Package ‘Neve2006’

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Title  expression and CGH data on breast cancer cell lines

Version  0.12.0

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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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License  Artistic-2.0

LazyLoad  yes

biocViews  ExperimentData, CancerData, BreastCancerData

NeedsCompilation  no

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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
Argument

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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**logRatios**

**References**

R. M. Neve Cancer Cell Dec 2006

**Examples**

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

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**Description**

extractor for cghSet assay data

**Usage**

```r
logRatios(cghSet)
```

**Arguments**

- `cghSet` instance of `cghSet` class

**Details**

gets the AssayData element

**Value**

matrix

**Author(s)**

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**Examples**

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