Neve2006

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R topics documented:

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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).

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Slots

    cghAssays: Object of class `"AssayData"` rectangular representation of logRatio data from CGH

    cloneMeta: Object of class `"AnnotatedDataFrame"` 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

    annotation: Object of class `"character"` identifiers for expression and CGH platforms, as a named vector with elements named 'exprs' and 'logRatios'

    .__classVersion__: Object of class `"Versions"`

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)

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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

Details

gets the AssayData element

Value

matrix

Author(s)

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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
```

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