Software Manual

Institute of Bioinformatics, Johannes Kepler University Linz

fabiaData (Gene Expression Data Sets for Biclustering)

— Manual for the R package —

Sepp Hochreiter

Institute of Bioinformatics, Johannes Kepler University Linz
Altenberger Str. 69, 4040 Linz, Austria
hochreit@bioinf.jku.at

Version 1.52.0, November 25, 2026

Contents

1 Introduction **3**

2 Getting Started: fabiaData **3**

3 Data Sets **4**
3.1 Breast_A 4
3.2 DLBCL_B 4
3.3 Multi_A 4

4 Demos **5**

1 Introduction

The `fabiaData` package is part of the Bioconductor (http://www.bioconductor.org) project. The package provides gene expression data sets for biclustering demos in the R package `fabia`. It is automatically loaded by `fabia` when needed.

The package `fabia` allows to extract biclusters from data sets based on a generative model according to the FABIA method (Hochreiter *et al.*, 2010). It has been designed especially for microarray data sets, but can be used for other kinds of data sets as well.

Please visit for additional information the FABIA homepage http://www.bioinf.jku.at/software/fabia/fabia.html.

2 Getting Started: fabiaData

First load the `fabia` package:

```
R> library(fabia)
```

Then load the `fabiaData` package

```
R> library(fabiaData)
```

Now biclusters can be extracted from these data sets in the fabia demos:

```
R> fabiaDemo()
```

1. demo2: Microarray data set of (van't Veer *et al.*, 2002) on breast cancer.

   ```
   R> fabiaDemo()
   ```

   Choose "2" to extract subclasses in the data set of van't Veer as biclusters.

2. demo3: Microarray data set of (Su *et al.*, 2002) on different mammalian.

   ```
   R> fabiaDemo()
   ```

   Choose "3" to check whether the different mouse and human tissue types can be extracted.

3. demo4: Microarray data set of (Rosenwald *et al.*, 2002) diffuse large-B-cell lymphoma. (Hoshida *et al.*, 2007) divided the data set into three classes

   - OxPhos: oxidative phosphorylation
   - BCR: B-cell response
   - HR: host response

   ```
   R> fabiaDemo()
   ```

   Choose "4" to check whether the different classes can be extracted.

3 Data Sets

3.1 Breast_A

Microarray data set of van't Veer breast cancer.

Microarray data from Broad Institute "Cancer Program Data Sets" which was produced by (van't Veer *et al.*, 2002) (`http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi`) Array S54 was removed because it is an outlier.

Goal was to find a gene signature to predict the outcome of a cancer therapy that is to predict whether metastasis will occur. A 70 gene signature has been discovered.

Here we want to find subclasses in the data set.

(Hoshida *et al.*, 2007) found 3 subclasses and verified that 50/61 cases from class 1 and 2 were ER positive and only in 3/36 from class 3.

`XBreast` is the data set with 97 samples and 1213 genes, `CBreast` give the three subclasses from (Hoshida *et al.*, 2007).

3.2 DLBCL_B

Microarray data set of Rosenwald diffuse large-B-cell lymphoma.

Microarray data from Broad Institute "Cancer Program Data Sets" which was produced by (Rosenwald *et al.*, 2002) (`http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi`)

Goal was to predict the survival after chemotherapy

(Hoshida *et al.*, 2007) divided the data set into three classes:

- OxPhos: oxidative phosphorylation
- BCR: B-cell response
- HR: host response

We want to identify these subclasses.

The data has 180 samples and 661 probe sets (genes).

`XDLBCL` is the data set with 180 samples and 661 genes, `CDLBCL` give the three subclasses from (Hoshida *et al.*, 2007).

3.3 Multi_A

Microarray data set of Su on different mammalian tissue types.

Microarray data from Broad Institute "Cancer Program Data Sets" which was produced by (Su *et al.*, 2002) (`http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi`)

Gene expression from human and mouse samples across a diverse array of tissues, organs, and cell lines have been profiled. The goal was to have a reference for the normal mammalian transcriptome.

Here we want to identify the subclasses which correspond to the tissue types.

The data has 102 samples and 5565 probe sets (genes).

`XMulti` is the data set with 102 samples and 5565 genes, `CMulti` give the four subclasses corresponding to the tissue types.

4 Demos

```
library(fabiaData)


#----------------------------------------
##########################################
# fabia Demos
##########################################
#----------------------------------------

#----------------------------------------
# DEMO1: Laura van't Veer's gene expression
#        data set for breast cancer
#----------------------------------------

avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("#########################################################")
    message("Package 'fabia' is not available: please install.")
    message("#########################################################")
} else {

data(Breast_A)

X <- as.matrix(XBreast)


resBreast1 <- fabia(X,5,0.1,400,1.0,1.0)

rBreast1 <- extractPlot(resBreast1,ti="FABIA Breast cancer(Veer)")
```

```
raBreast1 <- extractBic(resBreast1)

if ((raBreast1$bic[[1]][1]>1) && (raBreast1$bic[[1]][2])>1) {
    plotBicluster(raBreast1,1)
}
if ((raBreast1$bic[[2]][1]>1) && (raBreast1$bic[[2]][2])>1) {
    plotBicluster(raBreast1,2)
}
if ((raBreast1$bic[[3]][1]>1) && (raBreast1$bic[[3]][2])>1) {
    plotBicluster(raBreast1,3)
}
if ((raBreast1$bic[[4]][1]>1) && (raBreast1$bic[[4]][2])>1) {
    plotBicluster(raBreast1,4)
}


plot(resBreast1,dim=c(1,2),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(1,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(1,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(1,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(2,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(2,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(2,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(3,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(3,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast1,dim=c(4,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)

}


#-----------------------------------
# DEMO2: Su's multiple tissue types
#        gene expression data set
#-----------------------------------


avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("#########################################################")
    message("Package 'fabia' is not available: please install.")
    message("#########################################################")
} else {
```

```
data(Multi_A)

X <- as.matrix(XMulti)

resMulti1 <- fabia(X,5,0.1,300,1.0,1.0)

rMulti1 <- extractPlot(resMulti1,ti="FABIA Multiple tissues(Su)")

raMulti1 <- extractBic(resMulti1)

if ((raMulti1$bic[[1]][1]>1) && (raMulti1$bic[[1]][2])>1) {
    plotBicluster(raMulti1,1)
}
if ((raMulti1$bic[[2]][1]>1) && (raMulti1$bic[[2]][2])>1) {
    plotBicluster(raMulti1,2)
}
if ((raMulti1$bic[[3]][1]>1) && (raMulti1$bic[[3]][2])>1) {
    plotBicluster(raMulti1,3)
}
if ((raMulti1$bic[[4]][1]>1) && (raMulti1$bic[[4]][2])>1) {
    plotBicluster(raMulti1,4)
}

plot(resMulti1,dim=c(1,2),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(1,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(1,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(1,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(2,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(2,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(2,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(3,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(3,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(4,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)

}



#----------------------------------------
# DEMO3: Rosenwald's diffuse large-B-cell
#        lymphoma gene expression data set
#----------------------------------------

avail <- require(fabia)
```

```
if (!avail) {
    message("")
    message("")
    message("########################################################")
    message("Package 'fabia' is not available: please install.")
    message("########################################################")
} else {

data(DLBCL_B)

X <- as.matrix(XDLBCL)

resDLBCL1 <- fabia(X,5,0.1,400,1.0,1.0)

rDLBCL1 <- extractPlot(resDLBCL1,ti="FABIA Lymphoma(Rosenwald)")

raDLBCL1 <- extractBic(resDLBCL1)

if ((raDLBCL1$bic[[1]][1]>1) && (raDLBCL1$bic[[1]][2])>1) {
    plotBicluster(raDLBCL1,1)
}
if ((raDLBCL1$bic[[2]][1]>1) && (raDLBCL1$bic[[2]][2])>1) {
    plotBicluster(raDLBCL1,2)
}
if ((raDLBCL1$bic[[3]][1]>1) && (raDLBCL1$bic[[3]][2])>1) {
    plotBicluster(raDLBCL1,3)
}
if ((raDLBCL1$bic[[4]][1]>1) && (raDLBCL1$bic[[4]][2])>1) {
    plotBicluster(raDLBCL1,4)
}

plot(resDLBCL1,dim=c(1,2),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(1,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(1,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(1,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(2,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(2,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(2,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(3,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(3,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL1,dim=c(4,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)

}


#----------------------------------------
```

```
##########################################
# fabias Demos
##########################################
#----------------------------------------

#----------------------------------------
# DEMO1: Laura van't Veer's gene expression
#        data set for breast cancer
#----------------------------------------

avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("#########################################################")
    message("Package 'fabia' is not available: please install.")
    message("#########################################################")
} else {


data(Breast_A)

X <- as.matrix(XBreast)

resBreast2 <- fabias(X,5,0.6,300,1.0)

rBreast2 <- extractPlot(resBreast2,ti="FABIAS Breast cancer(Veer)")


raBreast2 <- extractBic(resBreast2)

if ((raBreast2$bic[[1]][1]>1) && (raBreast2$bic[[1]][2])>1) {
    plotBicluster(raBreast2,1)
}
if ((raBreast2$bic[[2]][1]>1) && (raBreast2$bic[[2]][2])>1) {
    plotBicluster(raBreast2,2)
}
if ((raBreast2$bic[[3]][1]>1) && (raBreast2$bic[[3]][2])>1) {
    plotBicluster(raBreast2,3)
}
if ((raBreast2$bic[[4]][1]>1) && (raBreast2$bic[[4]][2])>1) {
    plotBicluster(raBreast2,4)
}

plot(resBreast2,dim=c(1,2),label.tol=0.03,col.group=CBreast,lab.size=0.6)
```

```
plot(resBreast2,dim=c(1,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(1,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(1,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(2,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(2,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(2,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(3,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(3,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast2,dim=c(4,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)

}


#-----------------------------------
# DEMO2: Su's multiple tisse types
#        gene expression data set
#-----------------------------------

avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("########################################################")
    message("Package 'fabia' is not available: please install.")
    message("########################################################")
} else {

data(Multi_A)

X <- as.matrix(XMulti)

resMulti2 <- fabias(X,5,0.6,300,1.0)

rMulti2 <- extractPlot(resMulti2,ti="FABIAS Multiple tissues(Su)")

raMulti2 <- extractBic(resMulti2)

if ((raMulti2$bic[[1]][1]>1) && (raMulti2$bic[[1]][2])>1) {
    plotBicluster(raMulti2,1)
}
if ((raMulti2$bic[[2]][1]>1) && (raMulti2$bic[[2]][2])>1) {
    plotBicluster(raMulti2,2)
}
if ((raMulti2$bic[[3]][1]>1) && (raMulti2$bic[[3]][2])>1) {
    plotBicluster(raMulti2,3)
```

```
}
if ((raMulti2$bic[[4]][1]>1) && (raMulti2$bic[[4]][2])>1) {
    plotBicluster(raMulti2,4)
}

plot(resMulti2,dim=c(1,2),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(1,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(1,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(1,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(2,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(2,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(2,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(3,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(3,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti2,dim=c(4,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)

}


#----------------------------------------
# DEMO3: Rosenwald's diffuse large-B-cell
#        lymphoma gene expression data set
#----------------------------------------

avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("#########################################################")
    message("Package 'fabia' is not available: please install.")
    message("#########################################################")
} else {

data(DLBCL_B)

X <- as.matrix(XDLBCL)

resDLBCL2 <- fabias(X,5,0.6,300,1.0)

rDLBCL2 <- extractPlot(resDLBCL2,ti="FABIAS Lymphoma(Rosenwald)")

raDLBCL2 <- extractBic(resDLBCL2)

if ((raDLBCL2$bic[[1]][1]>1) && (raDLBCL2$bic[[1]][2])>1) {
    plotBicluster(raDLBCL2,1)
```

```
}
if ((raDLBCL2$bic[[2]][1]>1) && (raDLBCL2$bic[[2]][2])>1) {
    plotBicluster(raDLBCL2,2)
}
if ((raDLBCL2$bic[[3]][1]>1) && (raDLBCL2$bic[[3]][2])>1) {
    plotBicluster(raDLBCL2,3)
}
if ((raDLBCL2$bic[[4]][1]>1) && (raDLBCL2$bic[[4]][2])>1) {
    plotBicluster(raDLBCL2,4)
}

plot(resDLBCL2,dim=c(1,2),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(1,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(1,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(1,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(2,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(2,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(2,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(3,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(3,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL2,dim=c(4,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)

}




#-----------------------------------------
##########################################
# MFSC Demos
##########################################
#-----------------------------------------



#-----------------------------------------
# DEMO1: Laura van't Veer's gene expression
#        data set for breast cancer
#-----------------------------------------

avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("########################################################")
```

```
    message("Package 'fabia' is not available: please install.")
    message("#########################################################")
} else {

data(Breast_A)

X <- as.matrix(XBreast)

resBreast4 <- mfsc(X,5,100,0.6,0.6)

rBreast4 <- extractPlot(resBreast4,ti="MFSC Breast cancer(Veer)")


raBreast4 <- extractBic(resBreast4,thresZ=0.01,thresL=0.05)

if ((raBreast4$bic[[1]][1]>1) && (raBreast4$bic[[1]][2])>1) {
    plotBicluster(raBreast4,1)
}
if ((raBreast4$bic[[2]][1]>1) && (raBreast4$bic[[2]][2])>1) {
    plotBicluster(raBreast4,2)
}
if ((raBreast4$bic[[3]][1]>1) && (raBreast4$bic[[3]][2])>1) {
    plotBicluster(raBreast4,3)
}
if ((raBreast4$bic[[4]][1]>1) && (raBreast4$bic[[4]][2])>1) {
    plotBicluster(raBreast4,4)
}

plot(resBreast4,dim=c(1,2),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(1,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(1,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(1,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(2,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(2,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(2,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(3,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(3,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(4,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)

}


#----------------------------------
# DEMO2: Su's multiple tissue types
#        gene expression data set
#----------------------------------
```

```
avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("#########################################################")
    message("Package 'fabia' is not available: please install.")
    message("#########################################################")
} else {

data(Multi_A)

X <- as.matrix(XMulti)

resMulti4 <- mfsc(X,5,100,0.6,0.6)

rMulti4 <- extractPlot(resMulti4,ti="MFSC Multiple tissues(Su)")


raMulti4 <- extractBic(resMulti4,thresZ=0.01,thresL=0.05)

if ((raMulti4$bic[[1]][1]>1) && (raMulti4$bic[[1]][2])>1) {
    plotBicluster(raMulti4,1)
}
if ((raMulti4$bic[[2]][1]>1) && (raMulti4$bic[[2]][2])>1) {
    plotBicluster(raMulti4,2)
}
if ((raMulti4$bic[[3]][1]>1) && (raMulti4$bic[[3]][2])>1) {
    plotBicluster(raMulti4,3)
}
if ((raMulti4$bic[[4]][1]>1) && (raMulti4$bic[[4]][2])>1) {
    plotBicluster(raMulti4,4)
}

plot(resMulti4,dim=c(1,2),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(1,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(1,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(1,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(2,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(2,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(2,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(3,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(3,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti4,dim=c(4,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
```

```
}


#----------------------------------------
# DEMO3: Rosenwald's diffuse large-B-cell
#        lymphoma gene expression data set
#----------------------------------------

avail <- require(fabia)

if (!avail) {
    message("")
    message("")
    message("#########################################################")
    message("Package 'fabia' is not available: please install.")
    message("#########################################################")
} else {

data(DLBCL_B)

X <- as.matrix(XDLBCL)


resDLBCL4 <- mfsc(X,5,100,0.6,0.6)

rDLBCL4 <- extractPlot(resDLBCL4,ti="MFSC Lymphoma(Rosenwald)")

raDLBCL4 <- extractBic(resDLBCL4,thresZ=0.01,thresL=0.05)

if ((raDLBCL4$bic[[1]][1]>1) && (raDLBCL4$bic[[1]][2])>1) {
    plotBicluster(raDLBCL4,1)
}
if ((raDLBCL4$bic[[2]][1]>1) && (raDLBCL4$bic[[2]][2])>1) {
    plotBicluster(raDLBCL4,2)
}
if ((raDLBCL4$bic[[3]][1]>1) && (raDLBCL4$bic[[3]][2])>1) {
    plotBicluster(raDLBCL4,3)
}
if ((raDLBCL4$bic[[4]][1]>1) && (raDLBCL4$bic[[4]][2])>1) {
    plotBicluster(raDLBCL4,4)
}

plot(resDLBCL4,dim=c(1,2),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(1,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(1,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
```

```
plot(resDLBCL4,dim=c(1,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(2,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(2,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(2,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(3,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(3,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resDLBCL4,dim=c(4,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)

}
```

References

Hochreiter, S., Bodenhofer, U., Heusel, M., Mayr, A., Mitterecker, A., Kasim, A., Khamiakova, T., Sanden, S. V., Lin, D., Talloen, W., Bijnens, L., Göhlmann, H. W. H., Shkedy, Z., and Clevert, D.-A. (2010). FABIA: Factor analysis for bicluster acquisition. *Bioinformatics*. doi:10.1093/bioinformatics/btq227, http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btq227.

Hoshida, Y., Brunet, J.-P., Tamayo, P., Golub, T. R., and Mesirov, J. P. (2007). Subclass mapping: Identifying common subtypes in independent disease data sets. *PLoS ONE*, **2**(11), e1195.

Rosenwald, A., Wright, G., Chan, W. C., Connors, J. M., Campo, E., Fisher, R. I., Gascoyne, R. D., Muller-Hermelink, H. K., Smeland, E. B., Giltnane, J. M., Hurt, E. M., Zhao, H., Averett, L., Yang, L., Wilson, W. H., Jaffe, E. S., Simon, R., Klausner, R. D., Powell, J., Duffey, P. L., Longo, D. L., Greiner, T. C., Weisenburger, D. D., Sanger, W. G., Dave, B. J., Lynch, J. C., Vose, J., Armitage, J. O., Montserrat, E., L'opez-Guillermo, A., Grogan, T. M., Miller, T. P., LeBlanc, M., Ott, G., Kvaloy, S., Delabie, J., Holte, H., Krajci, P., Stokke, T., and Staudt, L. M. (2002). The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma. *New Engl. J. Med.*, **346**, 1937–1947.

Su, A. I., Cooke, M. P., A.Ching, K., Hakak, Y., Walker, J. R., Wiltshire, T., Orth, A. P., Vega, R. G., Sapinoso, L. M., Moqrich, A., Patapoutian, A., Hampton, G. M., Schultz, P. G., and Hogenesch, J. B. (2002). Large-scale analysis of the human and mouse transcriptomes. *P. Natl. Acad. Sci. USA*, **99**(7), 4465–4470.

van't Veer, L. J., Dai, H., van de Vijver, M. J., He, Y. D., Hart, A. A., Mao, M., Peterse, H. L., van der Kooy, K., Marton, M. J., Witteveen, A. T., Schreiber, G. J., Kerkhoven, R. M., Roberts, C., Linsley, P. S., Bernards, R., and Friend, S. H. (2002). Gene expression profiling predicts clinical outcome of breast cancer. *Nature*, **415**, 530–536.