

# Package ‘AffyRNADegradation’

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**Type** Package

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

**Version** 1.57.0

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

**Suggests** AmpAffyExample, hgu133acdf

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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.

**License** GPL-2

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

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AffyDegradationBatch-class	
	<i>Class AffyDegradationBatch</i>

---

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