Package ‘MAQCsubset’

February 27, 2024

Title Experimental Data Package: MAQCsubset
Version 1.40.0
Author VJ Carey
Maintainer VJ Carey <stvjc@channing.harvard.edu>
Depends R (>= 2.10.0), affy (>= 1.23.4), Biobase (>= 2.5.5), lumi, methods
Suggests genefilter, codelink
License Artistic-2.0
biocViews ExperimentData, MicroarrayData, GEO
LazyLoad true
git_url https://git.bioconductor.org/packages/MAQCsubset
git_branch RELEASE_3_18
git_last_commit 708a5e9
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-02-27

R topics documented:

gehMAQCsubDef ......................................................... 2
gnfCerebHi ............................................................. 2
MAQCsubset .............................................................. 3
proboscis ................................................................. 4
proboStruct-class ..................................................... 5

Index 6
gehMAQCsubDef  

**Excerpt from GE Codelink array contributions to MAQC**

**Description**

Excerpt from GE Codelink contributions to MAQC

**Usage**

```r
data(gehSubRaw)
data(gehMAQCsubDef)
```

**Details**

`gehSubRaw` is a `codelink::Codelink` instance based on reading the raw GEO files: "GSM123122\_GEH\_I\_A1.TXT" "GSM123123\_GEH\_I\_A2.TXT" "GSM123127\_GEH\_I\_B1.TXT" "GSM123128\_GEH\_I\_B2.TXT" "GSM123132\_GEH\_I\_C1.TXT" "GSM123133\_GEH\_I\_C2.TXT" "GSM123137\_GEH\_I\_D1.TXT" "GSM123138\_GEH\_I\_D2.TXT"

`gehMAQCsubDef` is an `ExpressionSet` instance based on default background correction and normalization of the `codelink` package. The original feature names include duplicates; these were made unique by `make.names` with `unique=TRUE`.

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**Examples**

```r
data(gehMAQCsubDef)
gehMAQCsubDef
```

gnfCerebHi  

**Gene lists for hi or low abundance in cerebellum according to Novartis GNF symatlas**

**Description**

Data frames with gene lists for hi or low abundance in cerebellum according to Novartis GNF symatlas

**Usage**

```r
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)

Vince Carey <stvjc@channing.harvard.edu>

Examples

data(gnfCerebHi)
gnfCerebHi[1:3,]

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>es</td>
<td>ExpressionSet instance with MAQC assay results</td>
</tr>
<tr>
<td>site</td>
<td>numeric code – site to be assessed</td>
</tr>
<tr>
<td>ABp</td>
<td>ABp – p-value threshold to declare concentration of gene in sample A to be different from the concentration in sample B</td>
</tr>
<tr>
<td>CDp</td>
<td>CDp – p-value threshold to declare concentration of gene in sample C to be different from the concentration in sample D</td>
</tr>
<tr>
<td>mmrad</td>
<td>numeric radius of the moving mean used to smooth the proportions differentially expressed</td>
</tr>
</tbody>
</table>

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.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

References

PMID 16964226
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.

#### Author(s)

V Carey <stvjc@channing.harvard.edu>

#### 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")
```
Index

* classes
  proboStruct-class, 5

* datasets
  MAQCsubset, 3

* models
  gehMAQCsubDef, 2
  gnfCerebHi, 2
  proboscis, 4

afxsub (MAQCsubset), 3
afxsubRMA (MAQCsubset), 3
afxsubRMAES (MAQCsubset), 3
ExpressionSet, 4
gehMAQCsubDef, 2
gehSubRaw (gehMAQCsubDef), 2
gnfCerebHi, 2
gnfCerebLow (gnfCerebHi), 2
ilmMAQCsubR (MAQCsubset), 3
lines,proboStruct-method
  (proboStruct-class), 5
list, 5
make.names, 2
MAQCsubset, 3
plot,proboStruct,ANY-method
  (proboStruct-class), 5
plot,proboStruct-method
  (proboStruct-class), 5
proboscis, 4
proboStruct, 4
proboStruct-class, 5
show,proboStruct-method
  (proboStruct-class), 5
vector, 5