

# Package ‘diggitdata’

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**Type** Package

**Title** Example data for the diggit package

**Version** 1.39.0

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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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## Contents

|                              |          |
|------------------------------|----------|
| diggitdata-package . . . . . | 2        |
| gbm.aracne . . . . .         | 2        |
| gbm.cnv . . . . .            | 3        |
| gbm.cnv.normal . . . . .     | 3        |
| gbm.expression . . . . .     | 4        |
| gbm.mindy . . . . .          | 4        |
| <b>Index</b>                 | <b>5</b> |

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*

---

**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)
```

# Index

## \* datasets

- gbm.aracne, 2
- gbm.cnv, 3
- gbm.cnv.normal, 3
- gbm.expression, 4
- gbm.mindy, 4

diggitdata (diggitdata-package), 2  
diggitdata-package, 2

- gbm.aracne, 2
- gbm.cnv, 3
- gbm.cnv.normal, 3
- gbm.expression, 4
- gbm.mindy, 4
- gbmCNV (gbm.cnv), 3
- gbmCNVnormal (gbm.cnv.normal), 3
- gbmExprs (gbm.expression), 4
- gbmMindy (gbm.mindy), 4
- gbmTFregulon (gbm.aracne), 2