Package ‘MAQCsubset’

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1
Excerpt from GE Codelink array contributions to MAQC

data(gehSubRaw)
data(gehMAQCsubDef)

details

text

Author(s)

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Examples

data(gnfCerebHi)
data(gnfCerebLow)
**Details**

The symatlas.gnf.org database was searched using the gcrma version of human gene atlas for genes having expression in cerebellum at least 3 times (or at most 1/3 times) median expression over all organs surveyed. The resulting gene lists were intersected with genes present on GE codelink (version used in MAQCsubset) and hgu95a.

**Value**

data.frame instances with columns providing gene name, affy probe set identifier, codelink probe identifier, illuminaHumanv1 identifier.

**Author(s)**

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**Examples**

data(gnfCerebHi)
gnfCerebHi[1:3,]

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**MAQCsubset**

Experimental Data Package: MAQCsubset

**Description**

selected data from the MAQC project (Nature Biotechnology, Sept. 2006)

**Usage**

data(afxsubRMAES)
data(afxsubRMA)
data(afxsub)

**Format**

The format is: An ExpressionSetObject with covariates:

- site: from cel
- samp: rna src/mixture code
- repl: replicate

**Note**

afxsubRMA is an exprSet (deprecated) and afxsub is an AffyBatch. afxsubRMAES is a proper ExpressionSet instance.

ilmMAQCSubR is the result of applying lumiR to the files in the vicinity of GEO GSM122901 with filename suffixes matching those of the sampleNames in the set.
Examples

data(afxsubRMAES)

proboscis

Produce a plot similar to Figure 2 of the Shippy MAQC paper (PMID 16964226).

Description

Produce a plot similar to Figure 2 of the Shippy MAQC paper (PMID 16964226).

Usage

proboscis(es, site=1, ABp=0.001, CDp=0.01, mmrad=100)

Arguments

es ExpressionSet instance with MAQC assay results
site numeric code – site to be assessed
ABp ABp – p-value threshold to declare concentration of gene in sample A to be different from the concentration in sample B
CDp CDp – p-value threshold to declare concentration of gene in sample C to be different from the concentration in sample D
mmrad numeric radius of the moving mean used to smooth the proportions differentially expressed

Details

Figure 2 of the Shippy paper consists of a collection of plots of estimated probabilities of self-consistent monotone titration – briefly, samples are such that A has 100% USRNA, B has 100% Ambion brain, C has 75% USRNA+25% brain, D has 25% USRNA, 75% brain. Self-consistent monotone titration holds for gene g if microarray measures for that gene satisfy A > C > D > B or B > C > D > A. The estimated probability functions look like a creature sticking its nose over a wall, thus the name of this function.

Value

an instance of proboStruct, for which a plot and lines method are available.

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References

PMID 16964226
proboStruct-class

Examples

```r
data(afxsubRMAES)
NN2 = proboscis(afxsubRMAES, site=2)
plot(NN2)
```

proboStruct-class  Class "proboStruct"

Description

structure for managing proboscis plot data

Objects from the Class

Objects can be created by calls of the form `new("proboStruct", ...)`. 

Slots

`.Data`: Object of class "list" ~~
`call`: Object of class "call" ~~

Extends

Class "list", from data part. Class "vector", by class "list", distance 2. Class AssayData-class, by class "list", distance 2.

Methods

plot

Note

The proboscis plot shows how the probability of self-consistent monotone titration (SCMT) varies with the spiked difference in concentrations of two mRNA preparations in an MAQC dataset.

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References

For Figure 2 of Shippy et al., Using RNA sample titrations... (Nat Biotech, 24(9):1123-1131, Sep 2006)

Examples

```r
data(afxsubRMAES)
NN1 = proboscis(afxsubRMAES)
plot(NN1)
showClass("proboStruct")
```
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