Package 'plier'

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Title Implements the Affymetrix PLIER algorithm

Version 1.82.0

Author Affymetrix Inc., Crispin J Miller, PICR

Description The PLIER (Probe Logarithmic Error Intensity Estimate) method produces an improved signal by accounting for experimentally observed patterns in probe behavior and handling error at the appropriately at low and high signal values.

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Depends R (>= 2.0), methods

Imports affy, Biobase, methods

License GPL (>= 2)

biocViews Software

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justPlier *Implements the PLIER algorithm*

Description

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

Usage

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

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.

Value

An Expression set containing PLIER generated expression calls

Author(s)

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

References

bioinf.picr.man.ac.uk www.affymetrix.com

See Also

normalize.AffyBatch.quantiles

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