Package 'Neve2006'

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Title expression and CGH data on breast cancer cell lines

Version 0.46.0

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Description Experimental organization of combined expression and CGH data

Depends R (>= 2.14.0), tools, methods, utils, Biobase (>= 1.14.0), hgu133a.db, annotate

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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 AnnotatedDataFrame, mi is MIAME
```

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

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 *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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