

Package ‘netDx.examples’

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Title Companion data package to netDx

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Description Companion data package to run vignettes for netDx.

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cnv_GR	<i>CNV locations for breast cancer (subset)</i>
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Description

Subset of CNV locations for TCGA breast tumour. Each range is associated with a patient (ID)

Source

The Cancer Genome Atlas. (2012). Nature 490:61-70.

References

The Cancer Genome Atlas. (2012). Nature 490:61-70.

Examples

```
data(TCGA_BRCA)
head(cnv_GR)
```

genes	<i>Table of gene definitions (small subsample of human genes)</i>
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Description

data.frame object with columns of (gene) RefSeq ID (name), chromosome (chrom), strand, transcription start site (txStart), transcription end site (txEnd), and gene symbol (name2)

Usage

```
data(genes)
```

Examples

```
data(genes)
head(genes)
```

`KIRC_dat`*Clinical and gene expression data for kidney cancer survival.*

Description

List with one entry for clinical data ("clinical") and one for gene expression ("rna"). Each entry contains a data.frame with patient-level measures (columns) for clinical variables or genes (rows).

Usage

```
data(KIRC_dat)
```

References

Yuan Y, Van Allen EM, Omberg L, Wagle N, Amin-Mansour A, Sokolov A, Byers LA, Xu Y, Hess KR, Diao L, Han L, Huang X, Lawrence MS, Weinstein JN, Stuart JM, Mills GB, Garraway LA, Margolin AA, Getz G, Liang H (2014b) Synapse syn1710286.

Examples

```
data(KIRC_dat)
head(KIRC_dat)
```

`KIRC_group`*Variable groupings for kidney cancer survival data (clinical and gene expression)*

Description

List with one entry for clinical data ("clinical") and one for gene expression ("rna"). Each entry contains a list with keys being group names, and values containing members for the corresponding groups. Correspond to data present in KIRC_dat

Usage

```
data(KIRC_group)
```

References

Yuan Y, Van Allen EM, Omberg L, Wagle N, Amin-Mansour A, Sokolov A, Byers LA, Xu Y, Hess KR, Diao L, Han L, Huang X, Lawrence MS, Weinstein JN, Stuart JM, Mills GB, Garraway LA, Margolin AA, Getz G, Liang H (2014b) Synapse syn1710286.

Examples

```
data(KIRC_group)
head(KIRC_group)
```

`KIRC_pheno`*Sample metadata table for kidney cancer example*

Description

data.frame with patient ID (ID), survival status (STATUS) and covariates. Data from the PanCancer Survival project.

Usage

```
data(KIRC_pheno)
```

References

Yuan Y, Van Allen EM, Omberg L, Wagle N, Amin-Mansour A, Sokolov A, Byers LA, Xu Y, Hess KR, Diao L, Han L, Huang X, Lawrence MS, Weinstein JN, Stuart JM, Mills GB, Garraway LA, Margolin AA, Getz G, Liang H (2014b) Synapse syn1710286.

Examples

```
data(KIRC_pheno)
head(KIRC_pheno)
```

`MB.pheno`*Gene expression for medulloblastoma example*

Description

data.frame with gene expression values (rows) for all patients (columns)

Source

Northcott et al. (2011). J Clin Oncol. 29 (11):1408.

References

Northcott et al. (2011). J Clin Oncol. 29 (11):1408.

Examples

```
data(MBblastoma)
head(MB.pheno)
```

`MB.xpr`*Sample metadata table for medulloblastoma dataset.*

Description

data.frame with patient ID and tumour subtype (STATUS)

Usage

```
data(MB.xpr)
```

Source

Northcott et al. (2011). J Clin Oncol. 29 (11):1408.

References

Northcott et al. (2011). J Clin Oncol. 29 (11):1408.

Examples

```
data(MBblastoma)
head(MB.xpr)
```

`MB.xpr_names`*Gene names for medulloblastoma expression data*

Description

Vector of gene symbols

Source

Northcott et al. (2011). J Clin Oncol. 29 (11):1408.

References

Northcott et al. (2011). J Clin Oncol. 29 (11):1408.

Examples

```
data(MBblastoma)
head(MB.xpr_names)
```

pheno	<i>Sample metadata table</i>
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Description

data.frame with patient ID (ID), sample type (Type), tumour subtype (STATUS). From TCGA 2012 breast cancer paper (see reference).

Source

The Cancer Genome Atlas. (2012). Nature 490:61-70.

References

The Cancer Genome Atlas. (2012). Nature 490:61-70.

Examples

```
data(TCGA_BRCA)
head(pheno)
```

TCGA_BRCA	<i>Breast cancer sample data</i>
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Description

Contains three objects: 1) pheno: data frame with sample metadata. data.frame with patient ID (ID), sample type (Type), tumour subtype (STATUS). 2) xpr: gene expression table 3) cnv_GR: GenomicRanges object with patient CNVs

Source

The Cancer Genome Atlas. (2012). Nature 490:61-70.

References

The Cancer Genome Atlas. (2012). Nature 490:61-70.

Examples

```
data(TCGA_BRCA)
head(pheno)
head(xpr)
head(cnv_GR)
```

`xpr`*Example expression matrix*

Description

data.frame with gene expression for 727 genes (rows) and 40 patients (columns). Data from TCGA breast cancer subtyping study.

Source

The Cancer Genome Atlas. (2012). Nature 490:61-70.

References

The Cancer Genome Atlas. (2012). Nature 490:61-70.

Examples

```
data(TCGA_BRCA)
head(xpr)
```

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