Package ‘spkTools’

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Title Methods for Spike-in Arrays
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        expression measures on different array platforms.
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R topics documented:

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affy  
SpikeInExpressionSet of Affymetrix Spike-in Experiment Data

Description

This is a SpikeInExpressionSet object containing the data from the Affymetrix HGU133A Spike-in Experiment.

Usage

data(affy)

Format

It contains a matrix of expression values and a matrix of nominal concentrations.

Source


plotSpkBox  
Boxplots of Fold Changes Calculated by spkBox

Description

Plots boxplots of the data resulting from a call to spkBox.

Usage

plotSpkBox(boxs, fc=2, box.names=NULL, ...)

Arguments

boxs       the output of a call to spkBox
fc          expected fold change
box.names   names to be printed below each boxplot
...         parameters passed to boxplot

Value

Boxplots for spike-in and non-spike-in comparisons stratified by ALE strata are produced.
**SpikeInExpressionSet-class**

**Author(s)**  
Matthew N. McCall

**Examples**
```r
data(affy)  
affySlope <- spkSlope(affy)  
affyBox <- spkBox(affy, affySlope)  
plotSpkBox(affyBox)
```

---

**SpikeInExpressionSet-class**

Class to Contain and Describe High-Throughput Expression Level Assays with Spike-in Data

**Description**

This is a class representation for spike-in expression data. SpikeInExpressionSet class is derived from ExpressionSet, and requires a matrix names `exprs` and a matrix named `spikeIn`.

**Extends**

Extends class ExpressionSet.

**Creating Objects**

```r
createSpikeInExpressionSet(exprs, spikeIn, ...)  
new("SpikeInExpressionSet", phenoData = new("AnnotatedDataFrame"), featureData = new("AnnotatedDataFrame"), experimentData = new("MIAME"), annotation = character(0), exprs = new("matrix"), spikeIn = new("matrix"))
```

This creates a SpikeInExpressionSet with assayData implicitly created to contain `exprs` and `spikeIn`. Additional named matrix arguments with the same dimensions as `exprs` are added to assayData; the row and column names of these additional matrices should match those of `exprs` and `spikeIn`.

```r
new("SpikeInExpressionSet", assayData = assayDataNew(exprs=new("matrix"),spikeIn=new("matrix"))
```

This creates a SpikeInExpressionSet with assayData provided explicitly. In this form, the only required named argument is assayData.

**Slots**

Inherited from ExpressionSet:

- `assayData`: Contains matrices with equal dimensions, and with column number equal to `nrow(phenoData)`. `assayData` must contain a matrix `exprs` and a matrix `spikeIn` with rows representing features and columns representing samples.

- `phenoData`: See eSet
- `annotation` See eSet
- `featureData` See eSet
- `experimentData`: See eSet
Methods

Class-specific methods:

spikeIn(SpikeInExpressionSet), spikeIn(SpikeInExpressionSet)<-  Access and set elements named spikeIn in the AssayData-class slot.

spkSplit(SpikeInExpressionSet) creates two SpikeInExpressionSet objects – one with the spike-in probes and one with the non-spike-in probes.

For derived methods (see ExpressionSet).

See Also

eSet-class, ExpressionSet-class.

Examples

# create an instance of SpikeInExpressionSet
new("SpikeInExpressionSet")

new("SpikeInExpressionSet", exprs=matrix(runif(1000), nrow=100), spikeIn=matrix(rep(1:10,100), nrow=100))

# class specific methods
data(affy)
affySpikes <- spikeIn(affy)
affySplit <- spkSplit(affy)

<table>
<thead>
<tr>
<th>spkAccSD</th>
<th>Accuracy Standard Deviation</th>
</tr>
</thead>
</table>

Description

Estimates the standard deviation for spike-ins at the lowest possible fold change in each bin.

Usage

spkAccSD(object, spkSlopeOut, tol=3)

Arguments

object       a SpikeInExpressionSet object
spkSlopeOut  the output from the spkSlope function
tol          number of digits after decimal point

Value

returns the median absolute deviation (MAD) for each bin.

Author(s)

Matthew N. McCall
spkAll

Examples

data(affy)
affySlope <- spkSlope(affy)
spkAccSD <- spkAccSD(affy, affySlope)

spkAll

Spike-in Functions Wrapper

Description

A wrapper for the functions contained in the spkTools package, which calls each function.

Usage

spkAll(object, label, model=expr~spike+probe+array, fc=NULL, tol=3,
xrngs=NULL, yrngs=NULL, cuts=c(.6,.99), potQuantile=.995,
gnn=c(25,100,10000), pch=".", output="eps")

Arguments

object a SpikeInExpressionSet object
label a character string to insert into the graphs and tables produced
model model to be passed to spkAnova
fc the fold change for which fold change plots will be produced
tol the number of digits after the decimal point in fc
xrngs ranges for the x-axis of each plot. d=density, s=slope, v=box, m=M vs A
yrngs ranges for the y-axis of each plot. d=density, s=slope, v=box, m=M vs A
cuts quantiles used to make the low, medium, and high bins
potQuantile the desired quantile to compute the probability of being above
gnn a vector of 3 numbers passed to spkGNN: the desired number of true positives,
the number of truly expressed genes, and the number of truly unexpressed genes
pch plotting point to be used in spkSlope
output the format in which to save the plots produced. Options are "pdf" and "eps"

Value

The full complement of plots and tables described in the vignette are created and saved in the current working directory.

Author(s)

Matthew N. McCall

Examples

data(affy)
spkAll(affy, label="affy", fc=2)
**spkAnova**  
*Anova Model for Microarray Spike-in Data*

**Description**
Computes the mean squared errors of a microarray spike-in design due to concentration, probe, array, and error.

**Usage**
```
spkAnova(object, model=expr~spike+probe+array)
```

**Arguments**
- **object**: a SpikeInExpressionSet object
- **model**: the anova model

**Value**
A vector of the mean squared errors from the anova model.

**Author(s)**
Matthew N. McCall

**Examples**
```
data(affy)
spkAnova(affy)
```

---

**spkBala**  
*Quantify Microarray Spike-in Design Imbalance*

**Description**
Computes the imbalance of a microarray spike-in design due to probes and arrays.

**Usage**
```
spkBala(object)
```

**Arguments**
- **object**: a SpikeInExpressionSet object

**Value**
The probe and array imbalances.
Author(s)

Matthew N. McCall

References


Examples

data(affy)
spkBal(affy)

spkBox

Fold Change Calculations

Description

A function to calculate the log-ratios stratified by which ALE groups yield the comparison. They are stratified by which bins are being compared to produce the given fold change.

Usage

spkBox(object, spkSlopeOut, fc = 2, tol = 3, reduce = TRUE)

Arguments

object a SpikeInExpressionSet object
spkSlopeOut the output of the spkSlope function
fc the fold change of interest
tol the precision (number of digits after decimal point) in fc
reduce if TRUE the number of points plotted in the null bins is reduced

Details

This function requires the output of spkSlope.

Value

A list with the log-ratios separated by ALE strata comparison.

Author(s)

Matthew N. McCall

Examples

data(affy)
affySlope <- spkSlope(affy)
spkBox(affy, affySlope)
**spkDensity**

*Description*

A density plot of the non-spike-in expression with a rug of the average expression at each spike-in level.

**Usage**

```r
spkDensity(object, spkSlopeOut, cuts=TRUE, label = NULL, ...)
```

**Arguments**

- `object`: a `SpikeInExpressionSet` object
- `spkSlopeOut`: the output from the `spkSlope` function
- `cuts`: if TRUE vertical lines are drawn at the expression values separating low vs medium and medium vs high ALE strata
- `label`: a character string to insert into the plot title
- `...`: arguments passed to the plot function

**Details**

This function requires the output of `spkSlope`.

**Value**

Density plot is produced.

**Author(s)**

Matthew N. McCall

**Examples**

```r
data(affy)
affySlope <- spkSlope(affy)
spkDensity(affy, affySlope)
```
spkGNN

Genes Needed to Detect N True Positives

Description

Computes the number of genes one would need to consider to obtain a given number of truly positive genes if one considered genes in order of decreasing observed fold change.

Usage

spkGNN(n, n.expr, n.unexpr, AccuracySlope, AccuracySD, nullfc)

Arguments

n  the desired number of true positives
n.expr  the actual number of truly expressed genes
n.unexpr  the actual number of truly unexpressed genes
AccuracySlope  the signal detect slope from the spkSlope function
AccuracySD  the standard deviation of the signal detect slope from the spkAccSD function
nullfc  a vector of null fold changes from the spkBox function

Value

This function returns the expected number of genes one would have to consider to obtain N true positives under the given conditions.

Author(s)

Matthew N. McCall

Examples

data(affy)
spkSlopeOut <- spkSlope(affy)
spkBoxOut <- spkBox(affy, spkSlopeOut, fc=2)
AccuracySlope <- round(spkSlopeOut$slope[-1], digits=2)
AccuracySD <- round(spkAccSD(affy, spkSlopeOut), digits=2)
spkGNN(n=25, n.expr=100, n.unexpr=10000, AccuracySlope[2],
AccuracySD[2], spkBoxOut[[2]])
spkMA  MA Plots

Description

Plots log-ratios (M) vs. average log expression (A) for a SpikeInExpressionSet object.

Usage

spkMA(object, spkSlopeOut, fc=2, tol=3, label=NULL, ylim=NULL, outlier=1, reduce=TRUE, plot.legend=TRUE)

Arguments

object  a SpikeInExpressionSet object
spkSlopeOut  the output from the spkSlope function
fc  the fold change of interest
tol  the precision (number of digits after decimal point) in fc
label  a character string to insert into the plot title
ylim  limits of y-axis
outlier  log fold change cut-off for outliers
reduce  if TRUE some points are removed from the background to speed plotting
plot.legend  if TRUE a legend is plotted

Value

The MA plot is produced.

Author(s)

Matthew N. McCall

Examples

data(affy)
affySlope <- spkSlope(affy)
spkMA(affy, affySlope)
**spkPair**

*Pairwise Comparisons for Spike-in Genes*

**Description**

Compute log-ratios among spike-in genes.

**Usage**

```r
spkPair(object)
```

**Arguments**

- `object` a `SpikeInExpressionSet` object

**Value**

An array containing either log-ratios (M), average log expression (A), and nominal concentrations (N1 & N2). Dimension one is genes, dimension two is array pairings, dimension three is M, A, N1, and N2.

**Author(s)**

Matthew N. McCall

**Examples**

```r
data(affy)
affyPair <- spkPair(affy)
```

---

**spkPairNS**

*Pairwise Comparisons for Non-Spike-in Genes*

**Description**

Compute log-ratios among non-spike-in genes.

**Usage**

```r
spkPairNS(object, output="M")
```

**Arguments**

- `object` a `SpikeInExpressionSet` object
- `output` what to return; either "M" for log-ratios or "A" for average log expression.

**Value**

A matrix containing either log-ratios (M) or average log expression (A). Rows are genes and columns are array pairings.
spkPot

Author(s)
Matthew N. McCall

Examples

```r
data(affy)
affyPairNS <- spkPairNS(affy)
```

---

**Description**

Compute the probability that a spike-in with a nominal fold change of 2 appears in the top 0.5% (default) of log-ratios.

**Usage**

```r
spkPot(object, spkSlopeOut, sig, SD, precisionQuantile)
```

**Arguments**

- `object`: a SpikeInExpressionSet object
- `spkSlopeOut`: the output from the spkSlope function
- `sig`: the signal detect slopes from a call to spkSlope
- `SD`: the standard deviation from spkAccSD
- `precisionQuantile`: the desired quantile to compute the probability of being above

**Value**

A vector of probabilities for each ALE strata.

Author(s)
Matthew N. McCall

Examples

```r
data(affy)
affySlope <- spkSlope(affy)
affyAccSD <- spkAccSD(affy, affySlope)
spkPot(affy, affySlope, affySlope$slopes, affyAccSD, .995)
```
### spkQuantile

#### Description
An internal function called by spkSlope.

#### Usage
```r
spkQuantile(amt, avgE, ens, p)
```

#### Arguments
- `amt`: a vector of nominal concentrations
- `avgE`: the observed average expression corresponding to each nominal concentration
- `ens`: the average expression across arrays of unexpressed genes
- `p`: the quantiles to make the bins

#### Author(s)
Matthew N. McCall

#### Examples
```r
data(affy)
affySlope <- spkSlope(affy)
```

---

### spkSlope

#### Description
Plots observed expression vs. nominal concentration. The overall regression slope, as well as, regression slopes for low, medium, and high bins are computed and the regression lines plotted.

#### Usage
```r
spkSlope(object, label = NULL, cuts=c(.6,.99), ...)
```

#### Arguments
- `object`: a SpikeInExpressionSet object
- `label`: a character string to insert into the plot title
- `cuts`: quantiles used to make the low, medium, and high bins
- `...`: arguments passed to the plot function
Details

The bins are created by computing the proportion of non-spike-in genes with expression values less than or equal to the average expression value at each nominal concentration. Using the default value of cuts, the high bin contains nominal concentrations with 99 percent or more of the non-spike-in expression values lower than it. The medium bin contains nominal concentrations with between 60 and 99 percent of the non-spike-in expression values lower than it. The low bin contains nominal concentrations with less than 60 percent of the non-spike-in expression values lower than it.

Value

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>avgExp</td>
<td>average expression at each nominal concentration</td>
</tr>
<tr>
<td>slopes</td>
<td>the regression slopes - overall and for each bin</td>
</tr>
<tr>
<td>breaks</td>
<td>which spike-in levels fall in each bin</td>
</tr>
<tr>
<td>brkpts</td>
<td>the expression value of the cut points between bins</td>
</tr>
<tr>
<td>prop</td>
<td>the proportion of non-spike-in probes with expression less than the average expression at each nominal concentration</td>
</tr>
</tbody>
</table>

Author(s)

Matthew N. McCall

Examples

data(affy)
spkSlope(affy)

Description

A collection of functions to examine microarray datasets that include spike-ins. In particular, it allows one to explore the distribution of spike-ins within the range of possible expression values, the relationship between nominal concentration and expression, and the relationship between expected and observed fold change for different levels of comparison.

Details

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<th>Type</th>
<th>Version</th>
<th>Date</th>
<th>License</th>
</tr>
</thead>
<tbody>
<tr>
<td>spkTools</td>
<td>Package</td>
<td>0.0.1</td>
<td>2007-10-9</td>
<td>GPL version 2 or newer</td>
</tr>
</tbody>
</table>
**spkVar**

**Author(s)**

Matthew N. McCall

Maintainer: Matthew N. McCall <mmccall@jhsph.edu>

**Examples**

```r
## The Three Plots
data(affy)
par(mfrow=c(2,2))
affySlope <- spkSlope(affy)
spkDensity(affy, affySlope)
spkBox(affy, affySlope)

## The Full Wrapper
data(affy)
spkAll(affy, label="Affymetrix", fc=2)
```

---

### spkVar

**Spike-in Variance**

**Description**

Compute an estimate of the standard deviation in expression at each nominal concentration.

**Usage**

```r
spkVar(object)
```

**Arguments**

- `object`: a SpikeInExpressionSet object

**Value**

A matrix containing spike-in levels and corresponding MADs.

**Author(s)**

Matthew N. McCall

**Examples**

```r
data(affy)
spkVar(affy)
```
summarySpkBox

Summary of Fold Changes Calculated by spkBox

Description
Prints a summary table of the data resulting from a call to spkBox.

Usage

summarySpkBox(boxs)

Arguments

boxs the output of a call to spkBox

Value
A dataframe with 2 columns: the mean fold change and the median average distance of the fold changes.

Author(s)
Matthew N. McCall

Examples

data(affy)
affySlope <- spkSlope(affy)
affyBox <- spkBox(affy, affySlope)
plotSpkBox(affyBox)
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