

panp

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`gcrma.ExpressionSet`
ExpressionSet resulting from gcrma processing of 3 HG-U133A chips

Description

An `ExpressionSet` object resulting from `gcrma` processing of three HG-U133A chips from the 28-chip `affyCOMP II` dataset, derived from the `AffyMetrix Latin Squares` dataset. The `gcrma.ExpressionSet` can be used as example input for `panp`'s `pa.calls()` function, and it is used for this purpose in the `panp` vignette.

Usage

```
data(gcrma.ExpressionSet)
```

Format

An `ExpressionSet` object comprising three `gcrma`-processed HG-U133A chips

Source

The 3 HG-U133A chips are the first three of `affyCOMP II Latin Squares` set

NSMPnames.hgu133a *Negative Strand Matching Probeset (NSMP) names for HG-U133A chip type*

Description

This list of NSMP probeset names is used by `pa.calls()` in calculating the NSMP expression distribution. It is specific to the chip type; the correct version is automatically loaded for the detected chip type, if supported. The user does not load or use this data directly.

Usage

```
data(NSMPnames.hgu133a)
```

Format

A vector containing probeset names

Source

October 2004 AffyMetrix chip annotation files, filtered, with outliers removed

NSMPnames.hgu133plus2
Negative Strand Matching Probeset (NSMP) names for HG-U133 Plus 2.0 chip type

Description

This list of NSMP probeset names is used by `pa.calls()` in calculating the NSMP expression distribution. It is specific to the chip type; the correct version is automatically loaded for the detected chip type, if supported. The user does not load or use this data directly.

Usage

```
data(NSMPnames.hgu133plus2)
```

Format

A vector containing probeset names

Source

October 2004 AffyMetrix chip annotation files, filtered, with outliers removed

pa.calls

*Presence-Absence Calls from Negative Strand Matching Probesets***Description**

Function to make gene presence/absence calls based on distance from empirical distribution of chip-specific negative strand matching probesets (NSMP).

Usage

```
pa.calls(object, looseCutoff = 0.02, tightCutoff = 0.01, verbose = FALSE)
```

Arguments

object	an ExpressionSet object (result of running expression-generating function, like <code>expresso()</code> , <code>rma()</code> , <code>mas5()</code> , etc.) Currently, this must be of chip type HGU133A or HGU133 Plus 2.0
looseCutoff	the larger P-value cutoff (see details)
tightCutoff	the smaller, more strict P-value cutoff
verbose	logical. If 'TRUE' detailed progress messages are reported.

Details

The function calculates a matrix of P-values for the expression values in the input ExpressionSet. P-values are calculated based on the empirical survivor function (1-CDF) of the set of negative probesets identified by Affymetrix as negative strand matching probesets (NSMP) with no cross hybridization. These probesets are therefore assumed to show nothing but background/machine noise plus some occasional non-specific binding. The P-value returned for any probeset expression value in ExpressionSet is the value of the NSMP survivor function for that expression level.

Presence/Absence calls are derived by applying the two cutoff values to the matrix of P-values for all genes in the ExpressionSet, as follows:

Present ('P') P-values \leq tightCutoff

Absent ('A') P-values $>$ looseCutoff

Marginal ('M') P-values between tightCutoff and looseCutoff

Value

list	a new list containing two matrices: Pcalls and Pvals, as follows:
Pcalls	a matrix of Presence (P), Marginal (M), Absent (A) indicators
Pvals	a matrix of P-values. Each data point is the P-value for the expr at the same x, y coordinates.

Note

NSMP sets have been established for the HGU133A and HGU133-Plus-2.0 chipsets to date. Hence only these two are currently supported by PANP.

Author(s)

Peter Warren

References

Warren, P., Bienkowska, J., Martini, P., Jackson, J., and Taylor, D., PANP - a New Method of Gene Detection on Oligonucleotide Expression Arrays (2007), in preparation

Examples

```
## Load example ExpressionSet
data(gcrma.ExpressionSet)

## Generate Pvals and Pcalls matrices from ExpressionSet, using default cutoffs
PA <- pa.calls(gcrma.ExpressionSet)

## to access the Pcalls and Pvals:
myPcalls <- PA$Pcalls
myPvals <- PA$Pvals
```

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