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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LazyLoad yes

biocViews ExperimentData, CancerData, BreastCancerData

NeedsCompilation no

R topics documented:

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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
cghExSet-class

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

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logRatios

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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