Package ‘leukemiasEset’

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Type Package

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

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Maintainer Sara Aibar <saibar@usal.es>

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

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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: genemapperhg133plus2 (CDF from GATEXplorer)  
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 GATEXplorer (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)


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


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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