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).
cghExSet-class

Slots

cghAssays: Object of class "AssayData" rectangular representation of logRatio data from CGH

clonMeta: 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]

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**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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