Package 'a4Preproc'

July 23, 2025

Type Package	
Title Automated Affymetrix Array Analysis Preprocessing Package	
Version 1.56.0	
Date 2020-10-14	
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	
RoxygenNote 7.1.1	
VignetteBuilder knitr	
git_url https://git.bioconductor.org/packages/a4Preproc	
git_branch RELEASE_3_21	
git_last_commit 7ce40f8	
git_last_commit_date 2025-04-15	
Repository Bioconductor 3.21	
Date/Publication 2025-07-23	
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2 addGeneInfo

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) Tentrez 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`)</pre>
```

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```
* manip addGeneInfo, 2
```

 ${\tt addGeneInfo, 2}\\$