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

Description

ExpressionSet containing gene expresion 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 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)

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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, 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. 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))
```

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