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

Mariano J. Alvarez, James Chen, Andrea Califano
Department of Systems Biology, Columbia University, New York, USA

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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 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.