

Package ‘bionetdata’

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Type Package

Title Biological and chemical data networks

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Description Data Package that includes several examples of chemical and biological data networks, i.e. data graph structured.

License GPL (>= 2)

LazyLoad yes

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bionetdata-package *bionetdata: Biological and chemical data networks*

Description

Data Package that includes several examples of chemical and biological data networks represented through adjacency matrices of a graph

Details

Package:	bionetdata
Type:	Package
Version:	1.0
Date:	2011-11-13
License:	GPL (>= 2)
LazyLoad:	yes

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CGM.Cat

Cancer Gene Modules

Usage

```
data(CGM.Cat)
```

References

Segal E., Friedman N., Koller D. and Regev A., A module map showing conditional activity of expression modules in cancer, Nature Genetics, 36(10), 2004

Examples

```
data(CGM.Cat)
```

DD.chem.data	<i>Drug-drug chemical interaction data</i>
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Usage

```
data(DD.chem.data)
```

Format

The format is: chr "DD.chem.data"

References

Wishart, D., Knox, C., Guo, A., Shrivastava, S., Hassanali, M., Stothard, P., Chang, Z., Woolsey, J.: DrugBank: a comprehensive resource for in silico drug discovery and exploration. Nucleic Acids Res. 34(Jan), D668-D672 (2006)

Examples

```
data(DD.chem.data)
## maybe str(DD.chem.data) ; plot(DD.chem.data) ...
```

DrugBank.Cat	<i>DrugBank categories</i>
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Usage

```
data(DrugBank.Cat)
```

References

Knox, C., Law, V., Jewison, T., Liu, P., Ly, S., Frolkis, A., Pon, A., Banco, K., Mak, C., Neveu, V., Djoumbou, Y., Eisner, R., Guo, A., Wishart, D.: DrugBank 3.0: a comprehensive resource for "omics" research on drugs. Nucleic Acids Res. 39(Jan), D1035-41 (2011)

Examples

```
data(DrugBank.Cat)
```

FIN.data

Functional Interaction Network data for human

Usage

```
data(FIN.data)
```

References

Wu G., Feng X. and Stein L. A human functional protein interaction network and its application to cancer data analysis, *Genome Biology* 11:R53, 2010

Examples

```
data(FIN.data)
```

Yeast.Biogrid.data *Yeast BioGRID data*

Description

Protein-protein interaction (PPI) data (BioGRID) of yeast have been downloaded from the BioGRID database, that collects PPI data from both high-throughput studies and conventional focused studies (Stark et al. 2006). Data are represented through a binary named matrix and represent the presence or absence of protein-protein interactions. Names correspond to systematic names of yeast genes.

Usage

```
data(Yeast.Biogrid.data)
```

Format

Binary named matrix. Entry `Yeast.Biogrid.data[i, j]` = 1 if there is an interaction between gene *i* and *j*, otherwise `Yeast.Biogrid.data[i, j]` = 0.

Source

BioGRID data base: <http://thebiogrid.org>

References

Stark, C., Breitkreutz, B., Reguly, T., Boucher, L., Breitkreutz, A., and Tyers, M. (2006). BioGRID: a general repository for interaction datasets. *Nucleic Acids Res.*, 34, D535-D539.

Examples

```
data(Yeast.Biogrid.data);
Yeast.Biogrid.data[1:10, 1:5];
```

`Yeast.Biogrid.FunCat`*Yeast FunCat classes for 'BioGRID' data.*

Description

FunCat classes for the genes included in `Yeast.Biogrid.data`. Annotations refer the funcat-2.1 scheme, and funcat-2.1 data 20070316 data, available from the MIPS web site.

Usage

```
data(Yeast.Biogrid.FunCat)
```

Format

A named matrix where rows refer to yeast genes, columns to FunCat classes. Names of yeast genes are systematic names. Names of columns correspond to FunCat IDs.

Source

<http://mips.gsf.de/projects/funecat>

References

Ruepp, A., Zollner, A., Maier, D., Albermann, K., Hani, J., Mokrejs, M., Tetko, I., Guldener, U., Mannhaupt, G., Munsterkötter, M., and Mewes, H. (2004). The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. *Nucleic Acids Research*, 32(18), 5539-5545.

Examples

```
data(Yeast.Biogrid.FunCat)
Yeast.Biogrid.FunCat[1:10,1:6]
```

`Yeast.int.data`*Yeast integrated network data*

Description

Yeast data obtained by integrating 6 sources of data by a simple sum of linear kernels. Original data have been kernelized through a linear kernel and the corresponding Gram matrices have been simply added. Only genes common to all the considered sources of data have been included (1901 yeast genes).

Usage

```
data(Yeast.int.data)
```

Format

A real named matrix. Names correspond to systematic names of yeast genes.

Details

The following data sets have been integrated:

- Pfam-1: Domain data from Pfam database
- Pfam-2: enriched representation of Pfam domains by replacing the binary scoring with log E-values obtained with the HMMER software toolkit (Eddy, 1998)
- Expr: Gene expression data relative to two experiments described in (Gasch et al., 2000) and (Spellman et al, 1998).
- PPI-BG data set contains protein-protein interaction data downloaded from the BioGRID database (Stark et al. 2006).
- PPI-STRING protein-protein interactions from STRING database (Snel et al. 2000).
- SP-sim pairwise similarities between yeast genes represented by Smith and Waterman log-E values .

References

- Sean R. Eddy. Profile hidden Markov models. *Bioinformatics*, 14(9):755-763, 1998.
- P. Gasch et al. Genomic expression programs in the response of yeast cells to environmental changes. *Mol. Biol. Cell*, 11(12):4241-4257, 2000.
- P. T. Spellman et al. Comprehensive identification of cell cycle-regulated genes of the yeast *Saccharomyces cerevisiae* by microarray hybridization. *Molecular Biology of the Cell*, 9(12):3273-3297, 1998.
- Stark, C., Breitkreutz, B., Reguly, T., Boucher, L., Breitkreutz, A., and Tyers, M. (2006). BioGRID: a general repository for interaction datasets. *Nucleic Acids Res.*, 34, D535-D539.
- Snel B, Lehmann G, Bork P, Huynen MA. STRING: a web-server to retrieve and display the repeatedly occurring neighbourhood of a gene. *Nucleic Acids Res.* 2000 Sep 15;28(18):3442-4.

Examples

```
data(Yeast.int.data)
```

Yeast.int.FunCat	<i>Yeast FunCat classes for 'Yeast.int.data'</i>
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Description

FunCat classes for the genes included in [Yeast.int.data](#). Annotations refer the funcat-2.1 scheme, and funcat-2.1 data 20070316 data, available from the MIPS web site.

Usage

```
data(Yeast.int.FunCat)
```

Format

A named matrix where rows refer to yeast genes, columns to FunCat classes. Names of yeast genes are systematic names. Names of columns correspond to FunCat IDs.

Source

<http://mips.gsf.de/projects/funcat>

References

Ruepp, A., Zollner, A., Maier, D., Albermann, K., Hani, J., Mokrejs, M., Tetko, I., Guldener, U., Mannhaupt, G., Munsterkott, M., and Mewes, H. (2004). The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. *Nucleic Acids Research*, 32(18), 5539-5545.

Examples

```
data(Yeast.int.FunCat)
```

Yeast.STRING.data *Yeast interactions from STRING*

Description

Binary protein-protein interactions from the STRING data base (von Mering et al. 2002), representing interaction data from yeast two-hybrid assay, mass-spectrometry of purified complexes, correlated mRNA expression and genetic interactions.

Usage

```
data(Yeast.STRING.data)
```

Format

Binary named matrix. Entry `Yeast.Biogrid.STRING[i, j] = 1` if there is an interaction between gene `i` and `j`, otherwise `Yeast.STRING.data[i, j] = 0`.

Source

<http://string-db.org>

References

von Mering, C., Krause, R., Snel, B., Cornell, M., Oliver, S., Fields, S., and Bork, P. (2002). Comparative assessment of large-scale data sets of protein-protein interactions. *Nature*, 417, 399-403.

Examples

```
data(Yeast.STRING.data)
```

```
Yeast.STRING.FunCat
```

Yeast FunCat classes for 'STRING' data.

Description

FunCat classes for the genes included in `Yeast.STRING.data`. Annotations refer the funcat-2.1 scheme, and funcat-2.1 data 20070316 data, available from the MIPS web site.

Usage

```
data(Yeast.STRING.FunCat)
```

Format

A named matrix where rows refer to yeast genes, columns to FunCat classes. Names of yeast genes are systematic names. Names of columns correspond to FunCat IDs.

Source

<http://mips.gsf.de/projects/funecat>

References

Ruepp, A., Zollner, A., Maier, D., Albermann, K., Hani, J., Mokrejs, M., Tetko, I., Guldener, U., Mannhaupt, G., Munsterkotter, M., and Mewes, H. (2004). The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. *Nucleic Acids Research*, 32(18), 5539-5545.

Examples

```
data(Yeast.STRING.FunCat)
```


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