

Package ‘bcellViper’

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Type Package

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

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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 "

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bcellViper-package	<i>Human B-cell interactome and normal and tumor B-cell phenotypes expression data</i>
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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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