

Package ‘MetaGxPancreas’

June 30, 2022

Title Transcriptomic Pancreatic Cancer Datasets

Version 1.16.0

Description A collection of pancreatic Cancer transcriptomic datasets that are part of the MetaGxData package compendium. This package contains multiple pancreas cancer datasets that have been downloaded from various resources and turned into SummarizedExperiment objects. The details of how the authors normalized the data can be found in the experiment data section of the objects. Additionally, the location the data was obtained from can be found in the url variables of the experiment data portion of each SE.

License Artistic-2.0

Encoding UTF-8

Depends SummarizedExperiment, ExperimentHub, R (>= 3.6.0)

Imports stats, impute, S4Vectors, AnnotationHub

Suggests testthat, knitr, BiocStyle, rmarkdown, markdown

VignetteBuilder knitr

biocViews ExpressionData, ExperimentHub, CancerData,
Homo_sapiens_Data, ArrayExpress, GEO, NCI, MicroarrayData,
ExperimentData, SequencingData

LazyData yes

RoxygenNote 7.1.1

git_url <https://git.bioconductor.org/packages/MetaGxPancreas>

git_branch RELEASE_3_15

git_last_commit cc86cbb

git_last_commit_date 2022-04-26

Date/Publication 2022-06-30

Author Michael Zon [aut],
Vandana Sandhu [aut],
Christopher Eeles [ctb],
Benjamin Haibe-Kains [aut, cre]

Maintainer Benjamin Haibe-Kains <benjamin.haibe.kains@utoronto.ca>

R topics documented:

loadPancreasDatasets 2

Index 4

loadPancreasDatasets *Function to load pancreas cancer expression profiles from the Experiment Hub*

Description

This function returns pancreas cancer patient cohorts in SummarizedExperiment object from the hub and a vector of patients from the datasets that are duplicates

Usage

```
loadPancreasDatasets(
  removeDuplicates = TRUE,
  quantileCutoff = 0,
  rescale = FALSE,
  minNumberGenes = NA,
  minSampleSize = NA,
  minNumberEvents = NA,
  removeSeqSubset = FALSE,
  keepCommonOnly = FALSE,
  imputeMissing = FALSE
)
```

Arguments

removeDuplicates remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)

quantileCutoff A numeric between 0 and 1 specifying to remove genes with standard deviation below the required quantile (default 0)

rescale apply centering and scaling to the expression sets (default FALSE)

minNumberGenes an integer specifying to remove expression sets with less genes than this number (default 0)

minSampleSize an integer specifying the minimum number of patients required in an SE (default 0)

minNumberEvents an integer specifying how man survival events must be in the dataset to keep the dataset (default 0)

removeSeqSubset currently only removes the ICGSSEQ dataset as it contains the same patients as the ICGS microarray dataset (default TRUE, currently just ICGSSEQ)

`keepCommonOnly` remove probes not common to all datasets (default FALSE)
`imputeMissing` impute missing expression value via knn

Value

a list with two elements. The First element named `SummarizedExperiments` contains the datasets as Bioconductor `SummarizedExperiment` objects. The second element named `duplicates` contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

Examples

```
sumExptsAndDuplicates <- loadPancreasDatasets()
```

Index

loadPancreasDatasets, [2](#)