

# Package ‘MAQCsubset’

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**Title** Experimental Data Package: MAQCsubset

**Version** 1.43.0

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

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**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

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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 | <i>Produce a plot similar to Figure 2 of the Shippy MAQC paper (PMID 16964226).</i> |
|-----------|---|

---

**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    | <a href="#">ExpressionSet</a> 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.

**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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