Package 'CLL'

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Type Package

Title A Package for CLL Gene Expression Data

Version 1.52.0

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Description The CLL package contains the chronic lymphocytic leukemia (CLL) gene expression data. The CLL data had 24 samples that were either classified as progressive or stable in regards to disease progression. The data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Depends R (>= 2.10), affy (>= 1.23.4), Biobase (>= 2.5.5)

License LGPL

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`CLL-package` *A package for CLL gene expression data*

Description

The CLL package contains the chronic lymphocytic leukemia (CLL) gene expression data. The CLL data had 24 samples that were either classified as progressive or stable in regards to disease progression. The CLL microarray data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Details

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Version:	1.0
Date:	2006-07-10
License:	LGPL

Author(s)

Elizabeth Whalen

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Examples

```
data(sCLLex)
```

`CLLbatch` *The AffyBatch object for the CLL microarray data*

Description

The AffyBatch object has 24 samples that were affixed to Affymetrix hgu95av2 arrays. These 24 samples came from 24 CLL patients that were either classified as stable or progressive in regards to disease progression.

Usage

```
data(CLLbatch)
```

Format

An AffyBatch object with 24 samples and 12,625 genes. The Affymetrix hgu95av2 array was used.

`cdfName` the name of the CDF file: HG_U95Av2

`nrow` the number of rows for each chip: 640

`ncol` the number of columns for each chip: 640

`exprs` the matrix containing one probe per row and one array per column (dimensions: 409,600 by 24)

`se.exprs` the matrix for standard errors: not calculated yet so has dimensions 0 by 0

`description` no information is available for the description slot, which is of class MIAME

`annotation` "hgu95av2"

`notes` there are no notes for this object

`reporterInfo` unknown (NULL)

`phenoData` a data frame with one variable: sample (more phenotype data can be found in the disease data frame)

`classVersion` no version

Source

The CLL microarray data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Examples

```
data(CLLbatch)
```

---

disease *The phenotype data for the CLL microarray data*

Description

The disease data frame consists of two variables: SampleID, which is the CEL file for the sample, and Disease, which is whether the sample came from a patient that was stable or progressive in terms of CLL disease progression.

Usage

```
data(disease)
```

Format

A data frame with 24 observations on the following 2 variables.

`SampleID` a character string refer to the CEL file of the sample

`Disease` a factor with levels `progres. stable`; this variable refers to whether the patient was progressive or stable in regards to CLL disease progression

Source

The CLL microarray data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Examples

```
data(disease)
```

---

nsFilter *Nonspecific filtering boolean values for the sCLLex ExpressionSet object*

Description

nsFilter is the nonspecific filtering boolean values for the sCLLex ExpressionSet object. One filter was use: genes with an IQR greater than or equal to the median IQR (IQR performed on the rows of the expression matrix) have a TRUE value (passed the filter) and those that had an IQR less than the median have a FALSE value (did not pass the filter). We only filtered on variation.

Usage

```
data(nsFilter)
```

Format

A named vector of logicals. The names are the Affymetrix identifiers and the values are booleans.

Source

The CLL microarray data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Examples

```
data(nsFilter)
data(sCLLex)
sCLLexF<-sCLLex[nsFilter, ]
```

sCLLex *The ExpressionSet object for the CLL microarray data*

Description

The ExpressionSet object was obtained by performing gcrma on the AffyBatch object (CLLbatch). Two arrays were of questionable quality so these two arrays (CLL1 and CLL10) were removed before performing gcrma on CLLbatch. The sCLLex ExpressionSet object has 22 samples and 12,625 genes. The Affymetrix hug95av2 arrays were used and the 22 samples came from 22 CLL patients that were either classified as stable or progressive in regards to disease progression.

Usage

```
data(sCLLex)
```

Format

An ExpressionSet object with 22 samples and 12,625 genes. The Affymetrix hgu95av2 array was used and gcrma was used for preprocessing the AffyBatch object.

`exprs` the matrix containing estimates expression levels with rows as genes and columns as patients (dimensions: 12,625 by 22)

`se.exprs` the matrix with standard error estimates (gcrma returns a 0 by 0 matrix)

`description` no information is available for the description slot, which is of class MIAME

`annotation` "hgu95av2"

`notes` there are no notes for this object

`reporterInfo` unknown (NULL)

`phenoData` a data frame with two variables: SampleID and Disease (from the disease data frame); SampleID is the CEL file and Disease is a factor with 2 levels: progressive or stable, based on the patient's CLL disease progression

`classVersion` no version

Source

The CLL microarray data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Examples

```
data(sCLLex)
```

sFiltert — *Boolean values for specific filtering based on the t-test*

Description

sFiltert is a named vector of booleans indicating whether a gene passed the specific and non-specific filtering steps. The specific filtering was to perform row t-tests and a TRUE value was obtained if the p-value was less than 0.005. So to have a TRUE value in sFiltert, the gene must have a row t-test p-value less than 0.005, an interquartile range of at least 0.5 on the log2 scale, and at least 25% of the samples had an expression value greater than 100 on the normal scale (the last 2 criteria were the nonspecific filters).

A TRUE value indicates that the gene passed the filtering step and should be included in further analysis.

Usage

```
data(sFiltert)
```

Format

A named vector of logicals. The names correspond to the Affymetrix identifiers and the values are booleans indicating whether the gene passed the nonspecific and specific filtering (based on t-test p-values).

Source

The CLL microarray data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Examples

```
data(sFiltert)
data(sCLLex)
sCLLexSF<-sCLLex[sFiltert, ]
```

sFiltertBH — *Boolean values for specific filtering based on the t-test*

Description

sFiltert is a named vector of booleans indicating whether a gene passed the specific and non-specific filtering steps. The nonspecific filtering step was described in the nsFilter man page. The specific filtering was to perform row t-tests, then perform p-value adjustment using the Benjamini & Hochberg method (using the mt.rawp2adjp function in the multtest package with the "BH" procedure), and finally include the gene if its adjusted p-value was less than 0.35. So to have a TRUE value in sFiltertBH, the gene must have an IQR greater than or equal to the median IQR and must have a BH adjusted p-value less than 0.35.

A TRUE value indicates that the gene passed the filtering step and should be included in further analysis.

Usage

```
data(sFiltert)
```

Format

A named vector of logicals. The names correspond to the Affymetrix identifiers and the values are booleans indicating whether the gene passed the nonspecific and specific filtering (based on adjusted t-test p-values).

Source

The CLL microarray data came from Dr. Sabina Chiaretti at Division of Hematology, Department of Cellular Biotechnologies and Hematology, University La Sapienza, Rome, Italy and Dr. Jerome Ritz at Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts.

Examples

```
data(sFiltertBH)
data(sCLLex)
sCLLexSF<-sCLLex[sFiltertBH, ]
```

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