# Package ‘BHC’

## April 25, 2017

**Type** Package  
**Title** Bayesian Hierarchical Clustering  
**Version** 1.28.0  
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**Description**  
The method performs bottom-up hierarchical clustering, using a Dirichlet Process (infinite mixture) to model uncertainty in the data and Bayesian model selection to decide at each step which clusters to merge. This avoids several limitations of traditional methods, for example how many clusters there should be and how to choose a principled distance metric. This implementation accepts multinomial (i.e. discrete, with 2+ categories) or time-series data. This version also includes a randomised algorithm which is more efficient for larger data sets.

**License** GPL-3  
**biocViews** Microarray, Clustering  
**NeedsCompilation** yes

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<td>Function to perform Bayesian Hierarchical Clustering on a 2D array of discretised (i.e. multinomial) data</td>
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**Description**  
The method performs bottom-up hierarchical clustering, using a Dirichlet Process (infinite mixture) to model uncertainty in the data and Bayesian model selection to decide at each step which clusters to merge. This avoids several limitations of traditional methods, for example how many clusters there should be and how to choose a principled distance metric. This implementation accepts multinomial (i.e. discrete, with 2+ categories) or time-series data. This version also includes a randomised algorithm which is more efficient for larger data sets.
Usage

```
bhc(data, itemLabels, nFeatureValues, timePoints, dataType, 
    noise, numReps, noiseMode, robust, numThreads, randomised, m, verbose)
```

Arguments

data  
A 2D array containing discretised data. The dimensions of `data` should be `nDataItems * nFeatures`, and the algorithm will cluster the data items.

itemLabels  
A character array containing `nDataItems` entries, one for each data item in the analysis. The leaf nodes of the output dendrogram will be labelled with these labels.

nFeatureValues  
Deprecated. This is a legacy argument, retained for backwards compatibility. Any value passed to it will have no effect.

timePoints  
An array of length `nFeatures`, containing the time points of the measurements.

dataType  
A string specifying the data type. Either `"multinomial"`, `"time-course"`, or `"cubicspline"`.

noise  
Noise term for each gene, required only if `noiseMode=2`. The noise term for each gene is calculated as

\[
\frac{\sum (\text{residuals}^2)}{(\text{number of observations for gene} - 1)(\text{number of replicates})}
\]

where (number of observations for gene) is typically (number of time points * number of replicates).

numReps  
Number of replicates per observation.

noiseMode  
Noise mode. If 0 then fitted noise; 2 estimated noise from replicates.

robust  
0 to use single Gaussian likelihood, 1 to use mixture likelihood.

numThreads  
The BHC library has been parallelised using OpenMP (currently on UNIX systems only). Specify here the number of threads to use (the default value is 1).

randomised  
Set to TRUE if you wish to use the randomised algorithm.

m  
If randomised is set to TRUE, then this is the dimension of the randomly chosen subset $D_m$ in the randomised algorithm.

verbose  
If set to TRUE, the algorithm will output some information to screen as it runs.

Details

Typical usage for the multinomial case:

```
bhc(data, itemLabels).
```

To use the squared-exponential covariance:

```
bhc(data, itemLabels, 0, timePoints, "time-course", 
    noise, numReps, noiseMode),
```

and the cubic spline covariance:

```
bhc(data, itemLabels, 0, timePoints, "cubicspline", 
    noise, numReps, noiseMode).
```

To use the randomised algorithm, simply include the following two arguments:

```
bhc(data, itemLabels, 0, timePoints, "time-course", 
    noise, numReps, noiseMode, randomised=TRUE, m=10)
```
Value

A DENDROGRAM object (see the R stats package for details).

Author(s)

Rich Savage, Emma Cooke, Robert Darkins, and Yang Xu

References

Bayesian Hierarchical Clustering, Heller + Ghahramani, Gatsby Unit Technical Report GCNU-TR 2005-002 (2005); also see shorter version in ICML-2005; R/BHC: fast Bayesian hierarchical clustering for microarray data, Savage et al, BMC Bioinformatics 10:242 (2009); Bayesian hierarchical clustering for microarray time series data with replicates and outlier measurements, Cooke et al, currently under review

See Also

hclust

Examples

```r
##BUILD SAMPLE DATA AND LABELS
data <- matrix(0,15,10)
itemLabels <- vector("character",15)
data[1:5,] <- 1 ; itemLabels[1:5] <- "a"
data[6:10,] <- 2 ; itemLabels[6:10] <- "b"
timePoints <- 1:10 # for the time-course case

##DATA DIMENSIONS
nDataItems <- nrow(data)
nFeatures <- ncol(data)

##RUN MULTINOMIAL CLUSTERING
hc1 <- bhc(data, itemLabels, verbose=TRUE)
plot(hc1, axes=FALSE)

##RUN TIME-COURSE CLUSTERING
hc2 <- bhc(data, itemLabels, 0, timePoints, "time-course",
    numReps=1, noiseMode=0, numThreads=2, verbose=TRUE)
plot(hc2, axes=FALSE)

##OUTPUT CLUSTER LABELS TO FILE
WriteOutClusterLabels(hc1, "labels.txt", verbose=TRUE)

##FOR THE MULTINOMIAL CASE, THE DATA CAN BE DISCRETISED
newData <- data[] + rnorm(150, 0, 0.1);
percentiles <- FindOptimalBinning(newData, itemLabels, transposeData=TRUE, verbose=TRUE)
discreteData <- DiscretiseData(t(newData), percentiles=percentiles)
discreteData <- t(discreteData)
hc3 <- bhc(discreteData, itemLabels, verbose=TRUE)
plot(hc3, axes=FALSE)
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