

# Package ‘flowMerge’

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**Type** Package

**Title** Cluster Merging for Flow Cytometry Data

**Version** 2.54.0

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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                    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](mailto: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**

<code>x</code>	A "list" of <code>flowMerge</code> objects for 1 through K clusters derived from a single max BIC <code>flowObj</code> or <code>flowClust</code> object.
<code>plot</code>	A logical indicating whether to plot the fit or not. Default is <code>FALSE</code> .
<code>normalized</code>	A logical indicating whether the merging should be done using the normalized or unnormalized entropy
<code>...</code>	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	<i>Update the flagOutliers slot in a flowMerge object</i>
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---

### 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

object	An object of type flowMerge
...	Additional arguments, currently unused
.	

---

flagOutliers-methods	<i>Methods to update the flagOutliers slot in a flowMerge object.</i>
----------------------	---

---

### 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	<i>A flowClust model fitted to the rituximab data for 1:10 clusters.</i>
---------------	--

---

### 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,randomSt`

**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	<i>Class "flowMerge"</i>
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---

**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 covraiances 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](mailto: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)*



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flowObj	<i>Create a flowObj object from a flowClust and flowFrame object</i>
---------	--

---

### 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

flowC	A flowClust object representing the model fit
flowF	A flowFrame object on which the flowClust 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](mailto:greg.finak@ircm.qc.ca)», Raphael Gottardo «[raphael.gottardo@ircm.qc.ca](mailto: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	<i>Class "flowObj"</i>
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---

### 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"`): Retrieves 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](#)

---

initPFlowMerge

*Initialize a SNOW cluster for use with flowMerge*

---

**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**

cl                    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	<i>Map matrix of probabilities to class assignments.</i>
-----	--

---

**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**

<code>z</code>	A matrix of probabilities.
<code>...</code>	Additional arguments, not currently used.

**Value**

A vector of class assignments of length  $n$ .

**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**

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

**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.cq»

**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

*Merge mixture components*

---

**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

*Cluster merging not meant to be called by the user*

---

**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**

<code>object</code>	Internal function not meant to be called by the user.
<code>a</code>	Internal function not meant to be called by the user.
<code>b</code>	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`*Extract the Normalized Entropy*

---

**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**

flowData	The data object, must be a flowFrame, flowSet or list of flowFrames
cl	The snow cluster object
K	The number of clusters to try for each flowFrame. Can be a vector. This is what is parallelized across processors.
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**

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 kth 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);
```

---

plot-methods

*Methods for plotting flowMerge and flowObj classes*

---

**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](#).

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

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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 `flowMerge`

**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)**

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**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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