

# Bayesian Hierarchical Clustering

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This is a simple Sweave test of the Bayesian Hierarchical Clustering method, as implemented in the R package *BHC*. It runs the example code as given in the R help file and generates a resulting dendrogram plot, to show the sort of results one can expect.

```
> require(BHC)
> ##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)

[1] Running Bayesian Hierarchical Clustering....
[1] "DataType: multinomial"
[1] Optimising global hyperparameter...
[1] 0.7642338 -88.7830929
[1] 1.236254 -99.514068
[1] 0.4309005 -79.1391819
[1] 0.4309005 -79.1391819
[1] 0.4309005 -79.1391819
[1] Hyperparameter: 0.430900452187475
[1] Lower bound on overall LogEvidence: -7.9139e+01
[1] *****

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

[1] Running Bayesian Hierarchical Clustering....
[1] "DataType: time-course"
[1] 0.0000 242.4406
[1] Hyperparameter: 0
[1] Lower bound on overall LogEvidence: 2.4244e+02
[1] *****

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

```

[1] ---CLUSTER 1 ---
[1] c
[1] c
[1] c
[1] c
[1] c
[1] ---CLUSTER 2 ---
[1] a
[1] a
[1] a
[1] a
[1] a
[1] ---CLUSTER 3 ---
[1] b
[1] b
[1] b
[1] b
[1] b

> ##FOR THE MULTINOMIAL CASE, THE DATA CAN BE DISCRETISED
> newData      <- data[] + rnorm(150, 0, 0.1);
> percentiles  <- FindOptimalBinning(newData, itemLabels, transposeData=TRUE, verbose=TRUE)

DATA DISCRETISATION
-----
Percentiles: 0.1 0.8 0.1
We have the following parameters for the data array:
nGenes:      15
nExperiments: 10
***Please check that these are the right way round! (it affects the discretisation)***

Discretisation logEvidence: 245.593187777093
(Need to add this to the model logEvidence)
-----
[1] Running Bayesian Hierarchical Clustering....
[1] "DataType: multinomial"
[1] Optimising global hyperparameter...
[1] 782.5754 -100.3550
[1] 1265.9246 -100.3267
[1] 1564.651 -100.318
[1] 1806.2716 -100.3131
[1] 1898.6036 -100.3115
[1] 1955.6680 -100.3106
[1] 1990.9357 -100.3101
[1] 2012.7323 -100.3098
[1] 2026.2034 -100.3096
[1] 2034.5289 -100.3095
[1] 2039.6744 -100.3094
[1] 2042.8545 -100.3093
[1] 2044.8199 -100.3093
[1] 2046.0346 -100.3093
[1] 2046.7853 -100.3093
[1] 2047.2493 -100.3093
[1] 2047.5826 -100.3093

```

```
[1] 2047.5826 -100.3093
[1] 2047.5826 -100.3093
[1] Hyperparameter: 2047.58264717158
[1] Lower bound on overall LogEvidence: -1.0031e+02
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.15 0.7 0.15

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 314.954339639011

(Need to add this to the model logEvidence)

-----

```
[1] Running Bayesian Hierarchical Clustering....
```

```
[1] "DataType: multinomial"
```

```
[1] Optimising global hyperparameter...
```

```
[1] 782.5754 -143.8307
```

```
[1] 1265.9246 -143.7785
```

```
[1] 1564.6508 -143.7624
```

```
[1] 1808.0122 -143.7532
```

```
[1] 1715.0564 -143.7564
```

```
[1] 1899.6794 -143.7503
```

```
[1] 1956.3328 -143.7487
```

```
[1] 1991.3466 -143.7477
```

```
[1] 2012.9863 -143.7471
```

```
[1] 2026.3603 -143.7468
```

```
[1] 2034.6259 -143.7466
```

```
[1] 2039.7344 -143.7464
```

```
[1] 2042.8916 -143.7463
```

```
[1] 2044.8428 -143.7463
```

```
[1] 2046.0488 -143.7463
```

```
[1] 2046.7941 -143.7462
```

```
[1] 2047.2547 -143.7462
```

```
[1] 2047.5881 -143.7462
```

```
[1] 2047.5881 -143.7462
```

```
[1] 2047.5881 -143.7462
```

```
[1] Hyperparameter: 2047.58805303031
```

```
[1] Lower bound on overall LogEvidence: -1.4375e+02
```

```
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.2 0.6 0.2

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 314.954339639011

(Need to add this to the model logEvidence)

```

-----
[1] Running Bayesian Hierarchical Clustering....
[1] "DataType: multinomial"
[1] Optimising global hyperparameter...
[1] 782.5754 -143.8307
[1] 1265.9246 -143.7785
[1] 1564.6508 -143.7624
[1] 1808.0122 -143.7532
[1] 1715.0564 -143.7564
[1] 1899.6794 -143.7503
[1] 1956.3328 -143.7487
[1] 1991.3466 -143.7477
[1] 2012.9863 -143.7471
[1] 2026.3603 -143.7468
[1] 2034.6259 -143.7466
[1] 2039.7344 -143.7464
[1] 2042.8916 -143.7463
[1] 2044.8428 -143.7463
[1] 2046.0488 -143.7463
[1] 2046.7941 -143.7462
[1] 2047.2547 -143.7462
[1] 2047.5881 -143.7462
[1] 2047.5881 -143.7462
[1] 2047.5881 -143.7462
[1] Hyperparameter: 2047.58805303031
[1] Lower bound on overall LogEvidence: -1.4375e+02
[1] *****

```

DATA DISCRETISATION

```

-----
Percentiles: 0.25 0.5 0.25
We have the following parameters for the data array:
nGenes:      15
nExperiments: 10
***Please check that these are the right way round! (it affects the discretisation)***

```

```

Discretisation logEvidence: 314.954339639011
(Need to add this to the model logEvidence)

```

```

-----
[1] Running Bayesian Hierarchical Clustering....
[1] "DataType: multinomial"
[1] Optimising global hyperparameter...
[1] 782.5754 -143.8307
[1] 1265.9246 -143.7785
[1] 1564.6508 -143.7624
[1] 1808.0122 -143.7532
[1] 1715.0564 -143.7564
[1] 1899.6794 -143.7503
[1] 1956.3328 -143.7487
[1] 1991.3466 -143.7477
[1] 2012.9863 -143.7471
[1] 2026.3603 -143.7468
[1] 2034.6259 -143.7466
[1] 2039.7344 -143.7464

```

```
[1] 2042.8916 -143.7463
[1] 2044.8428 -143.7463
[1] 2046.0488 -143.7463
[1] 2046.7941 -143.7462
[1] 2047.2547 -143.7462
[1] 2047.5881 -143.7462
[1] 2047.5881 -143.7462
[1] 2047.5881 -143.7462
[1] Hyperparameter: 2047.58805303031
[1] Lower bound on overall LogEvidence: -1.4375e+02
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.3 0.4 0.3

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068

(Need to add this to the model logEvidence)

-----

```
[1] Running Bayesian Hierarchical Clustering....
```

```
[1] "DataType: multinomial"
```

```
[1] Optimising global hyperparameter...
```

```
[1] 782.5754 -163.5695
```

```
[1] 1265.9246 -163.5086
```

```
[1] 1564.6508 -163.4898
```

```
[1] 1808.379 -163.479
```

```
[1] 1715.2829 -163.4827
```

```
[1] 1899.9058 -163.4756
```

```
[1] 1956.4728 -163.4737
```

```
[1] 1991.4331 -163.4726
```

```
[1] 2013.0397 -163.4719
```

```
[1] 2026.3934 -163.4715
```

```
[1] 2034.6464 -163.4713
```

```
[1] 2039.7470 -163.4711
```

```
[1] 2042.899 -163.471
```

```
[1] 2044.848 -163.471
```

```
[1] 2046.0517 -163.4709
```

```
[1] 2046.7959 -163.4709
```

```
[1] 2047.2558 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] Hyperparameter: 2047.58919090977
```

```
[1] Lower bound on overall LogEvidence: -1.6347e+02
```

```
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.35 0.3 0.35

We have the following parameters for the data array:

nGenes: 15  
nExperiments: 10  
\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 330.762433206533  
(Need to add this to the model logEvidence)

-----  
[1] Running Bayesian Hierarchical Clustering....  
[1] "DataType: multinomial"  
[1] Optimising global hyperparameter...  
[1] 782.5754 -158.8043  
[1] 1265.9246 -158.7461  
[1] 1564.6508 -158.7281  
[1] 1808.2878 -158.7178  
[1] 1715.2267 -158.7214  
[1] 1899.8497 -158.7146  
[1] 1956.4381 -158.7128  
[1] 1991.4116 -158.7117  
[1] 2013.0265 -158.7111  
[1] 2026.3852 -158.7107  
[1] 2034.6413 -158.7104  
[1] 2039.7439 -158.7103  
[1] 2042.8974 -158.7102  
[1] 2044.8464 -158.7101  
[1] 2046.0510 -158.7101  
[1] 2046.7954 -158.7101  
[1] 2047.2555 -158.7101  
[1] 2047.5889 -158.7101  
[1] 2047.5889 -158.7101  
[1] 2047.5889 -158.7101  
[1] Hyperparameter: 2047.58890870463  
[1] Lower bound on overall LogEvidence: -1.5871e+02  
[1] \*\*\*\*\*

#### DATA DISCRETISATION

-----  
Percentiles: 0.26 0.48 0.26  
We have the following parameters for the data array:  
nGenes: 15  
nExperiments: 10  
\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068  
(Need to add this to the model logEvidence)

-----  
[1] Running Bayesian Hierarchical Clustering....  
[1] "DataType: multinomial"  
[1] Optimising global hyperparameter...  
[1] 782.5754 -163.5695  
[1] 1265.9246 -163.5086  
[1] 1564.6508 -163.4898  
[1] 1808.379 -163.479  
[1] 1715.2829 -163.4827  
[1] 1899.9058 -163.4756

```
[1] 1956.4728 -163.4737
[1] 1991.4331 -163.4726
[1] 2013.0397 -163.4719
[1] 2026.3934 -163.4715
[1] 2034.6464 -163.4713
[1] 2039.7470 -163.4711
[1] 2042.899 -163.471
[1] 2044.848 -163.471
[1] 2046.0517 -163.4709
[1] 2046.7959 -163.4709
[1] 2047.2558 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] Hyperparameter: 2047.58919090977
[1] Lower bound on overall LogEvidence: -1.6347e+02
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.27 0.46 0.27

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068

(Need to add this to the model logEvidence)

-----

```
[1] Running Bayesian Hierarchical Clustering....
```

```
[1] "DataType: multinomial"
```

```
[1] Optimising global hyperparameter...
```

```
[1] 782.5754 -163.5695
```

```
[1] 1265.9246 -163.5086
```

```
[1] 1564.6508 -163.4898
```

```
[1] 1808.379 -163.479
```

```
[1] 1715.2829 -163.4827
```

```
[1] 1899.9058 -163.4756
```

```
[1] 1956.4728 -163.4737
```

```
[1] 1991.4331 -163.4726
```

```
[1] 2013.0397 -163.4719
```

```
[1] 2026.3934 -163.4715
```

```
[1] 2034.6464 -163.4713
```

```
[1] 2039.7470 -163.4711
```

```
[1] 2042.899 -163.471
```

```
[1] 2044.848 -163.471
```

```
[1] 2046.0517 -163.4709
```

```
[1] 2046.7959 -163.4709
```

```
[1] 2047.2558 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] Hyperparameter: 2047.58919090977
```

```
[1] Lower bound on overall LogEvidence: -1.6347e+02
```

[1] \*\*\*\*\*

DATA DISCRETISATION

-----

Percentiles: 0.28 0.44 0.28

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068

(Need to add this to the model logEvidence)

-----

[1] Running Bayesian Hierarchical Clustering....

[1] "DataType: multinomial"

[1] Optimising global hyperparameter...

[1] 782.5754 -163.5695

[1] 1265.9246 -163.5086

[1] 1564.6508 -163.4898

[1] 1808.379 -163.479

[1] 1715.2829 -163.4827

[1] 1899.9058 -163.4756

[1] 1956.4728 -163.4737

[1] 1991.4331 -163.4726

[1] 2013.0397 -163.4719

[1] 2026.3934 -163.4715

[1] 2034.6464 -163.4713

[1] 2039.7470 -163.4711

[1] 2042.899 -163.471

[1] 2044.848 -163.471

[1] 2046.0517 -163.4709

[1] 2046.7959 -163.4709

[1] 2047.2558 -163.4709

[1] 2047.5892 -163.4709

[1] 2047.5892 -163.4709

[1] 2047.5892 -163.4709

[1] Hyperparameter: 2047.58919090977

[1] Lower bound on overall LogEvidence: -1.6347e+02

[1] \*\*\*\*\*

DATA DISCRETISATION

-----

Percentiles: 0.29 0.42 0.29

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068

(Need to add this to the model logEvidence)

-----

[1] Running Bayesian Hierarchical Clustering....

[1] "DataType: multinomial"

[1] Optimising global hyperparameter...



```

[1] 782.5754 -163.5695
[1] 1265.9246 -163.5086
[1] 1564.6508 -163.4898
[1] 1808.379 -163.479
[1] 1715.2829 -163.4827
[1] 1899.9058 -163.4756
[1] 1956.4728 -163.4737
[1] 1991.4331 -163.4726
[1] 2013.0397 -163.4719
[1] 2026.3934 -163.4715
[1] 2034.6464 -163.4713
[1] 2039.7470 -163.4711
[1] 2042.899 -163.471
[1] 2044.848 -163.471
[1] 2046.0517 -163.4709
[1] 2046.7959 -163.4709
[1] 2047.2558 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] Hyperparameter: 2047.58919090977
[1] Lower bound on overall LogEvidence: -1.6347e+02
[1] *****

```

#### DATA DISCRETISATION

-----

Percentiles: 0.3 0.4 0.3

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068

(Need to add this to the model logEvidence)

-----

```

[1] Running Bayesian Hierarchical Clustering....

```

```

[1] "DataType: multinomial"

```

```

[1] Optimising global hyperparameter...

```

```

[1] 782.5754 -163.5695

```

```

[1] 1265.9246 -163.5086

```

```

[1] 1564.6508 -163.4898

```

```

[1] 1808.379 -163.479

```

```

[1] 1715.2829 -163.4827

```

```

[1] 1899.9058 -163.4756

```

```

[1] 1956.4728 -163.4737

```

```

[1] 1991.4331 -163.4726

```

```

[1] 2013.0397 -163.4719

```

```

[1] 2026.3934 -163.4715

```

```

[1] 2034.6464 -163.4713

```

```

[1] 2039.7470 -163.4711

```

```

[1] 2042.899 -163.471

```

```

[1] 2044.848 -163.471

```

```

[1] 2046.0517 -163.4709

```

```

[1] 2046.7959 -163.4709

```

```
[1] 2047.2558 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] Hyperparameter: 2047.58919090977
[1] Lower bound on overall LogEvidence: -1.6347e+02
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.31 0.38 0.31

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068

(Need to add this to the model logEvidence)

-----

```
[1] Running Bayesian Hierarchical Clustering....
```

```
[1] "DataType: multinomial"
```

```
[1] Optimising global hyperparameter...
```

```
[1] 782.5754 -163.5695
```

```
[1] 1265.9246 -163.5086
```

```
[1] 1564.6508 -163.4898
```

```
[1] 1808.379 -163.479
```

```
[1] 1715.2829 -163.4827
```

```
[1] 1899.9058 -163.4756
```

```
[1] 1956.4728 -163.4737
```

```
[1] 1991.4331 -163.4726
```

```
[1] 2013.0397 -163.4719
```

```
[1] 2026.3934 -163.4715
```

```
[1] 2034.6464 -163.4713
```

```
[1] 2039.7470 -163.4711
```

```
[1] 2042.899 -163.471
```

```
[1] 2044.848 -163.471
```

```
[1] 2046.0517 -163.4709
```

```
[1] 2046.7959 -163.4709
```

```
[1] 2047.2558 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] 2047.5892 -163.4709
```

```
[1] Hyperparameter: 2047.58919090977
```

```
[1] Lower bound on overall LogEvidence: -1.6347e+02
```

```
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.32 0.36 0.32

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068  
(Need to add this to the model logEvidence)

```
-----  
[1] Running Bayesian Hierarchical Clustering....  
[1] "DataType: multinomial"  
[1] Optimising global hyperparameter...  
[1] 782.5754 -163.5695  
[1] 1265.9246 -163.5086  
[1] 1564.6508 -163.4898  
[1] 1808.379 -163.479  
[1] 1715.2829 -163.4827  
[1] 1899.9058 -163.4756  
[1] 1956.4728 -163.4737  
[1] 1991.4331 -163.4726  
[1] 2013.0397 -163.4719  
[1] 2026.3934 -163.4715  
[1] 2034.6464 -163.4713  
[1] 2039.7470 -163.4711  
[1] 2042.899 -163.471  
[1] 2044.848 -163.471  
[1] 2046.0517 -163.4709  
[1] 2046.7959 -163.4709  
[1] 2047.2558 -163.4709  
[1] 2047.5892 -163.4709  
[1] 2047.5892 -163.4709  
[1] 2047.5892 -163.4709  
[1] Hyperparameter: 2047.58919090977  
[1] Lower bound on overall LogEvidence: -1.6347e+02  
[1] *****
```

#### DATA DISCRETISATION

```
-----  
Percentiles: 0.33 0.34 0.33  
We have the following parameters for the data array:  
nGenes: 15  
nExperiments: 10  
***Please check that these are the right way round! (it affects the discretisation)***
```

Discretisation logEvidence: 341.970650993068  
(Need to add this to the model logEvidence)

```
-----  
[1] Running Bayesian Hierarchical Clustering....  
[1] "DataType: multinomial"  
[1] Optimising global hyperparameter...  
[1] 782.5754 -163.5695  
[1] 1265.9246 -163.5086  
[1] 1564.6508 -163.4898  
[1] 1808.379 -163.479  
[1] 1715.2829 -163.4827  
[1] 1899.9058 -163.4756  
[1] 1956.4728 -163.4737  
[1] 1991.4331 -163.4726  
[1] 2013.0397 -163.4719  
[1] 2026.3934 -163.4715
```

```
[1] 2034.6464 -163.4713
[1] 2039.7470 -163.4711
[1] 2042.899 -163.471
[1] 2044.848 -163.471
[1] 2046.0517 -163.4709
[1] 2046.7959 -163.4709
[1] 2047.2558 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] Hyperparameter: 2047.58919090977
[1] Lower bound on overall LogEvidence: -1.6347e+02
[1] *****
```

#### DATA DISCRETISATION

-----

Percentiles: 0.34 0.32 0.34

We have the following parameters for the data array:

nGenes: 15

nExperiments: 10

\*\*\*Please check that these are the right way round! (it affects the discretisation)\*\*\*

Discretisation logEvidence: 341.970650993068

(Need to add this to the model logEvidence)

-----

```
[1] Running Bayesian Hierarchical Clustering....
[1] "DataType: multinomial"
[1] Optimising global hyperparameter...
[1] 782.5754 -163.5695
[1] 1265.9246 -163.5086
[1] 1564.6508 -163.4898
[1] 1808.379 -163.479
[1] 1715.2829 -163.4827
[1] 1899.9058 -163.4756
[1] 1956.4728 -163.4737
[1] 1991.4331 -163.4726
[1] 2013.0397 -163.4719
[1] 2026.3934 -163.4715
[1] 2034.6464 -163.4713
[1] 2039.7470 -163.4711
[1] 2042.899 -163.471
[1] 2044.848 -163.471
[1] 2046.0517 -163.4709
[1] 2046.7959 -163.4709
[1] 2047.2558 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] 2047.5892 -163.4709
[1] Hyperparameter: 2047.58919090977
[1] Lower bound on overall LogEvidence: -1.6347e+02
[1] *****
```

#### OPTIMISED DISCRETISATION

-----

```

Percentiles: 0.3 0.4 0.3
LogEvidence: 178.4998

> discreteData <- DiscretiseData(t(newData), percentiles=percentiles)

DATA DISCRETISATION
-----
Percentiles: 0.3 0.4 0.3
We have the following parameters for the data array:
nGenes:      10
nExperiments: 15
***Please check that these are the right way round! (it affects the discretisation)***

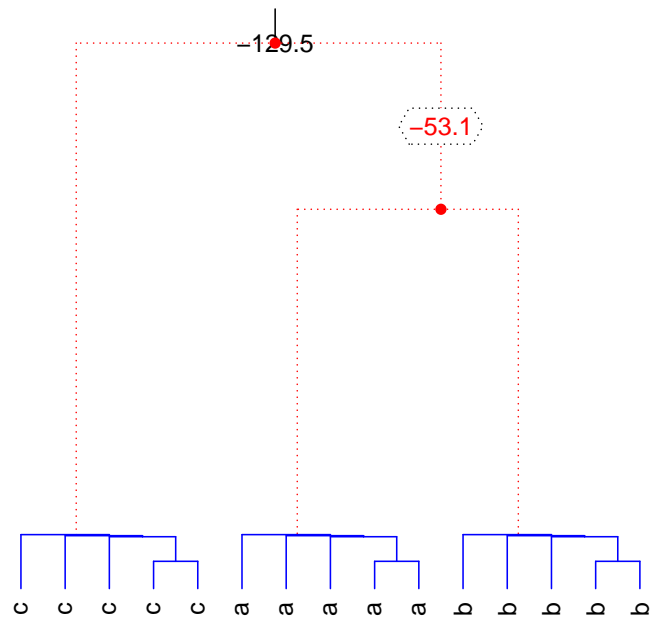
Discretisation logEvidence: 87.1282413568208
(Need to add this to the model logEvidence)
-----

> discreteData <- t(discreteData)
> hc3          <- bhc(discreteData, itemLabels, verbose=TRUE)

[1] Running Bayesian Hierarchical Clustering...
[1] "DataType: multinomial"
[1] Optimising global hyperparameter...
[1] 0.8411863 -115.5340881
[1] 1.283814 -121.370976
[1] 0.5078529 -111.1444609
[1] 0.5078529 -111.1444609
[1] 0.5078529 -111.1444609
[1] Hyperparameter: 0.507852925225962
[1] Lower bound on overall LogEvidence: -1.1114e+02
[1] *****

>

```



The plot shows a simple example dendrogram. (note that the structure is quite distinctive; this may be the result of discretising and analysing a small data-set).