

# Package ‘antiProfiles’

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**Title** Implementation of gene expression anti-profiles

**Description** Implements gene expression anti-profiles as described in Corrada Bravo et al., BMC Bioinformatics 2012, 13:272 doi:10.1186/1471-2105-13-272.

**Depends** R (>= 3.0), matrixStats (>= 0.50.0), methods (>= 2.14), locfit (>= 1.5)

**URL** <https://github.com/HCBravoLab/antiProfiles>

**biocViews** GeneExpression,Classification

**Suggests** antiProfilesData, RColorBrewer

**Collate** 'AllClasses.r' 'AllGenerics.r' 'show-methods.r'  
'antiProfiles-package.r' 'ap-methods.r' 'apCounts-methods.r'  
'apReorder-methods.r' 'apStats.r' 'accessors.r' 'ev.R'

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antiProfiles-package    *Gene Expression Anti-profiles*

### Description

This package implements the anti-profile method of Corrada Bravo et al., BMC Bioinformatics 2012, 13:272 doi:10.1186/1471-2105-13-272.

### Author(s)

Hector Corrada Bravo <hcorrada@gmail.com>

AntiProfile-class    *A gene expression anti-profile*

### Description

This class encapsulates anti-profiles. Objects of this class should be built from [AntiProfileStats](#) objects using the [buildAntiProfile](#) method. Anti-profile scores can be computed for new samples using the [apCount](#) method.

### Usage

## Accessors

```
getProbesetIds(object)
getNormalRegions(object)
```

### Arguments

object            Object of class (or inheriting from) [AntiProfile](#)

### Accessors

In the following code object is a [AntiProfile](#) object.

**getProbesetIds:** vector of Affymetrix ids for probesets included in the anti-profile (character)

**getNormalRegions:** median and upper boundary of normal expression regions (numeric matrix of dimension s-by-2, where s is the size of the anti-profile)

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**See Also**

[AntiProfileStats](#) for the class of objects from which anti-profiles are built. [buildAntiProfile](#) for the method used to construct objects of this class. [apCount](#) for the function used to calculate anti-profile scores from objects of this class.

**Examples**

```
if (require(antiProfilesData)) {
  data(apColonData)
  colonStats=apStats(exprs(apColonData), pData(apColonData)$Status)
  colonAP = buildAntiProfile(colonStats, tissueSpec=FALSE, sigsize=10)
  show(colonAP)

  head(getProbesetIds(colonAP))
  head(getNormalRegions(colonAP))
}
```

---

AntiProfileStats-class

*Statistics used to build anti-profiles*

---

**Description**

This class stores statistics required to build anti-profiles. Objects of this class should be built using the [apStats](#) function. To build anti-profiles from objects of this class, use the [buildAntiProfile](#) function.

**Usage**

```
## Accessors
getProbeStats(object)
```

**Arguments**

object            Object of class [AntiProfileStats](#)

**Accessors**

In the following code object is a [AntiProfileStats](#) object.

**getProbeStats:** Gets probeset statistics. A data.frame with columns

**affyid:** Affymetrix probeset id (character)

**SD0:** Normal expression standard deviation aggregated over tissue types (numeric)

**SD1:** Cancer expression standard deviation aggregated over tumor types (numeric)

**stat:** The log2-variance ratio statistic (numeric)  
**meds0:** Median normal expression aggregated over tissue types (numeric)  
**mads0:** Median absolute deviation of normal expression aggregate over tissue types (numeric)

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**See Also**

[apStats](#) to construct objects of this class, [buildAntiProfile](#) to build anti-profiles from objects of this class.

**Examples**

```
if (require(antiProfilesData)) {  
  data(apColonData)  
  colonStats = apStats(exprs(apColonData), pData(apColonData)$Status)  
  show(getProbeStats(colonStats))  
}
```

---

apCount

*Obtain the anti-profile score for a set of samples*

---

**Description**

This function applies the given anti-profile to a new set of samples. Rownames in the expression matrix are used to match probenames in the AntiProfile object.

**Arguments**

**fit** an object of class AntiProfile as produced by the buildAntiProfile method  
**expr** a matrix of gene expression, rownames are used as identifiers

**Value**

a numeric vector of anti-profile scores

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**Examples**

```

if (require(antiProfilesData)) {
  data(apColonData)

  # compute statistics
  colonStats = apStats(exprs(apColonData), pData(apColonData)$Status)

  # create an anti-profile, ignoring tissue-specificity of probesets, with 10 probesets
  ap = buildAntiProfile(colonStats, tissueSpec=FALSE, sigsize=10)

  # get counts for the original dataset
  counts = apCount(ap, exprs(apColonData))
}

```

---

apReorder

*Reorder an AntiProfileStats object*


---

**Description**

Reorders given AntiProfileStats object using provided ordering o

**Arguments**

stats            An object of class AntiProfileStats  
o                 A numeric vector giving new probe ordering

**Value**

A reordered AntiProfileStats object

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**Examples**

```

if (require(antiProfilesData)) {
  data(apColonData)
  colonStats = apStats(exprs(apColonData), pData(apColonData)$Status)
  o = sample(seq(len=nrow(slot(colonStats,"probes"))))
  newStats = apReorder(colonStats, o)
}

```

---

`apStats`*Compute statistics used to construct antiProfile*

---

**Description**

This function calculates normal ranges of expressions and variance ratios for all probesets. To create an anti-profile, call `buildAntiProfile` on the output of this function

**Usage**

```
apStats(e, cl, tiss = NULL, minL = 10, cutoff = 5,
        OnCutoff = 2.54)
```

**Arguments**

<code>e</code>	matrix of gene expression, with one column per sample
<code>cl</code>	vector of normal/cancer indicators as 0/1
<code>tiss</code>	vector of tissue types for each sample
<code>minL</code>	minimum number of samples of a given tissue/class to compute stats
<code>cutoff</code>	median absolute deviation multiplier used to determine proportion of samples within normal range of expression
<code>OnCutoff</code>	gene expression barcode z-score to determine if a gene is expressed

**Value**

An object of class `SuccsStats`

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**See Also**

[AntiProfileStats](#) for the type of object returned. [buildAntiProfile](#) to construct anti-profiles with objects returned by this function.

**Examples**

```
if (require(antiProfilesData)) {
  data(apColonData)
  colonStats = apStats(exprs(apColonData), pData(apColonData)$Status)
}
```

---

buildAntiProfile	<i>Create an anti-profile from a AntiProfileStats object</i>
------------------	--

---

**Description**

This function creates anti-profile using statistics stored in a AntiProfileStats object

**Arguments**

stats	an object of class AntiProfileStats as produced by the apStats function
tissueSpec	use tissue-specific regions of normal expression
tissueFilter	use only tissue-specific genes in the anti-profile
sigsize	desired size of signature, if NULL, computed from statCutoff
cutoff	median absolute deviation multiplier used to define normal regions of expression
statCutoff	cutoff used to include probesets in anti-profile

**Value**

an object of class AntiProfilesSig or AntiProfilesTissueSig depending on the tissueSpec argument

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**Examples**

```
if (require(antiProfilesData)) {  
  # create an anti-profile, ignoring tissue-specificity of probesets, with 10 probesets  
  data(apColonData)  
  colonStats = apStats(exprs(apColonData), pData(apColonData)$Status)  
  ap = buildAntiProfile(colonStats, tissueSpec=FALSE, sigsize=10)  
}
```

---

ev	<i>Compute expression variability measure</i>
----	---

---

**Description**

This function computes expression variability in a way that removes dependence on mean expression. It uses a local polynomial likelihood method to estimate variance as gamma distributed around given mean expression for each probeset. This function makes this calculation using all samples in argument. To calculate expression variability for samples in different groups, call this function for each subset of columns separately.

**Usage**

```
ev(x, cutoff = NULL, plot = FALSE, ...)
```

**Arguments**

<code>x</code>	matrix of gene expression, with one column per sample
<code>cutoff</code>	minimum expression value to be included in computation (for frma normalized data, we find 2.54 to be a good value for determining if a probeset is expressed in a given sample (default NULL))
<code>plot</code>	make a plot of local likelihood model using smoothScatter (default=FALSE)
<code>...</code>	arguments passed to smoothScatter

**Value**

numeric vector of length equal to number of rows of `x`

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**References**

E. Alemu, H. Corrada Bravo, S. Hannenhalli (2014). Determinants of Expression Variability. *Nucleic Acids Research*, 42 (6), 3503-14.

**See Also**

`frma` for normalization

**Examples**

```
if (require(antiProfilesData)) {
  data(apColonData)
  e <- exprs(apColonData)[,pData(apColonData)$Status==1]
  ev <- ev(e, cutoff=2.54)
}
```

---

TissueSpecAntiProfile-class

*A gene expression anti-profile using tissue-specific regions*

---

**Description**

This class encapsulates anti-profiles with tissue-specific normal expression regions. Objects of this class should be built from [AntiProfileStats](#) objects using the [buildAntiProfile](#) method. Anti-profile scores can be computed for new samples using the [apCount](#) method.



**Usage**

```
## Accessors

## S4 method for signature 'TissueSpecAntiProfile'
getProbesetIds(object)
## S4 method for signature 'TissueSpecAntiProfile'
getNormalRegions(object)
getNormalTissueRegions(object)
```

**Arguments**

object            Object of class [TissueSpecAntiProfile](#)

**Accessors**

In the following code object is a `TissueSpecAntiProfile` object.

`getProbesetIds`: vector of Affymetrix ids for probesets included in the anti-profile (character)  
`getNormalRegions`: median and upper boundary of normal expression regions (numeric matrix of dimension s-by-2, where s is the size of the anti-profile)  
`getNormalTissueRegions`: median and upper boundary of normal expression regions (numeric array of dimension s-by-2-by-t, where s is the size of the anti-profile, and t the number of normal tissues used in the anti-profile)

**Author(s)**

Hector Corrada Bravo <hcorrada@gmail.com>

**See Also**

[AntiProfileStats](#) for the class of objects from which anti-profiles are built. [buildAntiProfile](#) for the method used to construct objects of this class. [apCount](#) for the function used to calculate anti-profile scores from objects of this class. #'

**Examples**

```
if (require(antiProfilesData)) {
  data(apColonData)
  # fake tissues
  tissue=rep(c("colon","lung"), len=length(sampleNames(apColonData)))
  tissStats=apStats(exprs(apColonData), pData(apColonData)$Status, tiss=tissue, minL=3)
  tissAP=buildAntiProfile(tissStats, sigsize=10)
  show(tissAP)

  head(getProbesetIds(tissAP))
  head(getNormalRegions(tissAP))
  head(getNormalTissueRegions(tissAP))
}
```

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