

# Package ‘codelink’

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**Version** 1.81.0

**Title** Manipulation of Codelink microarray data

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**Imports** annotate

**Suggests** genefilter, parallel, knitr

**LazyLoad** yes

**Description** This package facilitates reading, preprocessing and manipulating Codelink microarray data. The raw data must be exported as text file using the Codelink software.

**License** GPL-2

**Collate** Codelink-class.R CodelinkSet-class.R file.R data.R norm.R  
plot.R CodelinkSet-methods.R CodelinkSet-tools.R  
CodelinkSetUnique-class.R CodelinkSetUnique-methods.R filter.R  
cluster.R

**biocViews** Microarray, OneChannel, DataImport, Preprocessing

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---

arrayNew

*Create a new x11 device*

---

### Description

Create a new x11 device with dimensions suited to be used with imageCodelink().

### Usage

```
arrayNew(f=2, chip="rwgcod")
```

**Arguments**

chip                    character; Codelink chip to be used in imageCodelink.  
 f                        numerical; scaling factor.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
  data(codelink.example)
  arrayNew()
  imageCodelink(codelink.example)

## End(Not run)
```

---

arraySize                    *Determine the size of the array*

---

**Description**

When loading Codelink arrays in text format (as exported from the Codelink software) this function retrieves the correct size of the array. This is useful because those files contain an indetermined number of empty lines at the end. Thus, reading the entire data matrix doesn't work.

**Note**

Not meant to be used directly.

**Author(s)**

Diego Diez

---

as.matrix.Codelink        *Return a matrix of intensity values*

---

**Description**

Takes a Codelink object and returns a matrix with the intensity values available.

**Usage**

```
## S3 method for class 'Codelink'
as.matrix(x, ...)
```

**Arguments**

x                        an object of class "Codelink".  
 ...                      additional arguments added to generic as.matrix since R-2.5.x

**Value**

A matrix with the intensity values.

**Author(s)**

Diego Diez

**See Also**

[as.matrix](#)

**Examples**

```
## Not run:
data(codelink.example)
mat <- as.matrix(codelink.example)
is(mat)

## End(Not run)
```

---

averageProbes

*averageProbes*

---

**Description**

Takes a CodelinkSet object and computes the average (mean) and sd of duplicated probes.

**Usage**

```
averageProbes(object, parallel = FALSE)
```

**Arguments**

object	an object of class "CodelinkSet".
parallel	whether to use a parallel version (requires package multicore).

**Details**

This function will compute the mean() and sd() on each duplicated probe (i.e. identical probe id as for probeNames()). CodelinkSet objects use the per-array index to enable unique identifiers needed for ExpressionSet derived objects. Although the method probeNames() provides access to Codelink probe ids, this is inconvenient when dealing with other packages that make use of featureNames() to obtain probe ids and feed them to the corresponding annotation package.

In such cases CodelinkSet objects are not compatible with methods working on ExpressionSet objects. To avoid this limitation it is possible to construct a CodelinkSet object containing unique identifiers (CodelinkSetUnique class) by averaging the intensities of all replicated probes. This is done by computing the mean(). The sd() is also computed and stored in the slot sd.

The current implementation takes a lot of time so a parallelized version of lapply() may be used through the package 'multicore'. This is controlled by the argument 'parallel' which is FALSE by default.

According to the authors it is not actually possible to use 'multicore' in a GUI environment like the R.app Cocoa application in R, because this interferes with the events loop. Therefore it is advised to use option 'parallel=TRUE' in an R session running in a shell.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
  data(codelink.example)
  foo <- averageProbes(codelink.example)

## End(Not run)
```

bkgdCorrect

*Background correction of intensity values.***Description**

Takes a CodelinkSet or Codelink object with Spot mean and Bkgd median values and performs background correction using one of the methods available.

**Usage**

```
bkgdCorrect(object, method = "half", preserve = FALSE, verbose = FALSE, offset = 0)

## S4 method for signature 'CodelinkSet'
codCorrect(object, method = "half", normexp.method="saddle", offset=0)
```

**Arguments**

object	an object of class CodelinkSet or Codelink.
method	the correction method to use, one of "none", "subtract", "half" and "normexp".
preserve	logical; if Smean and Bmedian slots should be preserved.
verbose	logical; if TRUE print some information with method normexp.
normexp.method	method used with normexp correction.
offset	numeric; value to add to intensities.

**Details**

Available methods are: . none: left intensities untouched. . subtract: simple subtraction of Bkgd median from Spot mean. . half: the same as above but avoid negative values setting all intensity values below zero to 0.5. . normexp: apply normexp background adjustment from package limma.

**Value**

An object of class Codelink with corrected intensity values, that is Ri slot.

**Author(s)**

Diego Diez

**Examples**

```
data(codset)
codset <- codCorrect(codset, method = "half")
```

---

Codelink-class	<i>Class Codelink</i>
----------------	-----------------------

---

### Description

This is the storage class for Codelink data

### Objects from the Class

Object are created after reading text codelink files with readCodelink()

### Description

Codelink objects contain a single "list", which contains the following elements:

**sample** Object of class "character" containing the sample names

**file** Object of class "character" containing the file names

**name** Object of class "character" containing the probe ID

**method** Object of class "list" containing log information

**Smean** Object of class "matrix" containing spot mean intensities

**Bmedian** Object of class "matrix" containing background median intensities

**Ri** Object of class "matrix" containing raw intensities

**Ni** Object of class "matrix" containing normalized intensities

**snr** Object of class "matrix" containing signal to noise ratio values

**flag** Object of class "character" containing assigned flags

### Note

More details are in the package vignette

### Author(s)

Diego Diez

### Examples

```
## Not run:  
  data(codelink.example)
```

```
## End(Not run)
```

---

codelink.example      *Dataset of class 'Codelink'*

---

**Description**

Dataset from a h20kcod (Codelink Human UniSet I 20k) array containing 2 samples and ~20000 probes.

**Usage**

```
data(codelink.example)
```

**Format**

A [Codelink](#) object containing 20469 probes and 2 samples.

**Author(s)**

Diego Diez

---

CodelinkSet-class      *Class CodelinkSet*

---

**Description**

This is the storage class for Codelink data

**Objects from the Class**

Object are created after reading text codelink files with `readCodelinkSet()`

**Description**

CodelinkSet objects are derived from ExpressionSet and therefore inherits all their methods. Additional methods are defined to extract information:

Old Codelink-class objects can be converted into CodelinkSet instances using the function `Codelink2CodelinkSet`.

**Extends**

Directly extends class [ExpressionSet](#).

**Methods**

Class-specific methods:

`getWeight` Get the matrix of weights.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:  
  data(codset)  
  
## End(Not run)
```

---

CodelinkSetUnique-class

*Class CodelinkSetUnique*

---

**Description**

This is the storage class for Codelink data– with unique probes

**Objects from the Class**

Object are created after applying `averageProbes()` on an object of the class `CodelinkSet`

**Description**

`CodelinkSetUnique` objects are derived from `ExpressionSet` and therefore inherits all the methods.

**Note**

More details are in the package vignette

**Author(s)**

Diego Diez

**Examples**

```
## Not run:  
  data(codelink.exprs)  
  foo <- averageProbes(codelink.exprs)  
  
## End(Not run)
```

---

codPlot

*Diagnostic plots for CodelinkSet object.*

---

**Description**

This function performs several types of diagnostic plots using information from `CodelinkSet` objects.

**Usage**

```
codPlot(object, array, what = "ma", ...)
```

**Arguments**

object	a CodelinkSet object.
array	The array to use for plotting (by default array=1).
what	the type of plot (by default ma).
...	additional arguments passed to the appropriate functions.

**Details**

Plot types:

scatter Scatter plot of the selected array intensities vs. the median array, or a second array if specified.

ma MA plot of the selected array intensities vs. the median array, or a second array if specified. In the x-axis the value of A (mean abundance;  $A = \text{Array1} + \text{Array2}$ ) is plotted. In the y-axis the value of M (difference;  $M = \text{Array1} - \text{Array2}$ ) is plotted.

density The distribution of intensities for each array in the dataset is plotted as a kernel density.

image If the logical position of the probes in the array are available, this plot produces a pseudoimage of the array. The values of the "intensity", "bg" or "snr" can be selected with the 'signal' parameter (default signal="bg"). Color range can be controlled with 'high' and 'low' parameters.

**Author(s)**

Diego Diez

---

codset                      *Dataset of class 'CodelinkSet'*

---

**Description**

Dataset from a h20kcod (Codelink Human UniSet I 20k) array containing 4 samples and ~20000 probes.

**Usage**

```
data(codelink.example)
```

**Format**

A [Codelink](#) object containing 20469 probes and 4 samples.

**Author(s)**

Diego Diez

---

createWeights	<i>Create weight for Codelink chips</i>
---------------	---

---

**Description**

Create a weight matrix based on probe type and flags.

**Usage**

```
createWeights(object, type.weights = NULL, flag.weights = NULL)
```

**Arguments**

object	an object of class "Codelink" or "CodelinkSet".
type.weights	named character vector of type weights used.
flag.weights	named character vector of flag weights used.

**Author(s)**

Diego Diez

**Examples**

```
data(codset)
w <- createWeights(codset)
```

---

cutCV	<i>Calculate cutoff based in CV.</i>
-------	--------------------------------------

---

**Description**

Takes a Codelink object and calculate cutoff based in CV.

**Usage**

```
cutCV(object, subset=c(1:dim(object)[2]))
```

**Arguments**

object	an object of class "Codelink".
subset	subset of arrays to calculate cutoff with

**Details**

First it computes the median of CV for each gene over all arrays. Then it computes the mean and sd of all medians. Finally:

```
cutoff = mean + 3 * sd
```

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
# data: Normalized Codelink object merged.
cutoff <- cutCV(data)

## End(Not run)
```

decDetect

*Determine decimal type of Codelink files***Description**

Determine decimal type of Codelink files.

**Usage**

```
decDetect(file, nlines)
```

**Arguments**

file	the file to be read.
nlines	number of lines to skip.

**Value**

Decimal type.

**Author(s)**

Diego Diez

dim.Codelink

*Return the dimension of a Codelink object.***Description**

Takes a Codelink object and returns the dimension (genes x samples).

**Usage**

```
## S3 method for class 'Codelink'
dim(x)
```

**Arguments**

x	an object of class "Codelink".
---	--------------------------------

**Value**

A numeric vector with the dimensions.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:  
data(codelink.example)  
dim(codelink.example)  
  
## End(Not run)
```

---

fc2Cond

*Select probes based on fold change calculation*

---

**Description**

Takes a Codelink object and calculate fold changes (M) between two conditions (samples). Then select genes based on those who pass the passed cutoff.

**Usage**

```
fc2Cond(object, cond1=NULL, cond2=NULL, fc=1.0, verbose=FALSE)
```

**Arguments**

object	an object of class "Codelink".
cond1	numeric or character; First condition to compute M.
cond2	numeric or character; Second condition to compute M.
fc	value of the fold change cutoff
verbose	logical; if some information is printed on the console.

**Details**

Conditions can be passed as characters or as numeric index from the sample slot. The intensities are internally transformed to log2 if needed. The M value is computed as:

$$M = \text{cond1} - \text{cond2}$$
**Value**

A logical vector indicating which genes pass the cutoff

**Author(s)**

Diego Diez

---

imageCodelink	<i>Image plot of Codelink arrays</i>
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---

### Description

Plot and image of a Codelink array if the layout information is found.

### Usage

```
imageCodelink(object, array = 1, what = "bg",  
              low="black", high="white", mar=c(1,1,1,1),  
              gr=1, gc=1, log.it=FALSE, ...)
```

### Arguments

object	an object of class "Codelink".
array	array to be used.
what	with data plot: bg, smean, ri, ni.
low	color used for low intensities.
high	color used for high intensities-
mar	character vector specifying margins.
gc	numerical; number of grid columns.
gr	numerical; number of grid rows.
log.it	logical; if TRUE data is log2 transformed (if not yet).
...	additional arguments passed to image.

### Author(s)

Diego Diez

### Examples

```
## Not run:  
data(codelink.example)  
imageCodelink(codelink.example)  
  
## End(Not run)
```

---

logCodelink	<i>Application of logCodelink to Codelink object</i>
-------------	--

---

**Description**

Takes a Codelink object and apply logCodelink to intensity values.

**Usage**

```
logCodelink(object)
```

**Arguments**

object            an object of class "Codelink" or a list of genes.

**Value**

A Codelink object with logCodelink intensities.

**Author(s)**

Diego Diez

**See Also**

[log2](#)

**Examples**

```
## Not run:  
data(codelink.example)  
codelink.example <- logCodelink(codelink.example)  
  
## End(Not run)
```

---

mergeArray	<i>Merge Codelink Bioarrays Data</i>
------------	--------------------------------------

---

**Description**

Merge data in a Codelink Object corresponding to same samples. Need a vector indicating the classes and an optional vector indicating the labels of the merged samples.

**Usage**

```
mergeArray(object, class, names=NULL, method="mean",  
          log.it=FALSE, merge.snr=TRUE)
```

**Arguments**

object	an object of class "Codelink".
class	a numeric vector indicating the classes.
names	an optional character vector indicating labels for each class.
method	the method used to summarize. Currently only "mean" supported.
log.it	logical; a logical indicating if log2 values should be returned.
merge.snr	logical; a logical indicating if SNR values should be merged.

**Value**

An object of class "Codelink".

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
data(codelink.example)
codelink.example <- bkgdCorrect(codelink.example)
codelink.example <- normalize(codelink.example, log.it = FALSE)
codelink.example <- mergeArray(codelink.example, class = c(1,1),
  names = "SAMPLE", log.it = TRUE)

## End(Not run)
```

---

na2false

*Set NAs to FALSE*

---

**Description**

Takes a logical vector as input and set all NAs to FALSE. This may happens when comparison is done on NA values.

**Usage**

```
na2false(x)
```

**Arguments**

x a logical vector.

**Value**

A logical vector without NAs.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
  a <- c(1, 2, 3, NA, 5)
  b <- c(5, 4, NA, 2, 1)
  sel <- a > b
  sel <- na2false(sel)

## End(Not run)
```

---

Nondocumented-objects *Here goes every undocumented function.*

---

**Description**

Every function without help page is redirected here. Either because it is not intended to have a help page or because it is a bug. If you think it is the later please contact the package maintainer.

NOTE: Actually it is none of that reasons but the fact that the package is under heavy development.

**Author(s)**

Diego Diez

---

normalize *Normalization wrapper for Codelink/CodelinkSet objects.*

---

**Description**

Takes a CodelinkSet or Codelink object and applies normalization to intensity values.

**Usage**

```
## S4 method for signature 'Codelink'
normalize(object, method="quantiles", log.it=TRUE, preserve=FALSE, weights=NULL, loess.method="fast")

## S4 method for signature 'CodelinkSet'
normalize(object, method="quantile", log.it=TRUE, weights=NULL, loess.method="fast")

## S4 method for signature 'CodelinkSet'
codNormalize(object, method="quantile", log.it=TRUE, weights=NULL, loess.method="fast")
```

**Arguments**

object	an object of class CodelinkSet or Codelink.
method	method to use in normalization.
log.it	logical; if data should be log2.
preserve	logical; if Ri slot should be preserved.
weights	weights for method CyclicLoess.
loess.method	loess method to be used, default to 'fast'.

**Details**

Currently supported methods include "median", "quantile" and "loess". Normalization functions are borrowed from the limma package.

If a matrix of weights is passed for CyclicLoess normalization, a vector is constructed taking the lowest weight for each probe.

**Value**

A CodelinkSet or Codelink object with normalized intensity values.

**Author(s)**

Diego Diez

**Examples**

```
data(codset)
# Background correction.
codset <- codCorrect(codset, method = "half")
# Normalization.
codset <- normalize(codset, method = "quantile")
```

---

plotCorrelation

*Plot correlation scatterplot between two arrays*

---

**Description**

Takes a Codelink object as argument and plot Correlation scatterplot of two arrays.

**Usage**

```
plotCorrelation(object, x=1, y=2, cutoff=FALSE, label="type", title=NULL, xlim=NULL, ylim=NULL)
```

**Arguments**

object	an object of class "Codelink".
x	array to be used in x axis.
y	array to be used in y axis.
cutoff	cutoff used to show fold change.
label	labels to shown.
title	The title of the plot.
xlim	range for the X axis.
ylim	range for the Y axis.

**Author(s)**

Diego Diez

**See Also**[plot](#)**Examples**

```
## Not run:
  data(codelink.example)
  plotCorrelation(codelink.example)

## End(Not run)
```

---

plotCV	<i>Plot of CV</i>
--------	-------------------

---

**Description**

Takes a Codelink object and plot de distribution of CV after applying mergeCodelink.

**Usage**

```
plotCV(object, subset=c(1:dim(object)[2]), cutoff=NULL, title=NULL, legend.cex=1)
```

**Arguments**

object	an object of class "Codelink".
subset	subset of arrays to plot
cutoff	cutoff of CV to be shown.
title	title of the plot.
legend.cex	factor to apply to the fonts in the legend to fit.

**Author(s)**

Diego Diez

---

plotDensities	<i>Plot Densities</i>
---------------	-----------------------

---

**Description**

Takes a Codelink object and plot the distributions of intensities.

**Usage**

```
plotDensities(object, what = NULL, title = NULL, col = NULL,
  legend.title = NULL, legend.cex=1, ...)
```

**Arguments**

object	an object of class "Codelink"
what	what data to plot, one of "bg", "smean", "snr", "ri" or "ni"
title	title of the plot
col	vector of colors
legend.title	if provided, a title for the legend
legend.cex	font factor use in legend
...	further arguments to be passed to plot() and line() functions (e.g. lwd, etc.)

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
  data(codelink.example)
  plotDensities(codelink.example)

## End(Not run)
```

---

plotMA

*MA plot*

---

**Description**

Takes a Codelink object and plot M vs A.

**Usage**

```
plotMA(object, array1 = 1, array2 = NULL, cutoff = c(-1, 1), label = NULL,
  type = NULL, high.list = NULL, high.col = "blue", high.pch = 21,
  high.bg = "cyan", snr = NULL, snr.cutoff = 1, legend.x = NULL, pch = ".",
  subset = NULL, title = NULL, xlim = NULL, ylim = NULL)
```

**Arguments**

object	an object of class "Codelink" or "MAarrayLM".
array1	first array to be used.
array2	second array to be used.
cutoff	cutoff to be used as fold change marker.
label	type of labeling used in legend.
type	spot type information.
high.list	list of genes highlighted.
high.col	color used for high genes.
high.pch	pch used for high genes.
high.bg	background color used for high genes.

snr	vector with SNR values, usually, taking rowMeans() from a SNR matrix.
snr.cutoff	SNR cutoff used for label spots.
legend.x	relative position of the legend.
pch	pch style used to main spots.
subset	subset of spots used to plot based on 'type' slot.
title	title of the plot.
xlim	range for the X axis.
ylim	range for the Y axis.

### Details

This function has suffered recent re-working, to increase the usability and to clean a little bit the code.

If array2 is NULL a median array is computed using all available arrays. Then the values of M and A are computed using the following formula:

$$M = \text{array2} - \text{array1}$$

$$A = (\text{array2} + \text{array1}) / 2$$

If type information is available in the Codelink object, or provided through the 'type' argument, spots are colored based on that. DISCOVERY spots are plotted black with pch = "." whereas the other classes are plotted with different background colors, using gray as border to increase contrasts. For that pch = 21 is used. If snr is specified as label option, the SNR is used to label spots, if available in the Codelink object. In this case, the mean SNR across all arrays is used when array2 = NULL.

Some parameters may not be working right now, as the new function is using a different method to labels spots.

The legend is 'automagically' located, but this can be overridden with the legend.x argument.

In addition, a subset of the spots can be plotted based on type information when available. This allows, for example, to plot only DISCOVERY spots.

### Author(s)

Diego Diez

### Examples

```
## Not run:
  data(codelink.example)
  plotMA(codelink.example)

## End(Not run)
```

---

printHead	<i>Print briefly a Codelink object</i>
-----------	--

---

**Description**

Takes a Codelink object and print a summary information of the data estored. It is based on printHead() from package limma.

**Usage**

```
printHead(x)
```

**Arguments**

x an object of class "Codelink".

**Author(s)**

Diego Diez

---

readCodelink	<i>Read Codelink Bioarrays Data</i>
--------------	-------------------------------------

---

**Description**

Read data exported as text by Codelink Software. It reads values (normalized by Codelink Software or not) flags and information about probes.

**Usage**

```
readCodelink(files = list.files(pattern = "TXT"), sample.name =
  NULL, flag, flag.weights, type.weights, dec = NULL,
  type = "Spot", preserve = FALSE, verbose = 2,
  file.type = "Codelink", check = TRUE, fix = FALSE, old
  = FALSE)
readCodelinkSet(filename, path, phenoData = NULL, ...)
```

**Arguments**

files	list of files to read.
sample.name	vector of same length as files with sample names.
flag	list with values to assign based on Flag quality values.
flag.weights	weights assigned to each probe flag.
type.weights	weights assigned to each probe type.
dec	character indicating the decimal character used in the files.
type	character indicating which base value to read from files.
preserve	logical, if TRUE Bkgd\stdev slot is not removed (if present).

verbose	numerical, set the level of information. Level 2 set as old behaviour. Level > 2 output some debug info.
file.type	exported file type, currently Codelink or XLS file formats supported.
check	logical, check for probe order consistency.
fix	logical, try to fix probe order consistency.
old	logical, whether NA is assigned to intensities based on flags.
filename	list of files.
path	path to the files.
phenoData	phenoData object with sample information.
...	further arguments to be passed.

**Value**

readCodelink returns an object of class "Codelink", whereas readCodelinkSet() returns a CodelinkSet object.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
# specify a different one.
f <- list.files(pattern = "TXT")
codset <- readCodelinkSet(filename = f)

# read a targets file with phenotypic information
# including sample names, file names and sample groups.
pdata = read.AnnotationDataFrame("targets.txt")
codset = readCodelinkSet(pdata$FileNames, phenoData=pdata)

data(codset)

## End(Not run)
```

---

readHeader

*Read Header from Codelink Bioarrays Files*

---

**Description**

Read the header of Codelink files and obtain useful information.

**Usage**

```
readHeader(file, dec=FALSE)
```

**Arguments**

file	File to read.
dec	logical; If TRUE determine decimal point.

**Value**

A list with header and other usefull information.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
  files <- list.files(pattern = "TXT")
  head <- readHeader(files[1])

## End(Not run)
```

---

readHeaderXLS

*Read Header from XLS exported Codelink Bioarrays Files*

---

**Description**

Read the header of Codelink files and obtain useful information.

**Usage**

```
readHeaderXLS(file, dec=FALSE)
```

**Arguments**

file	File to read.
dec	logical; If TRUE determine decimal point.

**Details**

This function is not meant to be used by normal users.

**Value**

A list with header and other usefull information.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:
  files <- list.files(pattern = "TXT")
  head <- readHeaderHeader(files[1])

## End(Not run)
```

---

reportCodelink	<i>Write a report of genes selected in HTML</i>
----------------	---

---

### Description

Takes a list of genes as argument and writes an HTML page containing information about these genes: Unigene, Genbank, Entrez Gene, etc.

### Usage

```
reportCodelink(object, chip, filename = NULL, title = "Main title",
               probe.type = FALSE, other = NULL, other.ord = NULL)
```

### Arguments

object	an object of class "Codelink" or a list of genes.
chip	the chip description package.
filename	file name used in the report.
title	title used in the report.
probe.type	logical; if TRUE Probe type information is written.
other	list of vectors containing additional values to add to the report.
other.ord	slot name in other to order genes by.

### Value

Nothing, only the HTML file generated.

### Author(s)

Diego Diez

### See Also

[htmlpage](#)

---

selCV	<i>Select based on CV cutoff.</i>
-------	-----------------------------------

---

### Description

Takes a Codelink object and select genes based on CV cutoff.

### Usage

```
selCV(object, cutoff)
```

**Arguments**

object            an object of class "Codelink".  
 cutoff           cutoff normally calculated with cutCV()

**Value**

A logical vector.

**Author(s)**

Diego Diez

---

SNR	<i>Calculate SNR</i>
-----	----------------------

---

**Description**

Compute SNR inside read.Codelink.

**Usage**

```
SNR(Smean, Bmedian, Bstdev)
```

**Arguments**

Smean            matrix of Smean intensities.  
 Bmedian          matrix of background median intensities.  
 Bstdev           matrix of background standard deviation.

**Author(s)**

Diego Diez

---

writeCodelink	<i>Write a Codelink object to file.</i>
---------------	---

---

**Description**

Export of the data from a codelink object to a text file.

**Usage**

```
writeCodelink(object, file, dec = ".", sep = "\t", flag = FALSE, chip)
```

**Arguments**

object	an object of class "Codelink".
file	filename to write object to.
dec	decimal character to use.
sep	delimiter character to use.
flag	should the Codelink flags be written.
chip	chip package to use, normally guessed.

**Details**

By default, intensities and SNR are wrote to the file. If set, the flag are also output. The header have "INTENSITY\\_\_", "SNR\\_\_" and "FLAG\\_\_" respectibely append to the sample name for those values. The default delimiter is the tab character, but that can be set with the sep argument. The default decimal character is the point.

**Author(s)**

Diego Diez

**Examples**

```
## Not run:  
  data(codelink.example)  
  writeCodelink(codelink.example, file = "foo.txt")  
  
## End(Not run)
```

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