Package `antiProfiles`

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Title  Implementation of gene expression anti-profiles
Description  Implements gene expression anti-profiles as described in Corrada
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(>= 1.5)
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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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R topics documented:

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antiProfiles-package  Gene Expression Anti-profiles

Description


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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

```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)

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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)

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See Also

`apStats` to construct objects of this class, `buildAntiProfile` to build anti-profiles from objects of this class.
Examples

```r
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)**

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**Examples**

```r
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)
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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
e
matrix of gene expression, with one column per sample

cl
vector of normal/cancer indicators as 0/1

tiss
vector of tissue types for each sample

minL
minimum number of samples of a given tissue/class to compute stats

cutoff
median absolute deviation multiplier used to determine proportion of samples within normal range of expression

OnCutoff
gene expression barcode z-score to determine if a gene is expressed
buildAntiProfile

Value
An object of class SuccsStats

Author(s)
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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 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)
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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

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

\texttt{ev(x, cutoff = NULL, plot = FALSE, \ldots)}

Arguments

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

Value

numeric vector of length equal to number of rows of \texttt{x}

Author(s)

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References


See Also

\texttt{frma} for normalization

Examples

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

```r
## Accessors
## S4 method for signature 'TissueSpecAntiProfile'
getProbesetIds(object)
```

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

```r
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)

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### 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)
}
TissueSpecAntiProfile-class

```r

tissAP = buildAntiProfile(tissStats, sigsize=10)
show(tissAP)

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

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