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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

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 off-set 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

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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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