

# Package ‘dynamicTreeCut’

November 22, 2009

**Version** 1.21

**Date** 2009-11-23

**Title** Methods for detection of clusters in hierarchical clustering dendrograms.

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**Depends** R (>= 2.3.0), stats

**ZipData** no

**License** GPL (>= 2)

**Description** Contains methods for detection of clusters in hierarchical clustering dendrograms.

**URL** [http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/  
BranchCutting/](http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/BranchCutting/)

**Repository** CRAN

**Date/Publication** 2009-11-22 19:39:26

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dynamicTreeCut-package

*Methods for detection of clusters in hierarchical clustering dendrograms.*

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## Description

Contains methods for detection of clusters in hierarchical clustering dendrograms.

## Details

Package: dynamicTreeCut  
 Version: 1.21  
 Date: 2009-11-23  
 Depends: R, stats  
 ZipData: no  
 License: GPL version 2 or newer  
 URL: <http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/BranchCutting/>

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indentSpaces	Spaces for indented output.
merge2Clusters	Merge two clusters
printFlush	Print arguments and flush the console.
treecut-package	Methods for detection of clusters in hierarchical clustering dendrograms.

## Author(s)

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cutreeDynamic

*Adaptive branch pruning of hierarchical clustering dendrograms.*

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## Description

This wrapper provides a common access point for two methods of adaptive branch pruning of hierarchical clustering dendrograms.

## Usage

```
cutreeDynamic(dendro, cutHeight = NULL, minClusterSize = 20, method = "hybrid",
             distM = NULL,
             deepSplit = (ifelse(method=="hybrid", 1, FALSE)),
             maxCoreScatter = NULL, minGap = NULL,
             maxAbsCoreScatter = NULL, minAbsGap = NULL,
             pamStage = TRUE, pamRespectsDendro = TRUE,
             useMedoids = FALSE, maxDistToLabel = cutHeight,
             respectSmallClusters = TRUE,
             verbose = 2, indent = 0)
```

## Arguments

dendro	A hierarchical clustering dendrogram such as one returned by <code>hclust</code> .
cutHeight	Maximum joining heights that will be considered. For <code>method=="tree"</code> it defaults to 0.99. For <code>method=="hybrid"</code> it defaults to 99 percentile and the maximum of the joining heights on the dendrogram.
minClusterSize	Minimum cluster size.
method	Chooses the method to use. Recognized values are "hybrid" and "tree".
distM	Only used for method "hybrid". The distance matrix used as input to <code>hclust</code> . If not given and <code>method == "hybrid"</code> , the function will issue a warning and default to <code>method = "tree"</code> .
deepSplit	For method "hybrid", can be either logical or integer in the range 0 to 4. For method "tree", must be logical. In both cases, provides a rough control over sensitivity to cluster splitting. The higher the value (or if TRUE), the more and smaller clusters will be produced. For the "hybrid" method, a finer control can be achieved via <code>maxCoreScatter</code> and <code>minGap</code> below.
maxCoreScatter	Only used for method "hybrid". Maximum scatter of the core for a branch to be a cluster, given as the fraction of <code>cutHeight</code> relative to the 5th percentile of joining heights. See Details.
minGap	Only used for method "hybrid". Minimum cluster gap given as the fraction of the difference between <code>cutHeight</code> and the 5th percentile of joining heights.
maxAbsCoreScatter	Only used for method "hybrid". Maximum scatter of the core for a branch to be a cluster given as absolute heights. If given, overrides <code>maxCoreScatter</code> .
minAbsGap	Only used for method "hybrid". Minimum cluster gap given as absolute height difference. If given, overrides <code>minGap</code> .

<code>pamStage</code>	Only used for method "hybrid". If TRUE, the second (PAM-like) stage will be performed.
<code>pamRespectsDendro</code>	Logical, only used for method "hybrid". If TRUE, the PAM stage will respect the dendrogram in the sense that objects and small clusters will only be assigned to clusters that belong to the same branch that the objects or small clusters being assigned belong to.
<code>useMedoids</code>	Only used for method "hybrid" and only if <code>labelUnlabeled==TRUE</code> . If TRUE, the second stage will be use object to medoid distance; if FALSE, it will use average object to cluster distance. The default (FALSE) is recommended.
<code>maxDistToLabel</code>	Only used for method "hybrid" and only if <code>labelUnlabeled==TRUE</code> . Maximum object distance to closest cluster that will result in the object assigned to that cluster.
<code>respectSmallClusters</code>	Only used for method "hybrid" and only if <code>labelUnlabeled==TRUE</code> . If TRUE, branches that failed to be clusters in stage 1 only because of insufficient size will be assigned together in stage 2. If FALSE, all objects will be assigned individually.
<code>verbose</code>	Controls the verbosity of the output. 0 will make the function completely quiet, values up to 4 gradually increase verbosity.
<code>indent</code>	Controls indentation of printed messages (see <code>verbose</code> above). Each unit adds two spaces before printed messages; useful when several functions' output is to be nested.

### Details

This is a wrapper for two related but different methods for cluster detection in hierarchical clustering dendrograms.

In order to make the shape parameters `maxCoreScatter` and `minGap` more universal, their values are interpreted relative to `cutHeight` and the 5th percetile of the merging heights (we arbitrarily chose the 5th percetile rather than the minimum for reasons of stability). Thus, the absolute maximum allowable core scatter is calculated as  $\text{maxCoreScatter} * (\text{cutHeight} - \text{refHeight}) + \text{refHeight}$  and the absolute minimum allowable gap as  $\text{minGap} * (\text{cutHeight} - \text{refHeight})$ , where `refHeight` is the 5th percentile of the merging heights.

### Value

A vector of numerical labels giving assignment of objects to modules. Unassigned objects are labeled 0, the largest module has label 1, next largest 2 etc.

### Author(s)

Peter Langfelder, <Peter.Langfelder@gmail.com>

### References

Langfelder P, Zhang B, Horvath S, 2007. <http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/BranchCutting>

**See Also**

[hclust](#), [cutreeHybrid](#), [cutreeDynamicTree](#).

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cutreeDynamicTree *Dynamic dendrogram pruning based on dendrogram only*

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**Description**

Detect clusters in a hierarchical dendrogram using a variable cut height approach. Uses only the information in the dendrogram itself is used (which may give incorrect assignment for outlying objects).

**Usage**

```
cutreeDynamicTree(dendro, maxTreeHeight = 1, deepSplit = TRUE, minModuleSize = 50)
```

**Arguments**

dendro	Hierarchical clustering dendrogram such produced by <a href="#">hclust</a> .
maxTreeHeight	Maximum joining height of objects to be considered part of clusters.
deepSplit	If TRUE, method will favor sensitivity and produce more smaller clusters. When FALSE, there will be fewer bigger clusters.
minModuleSize	Minimum module size. Branches containing fewer than minModuleSize objects will be left unlabeled.

**Details**

A variable height branch pruning technique for dendrograms produced by hierarchical clustering. Initially, branches are cut off at the height `maxTreeHeight`; the resulting clusters are then examined for substructure and if subclusters are detected, they are assigned separate labels. Subclusters are detected by structure and are required to have a minimum of `minModuleSize` objects on them to be assigned a separate label. A rough degree of control over what it means to be a subcluster is implemented by the parameter `deepSplit`.

**Value**

A vector of numerical labels giving assignment of objects to modules. Unassigned objects are labeled 0, the largest module has label 1, next largest 2 etc.

**Author(s)**

Bin Zhang, <[binzhang.ucla@gmail.com](mailto:binzhang.ucla@gmail.com)>, with contributions by Peter Langfelder, <[Peter.Langfelder@gmail.com](mailto:Peter.Langfelder@gmail.com)>

**References**

<http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/BranchCutting>

**See Also**

[hclust](#), [cutreeHybrid](#)

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cutreeHybrid	<i>Hybrid adaptive tree cut for hierarchical clustering dendrograms.</i>
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**Description**

Detect clusters in a dendrogram produced by the function `hclust`.

**Usage**

```
cutreeHybrid(dendro, distM, cutHeight = NULL, minClusterSize = 20,
             deepSplit = 1,
             maxCoreScatter = NULL, minGap = NULL,
             maxAbsCoreScatter = NULL, minAbsGap = NULL,
             pamStage = TRUE, pamRespectsDendro = TRUE,
             useMedoids = FALSE, maxDistToLabel = cutHeight,
             respectSmallClusters = TRUE, verbose = 2, indent = 0)
```

**Arguments**

<code>dendro</code>	a hierarchical clustering dendrogram such as one returned by <code>hclust</code> .
<code>distM</code>	Distance matrix that was used as input to <code>hclust</code> .
<code>cutHeight</code>	Maximum joining heights that will be considered. It defaults to 99 of the range between the 5th percentile and the maximum of the joining heights on the dendrogram.
<code>minClusterSize</code>	Minimum cluster size.
<code>deepSplit</code>	Either logical or integer in the range 0 to 4. Provides a rough control over sensitivity to cluster splitting. The higher the value, the more and smaller clusters will be produced. A finer control can be achieved via <code>maxCoreScatter</code> and <code>minGap</code> below.
<code>maxCoreScatter</code>	Maximum scatter of the core for a branch to be a cluster, given as the fraction of <code>cutHeight</code> relative to the 5th percentile of joining heights. See Details.
<code>minGap</code>	Minimum cluster gap given as the fraction of the difference between <code>cutHeight</code> and the 5th percentile of joining heights.
<code>maxAbsCoreScatter</code>	Maximum scatter of the core for a branch to be a cluster given as absolute heights. If given, overrides <code>maxCoreScatter</code> .

<code>minAbsGap</code>	Minimum cluster gap given as absolute height difference. If given, overrides <code>minGap</code> .
<code>pamStage</code>	Logical, only used for method "hybrid". If TRUE, the second (PAM-like) stage will be performed.
<code>pamRespectsDendro</code>	Logical, only used for method "hybrid". If TRUE, the PAM stage will respect the dendrogram in the sense an object can be PAM-assigned only to clusters that lie below it on the branch that the object is merged into. See <a href="#">cutreeDynamic</a> for more details.
<code>useMedoids</code>	if TRUE, the second stage will be use object to medoid distance; if FALSE, it will use average object to cluster distance. The default (FALSE) is recommended.
<code>maxDistToLabel</code>	Maximum object distance to closest cluster that will result in the object assigned to that cluster.
<code>respectSmallClusters</code>	If TRUE, branches that failed to be clusters in stage 1 only because of insufficient size will be assigned together in stage 2. If FALSE, all objects will be assigned individually.
<code>verbose</code>	Controls the verbosity of the output. 0 will make the function completely quiet, values up to 4 gradually increase verbosity.
<code>indent</code>	Controls indentation of printed messages (see <code>verbose</code> above). Each unit adds two spaces before printed messages; useful when several functions' output is to be nested.

## Details

The function detects clusters in a hierarchical dendrogram based on the shape of branches on the dendrogram. For details on the method, see <http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/BranchCutting>.

In order to make the shape parameters `maxCoreScatter` and `minGap` more universal, their values are interpreted relative to `cutHeight` and the 5th percetile of the merging heights (we arbitrarily chose the 5th percetile rather than the minimum for reasons of stability). Thus, the absolute maximum allowable core scatter is calculated as  $\text{maxCoreScatter} * (\text{cutHeight} - \text{refHeight}) + \text{refHeight}$  and the absolute minimum allowable gap as  $\text{minGap} * (\text{cutHeight} - \text{refHeight})$ , where `refHeight` is the 5th percentile of the merging heights.

## Value

A list containing the following elements:

<code>labels</code>	Numerical labels of clusters, with 0 meaning unassigned, label 1 labeling the largest cluster etc.
<code>cores</code>	Numerical labels indicating cores of found clusters.
<code>smallLabels</code>	Numerical labels for branches that failed to be recognized clusters only because of insufficient number of objects.
<code>trimmed</code>	Numerical labels indicating objects that have been trimmed from clusters.
<code>branches</code>	A list detailing the detected branch structure.

**Author(s)**

Peter Langfelder, <Peter.Langfelder@gmail.com>

**References**

Langfelder P, Zhang B, Horvath S, 2007. <http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/BranchCutting>

**See Also**

`hclust`, `as.dist`

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indentSpaces      *Spaces for indented output.*

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**Description**

Returns a character string containing two times indent spaces.

**Usage**

```
indentSpaces(indent = 0)
```

**Arguments**

indent      Desired level of indentation. The number of returned spaces will be twice this argument.

**Value**

A character string containing spaces, of length twice indent.

**Author(s)**

Peter Langfelder, <Peter.Langfelder@gmail.com>

**Examples**

```
spaces = indentSpaces(0);
print(paste(spaces, "This output is not indented..."));
spaces = indentSpaces(1);
print(paste(spaces, "...while this one is."))
```

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merge2Clusters      *Merge two clusters.*

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**Description**

Merge 2 clusters into 1.

**Usage**

```
merge2Clusters(labels, mainClusterLabel, minorClusterLabel)
```

**Arguments**

labels            a vector or factor giving the cluster labels  
mainClusterLabel            label of the first merged cluster. The merged cluster will have this label.  
minorClusterLabel            label of the second merged cluster.

**Value**

A vector or factor of the merged labels.

**Author(s)**

Bin Zhang and Peter Langfelder

**Examples**

```
options(stringsAsFactors = FALSE);

# Works with character labels:
labels = c(rep("grey", 5), rep("blue", 2), rep("red", 3))
merge2Clusters(labels, "blue", "red")

# Works with factor labels:
labelsF = factor(labels)
merge2Clusters(labelsF, "blue", "red")

# Works also with numeric labels:

labelsN = as.numeric(factor(labels))
labelsN
merge2Clusters(labelsF, 1, 3)
```

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<code>printFlush</code>	<i>Print arguments and flush the console.</i>
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**Description**

Passes all its arguments unchanged to the standard `print` function; after the execution of `print` it flushes the console, if possible.

**Usage**

```
printFlush(...)
```

**Arguments**

... Arguments to be passed to the standard `print` function.

**Details**

Passes all its arguments unchanged to the standard `print` function; after the execution of `print` it flushes the console, if possible.

**Value**

Returns the value of the `print` function.

**Author(s)**

Peter Langfelder, <Peter.Langfelder@gmail.com>

**See Also**

`print`

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