Package ‘a4Preproc’

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Type Package
Title Automated Affymetrix Array Analysis Preprocessing Package
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Description Automated Affymetrix Array Analysis Preprocessing Package
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License GPL-3
biocViews Microarray
NeedsCompilation no

R topics documented:

   addGeneInfo ................................................................. 1

Index

addGeneInfo Utility Function to Add Annotation to existing ExpressionSet Objects

Description

Add appropriate featureData, similar to the metadata added in the pipeline script, to the ExpressionSet object.

Usage

addGeneInfo(eset, annotationLibrary = NULL)
**Arguments**

- `eset` ExpressionSet object for which one wants to add additional annotation information.
- `annotationLibrary` Annotation Library to use. Must be specified when working with Entrez gene IDs. In this case, one can make use of the JnJ annotation packages such as `hgu133plus2hsentrezgJnJ`. If not specified, the annotation of the package will be automatically requested with `annotation()` of the expressionSet object `eset` and then Affymetrix probe set IDs are expected in `featureNames`.

**Details**

Slots of `featureData(a4ALL)` are:

- `Entrez ID~`: Entrez ID as retrieved from annotation package.
- `Ensembl ID~`: Ensembl ID as retrieved from annotation package.
- `Gene Symbol~`: Gene symbol as retrieved from annotation package.
- `Description~`: Description as retrieved from annotation package.

**Value**

A new ExpressionSet object with the additional information stored as feature data.

**Note**

One should always use subscripting of `featureData` by column name (e.g. `featureData(a4ALL)Entrez ID~`); as the pipeline ExpressionSets have one additional column compared to the `ExpressionSet` objects produced by `addGeneInfo`, i.e. column 2 of the pipeline ExpressionSets corresponds to column one of an `addGeneInfo` ExpressionSet.

**Author(s)**

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**Examples**

```r
library(ALL)
data(ALL)
a4ALL <- addGeneInfo(ALL)
head(featureData(a4ALL)Entrez ID~)
```
Index

*Topic manip
  addGeneInfo, 1

addGeneInfo, 1