Package 'GSBenchMark'

November 10, 2026

Version 1.32.0

Date 2014

Title Gene Set Benchmark

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Depends R (>= 2.13.1)

Description Benchmarks for Machine Learning Analysis of the Gene Sets. The package contains a list of pathways and gene expression data sets used in ``Identifying Tightly Regulated and Variably Expressed Networks by Differential Rank Conservation (DIRAC)'' (2010) by Eddy et al.

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biocViews MicroarrayData

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

git_branch RELEASE_3_23

git_last_commit 2e404c0

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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`GSBenchMark-package` *A list of pathways and 11 datasets consisting gene expressions and phenotypes as the benchmark for Gene Set Analysis. Most of this information was used to validate Differential Rank Conservation (DIRAC) in the first place. In addition the data in the Eddy et al. (2010) paper, we also provide two datasets.*

Description

The GSBenchMark package contains data for testing gene set analysis with two phenotypes. Specially, the user can use the datasets used for validating Differential Rank Conservation (DIRAC) (Eddy et al. 2010). This datasets are used in the package GSReg which implements DIRAC and a more efficient alternative called GSVReg.

GSBenchMark package features

The dataset are included:

leukemia_GSEA marfan_GDS2960 melanoma_GDS2735 parkinsons_GDS2519 prostate_GDS2545_m_nf prostate_GDS2545_m_p prostate_GDS2545_p_nf sarcoma_data squamous_GDS2520 breast_GDS807 bipolar_GDS2190 The phenotypes has also been provided and the pathways. For more details, please see the individual help of each dataset as well as (Eddy et al. 2010).

Author(s)

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

bipolar_GDS2190 *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Bipolar*

Description

Bipolar dataset: Gene expression matrix and a factor with binary ("Normal", "Bipolar") phenotypes corresponding to the samples.

Usage

```
data(bipolar_GDS2190)
```

Format

The `bipolar_GDS2190` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to Bipolar disorder (Bipolar or Normal) in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally from Ryan et al. (2006)

Author(s)

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5) Ryan, M. M., et al. "Gene expression analysis of bipolar disorder reveals downregulation of the ubiquitin cycle and alterations in synaptic genes." *Molecular psychiatry* 11.10 (2006): 965-978.

See Also

diracpathways

Examples

```
### Load gene expression data
data(squamous_GDS2520)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

`breast_GDS807` *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Breast cancer*

Description

Squamous dataset: Gene expression matrix and a factor with binary ("Responsive", "non-Responsive") phenotypes corresponding to the samples.

Usage

```
data(breast_GDS807)
```

Format

The `breast_GDS807` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the breast cancer data set in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally from Ma et al. (2004)

Author(s)

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Ma, Xiao-Jun, et al. "A two-gene expression ratio predicts clinical outcome in breast cancer patients treated with tamoxifen." *Cancer cell* 5.6 (2004): 607-616.

See Also

diracpathways

Examples

```
### Load gene expression data
data(squamous_GDS2520)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

---

diracpathways *The pathways downloaded from DIRAC paper*

Description

A list of gene sets representing pathways in Eddy et al (2010).

Usage

```
data(diracpathways)
```

Format

The diracpathways list contains the list of pathways. Each element is a vector of gene names.

Details

This list has been extracted from Eddy et al (2010).

Author(s)

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

See Also

GSBenchMarkDatasets

Examples

```
### Load pathways
data(diracpathways)

### The number of pathways coming from Eddy et al.
length(diracpathways)

### It is a list of pathways
class(diracpathways)

### Genes in the pathway TERCPATHWAY
diracpathways[["TERCPATHWAY"]]
```

---

exprsdata *Gene expression matrix from DIRAC paper*

Description

Gene expression matrices from different datasets will have this name. When the user loads a dataset from GSBenchMark, one of the variables loaded has this name.

Usage

```
exprsdata
```

Format

The exprsdata contains normalized of any dataset loaded from GSBenckMark package. The rows represent genes and the columns samples.

Details

This dataset corresponds to the Prostate cancer in Eddy and colleagues in PLoS Comp. Bio. (2010).

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

See Also

diracpathways, GSBenchMarkDatasets, phenotypes

Examples

```
### Load gene expression data
data(prostate_GDS2545_p_nf)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)
```

GSBenchMarkDatasets *The names of the datasets of gene expressions and phenotypes downloaded from DIRAC paper*

Description

The list of datasets used in Eddy et al (2010).

Usage

```
data(GSBenchMarkDatasets)
```

Format

The GSBenchMark.Dataset.names list contains the names of the datasets with gene expressions and phenotypes.

Details

This list gene expression datasets provided in Eddy et al (2010).

Author(s)

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

See Also

diracpathways

Examples

```
### Loading the names of the gene expression dataset
data(GSBenchMarkDatasets)

### The names of datasets
print(GSBenchMark.Dataset.names)

### Loading "leukemia_GSEA"
data(list=GSBenchMark.Dataset.names[[1]])
```

---

leukemia_GSEA *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Leukaemia*

Description

Leukaemia dataset: Gene expression matrix and a factor with binary (AML, ALL) phenotypes corresponding to the samples.

Usage

```
data(leukemia_GSEA)
```

Format

The `leukemia_GSEA` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the Leukemia in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally Armstrong and et al (2002).

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Armstrong, Scott A., et al. "MLL translocations specify a distinct gene expression profile that distinguishes a unique leukemia." *Nature genetics* 30.1 (2002): 41-47.

See Also

diracpathways

Examples

```
### Load gene expression data
data(leukemia_GSEA)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

logexprsdata *Gene expression matrix from DIRAC paper*

Description

The log of gene expressions are saved in matrices with this name. When the user loads a dataset from GSBenchMark, one of the variables loaded has this name.

Usage

```
logexprsdata
```

Format

The `logexprsdata` contains the log of normalized of any dataset loaded from GSBenckMark package. The rows represent genes and the columns samples.

Details

This dataset corresponds to the Prostate cancer in Eddy and colleagues in PLoS Comp. Bio. (2010).

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

See Also

diracpathways, GSBenchMarkDatasets, phenotypes, exprsdata

Examples

```
### Load gene expression data
data(prostate_GDS2545_p_nf)

### Number of genes
nrow(logexprsdata)

### Number of samples
ncol(logexprsdata)
```

```
### Show the first  10 gene names of the ``logexprsdata'' matrix
head(rownames(logexprsdata), n=10)
```

`marfan_GDS2960` *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Marfan*

Description

Marfan dataset: Gene expression matrix and a factor with binary ("non-MFS","MFS") phenotypes corresponding to the samples.

Usage

```
data(marfan_GDS2960)
```

Format

The `marfan_GDS2960` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to Marfan disease in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally Yao (2007).

Author(s)

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Yao, Zizhen, et al. "A Marfan syndrome gene expression phenotype in cultured skin fibroblasts." *BMC Genomics* 8.1 (2007): 319.

See Also

`diracpathways`

Examples

```
### Load gene expression data
data(marfan_GDS2960)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

`melanoma_GDS2735` *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Melanoma*

Description

Melanoma dataset: Gene expression matrix and a factor with binary phenotypes ("Normal", "Metastasis") corresponding to the samples.

Usage

```
data(melanoma_GDS2735)
```

Format

The `melanoma_GDS2735` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the melanoma cancer in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally from Critchley-Thorne (2007).

Author(s)

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Critchley-Thorne, Rebecca J., et al. "Down-regulation of the interferon signaling pathway in T lymphocytes from patients with metastatic melanoma." *PLoS Medicine* 4.5 (2007): e176.

See Also

diracpathways

Examples

```
### Load gene expression data
data(melanoma_GDS2735)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

---

parkinsons_GDS2519 *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Parkinson's*

Description

Parkinson's dataset: Gene expression matrix and a factor with binary ("Normal", "Parkinson's") phenotypes corresponding to the samples.

Usage

```
data(parkinsons_GDS2519)
```

Format

The `parkinsons_GDS2519` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the Parkinson's disease in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally Scherzer (2007).

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Scherzer, Clemens R., et al. "Molecular markers of early Parkinson's disease based on gene expression in blood." *Proceedings of the National Academy of Sciences* 104.3 (2007): 955-960.

See Also

diracpathways

Examples

```
### Load gene expression data
data(parkinsons_GDS2519)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

phenotypes *A factor for binary phenotypes from DIRAC paper*

Description

a factor for binary phenotypes corresponding to the samples and a two-element vector with the real label names. When the user loads one of data set from the GSBenchMark it will contain these two variables.

Usage

```
phenotypes
phenotypesLevels
```

Format

The `phenotypes` is a binary ("0" or "1") factor containing the phenotypes of the the samples in any dataset loaded from GSBenckMark package. "0" corresponds to less dangerous phenotype and "1" to more dangerous phenotype. The `phenotypesLevels` contains the real labels instead of "0" and "1".

Details

This dataset corresponds to the Prostate cancer in Eddy and colleagues in PLoS Comp. Bio. (2010).

Author(s)

Bahman Afsari <bahman@jhu.edu>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

See Also

diracpathways, GSBenchMarkDatasets, exprsdata

Examples

```
### Load gene expression data
data(prostate_GDS2545_p_nf)

### Show group variable
print(table(phenotypes))
print(phenotypesLevels)
```

`prostate_GDS2545_m_nf` *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Prostate*

Description

Prostate dataset: Gene expression matrix and a factor with binary phenotypes ("Normal" and "Metastasis") corresponding to the samples.

Usage

```
data(prostate_GDS2545_m_nf)
```

Format

The `prostate_GDS2545_m_nf` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the Prostate cancer in Eddy and colleagues in PLoS Comp. Bio. (2010).

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Chandran, Uma R., et al. "Gene expression profiles of prostate cancer reveal involvement of multiple molecular pathways in the metastatic process." *BMC cancer* 7.1 (2007): 64.

See Also

`diracpathways`

Examples

```
### Load gene expression data
data(prostate_GDS2545_m_nf)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

---

prostate_GDS2545_m_p *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Prostate*

Description

Prostate dataset: Gene expression matrix and a factor with binary phenotypes ("Primary" and "Metastasis") corresponding to the samples.

Usage

```
data(prostate_GDS2545_m_p)
```

Format

The `prostate_GDS2545_m_p` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the Prostate cancer in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally from Chandran (2007).

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Chandran, Uma R., et al. "Gene expression profiles of prostate cancer reveal involvement of multiple molecular pathways in the metastatic process." *BMC cancer* 7.1 (2007): 64.

See Also

diracpathways

Examples

```
### Load gene expression data
data(prostate_GDS2545_m_p)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

---

prostate_GDS2545_p_nf *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Prostate*

Description

Prostate dataset: Gene expression matrix and a factor with binary phenotypes ("Normal","Primary") corresponding to the samples.

Usage

```
data(prostate_GDS2545_p_nf)
```

Format

The `prostate_GDS2545_p_nf` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the Prostate cancer in Eddy and colleagues in PLoS Comp. Bio. (2010).

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Chandran, Uma R., et al. "Gene expression profiles of prostate cancer reveal involvement of multiple molecular pathways in the metastatic process." *BMC cancer* 7.1 (2007): 64.

See Also

diracpathways

Examples

```
### Load gene expression data
data(prostate_GDS2545_p_nf)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

---

sarcoma_data *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Sarcoma*

Description

Sarcoma (Gastrointestinal cancer) dataset: Gene expression matrix and a factor with binary phenotypes (GIST, LMS) corresponding to the samples.

Usage

```
data(sarcoma_data)
```

Format

The `sarcoma_data` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the Sarcoma cancer in Eddy and colleagues in PLoS Comp. Bio. (2010) abd originally data from Price et al.

Author(s)

Bahman Afsari <bahman.afsari@gmail.com>, Elana J. Fertig <ejfertig@jhmi.edu>

Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5)

Price, Nathan D., et al. "Highly accurate two-gene classifier for differentiating gastrointestinal stromal tumors and leiomyosarcomas." *Proceedings of the National Academy of Sciences* 104.9 (2007): 3414-3419.

See Also

`diracpathways`

Examples

```
### Load gene expression data
data(sarcoma_data)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

squamous_GDS2520 *Gene expression matrix and a factor for binary phenotypes from DIRAC paper: Squamous (Head and Neck Cancer)*

Description

Squamous dataset: Gene expression matrix and a factor with binary phenotypes (Normal, HNSCC) corresponding to the samples.

Usage

```
data(squamous_GDS2520)
```

Format

The `squamous_GDS2520` `exprsdata` contains normalized expression values (rows) across samples (columns). Group information is in the factor `phenotypes`.

Details

This dataset corresponds to the Squamous (Head and Neck) cancer in Eddy and colleagues in PLoS Comp. Bio. (2010) and originally from Kuriakose et al.

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Source

http://www.ncbi.nlm.nih.gov/pubmed/20523739

References

Eddy et al., "Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC).", *PLoS Comp. Bio.*, 2010, **6**(5) Kuriakose, M. A., et al. "Selection and validation of differentially expressed genes in head and neck cancer." *Cellular and Molecular Life Sciences CMLS* **61.11** (2004): 1372-1383.

See Also

diracpathways

Examples

```
### Load gene expression data
data(squamous_GDS2520)

### Number of genes
nrow(exprsdata)

### Number of samples
ncol(exprsdata)

### Show the first  10 gene names of the ``exprsdata'' matrix
head(rownames(exprsdata), n=10)


### Show group variable
table(phenotypes)
```

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