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

Author Mario Fasold

Maintainer Mario Fasold <`fasold@izbi.uni-leipzig.de`>

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.

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` contaning various statistical parameters from the analysis.
- `means.pm`**:** Object of class `matrix` containing the average PM probe intensites for probe locations of expressed genes.
- `means.mm`**:** Object of class `matrix` containing the average MM probe intensites for probe locations of expressed genes.

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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