

Package ‘a4Preproc’

April 15, 2024

Type Package

Title Automated Affymetrix Array Analysis Preprocessing Package

Version 1.50.0

Date 2020-10-14

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

git_url <https://git.bioconductor.org/packages/a4Preproc>

git_branch RELEASE_3_18

git_last_commit 7f02ff9

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-15

Author Willem Talloen [aut],
Tobias Verbeke [aut],
Laure Cougnaud [cre]

Maintainer Laure Cougnaud <laure.cougnaud@openanalytics.eu>

R topics documented:

addGeneInfo	2
Index	4

`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)

Tobias Verbeke, Steven Osselaer

Examples

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

Index

* **manip**

addGeneInfo, [2](#)

addGeneInfo, [2](#)