

# Package ‘diggitdata’

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**Type** Package

**Title** Example data for the diggit package

**Version** 1.37.0

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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

**Imports** viper

**LazyLoad** yes

**biocViews** ExperimentData, Cancer

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

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### 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 glioblastoma*

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### 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, summarized 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, summarized 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 glioblastoma*

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**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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