

Package ‘a4Preproc’

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Type Package

Title Automated Affymetrix Array Analysis Preprocessing Package

Version 1.49.0

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Description Utility functions to pre-process 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

RoxygenNote 7.1.1

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

| | |
|--------------------------------|---|
| <code>eset</code> | ExpressionSet object for to which one wants to add additional annotation information |
| <code>annotationLibrary</code> | 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 <code>hgu133plus2hsentrezgJnJ</code> . If not specified, the annotation of the package will be automatically requested with <code>annotation()</code> of the expressionSet object <code>eset</code> and then Affymetrix probe set IDs are expected in <code>featureNames</code> |

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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* **manip**

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