Package ‘mcsurvdata’

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Type Package
Version 1.4.0
Date 2018-07-20
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 knitr
Imports AnnotationHub, Biobase
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git_branch RELEASE_3_10
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**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"]]
```

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**nda.brca**

Processed gene expression data and clinical information of several breast cancer and colorectal 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()
nda.brca <- query(eh, "mcsurvdata")[["EH1497"]]

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

Description

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


Eklund A. and Szallasi Z. Correction of technical bias in clinical microarray data improves concordance with known biological information. Genome Biology 9, R26 (2008)


Examples

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

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