Package ‘Neve2006’

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Title expression and CGH data on breast cancer cell lines

Version 0.14.0

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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:

<table>
<thead>
<tr>
<th>Class</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cghExSet-class</td>
<td>Class “cghExSet” for combining CGH and expression data</td>
</tr>
</tbody>
</table>

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)

V Carey <stvjc@channing.harvard.edu>
**logRatios**

**References**

R. M. Neve Cancer Cell Dec 2006

**Examples**

```r
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**

```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]
```
neveCGHmatch

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
Index

*Topic classes
  cghExSet-class, 1
*Topic datasets
  neveCGHmatch, 4
*Topic models
  logRatios, 3
  [,cghExSet-method (cghExSet-class), 1
  cghExSet, 4
  cghExSet-class, 1
  cghSet, 3
  cghSet-class (logRatios), 3
  cloneMeta (cghExSet-class), 1
  cloneMeta, cghExSet-method (cghExSet-class), 1
  cloneNames (cghExSet-class), 1
  cloneNames, cghExSet-method (cghExSet-class), 1
  exprs, cghExSet-method (cghExSet-class), 1
  initialize, cghExSet-method (cghExSet-class), 1
  logRatios, 3
  logRatios, cghExSet-method (cghExSet-class), 1
  logRatios, cghSet-method (logRatios), 3
  make_cghExSet (cghExSet-class), 1
  MIAME, 2
  neveCGHmatch, 4
  neveExCGH (neveCGHmatch), 4
  neveRMAmatch (neveCGHmatch), 4
  show, cghExSet-method (cghExSet-class), 1