

Package ‘leukemiasEset’

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Type Package

Title Leukemia's microarray gene expression data (expressionSet).

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Depends R (>= 2.10.1), Biobase (>= 2.5.5)

Description Expressionset containing gene expression data from 60 bone marrow samples of patients with one of the four main types of leukemia (ALL, AML, CLL, CML) or non-leukemia.

License GPL (>= 2)

LazyLoad yes

biocViews Tissue, Genome, Homo_sapiens_Data, CancerData, LeukemiaCancerData, MicroarrayData, ChipOnChipData, TissueMicroarrayData, GEO

NeedsCompilation no

R topics documented:

leukemiasEset	1
Index	4

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Description

ExpressionSet containing gene expression data from 60 bone marrow samples of patients with one of the four main types of leukemia (ALL, AML, CLL, CML) or no-leukemia controls.

Platform: Affymetrix Human Genome U133 Plus 2.0
Annotation: genemapperhgu133plus2 (CDF from GATEExplorer)
Mapping: Gene Ensembl ID (20172 features)

Tissue: Bone Marrow

Cell type: Mononuclear cells isolated by Ficoll density centrifugation

Disease type:

1. Acute Lymphoblastic Leukemia (ALL). Subtype: c-ALL / pre-B-ALL without t(9;22)
2. Acute Myeloid Leukemia (AML). Subtype: Normal karyotype
3. Chronic Lymphocytic Leukemia (CLL)
4. Chronic Myeloid Leukemia (CML)
5. Non-leukemia and healthy bone marrow (NoL)

All samples were obtained from untreated patients at the time of diagnosis.

Preprocessing: The microarrays were normalized with [RMA](#) using a redefined probe mapping from *Affymetrix* probesets to *Ensembl* genes (Ensembl IDs ENSG). This alternative Chip Definition File (CDF) with complete unambiguous mapping of microarray probes to genes (GeneMapper) is available at GATEplorer (<http://bioinfow.dep.usal.es/xgate/mapping/mapping.php>) (Risueno *et al.* 2010).

Usage

```
data(leukemiasEset)
```

Format

`ExpressionSet` with `phenoData`:

- Project: "Mile1" for all samples
- Tissue: "BoneMarrow"
- LeukemiaType: Leukemia type acronym: "ALL", "AML", "CLL", "CML" or "NoL"
- LeukemiaTypeFullName: The full leukemia type name.
- Subtype: "AML with normal karyotype and other abnormalities", or "c_ALL/Pre_B_ALL without t(9 22)" if applies

Details

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Type:	Package
Version:	1.0
Date:	2013-03-13
License:	GPL (>=2)
LazyLoad:	yes

Author(s)

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Source

This is a subset of the samples collected by the Microarray Innovations in Leukemia (MILE) study (Kohlmann *et al.* 2008, Haferlach *et al.* 2010). Full study microarray raw data can be found at the NCBI Gene Expression Omnibus database (GEO, <http://www.ncbi.nlm.nih.gov/geo/>) under series accession number GSE13159. The selected samples are labelled keeping their source GEO IDs.

References

Kohlmann A, Kipps TJ, Rassenti LZ, Downing JR *et al.* An international standardization programme towards the application of gene expression profiling in routine leukaemia diagnostics: the Microarray Innovations in LEukemia study prephase. *Br J Haematol* (2008) 142(5):802-7. PMID: 18573112

Haferlach T, Kohlmann A, Wiczorek L, Basso G *et al.* Clinical utility of microarray-based gene expression profiling in the diagnosis and subclassification of leukemia: report from the International Microarray Innovations in Leukemia Study Group. *J Clin Oncol* (2010) 28(15):2529-37. PMID: 20406941

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. *BMC Bioinformatics* (2010) 11:221. PMID: 20429936.

See Also

This dataset is used in the examples on package [geNetClassifier](#).

Examples

```
# Load expression set:
library(leukemiasEset)
data(leukemiasEset)

# ExpressionSet overview:
leukemiasEset

# Phenodata:
pData(leukemiasEset)

# Number of samples per class:
summary(leukemiasEset$LeukemiaType)

# For adding a prefix with the disease to the sample name:
sampleNames(leukemiasEset) <- paste(leukemiasEset$LeukemiaType,
  sampleNames(leukemiasEset), sep="_")
colnames(exprs(leukemiasEset))
```

Index

- *Topic **cancer**
 - leukemiasEset, 1
- *Topic **datasets**
 - leukemiasEset, 1
- *Topic **expression**
 - leukemiasEset, 1
- *Topic **leukemia**
 - leukemiasEset, 1
- *Topic **microarrays**
 - leukemiasEset, 1

ExpressionSet, 2

geNetClassifier, 3

leukemiasEset, 1

leukemiasEset-package (leukemiasEset), 1

RMA, 2