

# Package ‘AffyRNADegradation’

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**Type** Package

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

**Version** 1.54.0

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**Depends** R (>= 2.9.0), methods, affy

**Suggests** AmpAffyExample, hgu133acdf

**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.

**License** GPL-2

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

**biocViews** GeneExpression, Microarray, OneChannel, Preprocessing, QualityControl

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AffyDegradationBatch-class

*Class AffyDegradationBatch*

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### 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.

`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 | <i>AffyRNADegradation: analyze and correct RNA degradation effects</i> |
|--------------------|------------------------------------------------------------------------|

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**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)
}

```

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GetTongs

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*Generate and visualize the tongs plot*


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**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**

|                       |                                               |
|-----------------------|-----------------------------------------------|
| <code>affyData</code> | an AffyBatch object.                          |
| <code>chip.idx</code> | index of the sample to compute the tongs for. |
| <code>tongs</code>    | the tongs plot data table.                    |
| <code>...</code>      | 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)])  
}
```

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RNADegradation*Compute degradation parameters and correct probe intensities*

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**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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