Package 'diggitdata'

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Type Package

Title Example data for the diggit package

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Description This package provides expression profile and CNV data for glioblastoma from TCGA, and transcriptional and post-translational regulatory networks assembled with the ARACNe and MINDy algorithms, respectively.

License GPL (>=2)

Depends R(>= 2.14.0), Biobase, methods

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`diggitdata-package` *Datasets and network models required for the examples in the diggit package*

Description

This package contains a human glioblastoma mRNA expression dataset, a human glioblastoma copy number variation (CNV) dataset, a glioblastoma context-specific transcriptional network, and a glioblastoma context-specific post-translational network.

Details

Package:	diggitdata
Type:	Package
Version:	0.99.0
Date:	2014-08-29
License:	GPL (>=2)
LazyLoad:	yes

Author(s)

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`gbm.aracne` *Transcriptional regulatory network for human glioblatoma*

Description

Human glioblastoma transcriptional regulatory network assembled by the ARACNe algorithm from TCGA expression data. The data is stored in a S3 class 'regulon' object.

Usage

```
data(gbm.aracne)
```

References

Margolin,A.A. et al. (2006) ARACNE: an algorithm for the reconstruction of gene regulatory networks in a mammalian cellular context. BMC Bioinformatics, 7 Suppl 1, S7.

Examples

```
data(gbm.aracne)
print(gbmTFregulon)
```

gbm.cnv *Human glioblastoma TCGA copy number variation (CNV) dataset*

Description

Normalized CNV data, sumarized at the gene level, for 230 samples from TCGA profiled by Agilent HG-CGH-244A arrays. The CNV data is in a matrix format, with samples in columns and genes in rows.

Usage

```
data(gbm.cnv)
```

Examples

```
data(gbm.cnv)
print(gbmCNV[1:5, 1:5])
```

gbm.cnv.normal *Human normal blood TCGA copy number variation (CNV) dataset*

Description

Normalized CNV data, sumarized at the gene level, for 33 blood samples from TCGA profiled by Agilent HG-CGH-244A arrays. The CNV data is in a matrix format, with samples in columns and genes in rows.

Usage

```
data(gbm.cnv.normal)
```

Examples

```
data(gbm.cnv.normal)
print(gbmCNVnormal[1:5, 1:5])
```

gbm.expression *Human glioblastoma mRNA expression dataset from TCGA*

Description

ExpressionSet object containing cleaner summarized and mas5 normalized mRNA expression data from 250 human glioblastoma samples profiled by TCGA on HT-HGU133A arrays.

Usage

```
data(gbm.expression)
```

References

Alvarez,M.J. et al. (2009) Correlating measurements across samples improves accuracy of large-scale expression profile experiments. Genome Biol., 10, R143.

Examples

```
data(gbm.expression)
print(gbmExprs)
```

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gbm.mindy *Post-translational regulatory network for human glioblatoma*

Description

Human glioblastoma post-translational regulatory network assembled by the MINDy algorithm from TCGA expression data. The data is stored in a S3 class 'regulon' object.

Usage

```
data(gbm.mindy)
```

References

Wang,K. et al. (2009) Genome-wide identification of post-translational modulators of transcription factor activity in human B cells. Nat. Biotechnol., 27, 829-39.

Examples

```
data(gbm.mindy)
print(gbmMindy)
```

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