

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

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biocViews Microarray

NeedsCompilation no

R topics documented:

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| addGeneInfo | <i>Utility Function to Add Annotation to existing ExpressionSet Objects</i> |
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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)
```

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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*Topic **manip**

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