Package ‘bcellViper’

May 26, 2026

Type Package

Title Human B-cell transcriptional interactome and normal human B-cell expression data

Version 1.48.0

Date 2013-04-15

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Description This package provides a human B-cell context-specific transcriptional regulatory network and a human normal B-cells dataset for the examples in package viper.

License GPL (>=2)

Depends R(>= 2.14.0), Biobase, methods

LazyLoad yes

biocViews ExperimentData, Genome, Homo_sapiens_Data, CancerData

Collate ''

git_url https://git.bioconductor.org/packages/bcellViper

git_branch RELEASE_3_23

git_last_commit a214acd

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-05-26

Contents

`bcellViper-package` *Human B-cell interactome and normal and tumor B-cell phenotypes expresion data*

Description

This package contains an interactome (regulon), expression data (dset), a list of normal sample IDs (normalSamples) and a short example of the ARACNE algorithm output (bcellaracne.adj file) required to run the examples of package viper.

Details

Package:	bcellViper
Type:	Package
Version:	0.99.2
Date:	2013-04-15
License:	GPL (>=2)
LazyLoad:	yes

Author(s)

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References

Basso, K. et al. Reverse engineering of regulatory networks in human B cells. Nature genetics 37, 382-90 (2005).

Gautier, L., Cope, L., Bolstad, B. M., and Irizarry, R. A. 2004. affy—analysis of Affymetrix GeneChip data at the probe level. Bioinformatics 20, 3 (Feb. 2004), 307-315.

Alvarez, M. J., Sumazin, P., Rajbhandari, P. & Califano, A. Correlating measurements across samples improves accuracy of large-scale expression profile experiments. Genome biology 10, R143 (2009).

`dset` *Human normal and tumor B-cell phenotypes expresion data*

Description

The expression data (dset) is a numeric matrix with genes (6,249) in rows and samples (211) in columns. Gene identifiers and sample names are contained in the rownames and colnames attributes, respectively. The samples represent several normal and tumor B-cell phenotypes, 5 naive B-cell, 5 memory B-cells, 5 centroblasts and 5 centrocytes phenotypes. The data is a subset from the Gene Expression Omnibus series GSE2350 (Basso et.al, 2005), where the original raw data (Affymetrix H-GU95Av2 gene arrays) was normalized by MAS5 (Gautier et.al, 2004) after generating custom probe-cluster with the cleaner algorithm (Alvarez et.al, 2009).

Usage

```
data(bcellViper)
```

References

Basso, K. et al. Reverse engineering of regulatory networks in human B cells. Nature genetics 37, 382-90 (2005).

Gautier, L., Cope, L., Bolstad, B. M., and Irizarry, R. A. 2004. affy—analysis of Affymetrix GeneChip data at the probe level. Bioinformatics 20, 3 (Feb. 2004), 307-315.

Alvarez, M. J., Sumazin, P., Rajbhandari, P. & Califano, A. Correlating measurements across samples improves accuracy of large-scale expression profile experiments. Genome biology 10, R143 (2009).

Examples

```
data(bcellViper)
dset
```

`regulon` *Human B-cell context-specific transcriptional interactome*

Description

The interactome is a human B-cell context-specific transcriptional regulatory network reverse engineered by the ARACNE algorithm from 254 normal and tumor B-cell phenotypes (Basso et.al, 2005). It represents 621 transcription factors (TF) and 6,249 target genes associated by 172,240 interactions. The interactome is contained in a list object of S3 class 'regulon' where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

```
data(bcellViper)
```

References

Basso, K. et al. Reverse engineering of regulatory networks in human B cells. Nature genetics 37, 382-90 (2005).

Examples

```
data(bcellViper)
print(regulon[1])
```

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