

# Neve2006

October 5, 2010

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`cghExSet-class`      *Class "cghExSet" for combining CGH and expression data*

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## Description

combination of an ExpressionSet and CGH assay results

## Usage

```
make_cghExSet(exprs, logRatios, cloneMeta, pd, mi, anno) # pd is AnnotatedDataFr
```

## Arguments

<code>exprs</code>	matrix of expression assay results
<code>logRatios</code>	matrix of aCGH assay results
<code>cloneMeta</code>	AnnotatedDataFrame for aCGH clone descriptions
<code>pd</code>	AnnotatedDataFrame for sample level data
<code>mi</code>	<a href="#">MIAME</a> instance for experiment documentation
<code>anno</code>	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



**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*

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**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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