

Package ‘Neve2006’

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Title expression and CGH data on breast cancer cell lines
Version 0.47.0
Author M. Neve et al. in Gray Lab at LBL
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Maintainer VJ Carey <stvjc@channing.harvard.edu>
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cghExSet-class	<i>Class "cghExSet" for combining CGH and expression data</i>
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Description

combination of an ExpressionSet and CGH assay results

Usage

```
make_cghExSet(exprs, logRatios, cloneMeta, pd, mi, anno) # pd is AnnotatedDataFrame, mi is MIAME
```

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)

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	<i>extractor for cghSet assay data</i>
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Description

extractor for cghSet assay data

Usage

```
logRatios(cghSet)
```

Arguments

cghSet instance of [cghSet](#) class

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
```

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