

# Package ‘diggitdata’

October 28, 2025

**Type** Package  
**Title** Example data for the diggit package  
**Version** 1.41.0  
**Date** 2014-08-29  
**Author** Mariano Javier Alvarez  
**Maintainer** Mariano Javier Alvarez <reef103@gmail.com>  
**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  
**git\_url** <https://git.bioconductor.org/packages/diggitdata>  
**git\_branch** devel  
**git\_last\_commit** f8f5c89  
**git\_last\_commit\_date** 2025-04-15  
**Repository** Bioconductor 3.23  
**Date/Publication** 2025-10-28

## 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 | <i>Datasets and network models required for the examples in the diggit package</i> |
|--------------------|------------------------------------------------------------------------------------|

---

## 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)

Mariano Javier Alvarez

Maintainer: Mariano Javier Alvarez <reef103@gmail.com>

---

|            |                                                                  |
|------------|------------------------------------------------------------------|
| gbm.aracne | <i>Transcriptional regulatory network for human glioblastoma</i> |
|------------|------------------------------------------------------------------|

---

## 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 | <i>Human glioblastoma mRNA expression dataset from TCGA</i> |
|----------------|-------------------------------------------------------------|

---

**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)
```

---

|           |                                                                     |
|-----------|---------------------------------------------------------------------|
| gbm.mindy | <i>Post-translational regulatory network for human glioblastoma</i> |
|-----------|---------------------------------------------------------------------|

---

**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](#)