

Neve2006

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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

| | |
|------------------------|--|
| <code>exprs</code> | matrix of expression assay results |
| <code>logRatios</code> | matrix of aCGH assay results |
| <code>cloneMeta</code> | AnnotatedDataFrame for aCGH clone descriptions |
| <code>pd</code> | AnnotatedDataFrame for sample level data |
| <code>mi</code> | MIAME instance for experiment documentation |
| <code>anno</code> | 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

`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

"[" signature (object = "cghExSet"): when first index is set, subset expression features; when second, subset samples

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 | <i>extractor for cghSet assay data</i> |
|-----------|--|

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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