Neve2006

April 2, 2010

cghExSet-class

Class "cghExSet" for combining CGH and expression data

Description

combination of an ExpressionSet and CGH assay results

Usage

make_cghExSet(exprs, logRatios, cloneMeta, pd, mi, anno) # pd is AnnotatedDataFr

Arguments

exprs matrix of expression assay results logRatios matrix of aCGH assay results

cloneMeta AnnotatedDataFrame for aCGH clone descriptions

pd AnnotatedDataFrame for sample level data
mi MIAME instance for experiment documentation

anno character string with annotation platform descriptor for expression data

Objects from the Class

Objects can be created by calls of the form new ("cghExSet", phenoData, experimentData, annotation, exprs, logRatios, cloneMeta).

Slots

 ${\tt cghAssays:} \begin{tabular}{l} {\tt CghAssays:} & {\tt Object of class "AssayData" rectangular representation of logRatio data from CGH \\ \end{tabular}$

 $\verb|cloneMeta|: Object of class "Annotated DataFrame" information on chromosome and offset of clones$

assayData: Object of class "AssayData" expression assay results

phenoData: Object of class "AnnotatedDataFrame" sample level data

featureData: Object of class "AnnotatedDataFrame" reporter level metadata for expression assay results

experimentData: Object of class "MIAME" container for experiment documentation

2 logRatios

Extends

```
Class eSet-class, directly. Class VersionedBiobase-class, by class "eSet", distance 2. Class Versioned-class, by class "eSet", distance 3.
```

Methods

```
cloneMeta signature(cghSet = "cghExSet"): extract annotated data frame on clone
    locations for CGH component

cloneNames signature(cghSet = "cghExSet"): extract character vector of clone IDs
    for CGH component

exprs signature(object = "cghExSet"): extract expression assay results
initialize signature(.Object = "cghExSet"): infrastructure
logRatios signature(cghSet = "cghExSet"): extract CGH assay results
```

show signature(object = "cghExSet"): display object in concise form

Author(s)

V Carey <stvjc@channing.harvard.edu>

References

R. M. Neve Cancer Cell Dec 2006

Examples

```
showClass("cghExSet")
data(neveExCGH)
logRatios(neveExCGH)[1:4,]
exprs(neveExCGH)[1:4,]
```

logRatios

extractor for cghSet assay data

Description

extractor for cghSet assay data

Usage

```
logRatios(cghSet)
```

Arguments

cghSet instance of cghSet class

neveCGHmatch 3

Details

gets the AssayData element

Value

matrix

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(neveCGHmatch)
logRatios(neveCGHmatch)[1:4,1:4]
```

neveCGHmatch

Neve Cancer Cell 2006 expression plus CGH data

Description

ExpressionSet and cghSet

Usage

```
data(neveCGHmatch)
data(neveRMAmatch)
data(neveExCGH)
```

Format

The individual datasets (aCGH and expression assays) take the form of a cghSet for neveCGHmatch and an ExpressionSet for neveRMAmatch. There are only 50 samples because only 50 could be aligned on the given sample name tokens in the caArrayDB data as of June 9 2007. Those sample name tokens are very mangled in the CEL files.

The combined data structure neveExCGH has a special container class cghExSet.

Source

links are provided in the pdf of the Cancer Cell paper; see the PMID of experimentData (neveCGHmatch)

References

PMID 17157791

Examples

```
data(neveCGHmatch)
neveCGHmatch
logRatios(neveCGHmatch) [1:4,1:4]
data(neveRMAmatch)
neveRMAmatch
```

Index

```
*Topic classes
    cghExSet-class, 1
*Topic datasets
   neveCGHmatch, 3
*Topic models
   logRatios, 2
cghExSet, 3
cghExSet-class, 1
cghSet, 2
cghSet-class (logRatios), 2
cloneMeta(cghExSet-class), 1
cloneMeta,cghExSet-method
       (cghExSet-class), 1
cloneNames (cghExSet-class), 1
cloneNames, cghExSet-method
       (cghExSet-class), 1
eSet-class, 2
exprs,cghExSet-method
       (cghExSet-class), 1
initialize, cghExSet-method
       (cghExSet-class), 1
logRatios, 2
logRatios,cghExSet-method
       (cghExSet-class), 1
logRatios,cghSet-method
       (logRatios), 2
make_cghExSet (cghExSet-class), 1
MIAME, 1
neveCGHmatch, 3
neveExCGH (neveCGHmatch), 3
neveRMAmatch (neveCGHmatch), 3
show, cghExSet-method
       (cghExSet-class), 1
Versioned-class, 2
VersionedBiobase-class, 2
```