Package ‘a4Preproc’

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Type Package

Title Automated Affymetrix Array Analysis Preprocessing Package

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Description Utility functions to preprocess data for the Automated Affymetrix Array Analysis set of packages.

Imports BiocGenerics, Biobase

Suggests ALL, hgu95av2.db, knitr, rmarkdown

License GPL-3

biocViews Microarray, Preprocessing

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VignetteBuilder knitr

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`addGeneInfo` *Utility Function to Add Annotation to existing ExpressionSet Objects*

Description

Adds 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 to 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

```
library(ALL)
data(ALL)
a4ALL <- addGeneInfo(ALL)
head(featureData(a4ALL)$`Entrez ID`)
```

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