

Package ‘ConsensusClusterPlus’

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Type Package

Imports Biobase, ALL, graphics, stats, utils

Title ConsensusClusterPlus

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Description algorithm for determining cluster count and membership by stability evidence in unsupervised analysis

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biocViews Software, Bioinformatics, Clustering

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ConsensusClusterPlus	<i>run ConsensusClusterPlus</i>
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Description

ConsensusClusterPlus function for determining cluster number and class membership by stability evidence. calcICL function for calculating cluster-consensus and item-consensus.

Usage

```
ConsensusClusterPlus(  
d=NULL, maxK = 3, reps=10, pItem=0.8, pFeature=1, clusterAlg="hc", title="untitled_consensus_clus  
innerLinkage="average", finalLinkage="average", distance="pearson", m1=NULL,  
tmyPal=NULL, seed=NULL, plot=NULL, writeTable=FALSE, weightsItem=NULL, weightsFeature=NULL, verbose=F)  
  
calcICL(res, title="untitled_consensus_cluster", plot=NULL, writeTable=FALSE)
```

Arguments

d	matrix where columns=items/samples and rows are features. For example, a gene expression matrix of genes in rows and microarrays in columns. OR ExpressionSet object.
maxK	integer value. maximum cluster number to evaluate.
reps	integer value. number of subsamples.
pItem	numerical value. proportion of items to sample.
pFeature	numerical value. proportion of features to sample.
clusterAlg	character value. cluster algorithm. "hc" heirarchical (hclust) or "km" for k-means. See Note.
title	character value for output directory. Directory is created only if plot is not NULL or writeTable is TRUE. This title can be an absolute or relative path.
innerLinkage	heirarchical linkage method for subsampling.
finalLinkage	heirarchical linkage method for consensus matrix.
distance	character value. sample distance measures: "pearson", "spearman", or "euclidean".
ml	optional. prior result, if supplied then only do graphics and tables.
tmyPal	optional character vector of colors for consensus matrix
seed	optional numerical value. sets random seed for reproducible results.
plot	character value. NULL - print to screen, 'pdf', 'png'.
writeTable	logical value. TRUE - write output and log to csv.
weightsItem	optional numerical vector. weights to be used for sampling items.
weightsFeature	optional numerical vector. weights to be used for sampling features.
res	result of consensusClusterPlus.
verbose	boolean. If TRUE, print messages to the screen to indicate progress. This is useful for large datasets.

Details

ConsensusClusterPlus implements the Consensus Clustering algorithm of Monti, et al (2003) and extends this method with new functionality and visualizations. Its utility is to provide quantitative stability evidence for determining a cluster count and cluster membership in an unsupervised analysis.

ConsensusClusterPlus takes a numerical data matrix of items as columns and rows as features. This function subsamples this matrix according to pItem, pFeature, weightsItem, and weightsFeature, and clusters the data into 2 to maxK clusters by clusterArg clusteringAlgorithm. Agglomerative heirarchical (hclust) and kmeans clustering are supported by an option see above. For users wishing to use a different clustering algorithm for which many are available in R, one can supply their own clustering algorithm as a simple programming hook - see the second commented-out example that uses divisive heirarchical clustering.

For a detailed description of usage, output and images, see the vignette by: openVignette().

Value

ConsensusClusterPlus returns a list of length maxK. Each element is a list containing consensusMatrix (numerical matrix), consensusTree (hclust), consensusClass (consensus class assignments). ConsensusClusterPlus also produces images.

calcICL returns a list of two elements clusterConsensus and itemConsensus corresponding to cluster-consensus and item-consensus. See Monti, et al (2003) for formulas.

Author(s)

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References

Monti, S., Tamayo, P., Mesirov, J., Golub, T. (2003) Consensus Clustering: A Resampling-Based Method for Class Discovery and Visualization of Gene Expression Microarray Data. *Machine Learning*, 52, 91-118.

Examples

```
## obtain gene expression data
library(Biobase)
data(geneData)
d=geneData
#median center genes
d = sweep(d,1, apply(d,1,median))

## run consensus cluster
rcc = ConsensusClusterPlus(d,maxK=4, reps=100, pItem=0.8, pFeature=1, title="example")

## ICL
resICL = calcICL(rcc, title="example")

##example of programming hook for clusterAlg:
#library(cluster)
#dianaHook = function(this_dist,k){
#  tmp = diana(this_dist,diss=TRUE)
#  assignment = cutree(tmp,k)
#  return(assignment)
#}
#ConsensusClusterPlus(d,maxK=6, reps=25, pItem=0.8, pFeature=1, title="example", plot="png", clusterAlg="dianaHook")
```

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