plier

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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,normaliz
```

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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