Package 'BHC'

April 12, 2022

Type Package

Title Bayesian Hierarchical Clustering

Version 1.46.0

Date 2011-09-07

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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.

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biocViews Microarray, Clustering

git_url https://git.bioconductor.org/packages/BHC

git_branch RELEASE_3_14

git_last_commit b3bffd8

git_last_commit_date 2021-10-26

Date/Publication 2022-04-12

R topics documented:

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bhc   *Function to perform Bayesian Hierarchical Clustering on a 2D array*
                             of discretised (i.e. multinomial) data

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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 UN*X 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

```
##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"
data[11:15,] <- 3 ; itemLabels[11:15] <- "c"
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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