

# 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

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addGeneInfo                      *Utility Function to Add Annotation to existing ExpressionSet Objects*

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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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