Package ‘mcsurvdata’

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**Type**  Package

**Version**  1.22.0

**Date**  2023-07-20

**Title**  Meta cohort survival data

**Description**  This package stores two merged expressionSet objects that contain
the gene expression profile and clinical information of -a- six breast
cancer cohorts and -b- four colorectal cancer cohorts. Breast cancer
data are employed in the vignette of the hrunbiased package for survival
analysis of gene signatures.

**VignetteBuilder**  knitr

**License**  GPL (>=2)

**NeedsCompilation**  no

**biocViews**  ExperimentData, Homo_sapiens_Data, GEO, MicroarrayData

**URL**  https://github.com/adricaba/mcsurvdata

**Depends**  R (>= 3.5), ExperimentHub

**Suggests**  BiocStyle, knitr

**Imports**  AnnotationHub, Biobase

**git_url**  https://git.bioconductor.org/packages/mcsurvdata

**git_branch**  RELEASE_3_19

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mcsurvdata  
Processed gene expression data and clinical information of several breast cancer and colorectal cancer cohorts

Description

Contains the processed gene expression data and clinical data from six breast cancer studies *nda.brca* as well as from four colon cancer studies *nda.crc*.

Details

ExpressionSet objects with merged data

Examples

```r
library(ExperimentHub)
eh <- ExperimentHub()
nda.brca <- query(eh, "mcsurvdata")[["EH1497"]]
nda.crc <- query(eh, "mcsurvdata")[["EH1498"]]
```

nda.brca  
Processed gene expression data and clinical information of six breast cancer cohorts

Description

Processed gene expression data and clinical data of 2294 patients from six breast cancer studies. These include GSE1456, GSE2034, GSE2990, GSE3494, GSE7390 and the metabric. Normalization is done by adjusting each gene by technical covariates such as Eklund metrics and scanning day in basis of a mixed effects model. Data merging is done by standardizing the gene expression matrix of GSE1456, GSE2034, GSE2990, GSE3494 and GSE7390 to a reference dataset (metabric). Only ER+ samples are included. Data in this package are used for the hrunbiased R package vignette
Details

ExpressionSet object with merged data from studies:

- GSE1456
- GSE2034
- GSE2990
- GSE3494
- GSE7390
- metabric

Author(s)

Adria Caballe Mestres, Antoni Berenguer Llergo, Camille Stephan-Otto Attolini.

References


Examples

```r
library(ExperimentHub)
eh <- ExperimentHub()
da.brca <- query(eh, "mcsurvdata")[["EH1497"]]

# survival info
cbind(da.brca$evn, da.brca$tev)
```
Processed gene expression data and clinical data of 914 patients from four colorectal cancer studies. These include GSE14333, GSE33113, GSE37892 and GSE39582. Normalization is done by adjusting each gene by technical covariates such as Eklund metrics and scanning day in basis of a mixed effects model. Data merging is done by standardizing the gene expression matrix of GSE14333, GSE33113 and GSE37892 to a reference dataset (GSE39582). Only MSS samples are included.

**Details**

ExpressionSet object with merged data from studies:

- GSE14333
- GSE33113
- GSE39582
- GSE37892

**Author(s)**

Adria Caballe Mestres, Antoni Berenguer Llergo, Camille Stephan-Otto Attolini.

**References**


Examples

```r
library(ExperimentHub)
eh <- ExperimentHub()
nda.crc <- query(eh, "mcsurvdata")[["EH1498"]]

# survival info
cbind(nda.crc$evn, nda.crc$tev)
```
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