

# Package ‘a4Preproc’

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**Type** Package

**Title** Automated Affymetrix Array Analysis Preprocessing Package

**Version** 1.55.0

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**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

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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

<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)

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**Examples**

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

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\* **manip**

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