Package ‘antiProfiles’

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Maintainer Hector Corrada Bravo <hcorrada@gmail.com>

Author Hector Corrada Bravo, Rafael A. Irizarry and Jeffrey T. Leek

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Title Implementation of gene expression anti-profiles


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'

RoxygenNote 5.0.1

NeedsCompilation no

R topics documented:

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Description


Author(s)

Hector Corrada Bravo <hcorrada@gmail.com>

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

```r
## 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

```r
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**

```r
## 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.
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)
    colonStats = apStats(exprs(apColonData), pData(apColonData)$Status)
    show(getProbeStats(colonStats))
}

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

\[
\begin{align*}
\text{stats} & \quad \text{An object of class AntiProfileStats} \\
o & \quad \text{A numeric vector giving new probe ordering}
\end{align*}
\]

Value

A reordered AntiProfileStats object

Author(s)

Hector Corrada Bravo <hcorrada@gmail.com>

Examples

```r
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

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

Arguments

\[
\begin{align*}
e & \quad \text{matrix of gene expression, with one column per sample} \\
cl & \quad \text{vector of normal/cancer indicators as 0/1} \\
tiss & \quad \text{vector of tissue types for each sample} \\
minL & \quad \text{minimum number of samples of a given tissue/class to compute stats} \\
cutoff & \quad \text{median absolute deviation multiplier used to determine proportion of samples within normal range of expression} \\
OnCutoff & \quad \text{gene expression barcode z-score to determine if a gene is expressed}
\end{align*}
\]
**buildAntiProfile**

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

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

---

**buildAntiProfile**

Create an anti-profile from a AntiProfileStats object

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

```r
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)
}
```
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
\[
ev(x, \text{cutoff} = \text{NULL}, \text{plot} = \text{FALSE}, \ldots)\]

Arguments
- \(x\): matrix of gene expression, with one column per sample
- \(\text{cutoff}\): minimum expression value to be included in computation (for \text{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)
- \(\text{plot}\): make a plot of local likelihood model using \text{smoothScatter} (default=FALSE)
- \(\ldots\): arguments passed to \text{smoothScatter}

Value
numeric vector of length equal to number of rows of \(x\)

Author(s)
Hector Corrada Bravo <hcorrada@gmail.com>

References

See Also
frma for normalization

Examples
```r
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

```r
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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