Package ‘GANPAdataset’

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Suggests GANPA
Description This is a dataset package for GANPA, which implements a network-based gene weighting approach to pathway analysis. This package includes data useful for GANPA, such as a functional association network, pathways, an expression dataset and multi-subunit proteins.
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R topics documented:

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GANPAdataset-package  The GANPA Datasets Package

Description

This is a dataset package for GANPA, which implements a network-based gene weighting approach to pathway analysis. This package includes data useful for GANPA, such as a functional association network, pathways, an expression dataset and multi-subunit proteins.

Details

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Author(s)

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Maintainer: Zhaozoyuan Fang <fangzhaoyuan@sibs.ac.cn>

References

Zhaozoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. Submitted.


gExprs.p53  Gene expression data for the P53 dataset

Description

The P53 dataset is consisted of gene expression profiling of 17 P53-wildtype (WT) and 33 P53-mutated (MUT) cancer cell lines.
gNET

Usage

data(gExprs.p53)

Format

A List of 2 matrices.
$gExprs : \text{num}[1:10100, 1:50]$
$sampleinfo : \text{chr}[1:50, 1:2]$

Source

http://www.broadinstitute.org/gsea/index.jsp

References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. Submitted.

Examples

data(gExprs.p53)

gNET: A comprehensive gene functional association network

description

This R documentation entry describes gNET, a comprehensive gene functional association network. It can be accessed via the command `data(gNET)`.

Usage

data(gNET)

Format

A List of 16979 character vectors.

References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. Submitted.
**Examples**

```r
data(gNET)
```

---

**gsets.msigdb.pnas**  
*Functional Gene Sets Used in GSEA PNAS Publication*

**Description**

A list of 522 C2 functional gene sets, see reference for details.

**Usage**

```r
data(gsets.msigdb.pnas)
```

**Format**

A List of 522 character vectors.

**Source**

http://www.broadinstitute.org/gsea/index.jsp

**References**


**Examples**

```r
data(gsets.msigdb.pnas)
```

---

**msp.groups**  
*A List of Human Multi-subunit Proteins*

**Description**

A list of genes encoding 82 multi-subunit proteins were extracted from human genes.

**Usage**

```r
data(msp.groups)
```

**Format**

A List of 82 character vectors.
msp.groups

Details

A multi-subunit protein is named in the format of Multi.XXX where XXX is a member gene picked arbitrarily from the subunit gene group. Note this naming rule is just for convenience.

References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. Submitted.

Examples

data(msp.groups)
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