

# Package ‘MetaGxPancreas’

June 28, 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** 2022-06-28

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## 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](#)