Package ‘leukemiasEset’

November 16, 2021

Type Package

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

Version 1.31.0

Date 2013-03-20


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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.

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LazyLoad yes

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

git_url https://git.bioconductor.org/packages/leukemiasEset

git_branch master

git_last_commit fb9e05d

git_last_commit_date 2021-10-26

Date/Publication 2021-11-16

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Leukemia's microarray gene expression data (expressionSet).

**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 GATEplorer)  
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**
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


See Also

This dataset is used in the examples on package geNetClassifier.

Examples

```r
# 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))
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