Package ‘a4Preproc’

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Type Package

Title Automated Affymetrix Array Analysis Preprocessing Package

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Author Willem Talloen, Tobias Verbeke

Maintainer Tobias Verbeke <tobias.verbeke@openanalytics.eu>, Willem Ligtenberg <willem.ligtenberg@openanalytics.eu>

Description Automated Affymetrix Array Analysis Preprocessing Package

Depends methods, AnnotationDbi

Suggests ALL, hgu95av2.db

License GPL-3

biocViews Microarray

NeedsCompilation no

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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)**

Tobias Verbeke, Steven Osselaer

**Examples**

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