**R topics documented:**

loadPancreasDatasets .............................................. 2

Index 4

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**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**

```r
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 many 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)
loadPancreasDatasets

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