

# Package ‘leukemiasEset’

October 18, 2022

**Type** Package

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

**Version** 1.32.0

**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.

**License** GPL (>= 2)

**LazyLoad** yes

**biocViews** Tissue, Genome, Homo\_sapiens\_Data, CancerData, LeukemiaCancerData, MicroarrayData, ChipOnChipData, TissueMicroarrayData, GEO

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leukemiasEset

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

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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 GATEExplorer (<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

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

### Author(s)

Author: Sara Aibar, Celia Fontanillo and Javier De Las Rivas. Bioinformatics and Functional Genomics Group. Cancer Research Center (CiC-IBMCC, CSIC/USAL). Salamanca. Spain.

Maintainer: Sara Aibar <saibar@usal.es>

### 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, Wieczorek 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.* GATEexplorer: 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))
```

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