

PROCESS

FUNCTION

Run microarrays to obtain the raw data files

Normalize the data using standard methods such as MAS5.0 or GCRMA as implemented in the Bioconductor affy package.

Import the data in the geneClassifiers packages by providing information on the preprocessing

Perform classification on the data

Export classification results

`setNormalizationMethod`

`runClassifier`

`getScores`
`getClassifications`