

# Package: AffyRNADegradation (via r-universe)

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**Type** Package

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

**Version** 1.51.0

**Date** 2023-10-17

**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

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

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/AffyRNADegradation>

**RemoteRef** HEAD

**RemoteSha** 69bae53d5fb74c7abe13d5e2fab54b184bc801ae

## Contents

AffyDegradationBatch-class . . . . .	2
AffyRNADegradation . . . . .	3
GetTongs . . . . .	4
RNADegradation . . . . .	5

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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` 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 <- abatch(affy.deg)  
}
```

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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

<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)])  
}
```

---

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])  
}
```

# Index

\* **classes**

AffyDegradationBatch-class, 2

\* **methods**

GetTongs, 4

RNADegradation, 5

\* **package**

AffyRNADegradation, 3

afbatch (AffyDegradationBatch-class), 2

afbatch, AffyDegradationBatch-method  
(AffyDegradationBatch-class), 2

AffyDegradationBatch  
(AffyDegradationBatch-class), 2

AffyDegradationBatch, ANY  
(AffyDegradationBatch-class), 2

AffyDegradationBatch-class, 2

AffyRNADegradation, 3

AffyRNADegradation-package  
(AffyRNADegradation), 3

d (AffyDegradationBatch-class), 2

d, AffyDegradationBatch-method  
(AffyDegradationBatch-class), 2

GetTongs, 4

PlotDegradationHooks (GetTongs), 4

plotDx (AffyDegradationBatch-class), 2

plotDx, AffyDegradationBatch-method  
(AffyDegradationBatch-class), 2

PlotTongs (GetTongs), 4

RNADegradation, 5