# Package ‘MAQCsubset’

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**Title** Experimental Data Package: MAQCsubset

**Version** 1.39.0

**Author** VJ Carey

**Description** Data Package automatically created on Sun Nov 19 15:59:29 2006.

**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

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## gehMAQCsubDef — *Excerpt from GE Codelink array contributions to MAQC*

### Description

Excerpt from GE Codelink contributions to MAQC

### Usage

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

### Details

gehSubRaw is a codelink::Codelink instance based on reading the raw GEO files: "GSM123122_GEH_1_A1.TXT" "GSM123123_GEH_1_A2.TXT" "GSM123127_GEH_1_B1.TXT" "GSM123128_GEH_1_B2.TXT" "GSM123132_GEH_1_C1.TXT" "GSM123133_GEH_1_C2.TXT" "GSM123137_GEH_1_D1.TXT" "GSM123138_GEH_1_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

```
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

```
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,]
```

---

## 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 ehe 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.

## Author(s)

Vince Carey <stvjc@channing.harvard.edu>

## References

PMID 16964226

## Examples

```
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

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

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