# Package 'codelink'

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**Version** 1.79.0

**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

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**ByteCompile** yes

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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 beacuse those files contain and indetermined number of empty lines at the end. Thus, reading the entire data matrix don't works.

### 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 adviced 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 performes 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 aboid 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` *Class Codelink*

## 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 = Array1 + Array2) is plotted. In the y-axis the value of M (difference; M = Array1 - 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 controled 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 *Create weight for Codelink chips*

### 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 *Calculate cutoff based in CV.*

### 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 = cond1 - cond2

## Value

A logical vector indicating which genes pass the cutoff

## Author(s)

Diego Diez

imageCodelink *Image plot of Codelink arrays*

## 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 specifiying margings. |
| 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 *Application of logCodelink to Codelink object*

### 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 *Merge Codelink Bioarrays Data*

### 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 mer- ged 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 isunder 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 *Plot of CV*

---

### 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` *Plot Densities*

---

### 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 markeer. |
| 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 = array2 - array1

A = (array2 + array1) / 2

If type information is available in the Codelink object, or provided throught 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 overrided 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` *Print briefly a Codelink object*

---

## Description

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

## Usage

```
printHead(x)
```

## Arguments

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

### Author(s)

Diego Diez

---

`readCodelink` *Read Codelink Bioarrays Data*

---

### 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 obtein usefull 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` *Write a report of genes selected in HTML*

## Description

Takes a list of genes as argument and writes an HTML page containing informa- tion 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 writen. |
| `other` | list of vectors containing aditional 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 *Select based on CV cutoff.*

## 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 normaly calculated with cutCV() |

## Value

A logical vector.

## Author(s)

Diego Diez

SNR *Calculate SNR*

## 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 *Write a Codelink object to file.*

## 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 appendend 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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