Package ‘Neve2006’

April 11, 2024

Title expression and CGH data on breast cancer cell lines

Version 0.40.0

Author M. Neve et al. in Gray Lab at LBL

Description Experimental organization of combined expression and CGH data

Depends R (>= 2.14.0), tools, methods, utils, Biobase (>= 1.14.0),
    hgu133a.db, annotate

Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

LazyLoad yes

biocViews ExperimentData, CancerData, BreastCancerData

git_url https://git.bioconductor.org/packages/Neve2006

git_branch RELEASE_3_18

git_last_commit 3cfc0a9

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-11

R topics documented:

cghExSet-class ......................................................... 2
logRatios ................................................................. 3
neveCGHmatch ......................................................... 4

Index 5
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

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>

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)**

Vince Carey <stvjc@channing.harvard.edu>

**Examples**

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

---

**Description**

ExpressionSet and cghSet

**Usage**

```r
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**

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

* classes
  cghExSet-class, 2

* datasets
  neveCGHmatch, 4

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