation of individual cell populations. `flowMerge` merges overlapping mixture components (based on the max BIC `flowClust` model fit) in an iterative manner based on an entropy criterion, allowing these cell populations to be represented by individual mixture components while retaining the good model fitting properties of the BIC solution. Estimates of the number of clusters from a `flowMerge` model more accurately represent the "true" number of cell populations in the data. Running `flowMerge` is relatively straightforward. A `flowClust` object is converted to a `flowObj` object, which groups the model and the data (a `flowFrame`) into a single object. This is done by a call to `flowObj(model, data)` with a call to `merge`, which takes a `flowObj` object. The algorithm may be run in parallel on a multi-core machine or a networked cluster of machines. It uses the functionality in the `snow` package to achieve this. Parallelized calls to `flowClust` are available via the `pFlowClust` and `pFlowMerge` functions.

`flowMerge` has functionality to automatically select the "correct" number of clusters by fitting a piecewise linear model to the entropy of clustering vs number of clusters, and locating the position of the changepoint. The piecewise linear model fitting is invoked by a call to `fitPiecewiseLinreg`, which returns the location of the changepoint.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>
Maintainer: Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; *Advances in Bioinformatics* (To Appear)

See Also

[flowClust](#), [flowObj](#), [pFlowMerge](#), [pFlowClust](#), [fitPiecewiseLinreg](#), [merge](#), [getData](#), [link{plot}](#)

Examples

```
#data(rituximab)
#data(RituximabFlowClustFit)
#o<-flowObj(flowClust.res[[which.max(flowMerge:::BIC(flowClust.res))]]),rituximab);
#m<-merge(o);
#i<-fitPiecewiseLinreg(m);
#m<-m[[i]];
#plot(m,pch=20,level=0.9);
```

checkForRemoteErrors *Check output of snow clusters for errors*

Description

Overrides the snow checkForRemoteErrors function. Try errors are returned when cluster nodes produce errors, rather than completely aborting the computation. Not meant to be called by the user.

Usage

```
checkForRemoteErrors(val)
```

Arguments

val **Result** The result returned from an individual cluster node.

Details

This function is meant to be called internally, but must be exported so that it can hide the native `checkForRemoteErrors` function in the snow package.

Value

The result from the snow cluster node, or an object of type `try-error` if there was an error.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; Advances in Bioinformatics (To Appear)

See Also

checkForRemoteErrors

fitPiecewiseLinreg*Fit Piecewise Linear Regression for a list of flowMerge Objects*

Description

Fits a two-component piecewise linear regression to the entropy vs number of clusters for a list of merged cluster solutions.

Usage

```
fitPiecewiseLinreg(x, plot=FALSE, normalized=TRUE, ...)
```

Arguments

x	A "list" of flowMerge objects for 1 through K clusters derived from a single max BIC flowObj or flowClust object.
plot	A logical indicating whether to plot the fit or not. Default is FALSE.
normalized	A logical indicating whether the merging should be done using the normalized or unnormalized entropy
...	Additional arguments not currently used.

Details

An S4 method that takes a list of flowMerge objects output by the `merge` method, extracts the entropy and fits a piecewise linear regression to the entropy vs number of clusters in order to find the position of the changepoint. The location of the changepoint corresponds to the optimal merged cluster solution. The piecewise linear regression now is fitted to the entropy vs cumulative sum of merged observations at each number of clusters. This normalizes the change in entropy for the number of data points as described in Baudry et al.

Value

An integer value corresponding to the position of the changepoint.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; *Advances in Bioinformatics* (To Appear)

See Also

[merge](#)

Examples

```
#data(rituximab)
#data(RituximabFlowClustFit)
#o<-flowObj(flowClust.res[[which.max(BIC(flowClust.res))]],rituximab);
#m<-merge(o)
#i<-fitPiecewiseLinreg(m);
```

fitPiecewiseLinreg-methods

Methods for fitPiecewiseLinreg in flowMerge package

Description

Methods for the function `fitPiecewiseLinreg` in the package `flowMerge`

Methods

x = "list" A list of `flowMerge` objectes derived from a call to the `merge` function.

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; *Advances in Bioinformatics* (To Appear)

flagOutliers

Update the flagOutliers slot in a flowMerge object

Description

Update the `flagOutliers` slot in a `flowMerge` object. This method is internal and called automatically from within the merging code.

Usage

```
flagOutliers(object,...)
```

Arguments

<code>object</code>	An object of type <code>flowMerge</code>
<code>...</code>	Additional arguments, currently unused
.	

flagOutliers-methods *Methods to update the flagOutliers slot in a flowMerge object.*

Description

Methods that update the `flagOutliers` slot in a `flowMerge` object so that they reflect the outliers in the new merged clustering. This is an internal function, not meant for user consumption. It is called from within the `merge` method.

Methods

object = "flowMerge" Update the `flagOutliers` slot for an object of type `flowMerge`

flowClust.res *A flowClust model fitted to the rituximab data for 1:10 clusters.*

Description

The Rituximab data set accessible via `data(rituximab)` in the `flowClust` package fitted to a `flowClust` model containing from one to ten components. The results are in the object `flowClust.res`.

Usage

```
data(RituximabFlowClustFit)
```

Format

The format is: `flowClust.res` is a `flowClustList`, where each element of the list is a `flowClust` model of the `rituximab` data, for $K=1$ through $K=10$ components, respectively. The structure of `flowClustList` and `flowClust` can be found in the corresponding documentation of the `flowClust` package. The format of the `rituximab` data is found in the documentation for that data set.

Details

The models have been precomputed for use in `flowMerge` examples to save computation time. `flowClust` was called on the `rituximab` data to generate these models with the following command:

```
flowClust.res<-flowClust(rituximab,K=1:10,B=1000,B.init=100,tol=1e-5,tol.init=1e-2,nu=4,randomStart=TRUE)
```

Source

Gasparetto, M., Gentry, T., Sebti, S., O'Bryan, E., Nimmanapalli, R., Blaskovich, M. A., Bhalla, K., Rizzieri, D., Haaland, P., Dunne, J. and Smith, C. (2004) Identification of compounds that enhance the anti-lymphoma activity of rituximab using flow cytometric high-content screening. *J. Immunol. Methods* **292**, 59-71.

Examples

```
#data(RituximabFlowClustFit)
#summary(flowClust.res);
```

flowMerge-class	Class "flowMerge"
-----------------	-------------------

Description

A class to represent flowMerge objects

Objects from the Class

The object unites the flowMerge model output and the data being modeled and contains additional slots for various characteristics of a merged cluster solution, including the entropy of clustering.

Slots

merged: The number of observations merged at the current step in the algorithm.

mtree: A tree-structured graph representing the order of merged components in the model. Inspired by SPADE. (Bendall et al.)

entropy: The entropy of clustering of the current solution.

DATA: An environment whose first element contains the flowFrame with the data modeled by this flowMerge object

expName: See the `flowClust` package for details

varNames: See the `flowClust` package for details

K: The number of clusters in the merged solution. See the `flowClust` package for details

w: The proportions for each component in the merged solution. See the `flowClust` package for details

mu: The means of the components in the merged solution. See the `flowClust` package for details

sigma: The covariances of the components in the merged solution. See the `flowClust` package for details

lambda: See the `flowClust` package for details

nu: See the `flowClust` package for details

z: See the `flowClust` package for details

u: The uncertainties for each data point.

label: See the `flowClust` package for details

uncertainty: See the `flowClust` package for details

ruleOutliers: See the `flowClust` package for details

flagOutliers: See the `flowClust` package for details

rm.min: See the `flowClust` package for details

rm.max: See the `flowClust` package for details
logLike: See the `flowClust` package for details
BIC: See the `flowClust` package for details
ICL: See the `flowClust` package for details

Extends

Class "[flowObj](#)", directly. Class "[flowClust](#)", by class "flowObj", distance 2.

Methods

getData `signature(obj = "flowMerge")`: Retrieves the `flowFrame` in the DATA environment slot.
plot `signature(x = "flowMerge", y = "missing")`: Plots the clusters in this object.
summary `signature(x = "flowMerge")`: Prints a summary of the object.
show `signature(x = "flowMerge")`: Prints information about the object.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data (Submitted)

See Also

[flowObj-class](#)

flowMerge-internal *Internal flowMerge functions*

Description

Internal functions for extracting the BIC, ICL or entropy from a list of `flowClus`, `flowObj`, or `flowMerge` objects.

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; *Advances in Bioinformatics* (To Appear)

flowObj*Create a flowObj object from a flowClust and flowFrame object*

Description

Convenience method that creates a `flowObj` object from a `flowClust` and `flowFrame` object, so as to group the model and data together. Useful for high-throughput analysis where one may want to access the data to compute other statistics.

Usage

```
flowObj(flowC = NULL, flowF = NULL)
```

Arguments

<code>flowC</code>	A <code>flowClust</code> object representing the model fit
<code>flowF</code>	A <code>flowFrame</code> object on which the <code>flowClust</code> model is based.

Details

Calls the `new("flowObj", ...)` constructor.

Value

An object of class `flowObj-class`

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; *Advances in Bioinformatics* (To Appear)

See Also

[flowObj-class](#)

Examples

```
#data(rituximab)
#data(RituximabFlowClustFit)
#o<-flowObj(flowClust.res[[which.max(flowMerge:::BIC(flowClust.res))]],rituximab);
#m<-merge(o);
```

flowObj-class *Class "flowObj"*

Description

A class inheriting from `flowClust` that groups the model and data in a single object.

Objects from the Class

Objects can be created by calls of the form `new("flowObj", ...)`. Has a convenience method `flowObj(flowClustObj, flowFrameObj)` for creating instances of the class.

Slots

DATA: An "environment" that holds a pointer to the `flowFrame` data in position `[[1]]`.
expName: As described in the `flowClust` documentation
varNames: As described in the `flowClust` documentation
K: As described in the `flowClust` documentation
w: As described in the `flowClust` documentation
mu: As described in the `flowClust` documentation
sigma: As described in the `flowClust` documentation
lambda: As described in the `flowClust` documentation
nu: As described in the `flowClust` documentation
z: As described in the `flowClust` documentation
u: As described in the `flowClust` documentation
label: As described in the `flowClust` documentation
uncertainty: As described in the `flowClust` documentation
ruleOutliers: As described in the `flowClust` documentation
flagOutliers: As described in the `flowClust` documentation
rm.min: As described in the `flowClust` documentation
rm.max: As described in the `flowClust` documentation
logLike: As described in the `flowClust` documentation
BIC: As described in the `flowClust` documentation
ICL: As described in the `flowClust` documentation

Extends

Class "[flowClust](#)", directly.

Methods

getData signature(obj = "flowObj"): Retreives the contents of the DATA environment

merge signature(x = "flowObj", y = "missing"): the flowMerge algorithm is called via this function on objects of type flowObj.

plot signature(x = "flowObj", y = "missing"): A simplified plotting method. Does not require specification of the data since it is contained in the flowObj object. Takes most of the same parameters as plot.flowClust, except the data parameter

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; Advances in Bioinformatics (To Appear)

See Also

[flowMerge-class](#), [flowObj](#)

<code>initPFlowMerge</code>	<i>Initialize a SNOW cluster for use with flowMerge</i>
-----------------------------	---

Description

Initializes a snow cluster for use with flowMerge, ensures that the flowMerge library is loaded in all environments. Not meant to be called by the user

Usage

`initPFlowMerge(cl)`

Arguments

<code>cl</code>	A snow cluster
-----------------	----------------

Details

A valid snow cluster.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; Advances in Bioinformatics (To Appear)

See Also

[pFlowMerge](#)

map

Map matrix of probabilities to class assignments.

Description

Traverse the rows of a matrix of probabilities of size $n \times k$, where the n rows are samples, and the k columns are the probability of assignment of the sample to each of k classes. The most probable class assignment is selected for each row and a vector of classes is returned.

Usage

```
map(z, ...)
```

Arguments

z	A matrix of probabilities.
...	Additional arguments, not currently used.

Value

A vector of class assignments of lenght n .

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>

Examples

```
z<-t(apply(t(replicate(100,rgamma(5,0.1,1))),1,function(x)x/sum(x)));
map(z);
```

merge	<i>Merge clusters in flow cytometry data</i>
-------	--

Description

Merge the clusters in a flowClust solution using the cluster merging algorithm and entropy criterion.

Usage

```
merge(x, y, ...)
```

Arguments

x	A flowObj object created from a flowClust object and a flowFrame using the flowObj constructor.
y	missing
...	Additional arguments. i.e. metric="entropy" "mahalanobis"

Details

Run the cluster merging algorithm on the max BIC solution from a call to flowClust. The optional argument, metric specifies the measure used for clustering. Either "mahalanobis" or "entropy". Defaults to "entropy".

Value

A list of unnamed flowMerge objects. The first element of the list corresponds to the 1-cluster merged solution. The second element corresponds to the 2-cluster merged solution, and so on.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data (Submitted)

See Also

[flowClust](#), [flowObj](#)

Examples

```
#data(rituximab)
#data(RituximabFlowClustFit)
#o<-flowObj(flowClust.res[[which.max(BIC(flowClust.res))]],rituximab)
#m<-merge(o);
```

merge-methods	<i>Merge mixture components</i>
---------------	---------------------------------

Description

Merge mixture components in a `flowObj` derived from a `flowClust` result and a `flowFrame` using the cluster merging algorithm.

Value

An unnamed list of `flowMerge` objects with the `k`th element corresponding to the `k`-cluster merged solution.

Methods

`x = "ANY", y = "ANY"` The generic method. Should not be called.
`x = "flowObj", y = "missing"` The merge method for a `flowObj`.

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data (To Appear)

Examples

```
#data(rituximab)
#data(RituximabFlowClustFit)
#o<-flowObj(flowClust.res[[which.max(flowMerge:::BIC(flowClust.res))]],rituximab);
#m<-merge(o);
```

mergeClusters	<i>Cluster merging not meant to be called by the user</i>
---------------	---

Description

Internal cluster merging function.

Usage

```
mergeClusters(object, metric)
```

Arguments

object	not meant to be called by the user
metric	not meant to be called by the user

Details

Not meant to be called by the user

Value

Not meant to be called by the user

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data (Submitted)

See Also

[merge](#)

mergeClusters2

Cluster merging not meant to be called by the user

Description

Internal function not meant to be called by the user.

Usage

`mergeClusters2(object, a, b)`

Arguments

object	Internal function not meant to be called by the user.
a	Internal function not meant to be called by the user.
b	Internal function not meant to be called by the user.

Details

Internal function not meant to be called by the user.

Value

Internal function not meant to be called by the user.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data (Submitted)

See Also

[merge](#)

NENT	<i>Extract the Normalized Entropy</i>
------	---------------------------------------

Description

Extracts the normalized entropy from a list of flowMerge objects.

Usage

`NENT(x)`

Arguments

`x` A list of flowMerge objects

Details

The normalized entropy is extracted from a flowMerge object by computing $\frac{E}{K*n}$ where E is the entropy, and K and n are the number of clusters and data points, respectively.

Value

Returns a vector of normalized entropy values for the flowMerge objects.

Warning

This function doesn't do enough error checking and will try to extract the entropy from a list of anything.

Author(s)

Greg Finak «greg.finak@ircm.qc.ca»

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data; Advances in Bioinformatics (To Appear)

See Also

[ENT,merge,flowMerge-class](#)

Examples

```
#data(RituximabFlowClustFit)
#data(rituximab)
#o<-flowObj(flowClust.res[[which.max(flowMerge:::BIC(flowClust.res))]],rituximab);
#m<-merge(o);
#flowMerge:::ENT(m);
#flowMerge:::NENT(m);
```

pFlowClust

Parallelized FlowClust

Description

A parallelized call to `flowClust` via the `snow` package and framework. Not called by the user.

Usage

```
pFlowClust(flowData,cl,K = 1:15,B.init = 100,
           tol.init = 0.01,tol = 1e-05,B = 1000,
           randomStart = 50,nu = 4,nu.est = 1,
           trans = 1,varNames = NA)
```

Arguments

<code>flowData</code>	The data object, must be a <code>flowFrame</code> , <code>flowSet</code> or list of <code>flowFrames</code>
<code>cl</code>	The <code>snow</code> cluster object
<code>K</code>	The number of clusters to try for each <code>flowFrame</code> . Can be a vector. This is what is parallelized across processors.
<code>B.init</code>	See <code>flowClust</code> documentation
<code>tol.init</code>	See <code>flowClust</code> documentation
<code>tol</code>	See <code>flowClust</code> documentation
<code>B</code>	See <code>flowClust</code> documentation
<code>randomStart</code>	See <code>flowClust</code> documentation
<code>nu</code>	See <code>flowClust</code> documentation
<code>nu.est</code>	See <code>flowClust</code> documentation
<code>trans</code>	See <code>flowClust</code> documentation
<code>varNames</code>	See <code>flowClust</code> documentation

Details

Calls flowClust via the `clusterMap` method of the `snow` package. Parallelizes the computation of multiple components for a single `flowFrame` in a loop over multiple `flowFrames`. If the `snow` cluster is `NULL`, will make the call via `mapply`.

Value

Returns a list of lists of `flowClust` objects. The outer list corresponds to the `flowFrames` passed into the method. The inner list corresponds to the `K` cluster solutions passed into the method, for each `flowFrame` (ie If the input is a list of two `flowFrames`, and `K=1:10`, then the result is a list of length 2. Each element of the list is itself a list of length 10. The `k`th element of the inner list is the `flowClust` `k` cluster solution.)

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data (Submitted)

See Also

[flowClust](#), [snow](#)

pFlowMerge

Parallel call to flowMerge

Description

Calls the `flowMerge` methods to compute the merged solution from a `flowClust` object or set of objects in a parallelized manner using the `snow` framework.

Usage

```
pFlowMerge(flowData, cl, K = 1:15,
           B.init = 100, tol.init = 0.01, tol = 1e-05,
           B = 500, randomStart = 10, nu = 4, nu.est = 0,
           trans = 1, varNames = NA)
```

Arguments

flowData	The data to be fit. A list of flowFrames, a flowSet or a flowFrame
cl	The snow cluster object. Can be NULL to call the non-parallel version of flowClust
K	See flowClust documentation
B.init	See flowClust documentation
tol.init	See flowClust documentation
tol	See flowClust documentation
B	See flowClust documentation
randomStart	See flowClust documentation
nu	See flowClust documentation
nu.est	See flowClust documentation
trans	See flowClust documentation
varNames	See flowClust documentation

Details

Makes a parallelized call to flowClust. Parses the results to extract the max BIC solution, merges clusters, finds the optimal k-cluster solution using the entropy and returns it. If cl is NULL, a non-parallel call is made to the flowClust function.

Value

A list of flowMerge objects. One per flowFrame passed into the method.

Warning

This function does not do any special memory management. A large data set will likely cause it to run out of memory and start swapping incessantly. If you have lots of data, it's best to feed it piecewise to pFlowClust.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Bashasharti A, Brinkmann R, Gottardo R. Merging Mixture Model Components for Improved Cell Population Identification in High Throughput Flow Cytometry Data (Submitted)

See Also

[pFlowClust](#), [flowClust](#), [merge](#), [snow](#), [fitPiecewiseLinreg](#)

Examples

```
data(rituximab)
#Parallelized call below:
## Not run: cl<-makeSOCKcluster(rep("finakg@localhost",7))
## Not run: result<-pFlowMerge(rituximab,cl,varNames=c("FSC.H","SSC.H"))
## Not run: plot(result)
#cl<-NULL;
#result<-pFlowMerge(rituximab,cl=NULL,varNames=c("FSC.H","SSC.H"),K=1:8);
#plot(result);
```

Description

Plots all possible two-dimensional projections of the parameters in a `flowMerge` or `flowObj` object and does not require specification of the `flowFrame` since a pointer to the data is stored in the object. Informative axis names are used, rather than the usual FL1/FL2/FS/SS channel names. This function can take most of the usual additional arguments provided to `plot` for the `flowClust` package, although some, like the axis names and the data are fixed. In order for `flowMerge` objects to display outliers correctly with `plot` (following merging), the `updateU` method must be called on them first.

Methods

`x = "flowMerge", y = "missing"` `x` is a `flowMerge` object.

`x = "flowObj", y = "missing"` `x` is a `flowObj` object.

See Also

[flowClust](#)

Examples

```
#data(rituximab)
#data(RituximabFlowClustFit)
#o<-flowObj(flowClust.res[[which.max(flowMerge:::BIC(flowClust.res))]],rituximab);
#m<-merge(o);
#i<-fitPiecewiseLinreg(m);
#m<-m[[i]];
#plot(m,pch=20,level=0.9);
```

ptree*Generate a Function to Plot The Merging Tree*

Description

This function generates and returns a new function which can be used to plot the merging tree for a flowMerge model, with nodes highlighted based on the expression of different parameters for each cell population.

Usage

```
ptree(x,y)
```

Arguments

x	A character string of the name of the variable holding the list of merged models returned from flowMerge
y	The index of the best fitting merged model in that list

Details

ptree will generate a function that will plot the merging tree from a flowMerge model. Nodes will be colored by the intensity of staining of that population in a given dimension. Calling `f<-ptree("model.name", fitPiecewiseLinreg(model.name))` will assign the function to `f`. Calling `f(3)` will plot the merging tree with nodes highlighted according to parameter 3, presuming that there are that many parameters in the model.

Value

Returns a function

Side Effects

A plot will be drawn on the current device.

Author(s)

Greg Finak <gfinak@fhcrc.org>

See Also

[merge.](#)

show-methods	<i>Describe a flowObj or flowMerge object</i>
--------------	---

Description

Accessors to describe a flowObj or flowMerge object.

Methods

object = "flowMerge" Describe a flowMerge object.

object = "flowObj" Describe a flowObj object.

split-methods	<i>Split data in a flowMerge object by cluster</i>
---------------	--

Description

Split method defined for flowMerge objects. Pulls out the population based on cluster number.

Methods

\itemx = "flowMerge", f = "missing" Split a flowMerge object into its component clusters.

summary-methods	<i>Summary methods for flowMerge</i>
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Description

Summary method for flowMerge objects.

Methods

object = "flowMerge" Summarize a flowMerge object.

object = "flowObj" Summarize a flowObj object

updateU

*Update uncertainties***Description**

Updates the uncertainties in a `flowMerge` object after merging clusters. This function is now internal and no longer exported. It is called automatically within the cluster merging method.

Usage

```
updateU(object)
```

Arguments

object	An object of type <code>flowMerge</code>
--------	--

Details

Updates the `u` slot of the `flowMerge` object following merging. The update is computation intensive, and so, is not automatically performed on each `flowMerge` object. Should only be done on objects used in further analysis.

Value

A `flowMerge` object with the `u` slot updated to reflect the new parameter values.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>

See Also

[flowMerge-class](#), [merge](#)

Examples

```
#data(rituximab)
#data(RituximabFlowClustFit)
#o<-flowObj(flowClust.res[[which.max(flowMerge:::BIC(flowClust.res))]],rituximab);
#m<-merge(o);
#i<-fitPiecewiseLinreg(m);
#m<-m[[i]];
#plot(m,pch=20,level=0.9);
```

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