Iyer517

October 25, 2011

`Iyer517` *exprSet instance Iyer517, time series on transcriptional response of*

Description

an expression set for timed measurements of transcriptional response of fibroblasts to serum in presence or absence of cycloheximide

Slots

`exprs`: Object of class matrix, value: 517 x 19 expression levels (normed to 1 at time 0)

`se.exprs`: Object of class matrix, value: absent

`description`: Object of class MIAME, value: string

`annotation`: Object of class character, value: ”

`notes`: Object of class character, value: ”

`phenoData`: Object of class phenoData, value: data frame with info on timing

`class`: Object of class character, value: ’exprSet’

References

Iyer et al 1999 Science v283 83-87

Examples

```
data(Iyer517)
show(Iyer517)
plot(apply(exprs(Iyer517)[1:100,1:13],2,mean),main="Cluster A",
xlab="index in time seq", ylab="ratio to time 0", log="y")
```

`IyerAnnotated` *Partly annotated version of Iyer517 data*

Description

GenBank ids, LocusLink ids (where available) and GO tags (where available) for the 517 cDNAs in the dataset.

Usage

```
data(IyerAnnotated); data(Iyer517GO)
```

Format

Iyer517GO: An environment with keys given by the 'GB' identifiers of probes and values given by vectors of GO tags (named by evidence codes) obtained via locuslink mapping

IyerAnnotated: A data frame with 517 observations on the following 9 variables.

Iclust a factor with levels `N A B` ... – the cluster groups A-J of the Iyer paper, with N for those rows that were not clustered

GB a factor with levels `AA001025 AA001722` ... accession numbers (often genbank) for probes

seqno a numeric vector indicating the order of the cDNA in the Iyer report on clustering. (Elements 2:101 formed cluster A, etc.)

locusid a numeric vector of locuslink ids, formed using AnnBuilder

GO1 a character vector of GO tags (there were up to five based on the LL:GO mapping available March 2003 – these should be ignored in favor of the new Iyer517GO environment

GO2 a character vector

GO3 a character vector

GO4 a character vector

GO5 a character vector

Details

Annotating this dataset is a good exercise for AnnBuilder. Many of the probes seem to have no annotation.

Source

http://genome-www.stanford.edu/serum/data.html

References

Iyer et al, Science v283: 83-87 (1999)

Examples

```
data(IyerAnnotated)
table(is.na(IyerAnnotated$GO1))
data(Iyer517GO)
get(ls(env=Iyer517GO)[1],env=Iyer517GO)
```

`get.dna2` *query genbank for an EST accession id*

Description

extends the get.dna function of E Paradis CRAN package "ape"

Usage

```
get.dna2(access.nb)
```

Arguments

`access.nb`	an EST accession id

Details

queries ncbi

Value

a vector of nucleotide codes

Note

try ape::get.dna if this fails

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

See Also

ape::get.dna

Examples

```
if (interactive())
{
data(IyerAnnotated)
get.dna2(IyerAnnotated$GB[1])
}
```

Index