

# Package ‘DLBCL’

April 4, 2014

**Type** Package

**Title** Diffuse large B-cell lymphoma expression data

**Version** 1.3.7

**Date** 2010-03-26

**Author** Marcus Dittrich and Daniela Beisser

**Maintainer** Marcus Dittrich <marcus.dittrich@biocentrum.uni-wuerzburg.de>

**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

**LazyLoad** yes

**URL** <http://bionet.bioapps.biozentrum.uni-wuerzburg.de/>

**biocViews** ExperimentData, Cancer

## R topics documented:

DLBCL-package . . . . .	2
dataLym . . . . .	2
exprLym . . . . .	3
interactome . . . . .	4
<b>Index</b>	<b>5</b>

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)**

Marcus Dittrich, Daniela Beisser

Maintainer: Marcus Dittrich <marcus.dittrich@biozentrum.uni-wuerzburg.de>

**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	<i>Expression set diffuse large B-cell lymphomas</i>
---------	--

---

**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 lymphoma 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
```

# Index

## \*Topic **datasets**

[dataLym](#), [2](#)

[exprLym](#), [3](#)

[interactome](#), [4](#)

[dataLym](#), [2](#)

[DLBCL \(DLBCL-package\)](#), [2](#)

[DLBCL-package](#), [2](#)

[exprLym](#), [3](#)

[interactome](#), [4](#)