

# plier

April 20, 2011

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justPlier

*Implements the PLIER algorithm*

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## Description

Provides a wrapper around Affymetrix's API to provide an implementation of the PLIER algorithm

## Usage

```
justPlier(eset=ReadAffy(), replicate=1:length(eset), get.affinities=FALSE, normalize=TRUE)
```

## Arguments

eset	An AffyBatch object containing the raw data
replicate	A factor containing the replicate structure to use for grouping samples
get.affinities	If TRUE, then return affinities in the description@preprocessing slot of the ExpressionSet object
normalize	If TRUE then apply quantile normalization to the probes before generating expression calls
norm.type	Can be 'separate', 'pmonly', 'mmonly' or 'together'
augmentation	Model parameter
defaultaffinity	Model parameter
defaultconcentration	Model parameter
attenuation	Model parameter
seaconvergence	Model parameter
seaiteration	Model parameter
gmcutoff	Model parameter
probepenalty	Model parameter
concpenalty	Model parameter
usemm	Model parameter

usemodel        Model parameter  
fitaffinity    Model parameter  
plierconvergence  
                  Model parameter  
plieriteration  
                  Model parameter  
dropmax        Model parameter  
lambdalimit   Model parameter  
optimization   Model parameter

### Details

This function is a thin wrapper around the Affymetrix implementation. For more details, including information about the meaning of the different model parameters, please see the plier documentation at [www.affymetrix.com](http://www.affymetrix.com).

### Value

An Expression set containing PLIER generated expression calls

### Author(s)

Crispin J Miller (wrapper), Earl Hubbell (algorithm)

### References

[bioinf.picr.man.ac.uk](http://bioinf.picr.man.ac.uk) [www.affymetrix.com](http://www.affymetrix.com)

### See Also

`normalize.AffyBatch.quantiles`

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