Package ‘DLBCL’

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Type Package

Title Diffuse large B-cell lymphoma expression data

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Description This package provides additional expression data on diffuse large B-cell lymphomas for the BioNet package.

License GPL (>=2)

Depends R(>= 2.11.0), Biobase, graph

LazyLoad yes

URL `http://bionet.bioapps.biozentrum.uni-wuerzburg.de/`

biocViews ExperimentData, CancerData, MicroarrayData, ChipOnChipData

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Contents

`DLBCL-package` *Routines for the functional analysis of biological networks*

Description

This package provides an expression set on diffuse large B-cell lymphoma and an protein-protein interaction network obtained from HPRD release 6. It accompanies the BioNet packages as example data. For further information on the data and the BioNet package, see references below.

Details

Package:	DLBCL
Type:	Package
Version:	1.2
Date:	2010-03-26
License:	GPL (>=2)
LazyLoad:	yes

Author(s)

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References

M. T. Dittrich, G. W. Klau, A. Rosenwald, T. Dandekar and T. Mueller (2008) Identifying functional modules in protein-protein interaction networks: an integrated exact approach. *(ISMB2008) Bioinformatics* 24: 13. i223-i231 Jul.

D. Beisser, G. W. Klau, T. Dandekar, T. Mueller and M. Dittrich (2009) BioNet: an R-package for the Functional Analysis of Biological Networks. *Bioinformatics*.

A. A. Alizadeh, M. B. Eisen, R. E. Davis et al. (2000) Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* 403: 503-11.

`dataLym` *Additional data for the lymphoma microarray chip (exprLym)*

Description

The dataset contains additional data for the exprLym dataset. It includes p-values for the gene expression, p-values for the survival data, an example score etc.

Usage

```
data(dataLym)
```

References

A. Rosenwald et al. (2002). The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma. *N Engl J Med*, 346(25), 1937-1947.

Examples

```
data(dataLym)
str(dataLym)
```

`exprLym` *Expression set diffuse large B-cell lymphomas*

Description

The dataset contains an expression set on diffuse large B-cell lymphoma. It accompanies the BioNet packages as example data. For further information on the data and the BioNet package see:

M. T. Dittrich, G. W. Klau, A. Rosenwald, T. Dandekar and T. Mueller (2008) Identifying functional modules in protein-protein interaction networks: an integrated exact approach. *(ISMB2008) Bioinformatics* 24: 13. i223-i231 Jul.

D. Beisser, G. W. Klau, T. Dandekar, T. Mueller and M. Dittrich (2009) BioNet: an R-package for the Functional Analysis of Biological Networks. *Bioinformatics*.

A. A. Alizadeh, M. B. Eisen, R. E. Davis et al. (2000) Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* 403: 503-11.

Usage

```
data(exprLym)
```

Examples

```
data(exprLym)
exprs(exprLym)[1:10,]
```

`interactome` *Human protein-protein interaction network*

Description

The dataset contains the human proteome, extracted from the Human Protein Reference Database (HPRD) from 2006 that is used in the ABC GCB diffuse large B-cell lymphma analysis. The format of the dataset is a graph object.

Usage

```
data(interactome)
```

References

M. T. Dittrich, G. W. Klau, A. Rosenwald, T. Dandekar, T. Mueller (2008) Identifying functional modules in protein-protein interaction networks: an integrated exact approach. *(ISMB2008) Bioinformatics*, 24: 13. i223-i231 Jul.

Examples

```
data(interactome)
interactome
```

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