

# a4Preproc

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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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