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
Depends methods, AnnotationDbi
Suggests ALL, hgu95av2.db
License GPL-3
biocViews Microarray
NeedsCompilation no

R topics documented:

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<th>Utility Function to Add Annotation to existing ExpressionSet Objects</th>
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Description

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

Usage

`addGeneInfo(eset, annotationLibrary = NULL)`
addGeneInfo

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

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