Package 'AffyRNADegradation'

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Type Package

Title Analyze and correct probe positional bias in microarray data due to RNA degradation

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Depends R (>= 2.9.0), methods, affy

Suggests AmpAffyExample

biocViews GeneExpression, Microarray, OneChannel, Preprocessing,QualityControl, Bioinformatics

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Description The package helps with the assessment and correction of RNA
degradation effects in Affymetrix 3' expression arrays. The parameter d
gives a robust and accurate measure of RNA integrity. The correction
removes the probe positional bias, and thus improves comparability of
samples that are affected by RNA degradation.

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Collate AllClasses.R decayFunction.R AffyRNADegradation.R probeInfo.R tongs.R

R topics documented:

AffyDegradationBatch-class

Class AffyDegradationBatch

Description

This class represents Affymetrix GeneChip probe level data that has been analysed and corrected for the probe location bias.

Objects from the Class

Objects can be created using the function RNADegradation.

Slots

location.type**:** Object of class character describing the type of probe position used for the analysis (probe index or probe location).

afbatch**:** Object of class AffyBatch containing corrected probe level data.

stats**:** Object of class matrix containg various statistical parameters from the analysis.

means.pm**:** Object of class matrix containing the average PM probe intensites for probe locations of expressed genes.

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Methods

afbatch signature(x = "AffyDegradationBatch"): returns as AffyBatch object containing corrected probe level data.

d signature(x = "AffyDegradationBatch"): returns a vector with a measure of RNA degradation for each sample

plotDx signature(x = "AffyDegradationBatch"): plots the probe location bias for all samples of the experiment.

Author(s)

Mario Fasold

See Also

AffyBatch

Examples

```
if (require(AmpAffyExample)) {
  # Get example data
  data(AmpData)

  affy.deg <- RNADegradation(AmpData[,4])

  ## Plot degradation
```

```
plotDx(affy.deg)

## Get degradation measure
d(affy.deg)

## Get AffyBatch object with corrected probe intensities
afbatch(affy.deg)
}
```

AffyRNADegradation   *AffyRNADegradation: analyze and correct RNA degradation effects*

Description

The AffyRNADegradation package helps in the assessment of RNA degradation effects in Affymetrix 3' expression arrays. The parameter d gives a robust and accurate measure of RNA integrity. The correction removes the probe positional bias, and thus improves comparability of samples that are affected by RNA degradation.

Details

Package:	AffyRNADegradation
Type:	Package
Version:	0.1.0
Date:	2011-10-13
License:	GPL >=2

The RNADegradation function performs both analysis and correction of RNA degradation effects, returning an object of type AffyDegradationBatch. The class provides accessor functions to obtain the degradation parameter d and a AffyBatch object containing corrected probe intensities. A more detailed look on the RNA degradation effects can be gained through the tongs plot, the Dx plot and further statistics.

Author(s)

Mario Fasold

Examples

```
if (require(AmpAffyExample)) {
 # Load example data (AmpData affybatch)
 data(AmpData)

 ## Compute and correct degradation for a single chip (for speed)
 affy.deg <- RNADegradation(AmpData[,4])

 ## Show degradation parameter d
 d(affy.deg)

 ## Replace data with corrected data for further analysis
 AmpData <- afbatch(affy.deg)
```

```
}
```

GetTongs   *Generate and visualize the tongs plot*

Description

The tongs plot and the related degradation hook show the relationship between expression level and probe location bias. They are required for the correct estimation of RNA degradation effects.

Usage

```
GetTongs(affyData, chip.idx = 1)
PlotTongs(tongs)
PlotDegradationHooks(affyData, ...)
```

Arguments

affyData	an AffyBatch object.
chip.idx	index of the sample to compute the tongs for.
tongs	the tongs plot data table.
...	optional graphical parameters.

Value

Tongs	a table containing Tongs plot values ordered by expression level.

Author(s)

Mario Fasold

Examples

```
if (require(AmpAffyExample)) {
  # Get example data
  data(AmpData)

  tongs <- GetTongs(AmpData, chip.idx = 4)
  PlotTongs(tongs)

  PlotDegradationHooks(AmpData[,c(3,4)])
}
```

RNADegradation　　　　　　*Compute degradation parameters and correct probe intensities*

Description

Given an AffyBatch object, the function RNADegradation computes the probe positional bias and several statistical parameters, including a robust and accurate measure of RNA degradation. Probe intensities are corrected for the bias for each sample within the AffyBatch object.

Usage

RNADegradation(affyData,
　　　　location.type = "index",
　　　　location.file.dir = NULL,
　　　　plot.images = FALSE)

Arguments

affyData　　　　an AffyBatch object containing the probe level microarray data.

location.type　　index-based probe alignment (x=k) if "index", or location-based alignment (x=L) if "absolute".

location.file.dir　directory containing the probe location file(s).

plot.images　　if TRUE plots a set of debug images.

Value

An AffyDegradationBatch object.

Author(s)

Mario Fasold

See Also

AffyDegradationBatch

Examples

```
if (require(AmpAffyExample)) {
  # Get example data
  data(AmpData)

  affy.deg <- RNADegradation(AmpData[,4])
}
```

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