Package ‘fabiaData’

March 26, 2024

Title  Data sets for FABIA (Factor Analysis for Bicluster Acquisition)
Version  1.40.0
Date  2012-08-15
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Depends  R (>= 2.10.0), Biobase
Imports  utils
Suggests  fabia

LinkingTo

Description  Supplying gene expression data sets for the demos of the biclustering method `Factor Analysis for Bicluster Acquisition' (FABIA). The following three data sets are provided: A) breast cancer (van't Veer, Nature, 2002), B) multiple tissues (Su, PNAS, 2002), and C) diffuse large-B-cell lymphoma (Rosenwald, N Engl J Med, 2002).

License  LGPL (>= 2.1)

URL  http://www.bioinf.jku.at/software/fabia/fabia.html
biocViews  CancerData, BreastCancerData, MicroarrayData
LazyLoad  yes

git_url  https://git.bioconductor.org/packages/fabiaData
git_branch  RELEASE_3_18
git_last_commit  b38972a
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Repository  Bioconductor 3.18
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Breast_A

Subclasses of van’t Veer breast cancer microarray data set

Description

Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by van’t Veer et al. 2002. 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.

Breast_A is the data set with 97 samples and 1213 genes, BRECT_B are the three subclasses from Hoshida et al. 2007.

Usage

Breast_A

Format

Matrix XBreast: 97 samples and 1213 probe sets, Vector CBreast: three subclasses from Hoshida

Source

Broad Institute “Cancer Program Data Sets”: http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi
CBreast

References


CBreast

Subclasses of van’t Veer breast cancer microarray data set

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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 are the three subclasses from Hoshida et al. 2007.

Usage

CBreast

Format

Vector CBreast of 97 samples giving the three subclasses from Hoshida.

Source

Broad Institute “Cancer Program Data Sets”: http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi

References


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

Description
Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by Rosenwald et al. 2002.
Goal was to predict the survival after chemotherapy
Hoshida divided the data set into three classes: “OxPhos” (oxidative phosphorylation), “BCR” (B-cell response), and “HR” (host response).
We want to identify these subclasses.

Usage
CDLBCL

Format
Vector CDLBCL of 180 samples giving the three subclasses according to Hoshida et al. 2007.

Source
Broad Institute “Cancer Program Data Sets”: http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi

References

CMulti Microarray data set of Su on different mammalian tissue types

Description
Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by Su et al. 2002.
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.
Usage

CMulti

Format

Vector CMulti of 102 samples giving the four classes of tissue types.

Source

Broad Institute “Cancer Program Data Sets”: http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi

References


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

Description

Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by Rosenwald et al. 2002.
Goal was to predict the survival after chemotherapy.
Hoshida divided the data set into three classes: “OxPhos” (oxidative phosphorylation), “BCR” (B-cell response), and “HR” (host response).
We want to identify these subclasses.

Usage

DLBCL_B

Format

Matrix XDLBCL: 180 samples and 661 probe sets, Vector CDLBCL: three subclasses according to Hoshida et al. 2007.

Source

Broad Institute “Cancer Program Data Sets”: http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi
References


fabiaData

Display available data sets

Description

fabiaData available data sets.

Usage

fabiaData()

Author(s)

Sepp Hochreiter

See Also

Breast_A, DLBCL_B, Multi_A,

Examples

fabiaData()

fabiaDataVersion

Display version info for package fabiaData

Description

fabiaDataVersion displays version information about the package.

Usage

fabiaDataVersion()

Author(s)

Sepp Hochreiter
Multi_A

See Also
  Breast_A, DLBCL_B, Multi_A,

Examples
  fabiaDataVersion()

| Multi_A | Microarray data set of Su on different mammalian tissue types |

Description
  Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by Su et al. 2002.
  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.

Usage
  Multi_A

Format
  Matrix XMulti: 102 samples and 5565 probe sets, Vector CMulti: four classes of tissue types.

Source
  Broad Institute “Cancer Program Data Sets”: http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi

References
**XBreast**  
*Subclasses of van’t Veer breast cancer microarray data set*

### Description

Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by van’t Veer et al. 2002. 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** are the three subclasses from Hoshida et al. 2007.

### Usage

**XBreast**

### Format

Matrix **XBreast**: 97 samples and 1213 probe sets.

### Source

Broad Institute “Cancer Program Data Sets”: [http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi](http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi)

### References


**XDLBCL**

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

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**Description**

Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by Rosenwald et al. 2002.

Goal was to predict the survival after chemotherapy

Hoshida divided the data set into three classes: “OxPhos” (oxidative phosphorylation), “BCR” (B-cell response), and “HR” (host response).

We want to identify these subclasses.

**Usage**

**Format**

Matrix XDLBCL: 180 samples and 661 probe sets.

**Source**

Broad Institute “Cancer Program Data Sets”: [http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi](http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi)

**References**


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**XMulti**

*Microarray data set of Su on different mammalian tissue types*

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**Description**

Microarray data from Broad Institute “Cancer Program Data Sets” which was produced by Su et al. 2002.

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.
XMulti

Usage

XMulti

Format

Matrix XMulti: 102 samples and 5565 probe sets

Source

Broad Institute “Cancer Program Data Sets”: http://www.broadinstitute.org/cgi-bin/cancer/datasets.cgi

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