

# Package ‘sparcl’

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**Title** Perform sparse hierarchical clustering and sparse k-means clustering

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**Description** Implements the sparse clustering methods of Witten and Tibshirani (2010): “A framework for feature selection in clustering”; published in Journal of the American Statistical Association 105(490): 713-726.

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sparcl-package

*Performs sparse hierarchical and sparse K-means clustering*


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### Description

Implements the sparse clustering methods of Witten and Tibshirani (2010) "A framework for feature selection in clustering", Journal Amer. Stat. Assocn. 105(490): 713-726.

### Details

Package: sparcl  
 Type: Package  
 Version: 1.0.3  
 Date: 2013-1-02  
 License: GPL-2  
 LazyLoad: yes

The main functions are KMeansSparseCluster and HierarchicalSparseCluster. Tuning parameters for these methods are chosen by KMeansSparseCluster.permute and HierarchicalSparseCluster.permute.

### Author(s)

Daniela M. Witten and Robert Tibshirani

Maintainer: Daniela Witten <dwitten@u.washington.edu>

### References

Witten and Tibshirani (2010) A framework for feature selection in clustering. Journal Amer. Stat. Assocn. 105(490): 713-726.

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ColorDendrogram

*Color the leaves in a hierarchical clustering dendrogram*


---

### Description

Pass in the output of "hclust" and a class label for each observation. A colored dendrogram will result, with the leaf colors indicating the classes.

### Usage

```
ColorDendrogram(hc, y, main = "", branchlength = 0.7, labels = NULL, xlab = NULL, sub = NULL, ylab = NULL)
```

**Arguments**

<code>hc</code>	The output of running "hclust" on a nxn dissimilarity matrix
<code>y</code>	A vector of n class labels for the observations that were clustered using "hclust". If labels are numeric from 1 to K, then colors will be determined automatically. Otherwise the labels can take the form of colors (e.g. <code>c("red", "red", "orange", "orange")</code> ).
<code>main</code>	The main title for the dendrogram.
<code>branchlength</code>	How long to make the colored part of the branches. Adjustment will be needed for each dissimilarity matrix
<code>labels</code>	The labels for the n observations.
<code>xlab</code>	X-axis label.
<code>sub</code>	Sub-x-axis label.
<code>ylab</code>	Y-axis label.
<code>cex.main</code>	The amount by which to enlarge the main title for the figure.

**Author(s)**

Daniela M. Witten and Robert Tibshirani

**References**

Witten and Tibshirani (2009) A framework for feature selection in clustering.

**See Also**

HierarchicalSparseCluster, HierarchicalSparseCluster.permute

**Examples**

```
# Generate 2-class data
set.seed(1)
x <- matrix(rnorm(100*20), ncol=20)
y <- c(rep(1,50), rep(2,50))
x[y==1,] <- x[y==1,]+2
# Perform hierarchical clustering
hc <- hclust(dist(x), method="complete")
# Plot
ColorDendrogram(hc, y=y, main="My Simulated Data", branchlength=3)
```

---

HierarchicalSparseCluster

*Hierarchical sparse clustering*


---

## Description

Performs sparse hierarchical clustering. If  $d_{ii'j}$  is the dissimilarity between observations  $i$  and  $i'$  for feature  $j$ , seek a sparse weight vector  $w$  and then use  $(\sum_j (d_{ii'j} w_j))_{ii'}$  as a  $n \times n$  dissimilarity matrix for hierarchical clustering.

## Usage

```
HierarchicalSparseCluster(x=NULL, dists=NULL, method=c("average", "complete", "single", "centroid"),
  wbound=NULL, niter=15, dissimilarity=c("squared.distance", "absolute.value"), uorth=NULL, silent=FALSE,
  cluster.features=FALSE, method.features=c("average", "complete",
  "single", "centroid"), output.cluster.files=FALSE,
  outputfile.prefix="output", genenames=NULL, genedesc=NULL, standardize.arrays=FALSE)
## S3 method for class 'HierarchicalSparseCluster'
print(x,...)
## S3 method for class 'HierarchicalSparseCluster'
plot(x,...)
```

## Arguments

<code>x</code>	A $n \times p$ data matrix; $n$ is the number of observations and $p$ the number of features. If NULL, then specify <code>dists</code> instead.
<code>dists</code>	For advanced users, can be entered instead of <code>x</code> . If <code>HierarchicalSparseCluster</code> has already been run on this data, then the <code>dists</code> value of the previous output can be entered here. Under normal circumstances, leave this argument NULL and pass in <code>x</code> instead.
<code>method</code>	The type of linkage to use in the hierarchical clustering - "single", "complete", "centroid", or "average".
<code>wbound</code>	The L1 bound on $w$ to use; this is the tuning parameter for sparse hierarchical clustering. Should be greater than 1.
<code>niter</code>	The number of iterations to perform in the sparse hierarchical clustering algorithm.
<code>dissimilarity</code>	The type of dissimilarity measure to use. One of "squared.distance" or "absolute.value". Only use this if <code>x</code> was passed in (rather than <code>dists</code> ).
<code>uorth</code>	If complementary sparse clustering is desired, then this is the $n \times n$ dissimilarity matrix obtained in the original sparse clustering.
<code>standardize.arrays</code>	Should the arrays be standardized? Default is FALSE.
<code>silent</code>	Print out progress?
<code>cluster.features</code>	Not for use.

method.features	Not for use.
output.cluster.files	Not for use.
outputfile.prefix	Not for use.
genenames	Not for use.
genedesc	Not for use.
...	not used.

### Details

We seek a p-vector of weights  $w$  (one per feature) and a  $n \times n$  matrix  $U$  that optimize

$\$maximize\_U, w \sum_j w_j \sum_{ii'} d_{ii'}^j U_{ii'}$  subject to  $\|w\|_2 \leq 1$ ,  $\|w\|_1 \leq wbound$ ,  $w_j \geq 0$ ,  $\sum_{ii'} U_{ii'}^2 \leq 1$ .

Here,  $d_{ii'}^j$  is the dissimilarity between observations  $i$  and  $i'$  with along feature  $j$ . The resulting matrix  $U$  is used as a dissimilarity matrix for hierarchical clustering. "wbound" is a tuning parameter for this method, which controls the L1 bound on  $w$ , and as a result the number of features with non-zero  $w_j$  weights. The non-zero elements of  $w$  indicate features that are used in the sparse clustering.

We optimize the above criterion with an iterative approach: hold  $U$  fixed and optimize with respect to  $w$ . Then, hold  $w$  fixed and optimize with respect to  $U$ .

Note that the arguments described as "Not for use" are included for the `sparcl` package to function with `GenePattern` but should be ignored by the R user.

### Value

hc	The output of a call to "hclust", giving the results of hierarchical sparse clustering.
ws	The p-vector of feature weights.
u	The $n \times n$ dissimilarity matrix passed into hclust, of the form $(\sum_j w_j d_{ii'}^j)_{ii'}$ .
dists	The $(n \times n) \times p$ dissimilarity matrix for the data matrix $x$ . This is useful if additional calls to <code>HierarchicalSparseCluster</code> will be made.

### Author(s)

Daniela M. Witten and Robert Tibshirani

### References

Witten and Tibshirani (2009) A framework for feature selection in clustering.

### See Also

[HierarchicalSparseCluster.permute](#), [KMeansSparseCluster](#), [KMeansSparseCluster.permute](#)

**Examples**

```

# Generate 2-class data
set.seed(1)
x <- matrix(rnorm(100*50),ncol=50)
y <- c(rep(1,50),rep(2,50))
x[y==1,1:25] <- x[y==1,1:25]+2
# Do tuning parameter selection for sparse hierarchical clustering
perm.out <- HierarchicalSparseCluster.permute(x, wbounds=c(1.5,2:6),
nperms=5)
print(perm.out)
plot(perm.out)
# Perform sparse hierarchical clustering
sparsehc <- HierarchicalSparseCluster(dists=perm.out$dists,
wbound=perm.out$bestw, method="complete")
# faster than sparsehc <- HierarchicalSparseCluster(x=x,wbound=perm.out$bestw, method="complete")
par(mfrow=c(1,2))
plot(sparsehc)
plot(sparsehc$hc, labels=rep("", length(y)))
print(sparsehc)
# Plot using knowledge of class labels in order to compare true class
# labels to clustering obtained
par(mfrow=c(1,1))
ColorDendrogram(sparsehc$hc,y=y,main="My Simulated Data",branchlength=.007)
# Now, what if we want to see if our data contains a *secondary*
# clustering after accounting for the first one obtained. We
# look for a complementary sparse clustering:
sparsehc.comp <- HierarchicalSparseCluster(x,wbound=perm.out$bestw,
method="complete",uorth=sparsehc$u)
# Redo the analysis, but this time use "absolute value" dissimilarity:
perm.out <- HierarchicalSparseCluster.permute(x, wbounds=c(1.5,2:6),
nperms=5, dissimilarity="absolute.value")
print(perm.out)
plot(perm.out)
# Perform sparse hierarchical clustering
sparsehc <- HierarchicalSparseCluster(dists=perm.out$dists, wbound=perm.out$bestw, method="complete", dissimilarity="absolute.value")
par(mfrow=c(1,2))
plot(sparsehc)

```

---

HierarchicalSparseCluster.permute

*Choose tuning parameter for sparse hierarchical clustering*


---

**Description**

The tuning parameter controls the L1 bound on  $w$ , the feature weights. A permutation approach is used to select the tuning parameter.

**Usage**

```
HierarchicalSparseCluster.permute(x, nperms = 10, wbounds = NULL,
dissimilarity=c("squared.distance",
"absolute.value"),standardize.arrays=FALSE)
## S3 method for class 'HierarchicalSparseCluster.permute'
plot(x,...)
## S3 method for class 'HierarchicalSparseCluster.permute'
print(x,...)
```

**Arguments**

<code>x</code>	A $n \times p$ data matrix, with $n$ observations and $p$ features.
<code>nperms</code>	The number of permutations to perform.
<code>wbounds</code>	The sequence of tuning parameters to consider. The tuning parameters are the L1 bound on $w$ , the feature weights. If <code>NULL</code> , then a default sequence will be used. If non-null, should be greater than 1.
<code>dissimilarity</code>	How should dissimilarity be computed? Default is <code>squared.distance</code> .
<code>standardize.arrays</code>	Should the arrays first be standardized? Default is <code>FALSE</code> .
<code>...</code>	not used.

**Details**

Let  $d_{ii'j}$  denote the dissimilarity between observations  $i$  and  $i'$  along feature  $j$ .

Sparse hierarchical clustering seeks a  $p$ -vector of weights  $w$  (one per feature) and a  $n \times n$  matrix  $U$  that optimize  $\sum_j w_j \sum_{ii'} d_{ii'j} U_{ii'}$  subject to  $\|w\|_2 \leq 1$ ,  $\|w\|_1 \leq s$ ,  $w_j \geq 0$ ,  $\sum_{ii'} U_{ii'}^2 \leq 1$ , where  $s$  is a value for the L1 bound on  $w$ . Let  $O(s)$  denote the objective function with tuning parameter  $s$ : i.e.  $O(s) = \sum_j w_j \sum_{ii'} d_{ii'j} U_{ii'}$ .

We permute the data as follows: within each feature, we permute the observations. Using the permuted data, we can run sparse hierarchical clustering with tuning parameter  $s$ , yielding the objective function  $O^*(s)$ . If we do this repeatedly we can get a number of  $O^*(s)$  values.

Then, the Gap statistic is given by  $\text{Gap}(s) = \log(O(s)) - \text{mean}(\log(O^*(s)))$ . The optimal  $s$  is that which results in the highest Gap statistic. Or, we can choose the smallest  $s$  such that its Gap statistic is within  $s_d(\log(O^*(s)))$  of the largest Gap statistic.

**Value**

<code>gaps</code>	The gap statistics obtained (one for each of the tuning parameters tried). If $O(s)$ is the objective function evaluated at the tuning parameter $s$ , and $O^*(s)$ is the same quantity but for the permuted data, then $\text{Gap}(s) = \log(O(s)) - \text{mean}(\log(O^*(s)))$ .
<code>sdgaps</code>	The standard deviation of $\log(O^*(s))$ , for each value of the tuning parameter $s$ .
<code>nnonzerows</code>	The number of features with non-zero weights, for each value of the tuning parameter.
<code>wbounds</code>	The tuning parameters considered.
<code>bestw</code>	The value of the tuning parameter corresponding to the highest gap statistic.

**Author(s)**

Daniela M. Witten and Robert Tibshirani

**References**

Witten and Tibshirani (2009) A framework for feature selection in clustering.

**See Also**

[HierarchicalSparseCluster](#), [KMeansSparseCluster](#), [KMeansSparseCluster.permute](#)

**Examples**

```
# Generate 2-class data
set.seed(1)
x <- matrix(rnorm(100*50),ncol=50)
y <- c(rep(1,50),rep(2,50))
x[y==1,1:25] <- x[y==1,1:25]+2
# Do tuning parameter selection for sparse hierarchical clustering
perm.out <- HierarchicalSparseCluster.permute(x, wbounds=c(1.5,2:6),
nperms=5)
print(perm.out)
plot(perm.out)
# Perform sparse hierarchical clustering
sparsehc <- HierarchicalSparseCluster(dists=perm.out$dists, wbound=perm.out$bestw, method="complete")
par(mfrow=c(1,2))
plot(sparsehc)
plot(sparsehc$hc, labels=rep("", length(y)))
print(sparsehc)
# Plot using knowledge of class labels in order to compare true class
# labels to clustering obtained
par(mfrow=c(1,1))
ColorDendrogram(sparsehc$hc,y=y,main="My Simulated
Data",branchlength=.007)
```

---

HierarchicalSparseCluster.wrapper

*A wrapper for the hierarchical sparse clustering algorithm*

---

**Description**

A wrapper for HierarchicalSparseCluster which reads in the data in GCT file format, and then automatically chooses the optimal tuning parameter value using HierarchicalSparseCluster.permute if not specified.



**Usage**

```
HierarchicalSparseCluster.wrapper(file, method=c("average", "complete", "single", "centroid"),
wbound=NULL, silent=FALSE, cluster.features=FALSE,
method.features=c("average", "complete",
"single", "centroid"), output.cluster.files=TRUE, outputfile.prefix=NULL, maxnumgenes=5000, standardize.
```

**Arguments**

<code>file</code>	A GCT filename in the working directory containing the data to be clustered.
<code>method</code>	The type of linkage to use in the hierarchical clustering - "single", "complete", "average", or "centroid".
<code>wbound</code>	The L1 bound on $w$ to use; this is the tuning parameter for sparse hierarchical clustering. If NULL, then it will be chosen via <code>HierarchicalSparseCluster.permute</code> .
<code>silent</code>	Print out progress?
<code>cluster.features</code>	Is a clustering for the features with non-zero weights also desired? Default is FALSE.
<code>method.features</code>	If <code>cluster.features</code> is TRUE, then the type of linkage used to cluster the features with non-zero weights: one of "single", "complete", "average", or "centroid".
<code>output.cluster.files</code>	Should files containing the clustering be output? Default is TRUE.
<code>outputfile.prefix</code>	The prefix for the output files. If NULL, then the prefix of the input file is used.
<code>maxnumgenes</code>	Limit the analysis to some number of genes with highest marginal variance, for computational reasons. This is recommended when the number of genes is very large. If NULL, then all genes are used.
<code>standardize.arrays</code>	Should the arrays first be standardized? Default is TRUE.

**Value**

<code>hc</code>	The output of a call to "hclust", giving the results of hierarchical sparse clustering.
<code>ws</code>	The p-vector of feature weights.
<code>u</code>	The $n \times n$ dissimilarity matrix passed into <code>hclust</code> , of the form $(\sum_j w_j d_{ij}^2)_{ii}$ .
<code>dists</code>	The $(n \times n) \times p$ dissimilarity matrix for the data matrix $x$ . This is useful if additional calls to <code>HierarchicalSparseCluster</code> will be made.

**Author(s)**

Daniela M. Witten and Robert Tibshirani

**References**

Witten and Tibshirani (2009) A framework for feature selection in clustering.

**See Also**

[HierarchicalSparseCluster.permute](#), [KMeansSparseCluster](#), [KMeansSparseCluster.permute](#)

---

KMeansSparseCluster      *Performs sparse k-means clustering*

---

**Description**

This function performs sparse k-means clustering. You must specify a number of clusters  $K$  and an L1 bound on  $w$ , the feature weights.

**Usage**

```
KMeansSparseCluster(x, K=NULL, wbounds = NULL, nstart = 20, silent =
FALSE, maxiter=6, centers=NULL)
## S3 method for class 'KMeansSparseCluster'
plot(x,...)
## S3 method for class 'KMeansSparseCluster'
print(x,...)
```

**Arguments**

$x$	An $n \times p$ data matrix. There are $n$ observations and $p$ features.
$K$	The number of clusters desired ("K" in K-means clustering). Must provide either $K$ or centers.
wbounds	A single L1 bound on $w$ (the feature weights), or a vector of L1 bounds on $w$ . If wbound is small, then few features will have non-zero weights. If wbound is large then all features will have non-zero weights. Should be greater than 1.
nstart	The number of random starts for the k-means algorithm.
silent	Print out progress?
maxiter	The maximum number of iterations.
centers	Optional argument. If you want to run the k-means algorithm starting from a particular set of clusters, then you can enter the $K \times p$ matrix of cluster centers here. Default use case involves taking centers=NULL and instead specifying $K$ .
...	not used.

**Details**

We seek a  $p$ -vector of weights  $w$  (one per feature) and a set of clusters  $C_1, \dots, C_K$  that optimize  $\sum_{j=1}^p \sum_{i=1}^n \min_{k=1, \dots, K} \|x_i - C_k\|_2^2$  subject to  $\|w\|_1 \leq 1$ ,  $\|w\|_1 \leq w_{\text{bound}}$ ,  $w_j \geq 0$

where  $\sum_{i=1}^n \min_{k=1, \dots, K} \|x_i - C_k\|_2^2$  is the between cluster sum of squares for feature  $j$ . An iterative approach is taken: with  $w$  fixed, optimize with respect to  $C_1, \dots, C_K$ , and with  $C_1, \dots, C_K$  fixed, optimize with respect to  $w$ . Here, wbound is a tuning parameter which determines the L1 bound on  $w$ .

The non-zero elements of  $w$  indicate features that are used in the sparse clustering.

**Value**

If wbounds is a vector, then a list with elements as follows (one per element of wbounds). If wbounds is just a single value, then elements as follows:

ws	The p-vector of feature weights.
Cs	The clustering obtained.

**Author(s)**

Daniela M. Witten and Robert Tibshirani

**References**

Witten and Tibshirani (2009) A framework for feature selection in clustering.

**See Also**

[KMeansSparseCluster.permute](#), [HierarchicalSparseCluster](#)

**Examples**

```
# generate data
set.seed(11)
x <- matrix(rnorm(50*70),ncol=70)
x[1:25,1:20] <- x[1:25,1:20]+1
x <- scale(x, TRUE, TRUE)
# choose tuning parameter
km.perm <- KMeansSparseCluster.permute(x,K=2,wbounds=seq(3,7,len=15),nperms=5)
print(km.perm)
plot(km.perm)
# run sparse k-means
km.out <- KMeansSparseCluster(x,K=2,wbounds=km.perm$bestw)
print(km.out)
plot(km.out)
# run sparse k-means for a range of tuning parameter values
km.out <- KMeansSparseCluster(x,K=2,wbounds=seq(1.3,4,len=8))
print(km.out)
plot(km.out)
# Run sparse k-means starting from a particular set of cluster centers
#in the k-means algorithm.
km.out <- KMeansSparseCluster(x,wbounds=2:7,centers=x[c(1,3,5),])
```

---

KMeansSparseCluster.permute

*Choose tuning parameter for sparse k-means clustering*

---

**Description**

The tuning parameter controls the L1 bound on w, the feature weights. A permutation approach is used to select the tuning parameter.

**Usage**

```

KMeansSparseCluster.permute(x, K=NULL, nperms = 25, wbounds = NULL,
  silent = FALSE, nvals = 10, centers=NULL)
## S3 method for class 'KMeansSparseCluster.permute'
print(x,...)
## S3 method for class 'KMeansSparseCluster.permute'
plot(x,...)

```

**Arguments**

x	The nxp data matrix, n is the number of observations and p the number of features.
K	The number of clusters desired - that is, the "K" in K-means clustering. Must specify K or centers.
nperms	Number of permutations.
wbounds	The range of tuning parameters to consider. This is the L1 bound on w, the feature weights. If NULL, then a range of values will be chosen automatically. Should be greater than 1 if non-null.
silent	Print out progress?
nvals	If wbounds is NULL, then the number of candidate tuning parameter values to consider.
centers	Optional argument. If you want to run the k-means algorithm starting from a particular set of clusters, then you can enter the Kxp matrix of cluster centers here. Default use case involves taking centers=NULL and instead specifying K.
...	not used.

**Details**

Sparse k-means clustering seeks a p-vector of weights  $w$  (one per feature) and a set of clusters  $C_1, \dots, C_K$  that optimize  $\sum_j w_j \text{BCSS}_j$  subject to  $\|w\|_2 \leq 1, \|w\|_1 \leq s, w_j \geq 0$ , where  $\text{BCSS}_j$  is the between cluster sum of squares for feature  $j$ , and  $s$  is a value for the L1 bound on  $w$ . Let  $O(s)$  denote the objective function with tuning parameter  $s$ : i.e.  $O(s) = \sum_j w_j \text{BCSS}_j$ .

We permute the data as follows: within each feature, we permute the observations. Using the permuted data, we can run sparse K-means with tuning parameter  $s$ , yielding the objective function  $O^*(s)$ . If we do this repeatedly we can get a number of  $O^*(s)$  values.

Then, the Gap statistic is given by  $\text{Gap}(s) = \log(O(s)) - \text{mean}(\log(O^*(s)))$ . The optimal  $s$  is that which results in the highest Gap statistic. Or, we can choose the smallest  $s$  such that its Gap statistic is within  $\text{sd}(\log(O^*(s)))$  of the largest Gap statistic.

**Value**

gaps	The gap statistics obtained (one for each of the tuning parameters tried). If $O(s)$ is the objective function evaluated at the tuning parameter $s$ , and $O^*(s)$ is the same quantity but for the permuted data, then $\text{Gap}(s) = \log(O(s)) - \text{mean}(\log(O^*(s)))$ .
sdgaps	The standard deviation of $\log(O^*(s))$ , for each value of the tuning parameter $s$ .

nnonzerows	The number of features with non-zero weights, for each value of the tuning parameter.
wbounds	The tuning parameters considered.
bestw	The value of the tuning parameter corresponding to the highest gap statistic.

**Author(s)**

Daniela M. Witten and Robert Tibshirani

**References**

Witten and Tibshirani (2009) A framework for feature selection in clustering.

**See Also**

[KMeansSparseCluster](#), [HierarchicalSparseCluster](#), [HierarchicalSparseCluster.permute](#)

**Examples**

```
# generate data
set.seed(11)
x <- matrix(rnorm(50*70),ncol=70)
x[1:25,1:10] <- x[1:25,1:10]+1.5
x <- scale(x, TRUE, TRUE)
# choose tuning parameter
km.perm <-
KMeansSparseCluster.permute(x,K=2,wbounds=seq(2,5,len=8),nperms=3)
print(km.perm)
plot(km.perm)
# run sparse k-means
km.out <- KMeansSparseCluster(x,K=2,wbounds=km.perm$bestw)
print(km.out)
plot(km.out)
# run sparse k-means for a range of tuning parameter values
km.out <- KMeansSparseCluster(x,K=2,wbounds=2:7)
print(km.out)
plot(km.out)
# Repeat, but this time start with a particular choice of cluster
# centers.
# This will do 4-means clustering starting with this particular choice
# of cluster centers.
km.perm.out <- KMeansSparseCluster.permute(x,wbounds=2:6, centers=x[1:4,],nperms=3)
print(km.out)
plot(km.out)
```

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