

# diggitdata, a data package required for the examples and vignette of the diggit package

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## 1 Overview of diggitdata data package

The *diggitdata* data package provides some example datasets, including mRNA expression and copy number variation (CNV) profiles for human glioblastoma, CNV for normal blood samples, and two human glioma-context specific regulatory networks, including a transcriptional regulatory network assembled by the ARACNe algorithm[2] and a post-translational regulatory network reverse engineered by the MINDy algorithm[3].

**Human glioblastoma mRNA expression dataset** The human glioblastoma dataset consists of 250 human glioblastoma samples profiled by The Cancer Genome Atlas (TCGA) on Affymetrix HT-HGU133A arrays. The raw data was pre-processed by the cleaner algorithm [1] and then MAS5 normalized. The dataset is contained in an ExpressionSet object with 6,215 features (genes) x 250 samples. We can access this dataset with the following code:

```
> library(diggitdata)
> data(gbm.expression)
> print(gbmExprs)
```

```
ExpressionSet (storageMode: lockedEnvironment)
assayData: 9215 features, 245 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: TCGA-02-0071-01 TCGA-02-0086-01 ... TCGA-06-0747-01 (245
    total)
  varLabels: subtype
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation:
```

**Human glioblastoma Copy Number Variation (CNV) dataset** The human glioblastoma CNV dataset contains 230 human glioblastoma samples profiled by TCGA on Agilent HG-CGH-244A arrays. The arrays data was summarized at the gene level and stored in a numerical matrix format, with genes in rows and samples in columns. To access this dataset we can use the code:

```
> data(gbm.cnv)
> print(gbmCNV[1:3, 1:3])
```

|          | TCGA-02-0001-01 | TCGA-02-0002-01 | TCGA-02-0003-01 |
|----------|-----------------|-----------------|-----------------|
| B4GALNT1 | -0.01903801     | -0.008458616    | 1.251183        |
| DTX3     | -0.01391792     | -0.007144781    | 1.099719        |
| SEC61G   | 0.20503025      | -0.157275603    | 1.440273        |

**Human blood CNV dataset** The human blood CNV dataset contains 33 normal human blood samples profiled by TCGA on Agilent HG-CGH-244A arrays. The arrays data was summarized at the gene level and stored in a numerical matrix format, with genes in rows and samples in columns. To access this dataset we can use the code:

```
> data(gbm.cnv.normal)
> print(gbmCNVnormal[1:3, 1:3])
```

|           | TCGA-08-0344-11A | TCGA-08-0345-11A | TCGA-08-0349-11A |
|-----------|------------------|------------------|------------------|
| LOC440900 | 0.02076955       | 0.05375572       | 0.002933042      |
| FAM83D    | 0.03465642       | 0.01119457       | 0.049300981      |
| SLK       | 0.02287745       | -0.02443086      | -0.021355070     |

**Human glioma context-specific transcriptional network** The human glioma transcriptional regulatory network (transcriptional interactome) represents 183,774 inferred regulatory interactions between 835 transcription factors and 8,365 target genes. It is contained in a *regulon* class S3 object, and methods to access it are included in the *viper* package, which is available from Bioconductor and it is imported by the *diggitdata* package.

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

Object of class *regulon* with 835 regulators, 8365 targets and 183774 interactions

**Human glioma context-specific post-translational network for CEBPB, CEBPD and STAT3** The human glioma post-translational regulatory network (post-translational interactome) represents 43 inferred modulatory interactions between 38 signaling genes and the 3 considered transcription factors. It is contained in a *regulon* class S3 object, and methods to access it are included in the *viper* package, which is available from Bioconductor and it is imported by the *diggitdata* package.

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

Object of class *regulon* with 157 regulators, 3 targets and 178 interactions

## References

- [1] Alvarez,M.J. et al. (2009) Correlating measurements across samples improves accuracy of large-scale expression profile experiments. *Genome Biol.*, 10, R143.
- [2] 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.
- [3] 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.