

Package ‘wrMisc’

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Title Analyze Experimental High-Throughput (Omics) Data

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Description The efficient treatment and convenient analysis of experimental high-throughput (omics) data gets facilitated through this collection of diverse functions. Several functions address advanced object-conversions, like manipulating lists of lists or lists of arrays, reorganizing lists to arrays or into separate vectors, merging of multiple entries, etc. Another set of functions provides speed-optimized calculation of standard deviation (sd), coefficient of variance (CV) or standard error of the mean (SEM) for data in matrixes or means per line with respect to additional grouping (eg n groups of replicates). Other functions facilitate dealing with non-redundant information, by indexing unique, adding counters to redundant or eliminating lines with respect redundancy in a given reference-column, etc. Help is provided to identify very closely matching numeric values to generate (partial) distance matrixes for very big data in a memory efficient manner or to reduce the complexity of large data-sets by combining very close values. Many times large experimental datasets need some additional filtering, adequate functions are provided. Batch reading (or writing) of sets of files and combining data to arrays is supported, too. Convenient data normalization is supported in various different modes, parameter estimation via permutations or boot-strap as well as flexible testing of multiple pair-wise combinations using the framework of 'limma' is provided, too.

Depends R (>= 3.1.0)

Imports grDevices, graphics, MASS, stats

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addBeforFileExtension *Add text before file-extension*

Description

This function helps changing character strings like file-names and allows adding the character vector 'add' (length 1) before the extension (defined by last '.') of the input string 'x'. Used for easily creating variants/additional filenames but keeping current extension.

Usage

```
addBeforFileExtension(x, add, sep = "_")
```

Arguments

x	main character vector
add	character vector to be added
sep	(character) separator between 'x' & 'add' (character, length 1)

Value

modified character vector

Examples

```
addBeforeFileExtension(c("abd.txt", "ghg.ijij.txt", "kjh"), "new")
```

adjBy2ptReg

Linear rescaling of numeric vector or matrix

Description

adjBy2ptReg takes data within window defined by 'lims' and determines linear transformation so that these points get the regression characteristics 'regrTo', all other points (ie beyond the limits) will follow the same transformation. In other words, this function performs 'linear rescaling', by adjusting (normalizing) the vector 'dat' by linear regression so that points falling in 'lims' (list with upper & lower boundaries) will end up as 'regrTo'.

Usage

```
adjBy2ptReg(dat, lims, regrTo = c(0.1, 0.9), refLines = NULL,
  callFrom = NULL)
```

Arguments

dat	numeric vector, matrix or data.frame
lims	(list, length=2) should be list giving limits (list(lo=c(min,max),hi=c(min,max)) in data allowing identifying which points will be used for determining slope & offset
regrTo	(numeric, length=2) to which characteristics data should be regressed
refLines	(NULL or integer) optional subselection of lines of dat (will be used internal as refDat)
callFrom	(character) for better tracking of use of functions

Value

matrix with normalized values

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

```
set.seed(2016); dat1 <- round(runif(50,0,100),1)
## extreme values will be further away :
adjBy2ptReg(dat1,lims=list(c(5,9),c(60,90)))
plot(dat1,adjBy2ptReg(dat1,lims=list(c(5,9),c(60,90))))
```

arrayCV	<i>CV of array</i>
---------	--------------------

Description

arrayCV gets CVs for replicates in 2 or 3 dim array and returns CVs as matrix. This function may be used to calculate CVs from replicate microtiter plates (eg 8x12) where replicates are typically done as multiple plates, ie initial matrixes that are the organized into arrays.

Usage

```
arrayCV(arr, byDim = 3, silent = TRUE, callFrom = NULL)
```

Arguments

arr	(3-dim) array of numeric data like where replicates are along one dimesion of the array
byDim	(integer) over which dimension repliates are found
silent	(logical) suppres messages
callFrom	(character) allow easier tracking of message produced

Value

matrix of CV values

See Also[rowCVs](#), [rowGrpCV](#), [replPlateCV](#)**Examples**

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
head(arrayCV(dat1,byDim=2))
```

asSepList

Organize data as separate list-entries

Description

asSepList allows reorganizing list into separate numeric vectors. For example, matrixes or data.frames will be split into separate columns (differnt to [partUnlist](#) which maintains the original structure). This function also works with lists of lists. This function may be helpful for reorganizing data for plots.

Usage

```
asSepList(y, asNumeric = TRUE, minLen = 4, fxArg = NULL,
          silent = FALSE, callFrom = NULL)
```

Arguments

y	list to be separated/split in vectors
asNumeric	(logical) to transform all list-elements in simple numeric vectors (won't work if some entries are character)
minLen	(integer) (currently use of this argument not implemeneted!) min length (or number of rows), as add'l element to eliminate arguments given wo names when asSepList is called in vioplot2
fxArg	(character) optinal names to exclude if any (lazy matching) matches (to exclude other arguments be misinterpreted as data, used in wrGraph::vioplot2)
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

list, partially unlisted to vectors

See Also

[partUnlist](#), [unlist](#)

Examples

```
bb <- list(fa=gl(2,2),c=31:33,L2=matrix(21:24,nc=2),li=list(li1=11:14,li2=data.frame(41:44)))
asSepList(bb)
lapply(bb,.asDF2)
partUnlist(lapply(bb,.asDF2))
```

 buildTree

Connect edges to form tree and extract all possible branches

Description

It is assumed that multiple fragments from a common ancestor may be characterized by their start- and end-sites by integer values. For example, if 'abcdefg' is the ancestor, the fragments 'bcd' (from position 2 to 4) and 'efg' may then be assembled. To do so, all fragments must be presented as a matrix specifying all start- and end-sites (and fragment-names). buildTree searches contiguous fragments from columns 'posCo' (start/end) from 'disDat' to build tree & extract path information starting with line 'startFr'. Made for telling if dissociated fragments contribute to long assemblies. This function uses various functions of package [data.tree](#) which must be installed, too.

Usage

```
buildTree(disDat, startFr = NULL, posCo = c("beg", "end"),
  silent = FALSE, callFrom = NULL)
```

Arguments

disDat	(matrix or data.frame) integer values with 1st column, ie start site of fragment, 2nd column as end of fragments, rownames as unique IDs (node-names)
startFr	(integer) index for 1st node (typically =1 if 'disDat' sorted by "beg"), should point to a terminal node for consecutive growing of branches
posCo	(character) colnames specifying the begin & start sites in 'disDat', if NULL 1st & 2nd col will be used
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

list with \$paths (branches as matrix with columns 'sumLen' & 'n'), \$usedNodes (character vector of all names used to build tree) and \$tree (object from data.tree)

See Also

package [data.tree](#) original function used [Node](#); in this package : for exploiting edge/tree related issues [simpleFragFig](#), [countSameStartEnd](#) and [contribToContigPerFrag](#),

Examples

```
frag2 <- cbind(beg=c(2,3,7,13,13,15,7,9,7,3,7,5,7,3),end=c(6,12,8,18,20,20,19,12,12,4,12,7,12,4))
rownames(frag2) <- c("A","E","B","C","D","F","H","G","I","J","K","L","M","N")
buildTree(frag2)
countSameStartEnd(frag2)
```

cbindNR	<i>cbind to non-redundant</i>
---------	-------------------------------

Description

cbindNR combines all matrixes given as arguments to non-redundant column names (by ADDING the number of 'duplicated' columns !). Thus, this function works similar to cbind, but allows combining multiple matrix-objects containing redundant column-names. The output may be optional sorted.

Usage

```
cbindNR(..., convertDFtoMatr = TRUE, sortOutput = TRUE,  
        silent = FALSE, callFrom = NULL)
```

Arguments

...	all matrixes to get combined in cbind way
convertDFtoMatr	(logical) decide if output should be converted to matrix
sortOutput	(logical) optional sorting by column-names
silent	(logical) suppres messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix or data.frame (as cbind would return)

See Also

[cbind](#), [nonAmbiguousNum](#), [firstOfRepLines](#)

Examples

```
ma1 <- matrix(1:6,ncol=3,dimnames=list(1:2,LETTERS[3:1]))  
ma2 <- matrix(11:16,ncol=3,dimnames=list(1:2,LETTERS[3:5]))  
cbindNR(ma1,ma2)
```

checkAvSd	<i>Check how multiple groups of data separate or overlap based on mean +/- sd</i>
-----------	---

Description

checkAvSd compares if/how neighbour groups separate/overlap via the 'engineering approach' (+/- 2 standard-deviations is similar to $\alpha=0.05$ t. test). This approach may be used as less elegant alternative to (multi-group) logistic regression. The function uses 'daAv' as matrix of means (rows are tested for up/down character/progression) which get compared with boundaries taken from daSd (for Sd values of each mean in 'daAv').

Usage

```
checkAvSd(daAv, daSd, nByGr = NULL, multSd = 2, codeConst = "const",
  extSearch = FALSE, outAsLogical = TRUE, silent = FALSE,
  callFrom = NULL)
```

Arguments

daAv	matrix or data.frame
daSd	matrix or data.frame
nByGr	optinal specifying number of Elements per group, allows rather using SEM (adopt to variable n of different groups)
multSd	(numeric) the factor specifyin how many sd values should be used as margin
codeConst	(character) which term/word to use when specifying 'constant'
extSearch	(logical) if TRUE, extend search to one group further (will call result 'nearUp' or 'nearDw')
outAsLogical	to switch between 2col-output (separate col for 'up' and 'down') or simple categorical vector ('const','okDw','okUp')
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

vector describing character as 'const' or 'okUp','okDw' (or if extSearch=TRUE 'nearUp','nearDw')

See Also

[rowGrpMeans](#)

Examples

```
mat1 <- matrix(rep(11:24,3)[1:40],byrow=TRUE,ncol=8)
checkGrpOrderSEM(mat1,grp=gl(3,3)[-1])
checkAvSd(rowGrpMeans(mat1,gl(3,3)[-1]),rowGrpSds(mat1,gl(3,3)[-1]) )
# consider variable n :
checkAvSd(rowGrpMeans(mat1,gl(3,3)[-1]),rowGrpSds(mat1,gl(3,3)[-1]),nByGr=c(2,3,3))
```

checkGrpOrder	<i>checkGrpOrder</i>
---------------	----------------------

Description

checkGrpOrder tests each line of 'x' if expected order appears. Used for comparing groups of measures with expected profile (simply by matching expected order)

Usage

```
checkGrpOrder(x, rankExp = NULL, revRank = TRUE)
```

Arguments

x	matrix or data.frame
rankExp	(numeric) expected order for values in columns, default 'rankExp' =1:ncol(x)
revRank	(logical) if 'revRank'=TRUE, the initial ranks & reversed ranks will be tested

Value

vector of logical values

See Also

[checkGrpOrderSEM](#)

Examples

```
set.seed(2005); mat <- matrix(round(runif(40),1),ncol=4)
checkGrpOrder(mat)
checkGrpOrder(mat,c(1,4,3,2))
```

checkGrpOrderSEM	<i>Check order of multiple groups including non-overlapping SEM-margins</i>
------------------	---

Description

checkGrpOrderSEM tests each line of 'x' if expected order of (replicate-) groups (defined in 'grp') appears intact, while including SEM of groups (replicates) via a proportional weight 'sdFact' as $(avGr1 - gr1SEM) < (avGr1 + gr1SEM) < (avGr2 - gr2SEM) < (avGr2 + gr2SEM)$. Used for comparing groups of measures with expected profile (by matching expected order) to check if data in 'x' representing groups ('grp') as lines follow. Groups of size=1: The sd (and SEM) can't be estimated directly without any replicates, however, an estimate can be given by shrinking if 'shrink1sampSd'=TRUE under the hypothesis that the overall mechanisms determining the variances is constant across all samples.

Usage

```
checkGrpOrderSEM(x, grp, sdFact = 1, revRank = TRUE,
  shrink1sampSd = TRUE, silent = FALSE, callFrom = NULL)
```

Arguments

x	matrix or data.frame
grp	(factor) to organize replicate columns of (x)
sdFact	(numeric) is proportional factor how many units of SEM will be used for defining lower & upper bounds of each group
revRank	(logical) optionally revert ranks
shrink1sampSd	(logical)
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

logical vector if order correct (as expected based on ranks)

See Also

takes only 10

Examples

```
mat1 <- matrix(rep(11:24, 3)[1:40], byrow=TRUE, ncol=8)
checkGrpOrderSEM(mat1, grp=gl(3, 3)[-1])
```

checkSimValueInSer *Check for similar values in series*

Description

checkSimValueInSer checks all values of 'x' for similar values outside/within (relative) range of 'ppm' (ie ambiguous within given range). Return logical vector : FALSE for each entry of 'x' if value inside of ppm range to neighbour

Usage

```
checkSimValueInSer(x, ppm = 5, sortX = TRUE)
```

Arguments

x	numeric vector
ppm	(numeric) ppm-range for considering as similar
sortX	(logical) allows speeding up function when set to FALSE, for large data that are already sorted

Value

logical vector : FALSE for each entry of 'x' if value inside of ppm range to neighbour

See Also

similar with more options [withinRefRange](#)

Examples

```
va1 <- c(4:7,7,7,7,7,8:10)+(1:11)/28600; checkSimValueInSer(va1)
cbind(va=va1,simil=checkSimValueInSer(va1))
```

checkStrictOrder *Check for strict (ascending or descending) order*

Description

checkStrictOrder tests lines of 'dat' (matrix of data.frame) for strict order (ascending, descending or constant), each col of data is tested relative to the col on its left.

Usage

```
checkStrictOrder(dat, invertCount = TRUE)
```

Arguments

dat matrix or data.frame
invertCount (logical)

Value

matrix with counts of (non-)up pairs, (non-)down pairs, (non-)equal-pairs, if 'invertCount'=TRUE
resulting 0 means that all columns are following the described characteristics (with variable column numbers easier to count)

See Also

[order](#)

Examples

```
set.seed(2005); mat <- matrix(round(runif(40),1),nc=4)
checkStrictOrder(mat); mat[which(checkStrictOrder(mat)[,2]==0),]
```

checkVectLength *Check length of vector*

Description

checkVectLength checks argument 'x' for expected length 'expL' and return either message or error when expectation not met. Used for parameter ('sanity') checking in other user front-end functions.

Usage

```
checkVectLength(x, expL = 1, stopOnProblem = FALSE, silent = FALSE,
callFrom = NULL)
```

Arguments

x (numeric or character vector) input to check length
expL (numeric) expected length
stopOnProblem (logical) continue on problems with message or stop (as error message)
silent (logical) suppress messages if TRUE
callFrom (character) allows easier tracking of message(s) produced

Value

NULL (produces only optional message if length is OK or error-message if length is not OK)

Examples

```
aa <- 1:5; checkVectLength(aa,exp=3)
```

cleanReplicates	<i>Replace most distant values by NA</i>
-----------------	--

Description

This procedure aims to straighten (clean) the most extreme of noisy replicates by identifying the most distant points (among a set of replicates). The input 'x' (matrix or data.frame) is supposed to come from multiple different measures taken in replicates (eg weight of different individuals as rows taken as multiple replicate measures in subsequent columns). With the argument nOutl the user chooses the total number of most extreme values to replace by NA. how many of the most extreme replicates of the whole dataset will be replaced by NA, ie with nOutl=1 only the single most extreme outlier will be replaced by NA. Outlier points are determined as point(s) with highest distance to (row) center (median and mean choice via argument 'centrMeth'). Returns input data with "removed" points set to NA, or if retOffPos=TRUE the most extreme/outlier positions.

Usage

```
cleanReplicates(x, centrMeth = "median", nOutl = 2,  
               retOffPos = FALSE, silent = FALSE, callFrom = NULL)
```

Arguments

x	matrix (or data.frame)
centrMeth	(character) method to summarize (mean or median)
nOutl	(integer) determines how many points per line will be set to NA (with n=1 the worst row of replicates will be 'cleaned')
retOffPos	(logical) if TRUE, replace the most extreme outlier only
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

input data with "removed" points set as NA, or if retOffPos=TRUE the most extreme/outlier positions

Examples

```
mat3 <- matrix(c(19,20,30, 18,19,28, 16,14,35),ncol=3)  
cleanReplicates(mat3,nOutl=1)
```

closeMatchMatrix	<i>Reorganize results of search for close (similar) value values in matrix-view</i>
------------------	---

Description

closeMatchMatrix reorganizes/refines results from simple search of similar values of 2 sets of data by `findCloseMatch` (as list for one-to many relations) to more human friendly/readable matrix. This function returns results combining two sets of data which were initially compared (eg measured and theoretical values) as matrix-view using output of `findCloseMatch` and both original datasets. Additional information (covariables, annotation, ...) may be included as optional columns for either 'predMatr' or 'measMatr'. Note : It is important to run `findCloseMatch` with `sortMatch=FALSE` ! Note : Results presented based on view of 'predMatr', so if multiple 'measMatr' are at within tolerated distance, lines of 'measMatr' will be repeated; Note : Distances 'disToMeas' and 'ppmToPred' are oriented : neg value if measured is lower than predicted (and pos values if higher than predicted); Note : Returns NULL when nothing within given limits of comparison;

Usage

```
closeMatchMatrix(closeMatch, predMatr, measMatr, prefMatch = c("^x",
  "y"), colPred = 1, colMeas = 1, limitToBest = TRUE,
  asDataFrame = FALSE, origNa = TRUE, silent = FALSE,
  callFrom = NULL, debug = FALSE)
```

Arguments

closeMatch	(list) output from <code>findCloseMatch</code> , ie list with hits for each 'x' (1st argument) : named vectors of value & x index in name; run with 'sortMatch'=F
predMatr	(vector or matrix) predicted values, the column 'colPred' indicates which column is used for matching from <code>findCloseMatch</code> ; if column 'id' present this column will be used as identifier for matching
measMatr	(vector or matrix) measured values, the column 'colMeas' indicates which column is used for matching from <code>findCloseMatch</code> ; if column 'id' present this column will be used as identifier for matching
prefMatch	(character, length=2) prefixes ('^x' and/or '^y') they may have been added by <code>findCloseMatch</code>
colPred	(integer or text, length=1) column of 'predMatr' with main values of comparison
colMeas	(integer or text, length=1) column of 'measMatr' with main measures of comparison
limitToBest	(integer) column of 'measMatr' with main measures of comparison
asDataFrame	(logical) convert results to data.frame if non-numeric matrix produced (may slightly slow down big results)
origNa	(logical) will try to use original names of objects 'predMatr', 'measMatr', if they are not multi-column and not conflicting other output-names (otherwise 'predMatr', 'measMatr' will appear)

silent (logical) suppress messages
 callFrom (character) allows easier tracking of message(s) produced
 debug (logical) for bug-tracking: more/enhanced messages

Value

results as matrix-view based on initial results from [findCloseMatch](#), including optional columns of supplemental data for both sets of data for comparison. Returns NULL when nothing within limits

See Also

[findCloseMatch](#), [checkSimValueInSer](#)

Examples

```

aA <- c(11:17); bB <- c(12.001,13.999); cC <- c(16.2,8,9,12.5,15.9,13.5,15.7,14.1,5)
(cloMa <- findCloseMatch(aA,cC,com="diff",lim=0.5,sor=FALSE))
# all matches (of 2d arg) to/within limit for each of 1st arg ('x'); 'y' ..to 2nd arg = cC
(maAa <- closeMatchMatrix(cloMa,aA,cC,lim=TRUE)) #
(maAa <- closeMatchMatrix(cloMa,aA,cC,lim=FALSE,origN=TRUE)) #
(maAa <- closeMatchMatrix(cloMa,cbind(valA=81:87,aA),cbind(valC=91:99,cC),colM=2,
  colP=2,lim=FALSE))
(maAa <- closeMatchMatrix(cloMa,cbind(aA,valA=81:87),cC,lim=FALSE,deb=TRUE)) #
a2 <- aA; names(a2) <- letters[1:length(a2)]; c2 <- cC; names(c2) <- letters[10+1:length(c2)]
(cloM2 <- findCloseMatch(x=a2,y=c2,com="diff",lim=0.5,sor=FALSE))
(maA2 <- closeMatchMatrix(cloM2,predM=cbind(valA=81:87,a2),measM=cbind(valC=91:99,c2),
  colM=2,colP=2,lim=FALSE,asData=TRUE))
(maA2 <- closeMatchMatrix(cloM2,cbind(id=names(a2),valA=81:87,a2),cbind(id=names(c2),
  valC=91:99,c2),colM=3,colP=3,lim=FALSE,deb=FALSE))
  
```

coinPermTest

Compare means of two vectors by permutation test

Description

Run coin-flipping like permutation tests (to compare difference of 2 means: 'x1' and 'x2') without any distribution-assumptions. Uses the package [coin](#).

Usage

```

coinPermTest(x1, x2, orient = "two.sided", nPerm = 5000,
  silent = FALSE, callFrom = NULL)
  
```

Arguments

x1	numeric vector (to be compared with vector 'x2')
x2	numeric vector (to be compared with vector 'x1')
orient	(character) may be "two.sided", "greater" or "less"
nPerm	(integer) number of permutations
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

"MCp" class numeric output with p-values

See Also

oneway_test in [LocationTests](#)

Examples

```
coinPermTest(2,3)
```

colMedSds

Standard error of median for each column by bootstrap

Description

Determine standard error (sd) of median by bootstrapping for multiple sets of data (rows in input matrix 'dat'). Note: Uses the package [boot](#).

Usage

```
colMedSds(dat, nBoot = 99)
```

Arguments

dat	(numeric) matrix
nBoot	(integer) number of iterations

Value

(numeric) vector with estimated standard errors

See Also

[boot](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
colMedSds(dat1)
```

colorAccording2 *Transform numeric values to color-gradient*

Description

This function helps making color-gradients for plotting a numerical variable.

Usage

```
colorAccording2(x, gradTy = "rainbow", nStartOmit = NULL,
  nEndOmit = NULL, revCol = FALSE, alpha = 1, callFrom = NULL)
```

Arguments

x	(character) color input
gradTy	(character) type of gradeint may be 'rainbow', 'heat.colors', 'terrain.colors', 'cm.colors', 'grey.colors'
nStartOmit	(integer) omit n steps from beginnin of gradient range
nEndOmit	(integer) omit n steps from end of gradient range
revCol	(logical) reverse order
alpha	(numeric) optional transparency value (1 for no transparency, 0 for complete opaqueness)
callFrom	(character) allow easier tracking of message(s) produced

Value

character vector (of same length as x) with color encoding

See Also

[cut](#)

Examples

```
set.seed(2015); dat1 <- round(runif(15),2)
plot(1:15,dat1,pch=16,cex=2,col=colorAccording2(dat1))
plot(1:15,dat1,pch=16,cex=2,col=colorAccording2(dat1,nStart0=0,nEnd0=4,revCol=TRUE))
plot(1:9,pch=3)
points(1:9,1:9,col=.transpGraySca(st=0,en=0.8,nSt=9,trans=0.3),cex=42,pch=16)
```

colSds	<i>sd for each column</i>
--------	---------------------------

Description

colSds is a speed optimized sd for matrix or data.frames. It and treats each line as an independent set of data for calculating the sd (equiv to `apply(dat, 1, sd)`). NAs are ignored from data.

Usage

```
colSds(dat)
```

Arguments

dat matrix (or data.frame) with numeric values (may contain NAs)

Value

numeric vector of sd values

See Also

[sd](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),nc=10)
colSds(dat1)
```

combineByEitherFactor *Create factor-like column regrouping data regrouping simultaneously by two factors*

Description

This function aims to address the situation when two somehow different groupings (of the same data) exist and need to be joined. It is not necessary that both alternative groupings use the same labels, neither. `combineByEitherFactor` adds new (last) column named 'grp' to input matrix representing the combined factor relative to 2 specified columns from input matrix 'mat' (via 'refC1','refC2'). Optionally, the output may be sorted and a column giving n per factor-level may be added. The function treats selected columns of 'mat' as pairwise combination of 2 elements (that may occur multiple times over all lines of 'mat') and sorts/organizes all instances of such combined elements (ie from both selected columns) as repeats of a given group, who's class number is given in output column 'grp', the (total) number of repeats may be displayed in column 'nGrp' (`nByGrp=TRUE`). If groups are overlapping (after re-ordering), an iterative process of max 3x2 passes will be launched after initial matching. Works on numeric as well as character input.

Usage

```
combineByEitherFactor(mat, refC1, refC2, nByGrp = FALSE,
  convergeMax = TRUE, callFrom = NULL, silent = FALSE)
```

Arguments

mat	input matrix
refC1	(numeric) column-number of 'mat' to use as 1st set
refC2	(numeric) column-number of 'mat' to use as 2nd set
nByGrp	(logical) add last col with n by group
convergeMax	(logical) if TRUE, run 2 add'l iteartive steps to search convergence to stable result
callFrom	(character) allows easier tracking of message(s) produced
silent	(logical) suppres messages

Value

matrix containing both selected columns plus additional column(s) indicating group-number of the pair-wise combination (and optional the total n by group)

Examples

```
nn <- rep(c("a", "e", "b", "c", "d", "g", "f"), c(3, 1, 2, 2, 1, 2, 1))
qq <- rep(c("m", "n", "p", "o", "q"), c(2, 1, 1, 4, 4))
nq <- cbind(nn, qq)[c(4, 2, 9, 11, 6, 10, 7, 3, 5, 1, 12, 8), ]
combineByEitherFactor(nq, 1, 2, nBy=TRUE); combineByEitherFactor(nq, 1, 2, nBy=FALSE)
combineByEitherFactor(nq, 1, 2, conv=FALSE); combineByEitherFactor(nq, 1, 2, conv=TRUE)
##
mm <- rep(c("a", "b", "c", "d", "e"), c(3, 4, 2, 3, 1)); pp <- rep(c("m", "n", "o", "p", "q"), c(2, 2, 2, 2, 5))
combineByEitherFactor(cbind(mm, pp), 1, 2, con=FALSE, nBy=TRUE);
combineByEitherFactor(cbind(mm, pp), 1, 2, con=TRUE, nBy=TRUE)
```

combineOverlapInfo *Find and combine points located very close in x/y space*

Description

Search points in x,y space that are located very close and thus likely to overlap. In case of points close enough, various options for joining names (and shortening longer descriptions) are available.

Usage

```
combineOverlapInfo(dat, suplInfo = NULL, disThr = 0.01,
  addNsimil = TRUE, txtSepChar = ",", combSym = "+", maxOverl = 50,
  callFrom = NULL, debug = FALSE, silent = FALSE)
```

Arguments

dat	(matrix) matrix or data.frame with 2 cols (used ONLY 1st & 2nd column !), used as x & y coordinates
suplInfo	(NULL or character) when points are considered overlapping the text from 'suplInfo' will be reduced to fragment before 'txtSepChar' and combined (with others from overlapping text) using 'combSym', if NULL \$combInf will appear with row-numbers
disThr	(numeric) distance-threshold for considering as similar via searchDataPairs()
addNsimil	(logical) include number of fused points
txtSepChar	(character) for use with .retain1stPart(): where to cut (& keep 1st part) text from 'suplInfo' to return in out\$CombInf; only 1st element used !
combSym	(character) concatenation symbol (character, length=1) for points considered overlaying, see also 'suplInfo'
maxOverl	(integer) if NULL no limit or max limit of group/clu size (avoid condensing too many neighbour points to single cloud)
callFrom	(character) allow easier tracking of message(s) produced
debug	(logical) additional messages for debugging
silent	(logical) suppress messages

Value

matrix with fused (condensed) information for cluster of overlapping points

Examples

```
set.seed(2013)
datT2 <- matrix(round(rnorm(200)+3,1),ncol=2,dimnames=list(paste("li",1:100,sep=""),
  letters[23:24]))
# (mimick) some short and longer names for each line
inf2 <- cbind(sh=paste(rep(letters[1:4],each=26),rep(letters,4),1:(26*4),sep=""),
  lo=paste(rep(LETTERS[1:4],each=26),rep(LETTERS,4),1:(26*4),",",rep(letters[sample.int(26)],4),
  rep(letters[sample.int(26)],4),sep=""))[1:100,]
head(datT2,n=10)
head(combineOverlapInfo(datT2,disThr=0.03),n=10)
head(combineOverlapInfo(datT2,suplI=inf2[,2],disThr=0.03),n=10)
```

combineRedBasedOnCol *Combine/reduce redundant lines based on specified column*

Description

This function works similar to unique, but it takes a matrix as input and considers one specified column to find unique instances. It identifies 'repeated' lines of the input-matrix (or data.frame) 'mat' based on (repeated) elements in/of column with name 'colNa' (or column-number). Redundant lines (ie repeated lines) will disappear in output. Eg used with extracted annotation where 1 gene has many lines for different GO annotation.

Usage

```
combineRedBasedOnCol(mat, colNa, sep = ",", silent = FALSE,
  callFrom = NULL)
```

Arguments

mat	input matrix or data.frame
colNa	character vector (length 1) mactng 1 column name (if mult only 1st will be used), in case of mult matches only 1st used
sep	(character) separator (default=",")
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix containing the input matrix without lines considered repeated (unique-like)

See Also

[findRepeated](#), [firstOfReplLines](#), [organizeAsListOfRepl](#)

Examples

```
matr <- matrix(c(letters[1:6], "h", "h", "f", "e", LETTERS[1:5]), ncol=3,
  dimnames=list(letters[11:15], c("xA", "xB", "xC")))
combineRedBasedOnCol(matr, colN="xB")
combineRedBasedOnCol(rbind(matr[1,], matr), colN="xB")
```

combineReplFromListToMatr

Combine replicates from list to matrix

Description

Suppose multiple measures (like multiple chanel) are taken for subjects and these measures are organized as groups in a list, like multiple parameters (= channels) or types of measurements (typically many paramters are recorded when screening compounds in microtiter plates). Within one parameter/channel all replicate-data from separate list-entries ('lst') will get combined according to names of list-elements. The function will trim any redundant text in names of list-elements, try to isolate separator (may vary among replicate-groups, but should be 1 character long). eg names "hct116 1.1.xlsx" & "hct116 1.2.xlsx" will be combined as replicates, "hct116 2.1.xlsx" will be considered as new group.

Usage

```
combineReplFromListToMatr(lst, callFrom = NULL)
```

Arguments

lst (list) list of arrays (typically multi-parameter measures of micortiterplate data)
 callFrom (character) allows easier tracking of message(s) produced

Value

list of arrays now with same dimension of arrays (but shorter, since replicate-arrays were combined)

See Also

[extr1chan](#), [organizeAsListOfRepl](#)

Examples

```
lst2 <- list(aa_1x=matrix(1:12,nrow=4,byrow=TRUE),ab_2x=matrix(24:13,nrow=4,byrow=TRUE))
combineReplFromListToMatr(lst2)
```

combineSingleT *Get all combinations with TRUE from each column*

Description

This function addresses the case when multiple alternative ways exist to combine two elements. combineSingleT makes combinatory choices : if multiple TRUE in given column of 'mat' make all multiple selections with always one TRUE from each column The resultant output contains index for first and second input columns elements to be combined.

Usage

```
combineSingleT(mat)
```

Arguments

mat 2-column matrix of logical values

Value

matrix with indexes of combinations of TRUE

Examples

```
## Example: First column indicates which boys want to dance and second column
## which girls want to dance. So if several boys want to dance each of the girls
## will have the chance to dance with each of them.
matr <- matrix(c(TRUE,FALSE,TRUE,FALSE,TRUE,FALSE),ncol=2)
combineSingleT(matr)
```

completeArrLst	<i>Complete list of arrays for same dimensions</i>
----------------	--

Description

This functions aims to inspect repeaing structues of data given as list of arrays and will try to complete arrays with fewer lines or columns (as this may appear eg with the very last set of high-thourput scening data if fewer measures remain in the last set). Thus, the dimensions of the arrays are compared and cases with fewer (lost) columns (eg fewer experimental replicates) will be adjust/complete by adding column(s) of NA. Used eg when at reading mircotiterplate data the last set is not complete.

Usage

```
completeArrLst(arrLst, silent = FALSE, callFrom = NULL)
```

Arguments

arrLst	(list) list of arrays (typically 1st and 2nd dim for specific genes/objects, 3rd for different measures associated with)
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

list of arrays, now with same dimension of arrays

See Also

[organizeAsListOfRepl, extr1chan](#)

Examples

```
arr1 <- array(1:24,dim=c(4,3,2),dimnames=list(c(LETTERS[1:4]),
  paste("col",1:3,sep=""),c("ch1","ch2")))
arr3 <- array(81:96,dim=c(4,2,2),dimnames=list(c(LETTERS[1:4]),
  paste("col",1:2,sep=""),c("ch1","ch2")))
arrL3 <- list(p1=arr1,p13=arr3)
completeArrLst(arrL3)
```

 contribToContigPerFrag

Characterize individual contribution of single edges in tree-structures

Description

This function helps investigating tree-like structures with the aim of indicating how much individual tree components contribute to compose long stretches. `contribToContigPerFrag` characterizes individual (isolated) contribution of single edges in tree-structures. Typically used to process/exploit summarized trees (as matrix) made by `buildTree` which makes use of the package `data.tree`. For example if A,B and C can be joined as well and B +D, this function will check if A+B+C is longer and if A contributes to the longest tree.

Usage

```
contribToContigPerFrag(joinMat, fullLength = NULL, nDig = 3)
```

Arguments

<code>joinMat</code>	(matrix) matrix with concatenated edges as rownames (separated by slashes), column <code>sumLen</code> for total length and column <code>n</code> for number of edges
<code>fullLength</code>	(integer) custom total length (useful if the concatenated edges do not cover 100 percent of the original precursor whose fragments are studied)
<code>nDig</code>	(integer) rounding: number of digits for 3rd column <code>len.rat</code> in output

Value

matrix of 3 columns: with length of longest tree-branches where given edge participates (column `sumLen`), the (total) number of edges therein (col `n.frag`) and a relative value (`len.rat`)

See Also

to build tree `buildTree`

Examples

```
path1 <- matrix(c(17,19,18,17, 4,4,2,3), ncol=2,
  dimnames=list(c("A/B/C/D", "A/B/G/D", "A/H", "A/H/I"), c("sumLen", "n")))
contribToContigPerFrag(path1)
```

conv01toColNa	<i>Convert matrix of integer to matrix of x-times repeated column-names</i>
---------------	---

Description

conv01toColNa transforms matrix of integers (eg 0 and 1) to repeated & concatenated text from 'colNa', the character string for 0 occurrences 'zeroTex' may be customized. Used eg when specifying (and concatenating) various counted elements (eg properties) along a vector like variable peptide modifications in proteomics.

Usage

```
conv01toColNa(mat, colNa = NULL, zeroTex = "", pasteCol = FALSE)
```

Arguments

mat	input matrix (with integer values)
colNa	alternative (column-)names to the ones from 'mat' (default colnames of mat)
zeroTex	text to display if 0 (default "")
pasteCol	(logical) allows to collapse all columns to single chain of characters in output

Value

character vector

Examples

```
(ma1 <- matrix(sample(0:3,40,rep1=TRUE),ncol=4,dimnames=list(NULL,letters[11:14])))
conv01toColNa(ma1)
conv01toColNa(ma1,colNa=LETTERS[1:4],ze=" .")
conv01toColNa(ma1,colNa=LETTERS[1:4],pasteCol=TRUE)
```

convMatr2df	<i>Convert matrix (eg with redundant) row-names to data.frame</i>
-------------	---

Description

convMatr2df provides flexible converting of matrix to data.frame. For example repeated/redundant rownames are not allowed in data.frame(), thus the corresponding column-names have to be re-named using a counter-suffix. In case of non-redundant rownames, a new column 'addIniNa' will be introduced at beginning to document the initial (redundant) rownames, non-redundant rownames will be created. Finally, this functions converts the corrected matrix to data.frame and checks/converts columns for transforming character to numeric. If the input is a data.frame containing factors, they will be converted to character before potential conversion. Note: for simpler version (only text to numeric) see from this package .convertMatrToNum .

Usage

```
convMatr2df(mat, addIniNa = TRUE, duplTxtSep = "_", silent = FALSE,
            callFrom = NULL)
```

Arguments

mat	matrix (or data.frame) to be converted
addIniNa	(logical) add initial name
duplTxtSep	(character) separator for enumerating replicated names
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

data.frame

See Also

for simpler version (only text to numeric) see from this package `.convertMatrToNum`

Examples

```
dat1 <- matrix(1:10, ncol=2)
rownames(dat1) <- letters[c(1:3,2,5)]
## as.data.frame(dat1) ... would result in an error
convMatr2df(dat1)
convMatr2df(data.frame(a=as.character((1:3)/2), b=LETTERS[1:3], c=1:3))
tmp <- data.frame(a=as.character((1:3)/2), b=LETTERS[1:3], c=1:3, stringsAsFactors=FALSE)
convMatr2df(tmp)
tmp <- data.frame(a=as.character((1:3)/2), b=1:3, stringsAsFactors=FALSE)
convMatr2df(tmp)
```

convToNum

Convert to numeric

Description

convToNum checks if input vector/character string contains numbers (with or without comma) and attempts converting to numeric. This function was designed for extracting the numeric part of character-vectors (or matrix) containing both numbers and character-elements. Depending on the parameters `convert` and `remove` text-entries can be converted to NA (in resulting numeric objects) or removed (the number of elements/lines gets reduced, in consequence). Note: if 'x' is a matrix, its matrix-dimensions & -names will be preserved. Note: so far Inf and -Inf do not get recognized as numeric.

Usage

```
convToNum(x, spaceRemove = TRUE, convert = c(NA, "sparseChar"),
  remove = NULL, euroStyle = TRUE, sciIncl = TRUE, callFrom = NULL,
  silent = TRUE)
```

Arguments

x	vector to be converted
spaceRemove	(logical) to remove all heading and trailing (white) space (until first non-space character)
convert	(character) define which type of non-conform entries to convert to NAs. Note, if remove is selected to eliminate character-entries they cannot be converted any more. Use 'allChar' for all character-entries; 'sparseChar' sparse (ie rare) character entries; NA for converting 'Na' or 'na' to NA; if 'none' or NULL no conversions at all.
remove	(character) define which type of non-conform entries to remove, removed items cannot be converted to NA any more. Use 'allChar' for removing all character entries; NA for removing all instances of NA (except those created by converting text); all elements will be kept if 'none' or NULL.
euroStyle	(logical) if TRUE will convert all ',' (eg used as European decimal-separator) to '.' (as internally used by R as decimal-separator), thus allowing converting the European decimal format.
sciIncl	(logical) include recognizing scientific notation (eg 2e-4)
callFrom	(character) allow easier tracking of message(s) produced
silent	(logical) suppress messages

Value

numeric vector (or matrix (if 'x' is matrix))

See Also

[numeric](#)

Examples

```
x1 <- c("+4", " + 5", "6", "-7", " - 8", "1e6", "+ 2.3e4", "-3E4", "- 4E5")
convToNum(x1, convert=NA, remove=c("allChar", NA))
convToNum(x1, convert=NA, remove=c("allChar", NA), sciIncl=FALSE)
```

correctToUnique	<i>Correct vector to unique</i>
-----------------	---------------------------------

Description

correctToUnique checks 'x' for unique entries, while maintaining the original length. If necessary a counter will added to non-unique entries.

Usage

```
correctToUnique(x, sep = "_", atEnd = TRUE, maxIter = 4,  
  NAenum = TRUE)
```

Arguments

x	input character vector
sep	(character) separator used when adding counter
atEnd	(logical) decide location of placing the counter (at end or at beginning of initial text)
maxIter	(numeric) max number of iterations
NAenum	(logical) if TRUE NAs will be enumerated (NA_1,NA_2,...)

Value

character vector

See Also

[unique](#) will simply remove repeated elements, ie length of 'x' won't remain constant, [filtSizeUniq](#) is more complex and slower, [treatTxtDuplicat](#)es

Examples

```
correctToUnique(c("li0", "n", NA, NA, rep(c("li2", "li3"), 2), rep("n", 4)))
```

countCloseToLimits *Count from two vectors number of values close within given limits*

Description

This functions summarizes the serach of similar (or identical) numeric values from 2 initial vectors, it evaluates the result from initial search run by findCloseMatch(), whose output is a less convenient list. countCloseToLimits checks furthermore how many results within additional (more stringent) distance-limits may be found and returns the number of distance values within the limits tested. Designed for checking if threshold used with findCloseMatch() may be set more stringent, eg when searching reasonable FDR limits ...

Usage

```
countCloseToLimits(closeMatch, limitIdent = 5, prefix = "lim_")
```

Arguments

closeMatch	(list) output from findCloseMatch(), ie list indicating which instances of 2 series of data have close matches
limitIdent	(numeric) max limit or panel of threshold values to test (if single value, in addition a panel with values below will be tested)
prefix	(character) prefix for names of output

Value

integer vector with counts for number of list-elements with at least one absolue value below threshold, names

See Also

[findCloseMatch](#)

Examples

```
set.seed(2019); aa <- sample(12:15,20, repl=TRUE) +round(runif(20),2)-0.5
bb <- 11:18
match1 <- findCloseMatch(aa,bb,com="diff",lim=0.65)
head(match1)
(tmp3 <- countCloseToLimits(match1,lim=c(0.5,0.35,0.2)))
(tmp4 <- countCloseToLimits(match1,lim=0.7))
```

countSameStartEnd	<i>Count same start- and end- sites of edges (or fragments)</i>
-------------------	---

Description

Suppose a parent sequence/string 'ABCDE' gets cut in various fragments (eg 'ABC', 'AB' ...). countSameStartEnd counts how many (ie re-occurring) start- and end- sites of edges do occur in the input-data. The input is presented as matrix of/indicating start- and end-sites of edges. The function is used to characterize partially redundant edges and accumulation of cutting/breakage sites.

Usage

```
countSameStartEnd(frag, minFreq = 2, nDig = 4)
```

Arguments

frag	(matrix) 1st column beg start-sites, 2nd column end end-sites of edges, row-names to precise fragment identities are recommended
minFreq	(integer) min number of accumulated sites for taking into account (allows filtering with large datasets)
nDig	(integer) rounding: number of digits for columns beg.rat and end.rat in output

Value

matrix of 6 columns: input (beg and end), beg.n, beg.rat, end.n, end.rat

See Also

to build initial tree [buildTree](#), [contribToContigPerFrag](#), [simpleFragFig](#)

Examples

```
frag1 <- cbind(beg=c(2,3,7,13,13,15,7,9,7, 3,3,5), end=c(6,12,8,18,20,20,19,12,12, 4,5,7))
rownames(frag1) <- letters[1:nrow(frag1)]
countSameStartEnd(frag1)
simpleFragFig(frag1)
```

cutArrayInCluLike *Cut 3-dim array in list of matrixes (or arrays) similar to organizing into clusters*

Description

cutArrayInCluLike cuts 'dat' (matrix,data.frame or 3-dim array) in list (of appended lines) according to 'cluOrg', which serves as instruction which line of 'dat' should be placed in which list-element (like sorting according to cluster-numbers).

Usage

```
cutArrayInCluLike(dat, cluOrg, callFrom = NULL)
```

Arguments

dat array (3 dim)
cluOrg (factor) organization of lines to clusters
callFrom (character) allows easier tracking of message(s) produced

Value

list of matrixes (or arrays)

Examples

```
mat1 <- matrix(1:30,nc=3,dimnames=list(letters[1:10],1:3))
cutArrayInCluLike(mat1,cluOrg=factor(c(2,rep(1:4,2),5)))
```

cutAtMultSites *Cut character-vector at multiple sites*

Description

This function cuts character vector after 'cutAt' (ie keep the search substing 'cutAt', different to strsplit). Used for theoretical enzymatic digestion (eg in proteomics)

Usage

```
cutAtMultSites(y, cutAt)
```

Arguments

y character vector (better if of length=1, otherwise one won't know which fragment stems from which input)
cutAt (character) search substing, ie 'cutting rule'

Value

modified (ie cut) character vector

See Also

[strsplit](#), [nFragments0](#), [nFragments](#)

Examples

```
tmp <- "MSVSRTMEDSCELDLVYVTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLSERRPDITKLHAKVLEFGWPDLHTPALEKI"
cutAtMultSites(c(tmp,"ojioRij"),c("R","K"))
```

cutToNgrp

Cut numeric vector to n groups (ie convert to factor)

Description

cutToNgrp is a more elaborate version of [cut](#) for cutting a the content of a numeric vector 'x' into a given number of groups, taken from the length of 'lev'. Besides, this function provides the group borders/limits for convention use with legends.

Usage

```
cutToNgrp(x, lev, NAuse = FALSE, callFrom = NULL)
```

Arguments

x	numeric vector
lev	(character or numeric), the length of this argument tells the number of groups to be used for cutting
NAuse	(logical) include NAs as separate group
callFrom	(character) for better tracking of use of functions

Value

list with \$grouped telling which element of 'x' goes in which group and \$legTxt with group-borders for convenient use with legends

See Also

[cut](#)

Examples

```
set.seed(2019); dat <- runif(30) +(1:30)/2
cutToNgrp(dat,1:5)
plot(dat,col=(1:5)[as.numeric(cutToNgrp(dat,1:5)$grouped)])
```

diffCombin	<i>Compute matrix of differences for all pairwise combinations of numeric vector</i>
------------	--

Description

diffCombin returns matrix of differences (eg resulting from substitution) for all pairwise combinations of numeric vector 'x'.

Usage

```
diffCombin(x, diagAsNA = FALSE, prefix = TRUE, silent = FALSE,  
           callFrom = NULL)
```

Arguments

x	numeric vector to compute differences for all combinations
diagAsNA	(logical) return all self-self combinations as NA (otherwise 0)
prefix	(logical) if TRUE, dimnames of output will specify orientation (prefix='from.' and 'to.')
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

numeric matrix of all pairwise differences

See Also

[diff](#) for simple differences

Examples

```
diffCombin(c(10,11.1,13.3,16.6))
```

diffPPM	<i>difference in ppm between numeric values</i>
---------	---

Description

diff()-like function to return difference in ppm between psubsequent values. Result is oriented, ie neg ppm value means decrease (from higher to lower value). Note that if the absolute difference remains the same the difference in ppm will not remain same. Any difference to NA is returned as NA, thus a single NA will result in two NAs in output (unless NA is 1st or last).

Usage

```
diffPPM(dat, toPrev = FALSE, silent = FALSE, callFrom = NULL)
```

Arguments

dat	(numeric) vector for calculating difference to preceeding/following value in ppm
toPrev	(logical) determine orientation
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

list with close matches of 'x' to given 'y', the numeric value dependes on 'sortMatch' (if FALSE then always value of 'y' otherwise of longest of x&y)

See Also

[checkSimValueInSer](#) and (from this package) [.compareByDiff](#), [diff](#)

Examples

```
aa <- c(1000.01,1000.02,1000.05,1000.08,1000.09,1000.08)
.compareByPPM(list(aa,aa),30,TRUE)           # tabular 'long' version
diffPPM(aa)
```

elimCloseCoord	<i>Eliminate close (overlapping) points (in x & y space)</i>
----------------	--

Description

elimCloseCoord reduces number of rows in 'dat' by eliminating lines where x & y coordinates (columns of matrix 'dat' defined by 'useCol') are identical (overlay points) or very close. The stringency for 'close' values may be fine-tuned using nDig, this function uses internally [firstOfRepeated](#).

Usage

```
elimCloseCoord(dat, useCol = 1:2, elimIdentOnly = FALSE, refine = 2,
  nDig = 3, callFrom = NULL, silent = FALSE)
```

Arguments

dat	matrix (or data.frame) with main numeric input
useCol	(numeric) index for numeric columns of 'dat' to use/consider
elimIdentOnly	(logical) if TRUE, eliminate real duplicated points only (ie identical values only)
refine	(numeric) allows increasing stringency even further (higher 'refine' .. more lines considered equal)
nDig	(integer) number of significant digits used for rounding, if two 'similar' values are identical after this rounding the second will be eliminated.
callFrom	(character) allows easier tracking of message(s) produced
silent	(logical) suppress messages

Value

resultant matrix/data.frame

See Also

[findCloseMatch](#), [firstOfRepeated](#)

Examples

```
da1 <- matrix(c(rep(0:4,5),0.01,1.1,2.04,3.07,4.5),nc=2); da1[,1] <- da1[,1]*99; head(da1)
elimCloseCoord(da1)
```

equLenNumber	<i>Equal character-length number</i>
--------------	--------------------------------------

Description

equLenNumber convert numeric entry 'x' to text, with all elements getting the same number of characters (ie by adding preceding or tailing 0s, if needed). So far, the function cannot handle scientific annotations.

Usage

```
equLenNumber(x, silent = FALSE, callFrom = NULL)
```

Arguments

x	(character) input vector
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

character vector formatted as equal number of characters per value

See Also

[sprintf](#)

Examples

```
equLenNumber(c(12,-3,321))
equLenNumber(c(12,-3.3,321))
```

exclExtrValues	<i>Exclude extreme values (based on distance to mean)</i>
----------------	---

Description

This function aims to identify extreme values (values most distant to mean, thus potential outliers), mark them as NA or directly exclude them (depending on 'showNAs'). Note that every set of non-identical values will have at least one most extreme value. Extreme values are part of many distributions, they are not necessarily true outliers.

Usage

```
exclExtrValues(dat, result = "val", CVlim = NULL, maxExcl = 1,
  showNA = FALSE, goodValues = TRUE, silent = FALSE,
  callFrom = NULL)
```

Arguments

dat	numeric vector, main input
result	(character) may be 'val' for returning data without extreme values or 'pos' for returning position/index of extreme values
CVlim	(NULL or numeric) allows to retain extreme values only if a certain CV (for all 'dat') is exceeded (to avoid calling extreme values form homogenous data-sets)
maxExcl	(integer) max number of elments to explude
showNA	(logical) will display extrelme values as NA
goodValues	(logical) allows to display rather the good values instead of the extreme values
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

numeric vector wo extremle values or index-position of extreme values

See Also

[firstOfRepLines](#), [get1stOfRepeatedByCol](#) for treatment of matrix

Examples

```
x <- c(rnorm(30), -6, 20)
exclExtrValues(x)
```

exponNormalize	<i>Normalize by adjusting exponent</i>
----------------	--

Description

This function normalizes 'dat' by optimizing exponent function (ie dat^{exp}) to fit best to 'ref' (default: average of each line of 'dat').

Usage

```
exponNormalize(dat, useExpon, dynExp = TRUE, nStep = 20,
  startExp = 1, simMeas = "cor", refDat = NULL, refGrp = NULL,
  refLines = NULL, rSquare = FALSE, silent = FALSE,
  callFrom = NULL)
```

Arguments

<code>dat</code>	matrix or data.frame of numeric data to be normalized
<code>useExpon</code>	(numeric vector or matrix) exponent values to be tested
<code>dynExp</code>	(logical) require 'useExpon' as 2 values (matrix), will gradually increase exponent from 1st to 2nd; may be matrix or data.frame for dynamic, in this case 1st line for exp for lowest data, 2nd line for highest
<code>nStep</code>	(integer) number of exponent variations (steps) when testing range from-to
<code>startExp</code>	(numeric)
<code>simMeas</code>	(character) similarity metric to be used (so far only "cor"), if rSquare=TRUE, the r-squared will be returned
<code>refDat</code>	(matrix or data.frame) if null average of each line from 'dat' will be used as reference in similarity measure
<code>refGrp</code>	(factor) designating which col of 'ref' should be used with which col of 'dat' (length equal to number of cols in 'dat'). Note: 'refGrp' not yet coded optimally to extract numeric part of character vector, potential problems when all lines or cols of dat are NA
<code>refLines</code>	(NULL or integer) optional subset of lines to be considered (only) when determining normalization factors
<code>rSquare</code>	(logical) if TRUE, add r-squared
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

Value

matrix of normalized data

See Also

more evolved than [normalizeThis](#) with argument set to 'exponent'

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),nc=10)
head(rowGrpCV(dat1,gr=gl(4,3,labels=LETTERS[1:4])[2:11]))
set.seed(2016); dat1 <- c(0.1,0.2,0.3,0.5)*rep(c(1,10),each=4)
dat1 <- matrix(round(c(sqrt(dat1),dat1^1.5,3*dat1+runif(length(dat1))),2),nc=3)
dat2a <- exponNormalize(dat1[,1],useExpon=2,nSte=1,refD=dat1[,3])
layout(matrix(1:2,nc=2))
plot(dat1[,1],dat1[,3],type="b",main="init",ylab="ref")
plot(dat2a$datNor[,1],dat1[,3],type="b",main="norm",ylab="ref")
dat2b <- exponNormalize(dat1[,1],useExpon=c(1.7,2.3),nSte=5,refD=dat1[,3])
plot(dat1[,1],dat1[,3],type="b",main="init",ylab="ref")
plot(dat2b$datNor[,1],dat1[,3],type="b",main="norm",ylab="ref")

dat2c <- exponNormalize(dat1[, -3],useExpon=matrix(c(1.7,2.3,0.6,0.8),nc=2),nSte=5,refD=dat1[,3]);
plot(dat1[,1],dat1[,3],type="b",main="init",ylab="ref ")
```



```
plot(dat2c$datNor[,1],dat1[,3],type="b",main="norm 1",ylab="ref")
plot(dat1[,2],dat1[,3],type="b",main="init",ylab="ref")
plot(dat2c$datNor[,2],dat1[,3],type="b",main="norm 2",ylab="ref");
```

extr1chan *Extract just one series, ie channel, of list of arrays*

Description

This function was designed for handling measurements stored as list of multiple arrays, like eg compound-screens using microtiter-plates where multiple parameters ('channels') were recorded for each well (element). The elements (eg compounds screened) are typically stored in the 1st dimension of the arrays, the replicated in the second dimension and different measure types/parameters in the 3rd channel. In order to keep the structure of individual microtiter-plates, typically each plate forms a separate array (of same dimensions) in a list. The this function allows extracting a single channel of the list of arrays (3rd dim of each array) and return row-appended matrix.

Usage

```
extr1chan(arrLst, cha, na.rm = TRUE, rowSep = "__")
```

Arguments

arrLst	(list) list of arrays (typically 1st and 2nd dim for specific genes/objects, 3rd for different measures associated with)
cha	(integer) channel number
na.rm	(logical) default =TRUE to remove NAs
rowSep	(character) separator for rows

Value

list with just single channel extracted

See Also

[organizeAsListOfRepl](#)

Examples

```
arr1 <- array(1:24,dim=c(4,3,2),dimnames=list(c(LETTERS[1:4]),
  paste("col",1:3,sep=""),c("ch1","ch2")))
arr2 <- array(74:51,dim=c(4,3,2),dimnames=list(c(LETTERS[1:4]),
  paste("col",1:3,sep=""),c("ch1","ch2")))
arrL1 <- list(pl1=arr1,pl2=arr2)
extr1chan(arrL1,ch=2)
```

`extractLast2numericParts`*Extract last two numeric parts from character vector*

Description

`extractLast2numericParts` extracts last 2 (integer) numeric parts between punctuations out of character vector 'x'. Runs faster than `gregexpr`. Note: won't work correctly with decimals or exponential signs !! (such characters will be considered as punctuation, ie as separator)

Usage

```
extractLast2numericParts(x, silent = FALSE, callFrom = NULL)
```

Arguments

x	main character input
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

(numeric) matrix with 2 columns (eg from initial concatenated coordinates)

See Also

`gregexpr` from [grep](#)

Examples

```
extractLast2numericParts(c("M01.1-4", "M001/2.5", "M_0001_03-16", "zyx", "012", "a1.b2.3-7,2"))
```

`extrNumericFromMatr`*Extract numeric part of matrix or data.frame*

Description

`extrNumericFromMatr` extracts numeric part of matrix or data.frame, removing remaining non-numeric elements if `trimToData` is set to TRUE. Note, that cropping entire lines where a (single) text element appeared may quickly reduce the overall content of the input data.

Usage

```
extrNumericFromMatr(dat, trimToData = TRUE, silent = FALSE,  
  callFrom = NULL)
```

Arguments

dat	matrix (or data.frame) for extracting numeric parts
trimToData	(logical) default to remove (crop) lines and cols contributing to NA, non-numeric data is transformed to NA
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix of numeric data

Examples

```
mat <- matrix(c(letters[1:7],14:16,LETTERS[1:6]),nrow=4,dimnames=list(1:4,letters[1:4]))
mat; extrNumericFromMatr(mat)
mat <- matrix(c(letters[1:4],1,"e",12:19,LETTERS[1:6]),nr=5,dimnames=list(11:15,letters[1:4]))
mat; extrNumericFromMatr(mat)
```

extrSpcText	<i>Extract specific text</i>
-------------	------------------------------

Description

extrSpcText extracts/cuts text-fragments out of 'txt' following specific anchors 'cutFrom' and 'cutTo'. In case 'cutFrom' not found 'missingAs' will be returned. In case 'cutTo' not found text gets extracted with 'chaMaxEl' characters.

Usage

```
extrSpcText(txt, cutFrom = " GN=", cutTo = " PE=", missingAs = NA,
  exclFromTag = TRUE, silent = FALSE, callFrom = NULL)
```

Arguments

txt	character vector to be treated
cutFrom	(character) text where to start cutting
cutTo	(character) text where to stop cutting
missingAs	(character) specific content of output at line/location of 'exclLi'
exclFromTag	(logical) to exclude text given in 'cutFrom' from result
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

modified character vector

Examples

```
extrSpcText(c(" ghjg GN=thisText PE=001", " GN=_ PE=", NA, "abcd"))
extrSpcText(c("ABCDEF.3-6", "05g", "bc.4-5"), cutFr="\.", cutT="-")
```

 filt3dimArr

Filter a three-dimensional array of numeric data

Description

Filtering of 3-dim array ('x'): filter column 'filtCrit' as 'larger as' (according to 'filtTy') 'filtVal' and extract/display all col matching 'displCrit'.

Usage

```
filt3dimArr(x, displCrit, filtCrit, filtVal, filtTy = ">")
```

Arguments

x	array (3-dim) of numeric data
displCrit	(character) column-name(s) to display
filtCrit	(character, length=1) which column-name consider when filtering filter with 'filtVal' and 'filtTy'
filtVal	(numeric) for testing inferior/superor/equal condition
filtTy	(character) which type of testing to perform ('eq', 'inf', 'infeq', 'sup', 'supeq', ">", '<', '>=', '<=', '==')

Value

list of filtered matrixes (by 3rd dim)

Examples

```
arr1 <- array(1:24, dim=c(4,3,2), dimnames=list(c(LETTERS[1:4]),
  paste("col", 1:3, sep=""), c("ch1", "ch2")))
filt3dimArr(arr1, displCrit=c("col1", "col2"), filtCrit="col2", filtVal=7)
```

filtSizeUniq	<i>Filter for unique elements</i>
--------------	-----------------------------------

Description

This function aims to identify and remove duplicated elements in list and maintaining the list-structure in the output. `filtSizeUniq` filters 'lst' (list of character-vectors or character-vector) for elements being unique (to 'ref' or if NULL to all 'lst') and of character length.

Usage

```
filtSizeUniq(lst, ref = NULL, minSize = 6, maxSize = 36,
  filtUnique = TRUE, byProt = TRUE, inclEmpty = TRUE,
  silent = FALSE, callFrom = NULL)
```

Arguments

<code>lst</code>	list of character-vectors or character-vector
<code>ref</code>	(character) optional alternative 'reference', if not NULL used in addition to 'lst' for considering elements of 'lst' as unique
<code>minSize</code>	(integer) minimum number of characters, if NULL set to 0
<code>maxSize</code>	(integer) maximum number of characters
<code>filtUnique</code>	(logical) if TRUE return unique-only character-strings
<code>byProt</code>	(logical) if TRUE organize output as list (by names of input, eg protein-names) - if 'lst' was named list
<code>inclEmpty</code>	(logical) optional including empty list-elements when all elements have been filtered away - if 'lst' was named list
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

Value

list of filtered input

See Also

[correctToUnique](#), [unique](#), [duplicated](#)

Examples

```
filtSizeUniq(list(A="a",B=c("b","bb","c"),D=c("dd","d","ddd","c")),filtUn=TRUE,minSi=NULL)
# input: c and dd are repeated
filtSizeUniq(list(A="a",B=c("b","bb","c"),D=c("dd","d","ddd","c")),ref=c(letters[c(1:26,1:3)]),
  "dd","dd","bb","ddd"),filtUn=TRUE,minSi=NULL) # a,b,c,dd repeated
```

findCloseMatch *Find close numeric values between two vectors*

Description

findCloseMatch finds close matches (similar values) between two numeric vectors ('x','y') based on method 'compTy' and threshold 'limit'. Return list with close matches of 'x' to given 'y', the numeric value depends on 'sortMatch' (if FALSE then always value of 'y' otherwise of longest of x&y). Note: Speed & memory improvement if 'sortMatch'=TRUE (but result might be inverted!): adopt search of x->y or y->x to searching matches of each longest to each shorter (ie flip x &y). Otherwise, if length of 'x' & 'y' are very different, it may be advantageous to use a long(er) 'x' and short(er) 'y' (with 'sortMatch'=FALSE). Note: Names of 'x' & 'y' or (if no names) prefix letters 'x' & 'y' are always added as names to results.

Usage

```
findCloseMatch(x, y, compTy = "ppm", limit = 5, asIndex = FALSE,
               maxFitShort = 100, sortMatch = FALSE, silent = FALSE,
               callFrom = NULL)
```

Arguments

x	numeric vector for comparison
y	numeric vector for comparison
compTy	(character) may be 'diff' or 'ppm', will be used with threshold from argument 'limit'
limit	(numeric) threshold value for retaining values, used with distace-type specified in argument 'compTy'
asIndex	(logical) optionally rather report index of retained values
maxFitShort	(numeric) limit output to max number of elements (avoid returning high number of results if filtering was not enough stringent)
sortMatch	(logical) if TRUE than matching will be preformed as 'match longer (of x & y) to closer', this may process slightly faster (eg 'x' longer: list for each 'y' all 'x' that are close, otherwise list of each 'x'),
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

list with close matches of 'x' to given 'y', the numeric value depends on 'sortMatch' (if FALSE then always value of 'y' otherwise of longest of x&y)

See Also

[checkSimValueInSer](#) and (from this package) [.compareByDiff](#), for convient output [countCloseToLimits](#)

Examples

```

aa <- 11:14 ; bb <- c(13.1,11.5,14.3,20:21)
findCloseMatch(aa,bb,com="diff",lim=0.6)
findCloseMatch(c(a=5,b=11,c=12,d=18),c(G=2,H=11,I=12,J=13)+0.5,comp="diff",lim=2)
findCloseMatch(c(4,5,11,12,18),c(2,11,12,13,33)+0.5,comp="diff",lim=2)
findCloseMatch(c(4,5,11,12,18),c(2,11,12,13,33)+0.5,comp="diff",lim=2,sort=FALSE)
.compareByDiff(list(c(a=10,b=11,c=12,d=13),c(H=11,I=12,J=13,K=33)+0.5),limit=1) #' return matrix

a2 <- c(11:20); names(a2) <- letters[11:20]
b2 <- c(25:5)+c(rep(0,5),(1:10)/50000,rep(0,6)); names(b2) <- LETTERS[25:5]
which(abs(b2-a2[8]) < a2[8]*1e-6*5) #' find R=18 : no10
findCloseMatch(a2,b2,com="ppm",lim=5) #' find Q,R,S,T
findCloseMatch(a2,b2,com="ppm",lim=5,asI=TRUE) #' find Q,R,S,T
findCloseMatch(b2,a2,com="ppm",lim=5,asI=TRUE,sort=FALSE)
findCloseMatch(a2,b2,com="ratio",lim=1.000005) #' find Q,R,S,T
findCloseMatch(a2,b2,com="diff",lim=0.00005) #' find S,T

```

findRepeated

*Find repeated elements***Description**

findRepeated gets index of repeated items/values in vector 'x' (will be treated as character). Return (named) list of indexes for each of the repeated values, or NULL if all values are unique. This approach is similar but more basic compared to [get1stOfRepeatedByCol](#).

Usage

```
findRepeated(x, nonRepeated = FALSE, silent = FALSE, callFrom = NULL)
```

Arguments

x	character vector
nonRepeated	(logical) if =TRUE, return list with elements \$rep and \$nonrep
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

(named) list of indexes for each of the repeated values, or NULL if all values unique

See Also

similar approach but more basic than [get1stOfRepeatedByCol](#)

Examples

```
aa <- c(11:16,14:12,14); findRepeated(aa)
```

findSimilFrom2sets *Find similar numeric values from two vectors/matrixes*

Description

findSimilFrom2sets compares two vectors or matrixes and returns combined view including only all close (by [findCloseMatch](#)). Return matrix (predMatr) with add'l columns for index to and 'grp' (group of similar values (1-to-many)), 'nGrp' (n of grp), 'isBest' or 'nBest', 'disToMeas' (distance/difference between pair) & 'ppmToPred' (distance in ppm). Note: too wide 'limitComp' will result in large window and many 'good' hits will compete (and be mutually excluded) if selection 'bestOnly' is selected

Usage

```
findSimilFrom2sets(predMatr, measMatr, colMeas = 1, colPre = 1,
  compareTy = "diff", limitComp = 0.5, bestOnly = FALSE,
  silent = FALSE, callFrom = NULL, debug = FALSE)
```

Arguments

predMatr	(matrix or numeric vector) dataset number 1, referred to as 'predicted', the column speified in argument colPre points to the data to be used
measMatr	(matrix or numeric vector) dataset number 2, referred to as 'measured', the column speified in argument colMeas points to the data to be used
colMeas	(integer) which column number of 'measMatr' to consider
colPre	(integer) which column number of 'predMatr' to consider
compareTy	(character) 'diff' (difference) 'ppm' (relative difference)
limitComp	(numeric) limit used by 'compareTy'
bestOnly	(logical) allows to filter only hits with min distance (defined by 'compareTy'), 3rd last col will be 'nBest' - otherwise 3rd last col 'isBest'
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced
debug	(logical) for bug-tracking: more/enhanced messages

Value

matrix (predMatr) with add'l columns for index to and 'grp' (group of similar values (1-to-many)), 'nGrp' (n of grp), 'isBest' or 'nBest', 'disToMeas' (distance/difference between pair) & 'ppmToPred' (distance in ppm)

See Also

[checkSimValueInSer](#) [findCloseMatch](#) [closeMatchMatrix](#)

Examples

```

aA <- c(11:17); bB <- c(12.001,13.999); cC <- c(16.2,8,9,12.5,12.6,15.9,14.1)
aZ <- matrix(c(aA,aA+20),ncol=2,dimnames=list(letters[1:length(aA)],c("aA","aZ")))
cZ <- matrix(c(cC,cC+20),ncol=2,dimnames=list(letters[1:length(cC)],c("cC","cZ")))
findCloseMatch(cC,aA,com="diff",lim=0.5,sor=FALSE)
findSimilFrom2sets(aA,cC)
findSimilFrom2sets(cC,aA)
findSimilFrom2sets(aA,cC,best=FALSE)
findSimilFrom2sets(aA,cC,comp="ppm",lim=5e4,deb=TRUE)
findSimilFrom2sets(aA,cC,comp="ppm",lim=9e4,best0=FALSE)
# below: find fewer 'best matches' since search window larger (ie more good hits compete !)
findSimilFrom2sets(aA,cC,comp="ppm",lim=9e4,best0=TRUE)

```

findUsableGroupRange *Select groups within given range*

Description

This function aims to help finding stretches/segments of data with a given maximum number of NA-instances. This function is used to inspect/filter each lines of 'dat' for a subset with sufficient presence/absence of NA values (ie limit number of NAs per level of 'grp'). Note : optimal performance with n.lines » n.groups

Usage

```
findUsableGroupRange(dat, grp, maxNA = 1, callFrom = NULL)
```

Arguments

dat	(matrix or data.frame) main input
grp	(factor) information which column of 'dat' is replicate of whom
maxNA	(interger) max number of tolerated NAs
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix with boundaries of 1st and last usable column (NA if there were no suitable groups found)

Examples

```

dat1 <- matrix(1:56,nc=7)
dat1[c(2,3,4,5,6,10,12,18,19,20,22,23,26,27,28,30,31,34,38,39,50,54)] <- NA
rownames(dat1) <- letters[1:nrow(dat1)]
findUsableGroupRange(dat1,gl(3,3)[- (3:4)])

```

firstLineOfDat *Filter matrix to keep only first of repeated lines*

Description

This function aims to reduce the complexity of a matrix (or data.frame) in case column 'refCol' has multiple lines with same value. In this case, it reduces the input-data to 1st line of redundant entries and returns a matrix (or data.frame) without lines identified as redundant entries for 'refCol'. In sum, this function works like using unique on a given column, and propagates the same treatment to all other columns.

Usage

```
firstLineOfDat(dat, refCol = 2, silent = FALSE, callFrom = NULL)
```

Arguments

dat	(matrix or data.frame) main input
refCol	(integer) column number of reference-column
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix (same number of columns as input)

See Also

[firstOfRepeated](#), [unique](#), [duplicated](#)

Examples

```
(mat1 <- matrix(c(1:6,rep(1:3,1:3)),ncol=2,dimnames=list(letters[1:6],LETTERS[1:2])))
firstLineOfDat(mat1)
```

firstOfRepeated *Find first of repeated elements*

Description

This function works similar to unique, but provides additional information about which elements of original input 'x' are repeated by providing indexes relative to the input. firstOfRepeated makes list with 3 elements: \$indRepeated.. index for first of repeated 'x', \$indUniq.. index of all unique + first of repeated, \$indRedund.. index of all redundant entries, ie non-unique (wo 1st). Used for reducing data to non-redundant status, however, for large numeric input the function nonAmbiguousNum() may perform better/faster. NAs won't be considered (NAs do not appear in reported index of results), see also firstOfRepLines().

Usage

```
firstOfRepeated(x)
```

Arguments

x (character or numeric) main input

Value

list with indices: \$indRepeated, \$indUniq, \$indRedund

See Also

[duplicated](#), [nonAmbiguousNum](#), [firstOfRepLines](#) gives less detail in output (lines/elements/indexes of omitted not directly accessible) and works faster

Examples

```
x <- c(letters[c(3,2:4,8,NA,3:1,NA,5:4)]); names(x) <- 100+(1:length(x))
firstOfRepeated(x)
x[firstOfRepeated(x)$indUniq] # only unique with names
```

firstOfRepLines	<i>Reduce to first occurrence of repeated lines</i>
-----------------	---

Description

This function concatenates all columns of input-matrix and then searches like unique for unique elements, optionally the indexes of unique elements may get returned. Note: This function treats input as character (thus won't understand 10==10.0). Returns simplified/non-redundant vector/matrix (ie fewer lines), or respective index. faster than [firstOfRepeated](#)

Usage

```
firstOfRepLines(mat, outTy = "ind", useCol = NULL, callFrom = NULL)
```

Arguments

mat initial matrix to treat

outTy for output type: 'ind'.. index to 1st occurrence (non-red), 'orig'..non-red lines of mat, 'conc'.. non-red concatenated values, 'num'.. index to which group/category the lines belong

useCol (integer) custom choice of which columns to paste/concatenate

callFrom (character) allows easier tracking of messages produced

Value

simplified/non-redundant vector/matrix (ie fewer lines for matrix), or respective index

See Also

[unique, nonAmbiguousNum](#), faster than [firstOfRepeated](#) which gives more detail in output (lines/elements/indexes of omitted)

Examples

```
mat <- matrix(c("e", "n", "a", "n", "z", "z", "n", "z", "z", "b",
               "", "n", "c", "n", "", "", "n", "", "", "z"), ncol=2)
firstOfRepLines(mat, out="conc")
```

 fuseAnnotMatr

Fuse annotation matrix to initial matrix

Description

In a number of instances experimental measurements and additional information (annotation) are provided by separate objects (matrixes) as they may not be generated the same time. The aim of this function is provide help when matching appropriate lines for 2 sets of data (experimental measures in `iniTab` and annotation from `annotTab`) for fusing. `fuseAnnotMatr` adds supplemental columns/annotation to an initial matrix `iniTab`: using column `'refIniT'` as key (in `iniTab`) to compare with key `'refAnnotT'` (from `'annotTab'`). The columns to be added from `annotTab` must be chosen explicitly. Note: if non-unique IDs in `iniTab`: runs slow (but save) due to use of loop for each unique ID.

Usage

```
fuseAnnotMatr(iniTab, annotTab, refIniT = "Uniprot",
              refAnnotT = "combName", addCol = c("ensembl_gene_id", "description",
              "geneName", "combName"), debug = TRUE, silent = FALSE,
              callFrom = NULL)
```

Arguments

<code>iniTab</code>	(matrix), that may have lines with multiple (=repeated) key entries
<code>annotTab</code>	(matrix) containing reference annotation
<code>refIniT</code>	(character) type of reference (eg <code>'Uniprot'</code>)
<code>refAnnotT</code>	(character) column name to use for reference-annotation
<code>addCol</code>	(character) column-namess of <code>'annotTab'</code> to use/extract (if no matches found, use all)
<code>debug</code>	(logical) for bug-tracking: more/enhanced messages
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

Value

combined matrix (elements not found in `'annotTab'` are displayed as NA)

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

```

tab0 <- matrix(rep(letters[1:25],8),ncol=10)
tab1 <- cbind(Uniprot=paste(tab0[,1],tab0[,2]),col1=paste(tab0[,3],
  tab0[,4],tab0[,5]," ",tab0[,7],tab0[,6]))
tab2 <- cbind(combName=paste(tab0[,1],tab0[,2]),col2=paste(tab0[,8],tab0[,9],tab0[,10]))
fuseAnnotMatr(tab1,tab2[c(20:11,2:5),],refIni="Uniprot",refAnnotT="combName",addCol="col2")
fuseAnnotMatr(tab2[c(20:11,2:5),],tab1,refAnnotT="Uniprot",refIni="combName",addCol="col1")

```

fuseCommonListElem	<i>Fuse content of list-elements with redundant (duplicated) names</i>
--------------------	--

Description

fuseCommonListElem fuses (character or numeric) elements of list re-occurring under same name, so that resultant list has unique names. Note : will not work with list of matrixes

Usage

```

fuseCommonListElem(lst, initOrd = TRUE, removeDuplicates = FALSE,
  callFrom = NULL)

```

Arguments

lst	(list) main input, list of numeric vectors
initOrd	(logical) preserve initial order in output (if TRUE) or otherwise sort alphabetically
removeDuplicates	(logical) allow to remove duplicate entries (if vector contains names, both the name and the value need to be identical to be removed; note: all names must have names with more than 0 characters to be considered as names)
callFrom	(character) allows easier tracking of message(s) produced

Value

fused list (same names as elements of input)

See Also[unlist](#)

Examples

```
val1 <- 10 +1:26
names(val1) <- letters
lst1 <- list(c=val1[3:6],a=val1[1:3],b=val1[2:3],a=val1[12],c=val1[13])
fuseCommonListElem(lst1)
```

 fusePairs

Fuse pairs to generate cluster-names

Description

Fuse previously identified pairs to 'clusters', return vector with cluster-numbers.

Usage

```
fusePairs(datPair, refDatNames = NULL, inclRepLst = FALSE,
          maxFuse = NULL, debug = FALSE, silent = TRUE, callFrom = NULL)
```

Arguments

datPair	2-column matrix where each line represents 1 pair
refDatNames	(NULL or character) allows placing selected pairs in context of larger data-set (names to match those of 'datPair')
inclRepLst	(logical) if TRUE, return list with 'clu' (clu-numbers, default output) and 'refLst' (list of clustered elements, only n>1)
maxFuse	(integer, default NULL) maximal number of groups/clusters
debug	(logical) for bug-tracking: more/enhanced messages and intermediate objects written in global name-space
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

vector with cluster-numbers

Examples

```
daPa <- matrix(c(1:5,8,2:6,9),ncol=2)
fusePairs(daPa,maxFuse=4)
```

get1stOfRepeatedByCol *Get first of repeated by column*

Description

get1stOfRepeatedByCol sorts matrix 'mat' and extracts only 1st occurrence of values in column 'sortBy'. Returns then non-redundant matrix (ie for column 'sortBy', if 'markIfAmbig' specifies existing col, mark ambig there). Note : problem when sortSupl or sortBy not present (or not intended for use)

Usage

```
get1stOfRepeatedByCol(mat, sortBy = "seq", sortSupl = "ty",
  asFirstLast = c("full", "inter"), markIfAmbig = c("ambig", "seqNa"),
  asList = FALSE, abmiPref = "_")
```

Arguments

mat	(matrix or data.frame) numeric vector to be tested
sortBy	column name for which elements should be made unique, numeric or character column; 'sortSupl' .. add'l colname to always select specific 1st)
sortSupl	default="ty"
asFirstLast	(character,length=2) to force specific strings from coluln 'sortSupl' as first and last when selecting 1st of repeated terms, default=c("full","inter")
markIfAmbig	(character,length=2) 1st will be set to 'TRUE' if ambiguous/repeated, 2nd will get (heading) prefix, default=c("ambig","seqNa")
asList	(logical) to return list with non-redundant ('unique') and removed lines ('repeats')
abmiPref	(character) prefix to note ambiguous entries/terms, default="_"

Value

depending on 'asList' either list with non-redundant ('unique') and removed lines ('repeats')

See Also

[firstOfRepeated](#) for (more basic) treatment of simple vector, [nonAmbiguousNum](#) for numeric use (much faster !!!)

Examples

```
aa <- cbind(no=as.character(1:20), seq=sample(LETTERS[1:15], 20, repl=TRUE),
  ty=sample(c("full", "Nter", "inter"), 20, repl=TRUE), ambig=rep(NA, 20), seqNa=1:20)
get1stOfRepeatedByCol(aa)
```

getValuesByUnique *Print matrix-content as plot*

Description

When data have repeated elements (defined by names inside the vector), it may be advantageous to run some operations only on a unique set of the initial data, or sometimes all repeated occurrences need to be replaced by a common (summarizing) value. This function allows to re-introduce new values from on second vector with unique names, to return a final vector of initial input-length and order of names (elements) like initial, too. Normally the user would provide 'datUniq' (without repeated names) containing new values which will be expanded to structure of 'dat', if 'datUniq' is not provided a vector with unique names will be made using the first occurrence of repeated value(s). For more complex cases the indexing relative to 'datUniq' can be returned (setting asIndex=TRUE). Note: If not all names of 'dat' are found in 'datUniq' the missing spots will be returned as NA.

Usage

```
getValuesByUnique(dat, datUniq = NULL, asIndex = FALSE,
  silent = FALSE, callFrom = NULL)
```

Arguments

dat	(numeric or character) main long input, must have names
datUniq	(numeric or character) will be used to impose values on dat, must have names that should match names (at least partially) from dat
asIndex	(logical) if TRUE index values will be returned instead of replacing values
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

vector of length dat with imposed values, or index values if asIndex=TRUE

See Also

[unique](#), [findRepeated](#), [correctToUnique](#), [treatTxtDuplicates](#)

Examples

```
dat <- 11:19
names(dat) <- letters[c(6:3,2:4,8,3)]
## let's make a 'datUniq' with the mean of repeated values :
datUniq <- round(tapply(dat,names(dat),mean),1)
## now propagate the mean values to the full vector
getValuesByUnique(dat,datUniq)
cbind(ini=dat,firstOfRep=getValuesByUnique(dat,datUniq),
  indexUniq=getValuesByUnique(dat,datUniq,asIn=TRUE))
```

htmlSpecCharConv	<i>Html special character conversion</i>
------------------	--

Description

Converts 'txt' so that special characters (like 'beta', 'micro', 'square' etc) will be displayed correctly when used for display in html (eg at mouse-over). Note : uses package [stringi](#)

Usage

```
htmlSpecCharConv(txt)
```

Arguments

txt character vector including special characters

Value

corrected character vector adopted to html display

See Also

tables on <http://www.htmlhelp.com/reference/html40/entities/latin1.html>, <http://www.degraeve.com/reference/specialcharacters.php>, <http://www.ascii.cl/htmlcodes.htm>

Examples

```
(x <- stringi::stri_unescape_unicode("\u00b5\u003d\u0061\u0062"))
htmlSpecCharConv(x)
```

listBatchReplace	<i>Replacements in list</i>
------------------	-----------------------------

Description

listBatchReplace replaces in list 'lst' all entries with value 'searchValue' by 'replaceBy'

Usage

```
listBatchReplace(lst, searchValue, replaceBy, silent = FALSE,
  callFrom = NULL)
```

Arguments

`lst` input-list to be used for replacing
`searchValue` (character, length=1)
`replaceBy` (character, length=1)
`silent` (logical) suppress messages
`callFrom` (character) allow easier tracking of message(s) produced

Value

corrected list

See Also

basic replacement sub in [grep](#)

Examples

```
lst1 <- list(aa=1:4,bb=c("abc","efg","abhh","effge"),cc=c("abdc","efg"))
listBatchReplace(lst1,search="efg",repl="EFG",sil=FALSE)
```

listGroupsByNames *Organize values into list and sort by names*

Description

Sort values of 'x' by its names and organize as list by common names, the names until 'sep' are used for (re)grouping. Note that typical spearators occuring the initial names may need protection by '\ (this is automatically taken care of for the case of the dot ('.') separator).

Usage

```
listGroupsByNames(x, sep = ".", silent = FALSE, callFrom = NULL)
```

Arguments

`x` (list) main input
`sep` (character) separator (note that typical separators may need to be protected, only automatically added for '.')
`silent` (logical) suppress messages
`callFrom` (character) allows easier tracking of message(s) produced

Value

matrix or data.frame

See Also

rbind in [cbind](#)

Examples

```
listGroupsByNames((1:10)/5)
ser1 <- 1:6; names(ser1) <- c("AA", "BB", "AA.1", "CC", "AA.b", "BB.e")
listGroupsByNames(ser1)
```

 lmSelClu

Run lm on segmented data (from clustering)

Description

lmSelClu runs linear regression on data segmented previously (eg by clustering). This function offers various types of (2-coefficient) linear regression on 2 columns of 'dat' (matrix with 3rd col named 'clu' or 'cluID', numeric elements for cluster-number). If argument 'clu' is (default) 'max', the column 'clu' will be inspected to take most frequent value of 'clu', otherwise a numeric entry specifying the cluster to extract is expected. Note: this function was initially made for use with results from diagCheck() Note: this function lacks means of judging goodness of fit of the regression performed & means for plotting

Usage

```
lmSelClu(dat, useCol = 1:2, clu = "max", regTy = "lin",
  filt1 = NULL, filt2 = NULL, silent = FALSE, callFrom = NULL)
```

Arguments

dat	matrix or data.frame
useCol	(integer or character) specify which 2 columns of 'dat' to use for linear regression
clu	(character) name of cluster to be extracted and treated
regTy	(character) change type used for linear regression : 'lin' for 1st col ~ 2nd col, 'res' for residue ~ 2nd col, 'norRes' for residue/2nd col ~ 2nd col or 'sqNorRes', 'inv' for 1st col ~ 1/(2nd col), 'invRes' for residue ~ 1/(2nd col)
filt1	(logical or numerical) filter criteria for 1st of 'useCol' , if numeric then select all lines of dat less than max of filt1
filt2	(logical or numerical) filter criteria for 2nd of 'useCol' , if numeric then select all lines of dat less than max of filt2
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

lm object (or NULL if no data left)

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

```

set.seed(2016); ran1 <- runif(220)
mat1 <- round(rbind(matrix(c(1:100+ran1[1:100], rep(1, 50)), ncol=3),
  matrix(c(1:60, 68:9+ran1[101:160], rep(2, 60)), nc=3)), 1)
colnames(mat1) <- c("a", "BB", "clu")
lmSelClu(mat1)
plot(mat1[which(mat1[, 3]=="2"), 1:2], col=grey(0.6))
abline(lmSelClu(mat1), lty=2, lwd=2)
#
mat2 <- round(rbind(matrix(c(1:100+ran1[1:100], rep(1, 50)), ncol=3),
  matrix(c(1:60, (2:61+ran1[101:160])^2, rep(2, 60)), nc=3)), 1)
colnames(mat2) <- c("a", "BB", "clu")
(reg2 <- lmSelClu(mat2, regTy="sqNor"))
plot(function(x) coef(reg2)[2]+ (coef(reg2)[2]*x^2), xlim=c(1, 70))
points(mat2[which(mat2[, 3]=="2"), 1:2], col=2)

```

[lrbind](#)*rbind on lists*

Description

rbind-like function to append list-elements containing tables and return one long table. Accepts also list-entries with data.frames or vectors (of length of no of columns) as long as at least 1 list-entry is a matrix

Usage

```
lrbind(lst, silent = FALSE, callFrom = NULL)
```

Arguments

lst	(list) main input (each list-element should have same number of columns, numeric vectors will be converted to number of columns of other elements)
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix or data.frame

See Also

rbind in [cbind](#)

Examples

```
lst1 <- list(matrix(1:9,nc=3,dimnames=list(letters[1:3],c("AA","BB","CC"))),
  11:13,matrix(51:56,ncol=3))
lrbind(lst1)
```

makeMAList

make MA-List object

Description

makeMAList extracts sets of data-pairs (like R & G series) and makes MA objects as MA-List object (eg for ratio oriented analysis). The grouping of columns as sets of replicate-measurements is done according to argument 'MAfac'. The output is fully compatible to functions of package **limma** (Bioconductor).

Usage

```
makeMAList(mat, MAfac, useF = c("R", "G"), isLog = TRUE,
  silent = FALSE, callFrom = NULL)
```

Arguments

mat	main input matrix
MAfac	(factor) factor organizing columns of 'mat' (if useF contains the default 'R' and 'G', they should also be part of MAfac)
useF	(character) two specific factor-levels of MAfac that will be used/extracted
isLog	(logical) tell if data is already log2 (will be considered when computing M and A values)
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

limma-type "MAList" containing M and A values

See Also

MA.RG in [normalizeWithinArrays](#)

Examples

```
set.seed(2017); t4 <- matrix(round(runif(40,1,9),2),ncol=4,
  dimnames=list(letters[c(1:5,3:4,6:4)],c("AA1","BB1","AA2","BB2")))
makeMAList(t4,gl(2,2,labels=c("R","G")))
```

makeNRedMatr

*Make non-redundant matrix***Description**

makeNRedMatr takes matrix or data.frame 'dat' to summarize redundant lines (column argument iniID) along method specified in summarizeRedAs to treat all lines with redundant iniID by same approach (ie for all columns the line where specified column is at eg max = 'maxOfRef'). If no name given, the function will take the last numeric (factors may be used - they will be read as levels).

Usage

```
makeNRedMatr(dat, summarizeRedAs, iniID = "iniID", retDataFrame = TRUE,
  callFrom = NULL, silent = FALSE, debug = FALSE)
```

Arguments

dat	(matrix or data.frame) main input for making non-redundant
summarizeRedAs	(character) summarization method(s), typical choices 'median', 'mean', 'min' or 'maxOfRef', 'maxAbsOfRef' for summarizing according to 1 specified column, may be single method for all or different method for each column (besides col 'iniID') or special method looking at column (if found, first of special methods used, everything else not considered).
iniID	(character) column-name used as initial ID (default="iniID")
retDataFrame	(logical) if TRUE, check if text-columns may be converted to data.frame with numeric
callFrom	(character) allows easier tracking of message(s) produced
silent	(logical) suppress messages
debug	(logical) for bug-tracking: more/enhanced messages

Value

(numeric) matrix or data.frame with summarized data and add'l col with number of initial redundant lines

See Also

simple/partial functionality in [summarizeCols](#), [checkSimValueInSer](#)

Examples

```
t3 <- data.frame(ref=rep(11:15,3),tx=letters[1:15],
  matrix(round(runif(30,-3,2),1),nc=2),stringsAsFactors=FALSE)
by(t3,t3[,1],function(x) x)
t(sapply(by(t3,t3[,1],function(x) x), summarizeCols, me="maxAbsOfRef"))
(xt3 <- makeNRedMatr(t3, summ="mean", iniID="ref"))
(xt3 <- makeNRedMatr(t3, summ=unlist(list(X1="maxAbsOfRef")), iniID="ref"))
```

matr2list	<i>Transform matrix to list of vectors</i>
-----------	--

Description

convert matrix to list of vectors: each column of 'mat' as vector of list

Usage

```
matr2list(mat, concSym = ".", silent = FALSE, callFrom = NULL)
```

Arguments

mat	(matrix) main input
concSym	(character) symbol for concatenating: concatenation of named vectors in list names as colname(s)+'concSym'+rowname
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix or array (1st dim is intraplate-position, 2nd .. plate-group/type, 3rd .. channels)

See Also

[convToNum](#)

Examples

```
mat1 <- matrix(1:12, ncol=3, dimnames=list(letters[1:4], LETTERS[1:3]))
mat2 <- matrix(LETTERS[11:22], ncol=3, dimnames=list(letters[1:4], LETTERS[1:3]))
matr2list(mat1); matr2list(mat2)
```

mergeSelCol	<i>Merge selected columns out of 2 matrix or data.frames</i>
-------------	--

Description

mergeSelCol merges selected columns out of 2 matrix or data.frames. 'selCols' will be used to define columns to be used; optionally may be different for 'dat2' : define in 'supCols2'. Output-cols will get additions specified in newSuff (default '.x' and '.y')

Usage

```
mergeSelCol(dat1, dat2, selCols, supCols2 = NULL, byC = NULL,
  useAll = FALSE, setRownames = TRUE, newSuff = c(".x", ".y"),
  callFrom = NULL)
```

Arguments

dat1	matrix or data.frame for fusing
dat2	matrix or data.frame for fusing
selCols	will be used to define columns to be used; optionally may be different for 'dat2' : define in 'supCols2'
supCols2	if additional column-names should be extracted form dat2
byC	(character) 'by' value used in merge
useAll	(logical) use all lines (will produce NAs when given identifier not found un 2nd group of data)
setRownames	(logical) if TRUE, will use values of col used as 'by' as rownames instead of showing as add'l col in output
newSuff	(character) prefix (argument 'suffixes' in merge)
callFrom	(character) allow easier tracking of message(s) produced

Value

data.frame

See Also

[merge](#), merge 3 data.frames using [mergeSelCol3](#)

Examples

```
mat1 <- matrix(c(1:7, letters[1:7], 11:17), ncol=3, dimnames=list(LETTERS[1:7], c("x1", "x2", "x3")))
mat2 <- matrix(c(1:6, c("b", "a", "e", "f", "g", "k"), 31:36),
              ncol=3, dimnames=list(LETTERS[11:16], c("y1", "x2", "x3")))
mergeSelCol(mat1, mat2, selC=c("x2", "x3"))
```

mergeSelCol3

mergeSelCol3

Description

successive merge of selected columns out of 3 matrix or data.frames. 'selCols' will be used to define columns to be used; optionally may be different for 'dat2' : define in 'supCols2'. Output-cols will get additions specified in newSuff (default '.x' and '.y')

Usage

```
mergeSelCol3(dat1, dat2, dat3, selCols, supCols2 = NULL,
             supCols3 = NULL, byC = NULL, useAll = FALSE, setRownames = TRUE,
             newSuff = c(".x", ".y", ".z"), callFrom = NULL)
```


Arguments

dat1	matrix or data.frame for fusing
dat2	matrix or data.frame for fusing
dat3	matrix or data.frame for fusing
selCols	will be used to define columns to be used; optionally may be different for 'dat2' : define in 'supCols2'
supCols2	if additional column-names should be extracted form dat2
supCols3	if additional column-names should be extracted form dat3
byC	(character) 'by' value used in merge
useAll	(logical) use all lines (will produce NAs when given identifier not found un 2nd group of data)
setRownames	if TRUE, will use values of col used as 'by' as rownames instead of showing as add'l col in output
newSuff	(character) prefix (argument 'suffixes' in merge)
callFrom	(character) allow easier tracking of message(s) produced

Value

data.frame

See Also

[merge](#), [mergeSelCol](#)

Examples

```
mat1 <- matrix(c(1:7, letters[1:7], 11:17), ncol=3, dimnames=list(LETTERS[1:7], c("x1", "x2", "x3")))
mat2 <- matrix(c(1:6, c("b", "a", "e", "f", "g", "k"), 31:36), ncol=3,
  dimnames=list(LETTERS[11:16], c("y1", "x2", "x3")))
mat3 <- matrix(c(1:6, c("c", "a", "e", "b", "g", "k"), 51:56), ncol=3,
  dimnames=list(LETTERS[11:16], c("z1", "x2", "x3")))
mergeSelCol3(mat1, mat2, mat3, selC=c("x2", "x3"))
```

mergeW2

Extended version of merge for multiple objects (even without rownames)

Description

mergeW2 provides flexible merging out of 'MArrayLM'-object (if found, won't consider any other input-data) or of separate vectors or matrixes. The main idea was to have something not adding add'l lines as merge might do, but to stay within the frame of the 1st argument given, even when IDs are repeated, so the output follows the order of the 1st argument, non-redundant IDs are created (orig IDs as new column). If no 'MArrayLM'-object found: try to combine all elements of input '...', input-names must match predefined variants 'chInp'. IDs given in 1st argument and not found in later arguments will be displayed as NA in the output matrix of data.frame. Note : (non-data) arguments must be given with full name (so far no lazy evaluation, may conflict with names in 'inputNamesLst'). Note : special characters in colnames bound to give trouble. Note : when no names given, mergeW2 will presume order of elements (names) from 'inputNamesLst'. PROBLEM : error after xxMerg3 when several entries have matching (row)names but some entries match only partially (what to do : replace with NAs ??)

Usage

```
mergeW2(..., nonRedundID = TRUE, convertDF = TRUE, selMerg = TRUE,
  inputNamesLst = NULL, noMatchPursue = TRUE, standColNa = FALSE,
  lastOfMultCols = c("p.value", "Lfdr"), duplTxtSep = "_",
  silent = FALSE, debug = FALSE, callFrom = NULL)
```

Arguments

...	all data (vectors, matrixes or data.frames) intended for merge
nonRedundID	(logical) if TRUE, always add 1st column with non-redundant IDs (add anyway if non-redundant IDs found)
convertDF	(logical) allows converting output in data.frame, add new heading col with non-red rownames & check which cols should be numeric
selMerg	(logical) if FALSE toggle to classic merge() (will give more rows in output in case of redundant names)
inputNamesLst	(list) named list with character vectors (should be unique), search these names in input for extracting/merging elements use for 'lazy matching' when checking names of input, default : 7 groups ('Mvalue', 'Avalue', 'p.value', 'mouseInfo', 'Lfdr', 'link', 'filt') with common short versions
noMatchPursue	(logical) allows using entries where 0 names match (just as if no names given)
standColNa	(logical) if TRUE return standard colnames as defined in 'inputNamesLst' (ie 'chInp'), otherwise colnames as initially provided
lastOfMultCols	may specify input groups where only last col will be used/extracted
duplTxtSep	(character) separator for counting/denominating multiple occurrences of same name
silent	(logical) suppress messages
debug	(logical) for bug-tracking: more/enhanced messages and intermediate objects written in global name-space
callFrom	(character) allows easier tracking of message(s) produced

Value

matrix or data.frame of fused data

See Also

[merge](#)

Examples

```
t1 <- 1:10; names(t1) <- letters[c(1:7,3:4,8)]
t2 <- 20:11; names(t2) <- letters[c(1:7,3:4,8)]
t3 <- 101:110; names(t3) <- letters[c(11:20)]
t4 <- matrix(100:81,ncol=2,dimnames=list(letters[1:10],c("co1","co2")))
t5 <- cbind(t1=t1,t52=t1+20,t53=t1+30)
      t1; t2; t3; cbind(t1,t2)
mergeW2(Mval=t1,p.value=t2,debug=FALSE)
```

minDiff

Minimum distance/difference between values

Description

minDiff aims to find the min distance (ie closest point) to any other x (numeric value), ie intra 'x' and returns matrix with 'index','value','dif','ppm','ncur','nbest','best'. At equal distance to lower & upper neighbour point, the upper (following) point is chosen (as single best). In case of multiple ex-aequo distance returns 1st of multiple, may be different at various repeats.

Usage

```
minDiff(x, digSig = 3, ppm = TRUE, initOrder = TRUE,
        callFrom = NULL)
```

Arguments

x	(numeric) vector to search minimum difference
digSig	number of significant digits, used for ratio or ppm column
ppm	(logical) display distance as ppm (1e6*diff/refValue, ie normalized difference eg as used in mass spectrometry), otherwise the ratio is given as : value(from 'x') / closestValue (from 'x')
initOrder	(logical) return matrix so that 'x' matches exactly 2nd col of output
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix

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

```
set.seed(2017); aa <- 100*c(0.1+round(runif(20),2),0.53,0.53)
minDiff(aa); minDiff(aa,init0=TRUE,ppm=FALSE); .minDif(unique(aa))
```

moderTest2grp

Moderated pair-wise t-test from limma

Description

Runs moderated t-test from package 'limma' on each line of data. Note: This function requires the package [limma](#) from bioconductor. The limma contrast-matrix has to be read by column, the lines in the contrast-matrix containing '+1' will be compared to the '-1' lines, eg grpA-grpB .

Usage

```
moderTest2grp(dat, grp, limmaOutput = TRUE, addResults = c("lfd",
  "FDR", "Mval", "means"), testOrientation = "=", silent = FALSE,
  callFrom = NULL)
```

Arguments

dat	matrix or data.frame with rows for multiple (independent) tests, use ONLY with 2 groups; assumed as log2-data
grp	(factor) describes column-relationship of 'dat' (1st factor is considered as reference -> orientation of M-values !!)
limmaOutput	(logical) return full (or extended) MArrayLM-object from limma or 'FALSE' for only the (uncorrected) p.values
addResults	(character) types of results to add besides basic limma-output (eg "lfd" using fdrtools-package,"FDR" for BY-FDR,"Mval" (assumes that data are log2 !),"means" or "nonMod" for non-moderated test)
testOrientation	(character) for one-sided test (">","greater" or "<","less"), NOTE : 2nd grp is considered control/reference, '<' will identify grp1 < grp2
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

limma-type MA-object (list)

See Also

[lmFit](#) and [eBayes](#)

Examples

```
set.seed(2017); t8 <- matrix(round(rnorm(1600,10,0.4),2),ncol=8,
  dimnames=list(paste("1",1:200),c("AA1","BB1","CC1","DD1","AA2","BB2","CC2","DD2")))
t8[3:6,1:2] <- t8[3:6,1:2]+3 # augment lines 3:6 for AA1&BB1
t8[5:8,5:6] <- t8[5:8,5:6]+3 # augment lines 5:8 for AA2&BB2 (c,d,g,h should be found)
t4 <- log2(t8[,1:4]/t8[,5:8])
fit4 <- moderTest2grp(t4,gl(2,2))
limma::topTable(fit4,coef=1,n=5) # effect for 3,4,7,8
fit4in <- moderTest2grp(t4,gl(2,2),test0="<")
limma::topTable(fit4in,coef=1,n=5)
```

moderTestXgrp

Multiple moderated pair-wise t-tests from limma

Description

Runs all pair-wise combinations of moderated t-tests from package 'limma' on each line of data against 1st group from 'grp'. Note: This function requires the package **limma** from bioconductor. The limma contrast-matrix has to be read by column, the lines in the contrast-matrix containing '+1' will be compared to the '-1' lines, eg grpA-grpB .

Usage

```
moderTestXgrp(dat, grp, limmaOutput = TRUE, addResults = c("lfd",
  "FDR", "Mval", "means"), testOrientation = "=", silent = FALSE,
  callFrom = NULL)
```

Arguments

<code>dat</code>	matrix or data.frame with rows for multiple (independent) tests, use ONLY with 2 groups; assumed as log2-data !!!
<code>grp</code>	(factor) describes column-relationship of 'dat' (1st factor is considered as reference -> orientation of M-values !!)
<code>limmaOutput</code>	(logical) return full (or extended) MArrayLM-object from limma or 'FALSE' for only the (uncorrected) p.values
<code>addResults</code>	(character) types of results to add besides basic limma-output (eg "lfd" using fdrtools-package,"FDR" for BY-FDR,"Mval" (assumes that data are log2 !),"means" or "nonMod" for non-moderated test)
<code>testOrientation</code>	(character) for one-sided test (">","greater" or "<","less"), NOTE : 2nd grp is considered control/reference, '<' will identify grp1 < grp2
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

Value

limma-type MA-object (list)

See Also

[eBayes](#) for basal tool and [moderTest2grp](#) for single comparison

Examples

```
grp <- factor(rep(LETTERS[c(3,1,4)],c(2,3,3)))
set.seed(2017); t8 <- matrix(round(rnorm(208*8,10,0.4),2),ncol=8,
  dimnames=list(paste(letters[],rep(1:8,each=26),sep=""),paste(grp,c(1:2,1:3,1:3),sep="")))
t8[3:6,1:2] <- t8[3:6,1:2] +3 # augment lines 3:6 (c-f)
t8[5:8,c(1:2,6:8)] <- t8[5:8,c(1:2,6:8)] -1.5 # lower lines
t8[6:7,3:5] <- t8[6:7,3:5] +2.2 # augment lines
## expect to find C/A in c,d,g, (h)
## expect to find C/D in c,d,e,f
## expect to find A/D in f,g,(h)
test8 <- moderTestXgrp(t8,grp)
head(test8$p.value,n=8)
```

naOmit

Fast na.omit

Description

naOmit removes NAs from input vector. This function has no slot for removed elements while na.omit does so. Resulting objects from naOmit are smaller in size and subsequent execution (on large vectors) is faster (in particular if many NAs get encountered). Note : Behaves differently to na.omit with input other than plain vectors. Will not work with data.frames !

Usage

```
naOmit(x)
```

Arguments

x (vector or matrix) input

Value

vector without NAs (matrix input will be transformed to vector). Returns NULL if input consists only of NAs.

See Also

[na.fail](#), [na.omit](#)

Examples

```
aA <- c(11:13,NA,10,NA);  
naOmit(aA)
```

nFragments	<i>Number of fragments after cut at specific character(s) within size-range</i>
------------	---

Description

nFragments determines number of fragments /entry within range of 'sizeRa' (numeric,length=2) when cutting after 'cutAt'

Usage

```
nFragments(protSeq, cutAt, sizeRa)
```

Arguments

protSeq	(character) text to be cut
cutAt	(character) position to cut
sizeRa	(numeric,length=2) min and max size to consider

Value

numeric vector with number of fragments for each entry 'protSeq' (names are 'protSeq')

See Also

[cutAtMultSites](#), simple version {nFragments0} (no size-range)

Examples

```
tmp <- "MSVSREDSCELDLVYVTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGNYLLFNLSERRPDITKLHAKVLEFGWPDLHTPALEKI"  
nFragments(c(tmp,"ojioRij"),c("R","K"),c(4,31))
```

nFragments0	<i>Number of fragments after cut at specific character(s)</i>
-------------	---

Description

nFragments0 tells the number of fragments/entry when cutting after 'cutAt'

Usage

```
nFragments0(protSeq, cutAt)
```

Arguments

protSeq	(character) text to be cut
cutAt	(integer) position to cut

Value

numeric vector with number of fragments for each entry 'protSeq' (names are 'protSeq')

See Also

more elaborate {nFragments}; [cutAtMultSites](#)

Examples

```
tmp <- "MSVSRMEDSCELDLVYVTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGNYLLFNLSERRPDITKLHAKVLEFGWPDLHTPALEKI"
nFragments0(c(tmp, "ojoRij"), c("R", "K"))
```

nNonNumChar	<i>Count number of non-numeric characters</i>
-------------	---

Description

nNonNumChar counts number of non-numeric characters. Made for positive non-scientific values (eg won't count neg-sign, neither Euro comma ',')

Usage

```
nNonNumChar(txt)
```

Arguments

txt	character vector to be treated
-----	--------------------------------

Value

numeric vector with numer of non-numeric characters (ie not '.' or 0-9))

See Also

[nchar](#)

Examples

```
nNonNumChar("a1b "); sapply(c("aa", "12ab", "a1b2", "12", "0.5"), nNonNumChar)
```

nonAmbiguousMat	<i>Transform matrix to non-ambiguous matrix (in respect to given column)</i>
-----------------	--

Description

nonAmbiguousMat makes values of matrix 'mat' in col 'byCol' unique.

Usage

```
nonAmbiguousMat(mat, byCol, uniqOnly = FALSE, asList = FALSE,
  nameMod = "amb_", callFrom = NULL)
```

Arguments

mat	numeric or character matrix (or data.frame), column specified by 'byCol' must be/will be used as.numeric, 1st column of 'mat' will be considered like index & used for adding prefix 'nameMod' (unless byCol=1, then 2nd col will be used)
byCol	(character or integer-index) column by which ambiguity will be tested
uniqOnly	(logical) if =TRUE return unique only, if =FALSE return unique and single representative of non-unique values (with " added to name), selection of representative of repeated: first (of sorted) or middle if >2 instances
asList	(logical) return result as list
nameMod	(character) prefix added to 1st column of 'mat' (expect 'by') for indicating non-unique/ambiguous values
callFrom	(character) allow easier tracking of message(s) produced

Value

sorted non-ambiguous numeric vector (or list if 'asList'=TRUE and 'uniqOnly'=FALSE)

See Also

for non-numeric use [firstOfRepeated](#) - but 1000x much slower !; [get1stOfRepeatedByCol](#)

Examples

```
set.seed(2017); mat2 <- matrix(c(1:100,round(rnorm(200),2)),ncol=3,
  dimnames=list(1:100,LETTERS[1:3]));
head(mat2U <- nonAmbiguousMat(mat2,by="B",na="_",uniq0=FALSE),n=15)
head(get1stOfRepeatedByCol(mat2,sortB="B",sortS="B"))
```

nonAmbiguousNum	<i>make numeric vector non-ambiguous (ie unique)</i>
-----------------	--

Description

nonAmbiguousNum makes (named) values of numeric vector 'x' unique. Note: for non-numeric use [firstOfRepeated](#) - but 1000x slower ! Return sorted non-ambiguous numeric vector (or list if 'asList'=TRUE and 'uniqOnly'=FALSE)

Usage

```
nonAmbiguousNum(x, uniqOnly = FALSE, asList = FALSE,
  nameMod = "amb_", callFrom = NULL)
```

Arguments

x	(numeric) main input
uniqOnly	(logical) if=TRUE return unique only, if =FALSE return unique and single representative of non-unique values (with " added to name), selection of representative of repeated: first (of sorted) or middle if >2 instances
asList	(logical) return list
nameMod	(character) text to add in case on ambiguous values, default="amb_"
callFrom	(character) allow easier tracking of message(s) produced

Value

sorted non-ambiguous numeric vector (or list if 'asList'=TRUE and 'uniqOnly'=FALSE)

See Also

[firstOfRepeated](#) for non-numeric use (much slower !!!), [duplicated](#)

Examples

```
set.seed(2017); aa <- round(rnorm(100),2); names(aa) <- 1:length(aa)
str(nonAmbiguousNum(aa))
str(nonAmbiguousNum(aa,uniq=FALSE,asLi=TRUE))
```

nonredDataFrame	<i>Filter for unique elements</i>
-----------------	-----------------------------------

Description

nonredDataFrame filters 'x' (list of char-vectors or char-vector) for elements unique (to 'ref' or if NULL to all 'x') and of character length. May be used for different 'accession' for same pep sequence (same 'peptide_id'). Note : made for treating data.frames, may be slightly slower than matrix equivalent

Usage

```
nonredDataFrame(dataFr, useCol = c(pepID = "peptide_id", protID =
  "accession", seq = "sequence", mod = "modifications"),
  sepCollapse = "//", callFrom = NULL)
```

Arguments

dataFr	(data.frame) main input
useCol	(character,length=2) comlumn names of 'dataFr' to use : 1st value designates where redundant values should be gathered; 2nd value designes column of which information should be concatenated
sepCollapse	(character) conatenation symbol
callFrom	(character) allow easier tracking of messages produced

Value

data.frame of filtered (fewer lines) with additional 2 columns 'nSamePep' (number of redundant entries) and 'concID' (concatenated content)

See Also

[combineRedBasedOnCol](#), [correctToUnique](#), [unique](#)

Examples

```
df1 <- data.frame(cbind(xA=letters[1:5],xB=c("h","h","f","e","f"),xC=LETTERS[1:5]))
nonredDataFrame(df1,useCol=c("xB","xC"))
```

nonRedundLines	<i>Non-redundant lines of matrix</i>
----------------	--------------------------------------

Description

nonRedundLines reduces complexity of matrix (or data.frame) if multiple consecutive (!) lines with same values. Return matrix (or data.frame) without repeated lines (keep 1st occurrence)

Usage

```
nonRedundLines(dat, callFrom = NULL)
```

Arguments

dat	(matrix or data.frame) main input
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix (or data.frame) without repeated lines (keep 1st occurrence)..

See Also

[firstLineOfDat](#), [firstOfRepLines](#), [findRepeated](#), [firstOfRepeated](#), [get1stOfRepeatedByCol](#), [combineRedBasedOnCol](#), [correctToUnique](#)

Examples

```
mat2 <- matrix(rep(c(1,1:3,3,1),2),ncol=2,dimnames=list(letters[1:6],LETTERS[1:2]))
nonRedundLines(mat2)
```

normalizeThis	<i>Normalize data in various modes</i>
---------------	--

Description

Generic normalization of 'dat' (by columns), multiple methods may be applied. The choice of normalization procedures must be done with care, plotting the data before and after normalization may be critical to understanding the initial data structure and the effect of the procedure applied. Inappropriate methods chosen may render interpretation of (further) results incorrect. Note : the normalized data may appear (depending on the procedure chosen) on a different scale.

Usage

```
normalizeThis(dat, method = "mean", refLines = NULL, refGrp = NULL,
  trimFa = NULL, quantFa = NULL, expFa = NULL, silent = FALSE,
  callFrom = NULL)
```

Arguments

dat	matrix or data.frame
method	(character) may be "mean", "median", "NULL", "none", "trimMean", "slope", "exponent", "slope2Sections"; When NULL or 'none' is chosen the input will be returned
refLines	(NULL or numeric) allows to consider only specific lines of 'dat' when determining normalization factors (all data will be normalized)
refGrp	Only the columns indicated will be used as reference, default all columns (integer or colnames)
trimFa	(numeric, length=1) additional parameters for trimmed mean
quantFa	(numeric, length=2) additional parameters for quantiles to use with method='slope'
expFa	(numeric, length=1) additional parameters for method='exponent'
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message produced

Value

matrix of normalized data

See Also

[exponNormalize](#)

Examples

```
set.seed(2015); rand1 <- round(runif(300)+rnorm(300,0,2),3)
dat1 <- cbind(ser1=round(100:1+rand1[1:100]),ser2=round(1.2*(100:1+rand1[101:200])-2),
  ser3=round((100:1+rand1[201:300])^1.2-3))
dat1 <- cbind(dat1,ser4=round(dat1[,1]^seq(2,5,length.out=100)+rand1[11:110],1))
dat1[dat1 <1] <- NA
summary(dat1)
head( .normalize(dat1,"mean",list()))
dat1[c(1:5,50:54,95:100),]
no1 <- normalizeThis(dat1,refGrp=1:3,meth="mean")
no2 <- normalizeThis(dat1,refGrp=1:3,meth="trimMean",trim=0.4)
no3 <- normalizeThis(dat1,refGrp=1:3,meth="median")
no4 <- normalizeThis(dat1,refGrp=1:3,meth="slope",quantFa=c(0.2,0.8))
dat1[c(1:10,91:100),]
cor(dat1[,3],rowMeans(dat1[,1:2],na.rm=TRUE),use="complete.obs") # high
cor(dat1[,4],rowMeans(dat1[,1:2],na.rm=TRUE),use="complete.obs") # bad
cor(dat1[c(1:10,91:100),4],rowMeans(dat1[c(1:10,91:100),1:2],na.rm=TRUE),use="complete.obs")
cor(dat1[,3],rowMeans(dat1[,1:2],na.rm=TRUE)^(1/seq(2,5,length.out=100)),use="complete.obs")
```

organizeAsListOfRepl *(re)organize data of (3-dim) array as list of replicates*

Description

Organize array of all data ('arrIn', long table) into list of (replicate-)arrays (of similar type/layout) based on dimension number 'byDim' of 'arrIn' (eg 2nd or 3rd dim). Argument inspNChar defines the number of characters to consider, so if the beginning of names is the same they will be separated as list of multiple arrays. Default will search for '_' separator or trim from end if not found in the relevant dimnames

Usage

```
organizeAsListOfRepl(arrIn, inspNChar = 0, byDim = 3, silent = TRUE,
  callFrom = NULL)
```

Arguments

arrIn	(array) main input
inspNChar	(integer) if inspNChar=0 the array-names (2nd dim of 'arrIn') will be cut before last '_'
byDim	(integer, length=1) dimension number along which data will be split in separate elements (considering the first inspNChar characters)
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

list of arrays (typically 1st and 2nd dim for specific genes/objects, 3rd for different measures associated with)

Examples

```
arr1 <- array(1:24,dim=c(4,3,2),dimnames=list(c(LETTERS[1:4]),
  paste("col",1:3,sep=""),c("ch1","ch2")))
organizeAsListOfRepl(arr1)
```

partialDist	<i>Partial distance matrix (focus on closest)</i>
-------------	---

Description

partialDist calculates distance matrix like dist for 1- or 2-dim data, but only partially, ie only cases of small distances. This function was made for treating very large data-sets where only very close distances to a given point need to be found, it allows to overcome memory-problems with larger data (and faster execution with > 50 rows of 'dat').

Usage

```
partialDist(dat, groups, overLap = TRUE, method = "euclidean",
  silent = FALSE, callFrom = NULL)
```

Arguments

dat	(matrix of numeric values) main input
groups	(factor) to split using cut or specific custom grouping (length of dat)
overLap	(logical) if TRUE make groups overlapping by 1 value (ie maintain some context-information)
method	'character' name of method passed to dist
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix (not of class 'dist')

See Also

[dist](#)

Examples

```
set.seed(2016); mat3 <- matrix(runif(300),nr=30)
round(dist(mat3),1)
round(partialDist(mat3,gr=3),1)
```

partUnlist *Partial unlist of lists of lists*

Description

partUnlist does partial unlist for treating list of lists : New (returned) list has one level less of hierarchy (Highest level list will be appended). In case of conflicting (non-null) listnames a prefix will be added. Behaviour different to [unlist](#) when unlisting list of matrixes.

Usage

```
partUnlist(lst)
```

Arguments

lst list to be partailly unlisted

Value

list with partially reduced nested structure

See Also

[unlist](#), [asSeplist](#)

Examples

```
partUnlist(list(list(a=11:12,b=21:24),list(c=101:101,d=201:204)))
li4 <- list(c=1:3,L2=matrix(1:4,ncol=2),li3=list(L1=11:12,L2=matrix(21:26,ncol=2)))
partUnlist(li4)
unlist(li4,rec=FALSE)
```

pasteC *Advanced paste-collapse*

Description

pasteC is a variant of [paste](#) for convenient use of paste-collapse and separation of last element to paste (via 'lastCol'). This function was mode for more human like enumerating in output and messages. If multiple arguments are given without names they will all be concatenated, if they contain names lazy evaluation for names will be tried (with preference to longest match to argument names). Note that some special characters (like backslash) may need to be protected when used with 'collapse' or 'quoteC'. Returns character vector of length 1 (everything pasted together)

Usage

```
pasteC(..., collapse = ", ", lastCol = " and ", quoteC = "")
```


Arguments

...	(character) main input to be collapsed
collapse	(character,length=1) element to use for collapsing
lastCol	(character) text to use before last item enumerated element
quoteC	character to use for citing with quotations (default "")

Value

character vector of length=1 of the concatenated input/values.

See Also

[paste](#) for basic paste

Examples

```
pasteC(1:4)
```

presenceFilt	<i>Filter lines of matrix for max number of NAs</i>
--------------	---

Description

presenceFilt filters lines of 'dat' for sufficient presence/absence of NA values (ie limit number of NAs per line). Filter abundance/expression data for min number and/or ratio of values present/above threshold (incl NA) in at least 1 of multiple groups difference proteomics/RNAseq : if peptide was identified its quantity is more certain than based on spectral alignment.

Usage

```
presenceFilt(dat, grp, maxGrpMiss = 1, ratMaxNA = 0.8, minVal = NULL,
  silent = FALSE, callFrom = NULL)
```

Arguments

dat	matrix or data.frame
grp	factor of min 2 levels describing which col of 'dat' belongs to which group (levels 1 & 2 will be used)
maxGrpMiss	(numeric) at least 1 group has not more than this number of NAs (otherwise marke line as bad)
ratMaxNA	(numeric)
minVal	(default NULL or numeric), any value below will be treated like NA
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message produced

Value

logical matrix (with separate col for each pairwise combination of 'grp' levels) indicating if line of 'dat' acceptable based on NAs (and values minVal)

Examples

```
dat1 <- matrix(1:56,ncol=7)
dat1[c(2,3,4,5,6,10,12,18,19,20,22,23,26,27,28,30,31,34,38,39,50,54)] <- NA
dat1; presenceFilt(dat1,gr=gl(3,3)[-3:4],maxGr=0)
presenceFilt(dat1,gr=gl(2,4)[-1],maxGr=1,ratM=0.1)
presenceFilt(dat1,gr=gl(2,4)[-1],maxGr=2,rat=0.5)
```

pVal2lfdr

Convert p-values to lfdr

Description

This function takes a numeric vector of p-values and returns a vector of lfdr-values (local false discovery) using the package **fdrtool**. Multiple testing correction should be performed with caution, short series of p-values typically pose problems for transforming to lfdr. The transformation to lfdr values may give warning messages, in this case the resultant lfdr values may be invalid !

Usage

```
pVal2lfdr(x, silent = TRUE, callFrom = NULL)
```

Arguments

x (numeric) vector of p.values
 silent (logical) suppress messages
 callFrom (character) allow easier tracking of message(s) produced

Value

(numeric) vector of lfdr values (or NULL if data insufficient to run the function 'fdrtool')

See Also

lfdr from [fdrtool](#), other p-adjustments (multiple test correction, eg FDR) in [p.adjust](#)

Examples

```
## Note that this example is too small for estimating really meaningful fdr values
set.seed(2017); t8 <- matrix(round(rnorm(160,10,0.4),2),ncol=8,dimnames=list(letters[1:20],
  c("AA1","BB1","CC1","DD1","AA2","BB2","CC2","DD2")))
t8[3:6,1:2] <- t8[3:6,1:2]+3 # augment lines 3:6 (c-f) for AA1&BB1
t8[5:8,5:6] <- t8[5:8,5:6]+3 # augment lines 5:8 (e-h) for AA2&BB2 (c,d,g,h should be found)
head(pVal2lfdr(apply(t8,1,function(x) t.test(x[1:4],x[5:8])$p.value)))
```

randIndFx	<i>Distance of categorical data (Jaccard, Rand and adjusted Rand index)</i>
-----------	---

Description

randIndFx calculates distance of categorical data (as Rand Index, Adjusted Rand Index or Jaccard Index). Note: uses/requires package **flexclust** Methods so far available (via flexclust): "ARI" .. adjusted Rand Index, "RI" .. Rand index, "J" .. Jaccard, "FM" .. Fowlkes-Mallows.

Usage

```
randIndFx(ma, method = "ARI", adjSense = TRUE, silent = FALSE,
          callFrom = NULL)
```

Arguments

ma	(matrix) main input for distance calculation
method	(character) name of distance method (eg "ARI", "RI", "J", "FM")
adjSense	(logical) allows introducing correlation/anticorrelation (interpret neg distance results as anti)
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

distance matrix

See Also

comPart in [randIndex](#)

Examples

```
set.seed(2016); tab2 <- matrix(sample(1:2, size=42, replace=TRUE), ncol=7)
flexclust::comPart(tab2[1,], tab2[2,])
flexclust::comPart(tab2[1,], tab2[3,])
flexclust::comPart(tab2[1,], tab2[4,])
randIndFx(tab2, adjS=FALSE)
cor(t(tab2))
randIndFx(tab2, adjS=TRUE)
```

ratioAllComb	<i>Calculate all ratios between x and y</i>
--------------	---

Description

ratioAllComb calculates all possible pairwise ratios between all individual values of x and y.

Usage

```
ratioAllComb(x, y, maxLim = 10000, silent = FALSE, callFrom = NULL)
```

Arguments

x	(numeric) vector, numerator for constructing ratios
y	(numeric) vector, denominator for constructing ratios
maxLim	(integer) allows reducing complexity by drawing for very long x or y
silent	(logical) suppress (less important) messages
callFrom	(character) allow easier tracking of message(s) produced

Value

(numeric) vector with all ratios

Examples

```
set.seed(2014); ra1 <- c(rnorm(9,2,1),runif(8,1,2))
ratioAllComb(ra1[1:9],ra1[10:17])
boxplot(list(norm=ra1[1:9],unif=ra1[10:17],rat=ratioAllComb(ra1[1:9],ra1[10:17])))
```

ratioToPpm	<i>Convert ratio to ppm</i>
------------	-----------------------------

Description

ratioToPpm transforms ratio 'x' to ppm (parts per million). If 'y' not given (or different length as 'x'), then 'x' is assumed as ratio otherwise ratios are constructed as x/y is used lateron. Does additional checking : negative values not expected - will be made absolute !

Usage

```
ratioToPpm(x, y = NULL, nSign = NULL, silent = FALSE,
           callFrom = NULL)
```

Arguments

x	(numeric) main input
y	(numeric) optional value to construct ratios (x/y). If NULL (or different length as 'x'), then 'x' will be considered as ratio.
nSign	(numeric) number of significant digits
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

numeric vector of ppm values

See Also

[XYToDiffPpm](#) for ppm of difference as used in mass spectrometry

Examples

```
set.seed(2017); aa <- c(1.000001, 0.999999, 1+rnorm(10, 0, 0.001))
cbind(x=aa, ppm=ratioToPpm(aa, nSign=4))
```

readCsvBatch

Read batch of csv-files

Description

This function was designed to read screening data split in parts (with common structure) and saved to multiple files, to extract the numeric columns and to compile all (numeric) data to a single array (or list). Some screening platforms save results while progressing through a pile of microtiter-plates separately. The organization of the resultant files is structured through file-names and all files have exactly the same organization of lines and columns/ European or US-formatted csv files can be read, if argument fileFormat is NULL both types will be tested, otherwise it allows to specify a given format. The presence of headers (to be used as column-names) may be tested using checkFormat.

Usage

```
readCsvBatch(fileNames = NULL, path = ".", fileFormat = "Eur",
  checkFormat = TRUE, returnArray = TRUE, columns = c("Plate",
  "Well", "StainA"), excludeFiles = "All infected plates",
  simpleNames = TRUE, minNamesLe = 4, silent = FALSE,
  callFrom = NULL)
```

Arguments

fileNames	(character) names of files to be read, if NULL all files fitting 'fileFormat'
path	(character) where files should be read (folders should be written in R-style)
fileFormat	(character) may be NULL (both US and European formats will be tried), 'Eur' or 'US'
checkFormat	(logical) if TRUE: check header, remove empty columns, 1st line if all empty, set output format for each file to matrix, if rownames are increasing integers try to use 2nd of 'columns' as rownames
returnArray	(logical) allows switching from array to list-output
columns	(NULL or character) column-headers to be extracted (if specified), 2nd value may be column with rownames (if rownames are encountered as increasing rownames)
excludeFiles	(character) names of files to exclude (only used when reading all files of given directory)
simpleNames	(logical) allows truncating names (from beginning) to get to variable part (using .trimFromStart()), but keeping 'minNamesLe'
minNamesLe	(integer) min length of column-names if simpleNames=TRUE
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

array (or list if 'returnArray'=FALSE) of all numeric data read (numerical columns only) from individual files

See Also

[read.table](#), [writeCsv](#), [readXlsxBatch](#)

Examples

```
path1 <- system.file("extdata",package="wrMisc")
fiNa <- c("pl01_1.csv", "pl01_2.csv", "pl02_1.csv", "pl02_2.csv")
datAll <- readCsvBatch(fiNa,path1)
str(datAll)
## batch reading of all csv files in specified path :
datAll2 <- readCsvBatch(fileNames=NULL,path=path1,silent=TRUE)
```

readXlsxBatch	<i>Read batch of Excel xlsx-files</i>
---------------	---------------------------------------

Description

readXlsxBatch reads data out of multiple xlsx files, the sheet indicated by 'sheetInd' will be considered. All files must have a very similar organization of data, as this is typically the case when high-throughput measurements are automatically saved while the screen progresses. The file-names will be used to structure the data read. By default all columns with text-content may be eliminated to extract the numeric part only, which may then get organized to a 3-dim array. NOTE : requires package `xlsx` being installed ! Uses a considerable amount of RAM ! Reading multiple xlsx files does take some time.

Usage

```
readXlsxBatch(fileNames = NULL, path = ".", fileExtension = "xlsx",
  excludeFiles = NULL, sheetInd = 1, checkFormat = TRUE,
  returnArray = TRUE, columns = c("Plate", "Well", "StainA"),
  simpleNames = 3, silent = FALSE, callFrom = NULL)
```

Arguments

fileNames	(character) provide either explicit list of file-names to be read or leave NULL for reading all files ending with 'xlsx' in path specified with argument path
path	(character) there may be a different path for each file
fileExtension	(character) extension of files (default='xlsx')
excludeFiles	(character) names of files to exclude (only used when reading all files of given directory)
sheetInd	(integer) specify which sheet to extract (must be number, eg sheetInd=2 will extract always the 2nd sheet (no matter the name)
checkFormat	(logical) if TRUE: check header, remove empty columns, if rownames are increasing integers it will search for first column with different entries to use as rownames
returnArray	(logical) allows switching from array to list-output
columns	(NULL or character) column-headers to be extracted (if specified, otherwise all columns will be extracted)
simpleNames	(integer), if NULL all characters of fileNames will be maintained, otherwise allows truncating names (from beginning) to get to variable part (using <code>.trimFromStart()</code>), but keeping at least the number of characters indicated by this argument
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

list

See Also

[read.xlsx](#), for simple reading of xls-files under 32-bit R see also: [odbcConnectExcel](#) via [odbcConnect](#)

Examples

```
path1 <- system.file("extdata",package="wrMisc")
fiNa <- c("pl01_1.xlsx","pl01_2.xlsx","pl02_1.xlsx","pl02_2.xlsx")
datAll <- readXlsxBatch(fiNa,path1)
str(datAll)
datAll2 <- readXlsxBatch(path=path1,silent=TRUE)
identical(datAll,datAll2)
```

reduceTable

Reduce table by aggregating smaller groups

Description

reduceTable treats/reduces results from [table](#) to 'nGrp' groups, optional indiv resolution of 'separFirst' (numeric or NULL). Mainly made for reducing the number of classes for better plots with [pie](#)

Usage

```
reduceTable(tab, separFirst = 4, nGrp = 15)
```

Arguments

tab	output of table
separFirst	(integer or NULL) optional separation of n 'separFirst' groups (value <2 or NULL will privilege more uniform size of groups, higher values will cause small initial and larger tailing groups)
nGrp	(integer) number of groups expected

Value

numeric vector with number of counts and class-borders as names (like table).

See Also

[table](#)

Examples

```
set.seed(2018); dat <- sample(11:60,200, repl=TRUE)
pie(table(dat))
pie(reduceTable(table(dat), sep=NULL))
pie(reduceTable(table(dat), sep=NULL), init.angle=90, clockwise=TRUE, col=rainbow(20)[1:15], cex=0.8)
```

regrBy1or2point	<i>Rescaling according to reference data using linear regression.</i>
-----------------	---

Description

regrBy1or2point does rescaling: linear transform simple vector 'inDat' that (mean of) elements of names cited in 'refLst' will end up as values 'regrTo'. Regress single vector according to 'refLst' (describing names of inDat). If 'refLst' contains 2 groups, the 1st group will be set to the 1st value of 'regrTo' (and the 2nd group of 'refLst' to the 2nd 'regrTo')

Usage

```
regrBy1or2point(inDat, refLst, regrTo = c(1, 0.5), silent = FALSE,  
  callFrom = NULL)
```

Arguments

inDat	matrix or data.frame
refLst	list of names existing in inDat (one group of names for each value in 'regrTo'), to be transformed in values precised in 'regrTo'; if no matches to names of 'inDat' found, the 2 lowest and/or highest highest values will be chosen
regrTo	(numeric,length=2) range (at scale 0-1) of target-values for mean of elements cited in 'refLst'
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

normalized matrix

See Also

[adjBy2ptReg](#), [regrMultBy1or2point](#)

Examples

```
set.seed(2016); dat1 <- 1:50 +(1:50)*round(runif(50),1)  
names(dat1) <- 1:length(dat1)  
reg1 <- regrBy1or2point(dat1,refLst=c("2","49"))  
plot(reg1,dat1)
```

regrMultBy1or2point	<i>Rescaling of multiple data-sets according to reference data using regression</i>
---------------------	---

Description

regrMultBy1or2point regresses each col of matrix according to 'refLst'(describing rownames of inDat). If 'refLst' contains 2 groups, the 1st group will be set to the 1st value of 'regrTo' (and the 2nd group of 'refLst' to the 2nd 'regrTo')

Usage

```
regrMultBy1or2point(inDat, refLst, regrTo = c(1, 0.5), silent = FALSE,
  callFrom = NULL)
```

Arguments

inDat	matrix or data.frame
refLst	list of names existing in inDat (one group of names for each value in 'regrTo'), to be transformed in values precised in 'regrTo'; if no matches to names of 'inDat' found, the 2 lowest and/or highest values will be chosen
regrTo	(numeric,length=2) range (at scale 0-1) of target-values for mean of elements cited in 'refLst'
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

normalized matrix

See Also

[adjBy2ptReg](#), [regrBy1or2point](#)

Examples

```
set.seed(2016); dat2 <- round(cbind(1:50 +(1:50)*runif(50),2.2*(1:50) +rnorm(50,0,3)),1)
rownames(dat2) <- 1:nrow(dat2)
reg1 <- regrBy1or2point(dat2[,1],refLst=list(as.character(5:7),as.character(44:45)))
reg2 <- regrMultBy1or2point(dat2,refLst=list(as.character(5:7),as.character(44:45)))
plot(dat2[,1],reg2[,1])
identical(reg1,reg2[,1])
identical(dat2[,1],reg2[,1])
```

renameColumns	<i>Rename columns</i>
---------------	-----------------------

Description

renameColumns renames columns of 'refMatr' using 2-column matrix (or data.frame) indicating old and new names (for replacement).

Usage

```
renameColumns(refMatr, newName, silent = FALSE, callFrom = NULL)
```

Arguments

refMatr	matrix (or data.frame) where column-names should be changed
newName	(matrix of character) giving correspondence of old to new names (number of lines must match number of columns of 'refMatr')
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

Value

matrix (or data.frame) with renamed columns

Examples

```
ma <- matrix(1:8, ncol=4, dimnames=list(1:2, LETTERS[1:4]))
replBy1 <- cbind(new=c("dd", "bb", "z_"), old=c("D", "B", "zz"))
replBy2 <- matrix(c("D", "B", "zz", "dd", "bb", "z_"), ncol=2)
replBy3 <- matrix(c("X", "Y", "zz", "xx", "yy", "z_"), ncol=2)
renameColumns(ma, replBy1)
renameColumns(ma, replBy2)
renameColumns(ma, replBy3)
```

replNAbyLow	<i>Replace NAs by low values</i>
-------------	----------------------------------

Description

With several screening techniques used in high-throughput biology values at/below detection limit are returned as NA. However, the resultant NA-values may be difficult to analyse properly, simply ignoring NA-values may not be a good choice. When (technical) replicate measurements are available, one can look for cases where one gave an NA while the other did not with the aim of investigating such 'NA-neighbours'. replNAbyLow locates and replaces NA values by (random) values from same line & same group 'grp'. The origin of NAs should be predominantly absence of measure

(quantitation) due to signal below limit of detection and not saturation at upper detection limit or other technical problems. Note, this approach may be not optimal if the number of NA-neighbours is very low. Replacemet is done -depending on agrument 'unif'- by Gaussian random model based on neighbour values (within same group), using their means and sd, or a uniform random model (min and max of neighbour values) . Then numeric matrix (same dim as 'x') with NA replaced is returned.

Usage

```
replNAbyLow(x, grp, quant = 0.8, signific = 3, unif = TRUE,
  absOnly = FALSE, seed = NULL, silent = FALSE, callFrom = NULL)
```

Arguments

x	(numeric matrix or data.frame) main input
grp	(factor) to organize replicate columns of (x)
quant	(numeric) quantile form 'neighbour' values to use as upper limit for random values
signific	number of signif digits for random values
unif	(logical) toggle between uniform and Gaussian random values
absOnly	(logical) if TRUE, make negative NA-replacment values positive as absolute values
seed	(integer) for use with set.seed for reproducible output
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

numeric matrix (same dim as 'x') with NA replaced

See Also

[naOmit](#), [na.fail](#)

Examples

```
dat <- matrix(round(rnorm(30),2),ncol=6); grD <- gl(2,3)
dat[sort(sample(1:30,9,repl=FALSE))] <- NA
dat; replNAbyLow(dat,gr=grD)
```

replPlateCV	<i>CV of replicate plates (list of matrixes)</i>
-------------	--

Description

replPlateCV gets CVs of replicates from list of 2 or 3-dim arrays (where 2nd dim is replicates, 3rd dim may be channel). Note : all list-elements of must **MUST** have SAME dimensions ! When treating data from microtiter plates (eg 8x12) data are typically spread over multiple plates, ie initial matrixes that are the organized into arrays. Returns matrix or array (1st dim is intraplate-position, 2nd .. plate-group/type, 3rd .. channels)

Usage

```
replPlateCV(lst, callFrom = NULL)
```

Arguments

lst	list of matrixes : suppose lines are independent elements, columns are replicates of the 1st column. All matrixes must have same dimensions
callFrom	(character) allows easier tracking of messages produced

Value

matrix or array (1st dim is intraplate-position, 2nd .. plate-group/type, 3rd .. channels)

See Also

[rowCVs](#), @seealso [arrayCV](#)

Examples

```
set.seed(2016); ra1 <- matrix(rnorm(3*96),nrow=8)
pla1 <- list(ra1[,1:12],ra1[,13:24],ra1[,25:36])
replPlateCV(pla1)
arrL1 <- list(a=array(as.numeric(ra1)[1:192],dim=c(8,12,2)),
             b=array(as.numeric(ra1)[97:288],dim=c(8,12,2)))
replPlateCV(arrL1)
```

rmDupl2colMatr	<i>Remove lines of matrix redundant /duplicated for 1st and 2nd column</i>
----------------	--

Description

rmDupl2colMatr removes lines of matrix that are redundant /duplicated for 1st and 2nd column (irrespective of content of their columns). The first occurrence of redundant /duplicated elements is kept.

Usage

```
rmDupl2colMatr(mat, useCol = c(1, 2))
```

Arguments

mat	(matrix or data.frame) main input
useCol	(integer, length=2) columns to consider/use when looking for duplicated entries

Value

matrix with duplicated lines removed

See Also

[unlist](#)

Examples

```
mat <- matrix(1:12, ncol=3)
mat[3,1:2] <- mat[1,1:2]
rmDupl2colMatr(mat)
```

rowCVs	<i>rowCVs</i>
--------	---------------

Description

rowCVs returns CV for values in each row (using speed optimized standard deviation). Note : NaN values get replaced by NA.

Usage

```
rowCVs(dat, autoconvert = NULL)
```

Arguments

dat (numeric) matrix
 autoconvert (NULL or character) allows converting simple vectors in matrix of 1 row (autoconvert="row")

Value

(numeric) vector with CVs for each row of 'dat'

See Also

[colSums](#), [rowGrpCV](#), [rowSds](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
head(rowCVs(dat1))
```

rowGrpCV

row group CV

Description

rowGrpCV calculates CVs for matrix with multiple groups of data, ie one CV for each group of data. Groups are specified as columns of 'x' in 'grp' (so length of grp should match number of columns of 'x', NAs are allowed)

Usage

```
rowGrpCV(x, grp, means = NULL, listOutp = FALSE)
```

Arguments

x numeric matrix where replicates are organized into separate columns
 grp (factor) defining which columns should be grouped (considered as replicates)
 means (numeric) alternative values instead of means by .rowGrpMeans()
 listOutp (logical) if TRUE, provide output as list with \$CV, \$mean and \$n

Value

matrix of CV values

See Also

[rowCVs](#), [arrayCV](#), [replPlateCV](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
head(rowGrpCV(dat1,gr=g1(4,3,labels=LETTERS[1:4])[2:11]))
```

rowGrpMeans	<i>rowMeans with distinction of groups (of columns, eg groups of replicates)</i>
-------------	--

Description

rowGrpMeans calculates column-means for matrix with multiple groups of data, ie similar to rowMeans but one mean for each group of data. Groups are specified as columns of 'x' in 'grp' (so length of grp should match number of columns of 'x', NAs are allowed).

Usage

```
rowGrpMeans(x, grp)
```

Arguments

x	matrix or data.frame
grp	(factor) defining which columns should be grouped (considered as replicates)

Value

matrix with mean values

See Also

[rowSds](#), [colSums](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
head(rowGrpMeans(dat1,gr=g1(4,3,labels=LETTERS[1:4])[2:11]))
```

rowGrpSds	<i>Per line and per group sd-values</i>
-----------	---

Description

rowGrpSds calculate Sd (standard-deviation) for matrix with multiple groups of data, ie one sd for each group of data. Groups are specified as columns of 'x' in 'grp' (so length of grp should match number of columns of 'x', NAs are allowed).

Usage

```
rowGrpSds(x, grp)
```

Arguments

x	matrix where replicates are organized into seprate columns
grp	(factor) defining which columns should be grouped (considered as replicates)

Value

matrix of sd values

See Also

[rowGrpMeans](#), [rowCVs](#), [rowSEMs,sd](#),

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
head(rowGrpSds(dat1,grp=gl(4,3,labels=LETTERS[1:4])[2:11]))
```

rowMedSds	<i>sd of median for each row by bootstrap</i>
-----------	---

Description

rowMedSds determines the stand error (sd) of the median for each row by bootstraping each row of 'dat'. Note: requires package **boot**

Usage

```
rowMedSds(dat, nBoot = 99)
```

Arguments

dat	(numeric) matix, main input
nBoot	(integer) number if iterations for bootstrap

Value

(numeric) vector with estimated standard errors

See Also

[boot](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
rowMedSds(dat1) ; plot(rowSds(dat1),rowMedSds(dat1))
```

rowSds	<i>sd for each row (fast execution)</i>
--------	---

Description

rowSds is speed optimized sd (takes matrix or data.frame and treats each line as set of data for sd equiv to apply(dat,1,sd). NAs are ignored from data unless entire line NA). Speed improvements may be seen at more than 100 lines. Note: NaN instances will be transformed to NA

Usage

```
rowSds(dat)
```

Arguments

dat matrix (or data.frame) with numeric values (may contain NAs)

Value

numeric vector of sd values

See Also

[sd](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
rowSds(dat1)
```

rowSEMs	<i>SEM for each row</i>
---------	-------------------------

Description

rowSEMs speed optimized SEM (standard error of the mean) for each row. The function takes a matrix or data.frame and treats each row as set of data for SEM; NAs are ignored from data. Note: NaN instances will be transformed to NA

Usage

```
rowSEMs(dat)
```

Arguments

dat matrix or data.frame

Value

numeric vector with SEM values

See Also

[rowSds](#), [colSds](#), [colSums](#)

Examples

```
set.seed(2016); dat1 <- matrix(c(runif(200)+rep(1:10,20)),ncol=10)
head(rowSEMs(dat1))
```

searchDataPairs	<i>Search duplicated data over multiple columns, ie pairs of data</i>
-----------------	---

Description

searchDataPairs searches matrix for columns of similar data, ie 'duplicate' values in separate columns or very similar columns if 'realDupsOnly'=FALSE. Initial distance measures will be normalized either to diagonale (normRange=TRUE) of 'window' or to the real max distance observed (equal or less than diagonale). Return data.frame with names for sample-pair, percent of identical values (100 for complete identical pair) and relative (Euclidean) distance (ie max dist observed =1.0). Note, that low distance values do not necessarily imply correlating data.

Usage

```
searchDataPairs(dat, disThr = 0.01, byColumn = TRUE,
  normRange = TRUE, altNa = NULL, realDupsOnly = TRUE,
  silent = FALSE, callFrom = NULL)
```

Arguments

<code>dat</code>	matrix or data.frame
<code>disThr</code>	(numeric) threshold to decide when to report similar data (applied on normalized distances, low val fewer reported), applied on normalized distances (norm to diagonale of all data for best relative 'unbiased' view)
<code>byColumn</code>	(logical) rotates main input by 90 degrees (using <code>t</code>), thus allows to read by rows instead of by columns
<code>normRange</code>	(logical) normalize each columns separately if TRUE
<code>altNa</code>	(character, default NULL) vector with alternative names (for display)
<code>realDupsOnly</code>	(logical) if TRUE will consider equal values only, otherwise will also consider very close values (based on argument <code>disThr</code>)
<code>silent</code>	(logical) suppres messages
<code>callFrom</code>	(character) allows easier tracking of message(s) produced

Value

data.frame with names for sample-pair, percent of identical values (100 for complete identical pair) and rel (Euclidean) distance (ie max dist observed =1.0)

See Also

[duplicated](#), [dist](#)

Examples

```
mat <- round(matrix(c(11:40,runif(20)+12,11:19,17,runif(20)+18,11:20),nrow=10),1); colnames(mat)=1:9
searchDataPairs(mat,disThr=0.05)
```

searchLinesAtGivenSlope

Search points forming lines at given slope

Description

`searchLinesAtGivenSlope` searches among set of points (2-dim) those forming line(s) with user-defined slope ('coeff'), ie search optimal (slope-) offset parameter(s) for (regression) line(s) with given slope ('coef'). Note: larger data-sets : segment residuals to 'coeff' & select most homogenous

Usage

```
searchLinesAtGivenSlope(dat, coeff = 1.5, filtExtr = c(0, 1),
  minMaxDistThr = NULL, lmCompare = TRUE, indexPoints = TRUE,
  displHist = FALSE, displScat = FALSE, bestCluByDistRat = TRUE,
  neighbDiLim = NULL, silent = FALSE, debugM = FALSE,
  callFrom = NULL)
```

Arguments

dat	matrix or data.frame
coeff	(numeric) slope to consider
filtExtr	(integer) lower & upper quantile values, remove points with extreme deviation to offset=0, (if single value: everything up to or after will be used)
minMaxDistThr	(logical) optional minimum and maximum distance threshold
lmCompare	(logical) add'l fitting of linear regression to best results, return offset AND slope based on lm fit
indexPoints	(logical) return results as list with element 'index' specifying retained points
displHist	(logical) display histogram of residues
displScat	(logical) display (simple) scatter plot
bestCluByDistRat	(logical) initial selection of decent clusters based on ratio overallDist/averNeighbDist (or by CV & cor)
neighbDiLim	(numeric) additional threshold for (trimmed mean) neighbour-distance
silent	(logical) suppress messages
debugM	(logical) for bug-tracking: more/enhanced messages
callFrom	(character) allow easier tracking of message(s) produced

Value

matrix of line-characteristics (or if indexPoints is TRUE then list (line-characteristics & index & lm-results))

Examples

```
set.seed(2016); ra1 <- runif(300)
dat1 <- cbind(x=round(c(1:100+ra1[1:100]/5, 4*ra1[1:50]), 1),
             y=round(c(1:100+ra1[101:200]/5, 4*ra1[101:150]), 1))
(li1 <- searchLinesAtGivenSlope(dat1, coeff=1))
```

simpleFragFig	<i>Simple figure showing line from start- to end-sites of edges (or fragments) defined by their start- and end-sites simpleFragFig draws figure showing start- and end-sites of edges (or fragments)</i>
---------------	--

Description

Simple figure showing line from start- to end-sites of edges (or fragments) defined by their start- and end-sites

simpleFragFig draws figure showing start- and end-sites of edges (or fragments)

Usage

```
simpleFragFig(frag, fullSize = NULL, sortByHead = TRUE,
             useTit = NULL, useCol = NULL, displNa = TRUE, useCex = 0.7)
```

Arguments

frag	(matrix) 2 columns defining begin- and end-sites (as interger values)
fullSize	(integer) optional max size used for figure (x-axis)
sortByHead	(logical) sort by begin-sites (if TRUE) or sort by end-sites
useTit	(character) custom title
useCol	(character) specify colors, if numeric vector will be onsidered as score values
displNa	(character) display names of edges (figure may get crowded)
useCex	(numeric) expansion factor

Value

matrix with mean values

See Also

[buildTree](#), [countSameStartEnd](#), [contribToContigPerFrag](#),

Examples

```
frag2 <- cbind(beg=c(2,3,7,13,13,15,7,9,7, 3,7,5,7,3),end=c(6,12,8,18,20,20,19,12,12, 4,12,7,12,4))
rownames(frag2) <- c("A","E","B","C","D","F","H","G","I", "J","K","L","M","N")
simpleFragFig(frag2,fullSize=21,sortByHead=TRUE)
buildTree(frag2)
```

singleLineAnova	<i>2-factorial Anova on single line of data</i>
-----------------	---

Description

singleLineAnova runs 2-factorial Anova on a single line of data (using [aov](#) from package stats) using a model with two factors (without factor-interaction) and extracts the correponding p-value.

Usage

```
singleLineAnova(dat, fac1, fac2, inclInteraction = TRUE)
```

Arguments

dat	numeric vector
fac1	(character or factor) vector describing grouping elements of dat for first factor, must be of same length as fac2
fac2	(character or factor) vector describing grouping elements of dat for second factor, must be of same length as fac1
inclInteraction	(logical) decide if factor-interactions (eg synergy) should be included to model

Value

(uncorrected) p for factor 'Pr(>F)' (see [aov](#))

See Also

[aov](#), [anova](#); for repeated tests including [eBayes](#) see [test2factLimma](#)

Examples

```
set.seed(2012); dat <- round(runif(8),1)
singleLineAnova(dat,gl(2,4),rep(1:2,4))
```

sortBy2CategorAnd1IntCol

Sort matrix by two categorical and one integer columns

Description

sortBy2CategorAnd1IntCol sorts matrix 'mat' subsequently by categorical and numerical columns of 'mat', ie lines with identical values for categor are sorted by numeric value.

Usage

```
sortBy2CategorAnd1IntCol(mat, categCol, numCol, findNeighb = TRUE,
  decreasing = FALSE, silent = FALSE, callFrom = NULL)
```

Arguments

mat	matrix (or data.frame) from which by 2 columns will be selected for sorting
categCol	(integer or character) which columns of 'mat' to be used as categorical columns
numCol	(integer or character) which column of 'mat' to be used as integer columns
findNeighb	(logical) if 'findNeighb' neighbour cols according to 'numCol' will be identified as groups & marked in new col 'neiGr', orphans marked as NA
decreasing	(logical) order of sort
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

sorted matrix (same dimensions as 'mat')

Examples

```
mat <- cbind(aa=letters[c(3,rep(7:8,3:4),4,4:6,7)],bb=LETTERS[rep(1:5,c(1,3,4,4,1))],
  nu=c(23:21,23,21,22,18:12))
mat[c(3:5,1:2,6:9,13:10),]
sortBy2CategorAnd1IntCol(mat,cate=c("bb","aa"),num="nu",findN=FALSE,decr=TRUE)
sortBy2CategorAnd1IntCol(mat,cate=c("bb","aa"),num="nu",findN=TRUE,decr=FALSE)
```

stableMode	<i>Estimate mode (most frequent value)</i>
------------	--

Description

Estimate mode (most frequent value); rounding to range of numbers used as number of significant values ('rangeSign') to better estimate continuous data. This function uses the package **BBmisc**.

Usage

```
stableMode(x, histLike = FALSE, rangeSign = 1:6, nCl = 50,
  callFrom = NULL, silent = FALSE)
```

Arguments

x	numeric vector
histLike	(logical) if TRUE, will search context dependent, ie like most frequent class of histogram. Using this mode the search will be refined if either 80 percent of values in single class or >50 percent in single
rangeSign	(integer) range of numbers used as number of significant values
nCl	(integer) defines the number of classes used (if 'histLike'=TRUE), very 'critical' parameter, may change results in strong way !! Note: higher values for 'nCl' will finally loose advantage of histLike-type search of mode !
callFrom	(character) allow easier tracking of message(s) produced
silent	(logical) suppress messages

Value

mode value (numeric)

See Also

[cut](#), [hist](#)

Examples

```
set.seed(2012); dat <- round(c(rnorm(50),runif(100)),3)
stableMode(dat)
```

stdErrMedBoot	<i>Standard error of median by boot-strap</i>
---------------	---

Description

stdErrMedBoot estimate standard error of median by boot-strap approach. Note: requires package [boot](#)

Usage

```
stdErrMedBoot(x, nBoot = 99)
```

Arguments

x (numeric) vector to estimate median and it's standard error
nBoot (integer) number for iterations

Value

(numeric) vector with estimated standard error

See Also

[boot](#)

Examples

```
set.seed(2014); ra1 <- c(rnorm(9,2,1),runif(8,1,2))
rat1 <- ratioAllComb(ra1[1:9],ra1[10:17])
median(rat1); stdErrMedBoot(rat1)
```

summarizeCols	<i>Summarize columns (as median,mean,min,last or other methods)</i>
---------------	---

Description

summarizeCols summarizes all columns of matrix (or data.frame). In case of text-columns the sorted middle (~median) will be given, unless 'maxLast', 'minLast', 'maxLast','maxAbsLast' or 'minLast' .. consider only last column of 'matr' : choose from all columns the line where (max of) last col is at min; 'medianComplete' or 'meanComplete' considers only lines/rows where no NA occur (NA have influence other columns !)

Usage

```
summarizeCols(matr, meth = "median", silent = FALSE, callFrom = NULL)
```

Arguments

matr	data.frame matrix of data to be summarized by column (may do different method for text and numeric columns)
meth	(character) summarization method (eg 'maxLast','minLast','maxLast','maxAbsLast','minLast','medianComplete' or 'meanComplete')
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

vector with summary for each column

See Also

rowMeans in [colSums](#)

Examples

```
t1 <- matrix(round(runif(30,1,9)),nc=3); rownames(t1) <- letters[c(1:5,3:4,6:4)]
summarizeCols(t1,me="median")
t(sapply(by(t1,rownames(t1), function(x) x), summarizeCols,me="maxLast"))
t3 <- data.frame(ref=rep(11:15,3),tx=letters[1:15],
  matrix(round(runif(30,-3,2),1),ncol=2),stringsAsFactors=FALSE)
by(t3,t3[,1],function(x) x)
t(sapply(by(t3,t3[,1],function(x) x), summarizeCols,me="maxAbsLast"))
```

tableToPlot	<i>Print matrix-content as plot</i>
-------------	-------------------------------------

Description

tableToPlot prints all columns of matrix in plotting region for easier inclusion to reports (default values are set to work for output as A4-sized pdf). This function was made for integrating listings of text to graphical output to devices like png, jpeg or pdf. This function was initially designed for listings with small/medium 1st col (eg couner or index), 2nd & 3rd col small and long 3rd col (like file paths). Obviously, the final number of lines one can pack and still read correctly into the graphical output depends on the size of the device (on a pdf of size A4 one can pack up to apr. 110 lines). Of course, [Sweave](#), combined with LaTeX, provides a powerful alternative for wrapping text to pdf-output (and further combining text and graphics). Note: The final result on pdf devices may vary depending on screen-size (ie with of current device), the parameters 'colPos' and 'titOffS' may need some refinements. Note: In view of typical page/figure layouts like A4, the plotting region will be split to avoid too wide spacing between rows with less than 30 rows.

Usage

```
tableToPlot(matr, colPos = c(0.05, 0.35, 0.41, 0.56), useCex = 0.7,
  useAdj = c(0, 1, 1, 0), titOffS = 0, useCol = 1, silent = FALSE,
  callFrom = NULL)
```

Arguments

matr	(matrix) main (character) matrix to display
colPos	(numeric) postion of columns on x-scale (from 0 to 1)
useCex	(numeric) cex expansion factor forsize of text (may be different for each column)
useAdj	(numeric) left/center/right alignment for text (may be different for each column)
titOffS	(numeric) offset for title line (relative to 'colPos')
useCol	color specification for text (may be different for each column)
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

NULL (no R-object returned), print 'plot' in current device only

See Also

[Sweave](#) for more flexible framework

Examples

```
## as example let's make a listing of file-names and associated parameters in current directory
mat <- dir()
mat <- cbind(no=1:length(mat), fileName=mat, mode=file.mode(mat),
            si=round(file.size(mat)/1024), path=getwd())
## Now, we wrap all text into a figure (which could be saved as jpg etc)
tableToPlot(mat[, -1], colPos=c(0.01, 0.4, 0.46, 0.6), titOffS=c(0.05, -0.03, -0.01, 0.06))
tableToPlot(mat, colPos=c(0, 0.16, 0.36, 0.42, 0.75), useAdj=0.5, titOffS=c(-0.01, 0, -0.01, 0, -0.1))
```

test2factLimma	<i>2-factorial limma-style t-test</i>
----------------	---------------------------------------

Description

test2factLimma runs 2 fact test on data 'datMatr' which should already be organized as matrix (rows = genes) using [eBayes](#) Note: this function uses the Bioconductor package [limma](#)

Usage

```
test2factLimma(datMatr, fac1, fac2, testSynerg = TRUE,
               testOrientation = "=", addResults = c("lfd", "FDR", "Mval",
               "means"), addGenes = NULL, silent = FALSE, callFrom = NULL)
```

Arguments

datMatr	matrix or data.frame with lines as independent series of measures (eg different genes)
fac1	(character or factor) vector describing grouping elements of each line of 'datMatr' for first factor, must be of same length as fac2
fac2	(character or factor) vector describing grouping elements of each line of 'datMatr' for second factor, must be of same length as fac1
testSynerg	(logical) decide if factor-interactions (eg synergy) should be included to model
testOrientation	(character) default (or any non-recognized input) '=', otherwise either '>', 'greater', 'sup', 'upper' or '<', 'inf', 'lower'
addResults	(character) vector defining which types of information should be included to output, may be 'lfd', 'FDR' (for BY correction), 'Mval' (M values), 'means' (matrix with mean values for each group of replicates)
addGenes	(matrix or data.frame) additional information to add to output
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

object of class "MArrayLM" (from limma)

See Also

single line testing [eBayes](#), for single line testing without eBayes see [test2factLimma](#)

Examples

```
## example for testing change of ratio for 4 sets (AA-DD) of pairs of data
set.seed(2017); t8 <- matrix(round(rnorm(160,10,0.4),2),ncol=8,
  dimnames=list(letters[1:20],c("AA1","BB1","CC1","DD1","AA2","BB2","CC2","DD2")))
t8[3:6,1:2] <- t8[3:6,1:2]+3 # augment lines 3:6 (c-f) for AA1&BB1
t8[5:8,5:6] <- t8[5:8,5:6]+3 # augment lines 5:8 (e-h) for AA2&BB2 (c,d,g,h should be found)
## via MAobj
maOb8 <- makeMAList(t8,MAf=gl(2,4,labels=c("R","G")))
fit8b <- test2factLimma(maOb8,c(1,1,1,1),c(0,0,1,1),testS=FALSE) # same result as fit8e
limma::topTable(fit8b,coef=1,n=5) # effect for c,d,g&h
## explicit (long) way via limma:
fit8 <- limma::lmFit(maOb8, design= model.matrix(~ 0+factor(c(1,1,2,2))))
fit8e <- limma::eBayes(fit8)
limma::topTable(fit8e,coef=1,n=5) # effect for c,d,g&h
```

treatTxtDuplicates *Locate duplicates in text and make non-redundant*

Description

treatTxtDuplicates locates dupliques in character-vector 'x' and return list (length=3) : with \$init (initial), \$nRed .. non-redundant text by adding number at end or beginning, and \$nrLst .. list-version with indexes per unique entry. Note : NAs (if multiple) will be renamed to NA_1, NA_2

Usage

```
treatTxtDuplicates(x, atEnd = TRUE, sep = "_",
  onlyCorrectToUnique = FALSE, silent = FALSE, callFrom = NULL)
```

Arguments

x	(character) vector with character-entries to identify (and remove) duplicates
atEnd	(logical) decide location of placing the counter (at end or at beginning of ID) (see correctToUnique)
sep	(character) separator to add before counter when making non-redundant version
onlyCorrectToUnique	(logical) if TRUE, return only vector of non-redundant
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

list with \$init, \$nRed, \$nrLst

See Also

For simple correction use [correctToUnique](#)

Examples

```
treatTxtDuplicates(c("li0",NA,rep(c("li2","li3"),2)))
correctToUnique(c("li0",NA,rep(c("li2","li3"),2)))
```

 triCoord

Pairwise x,y combinations

Description

triCoord gets pairwise combinations for 'n' elements; returns matrix with x & y coordinates to form all pairwise groups for 1:n elements

Usage

```
triCoord(n, side = "upper")
```

Arguments

n (integer) number of elements for making all pair-wise combinations
 side (character) "upper" or "lower"

Value

2-column matrix with indexes for all pairwise combinations of 1:n

See Also

[lower.tri](#) or [upper.tri](#), simpler version [upperMaCoord](#)

Examples

```
triCoord(4)
```

tTestAllVal	<i>t.test on all individual values against all other values</i>
-------------	---

Description

Run `t.test` on each indiv value of `x` against all its neighbours (=remaining values of same vector) in order to test if tis value is likely to belong to vector `x`. This represents a repeated leave-one-out testing. Mutiple choices for multiple testing correction are available.

Usage

```
tTestAllVal(x, alph = 0.05, alternative = "two.sided", p.adj = NULL)
```

Arguments

<code>x</code>	matrix or data.frame
<code>alph</code>	(numeric) threshold alpha (passed to <code>t.test</code>)
<code>alternative</code>	(character) will be passed to <code>t.test</code> as argument 'alternative', may be "two.sided",..
<code>p.adj</code>	(character) multiple test correction : may be NULL (no correction), "BH", "BY", "holm", "hochberg" or "bonferroni" (but not 'fdr' since this may be confounded with local false discovery rate), see p.adjust

Value

numeric vector with p-values or FDR (depending on argument `p.adj`)

See Also

[t.test](#), [p.adjust](#)

Examples

```
set.seed(2016); x1 <- rnorm(100)
allTests1 <- tTestAllVal(x1)
hist(allTests1,breaks="FD")
```

uniqCountReport	<i>Report number of unique and redundant elements (optional figure)</i>
-----------------	---

Description

Make report about number of unique and redundant elements of vector 'dat'. Note : fairly slow for long vectors !!

Usage

```
uniqCountReport(dat, frL = NULL, plotDispl = FALSE, tit = NULL,
  col = NULL, radius = 0.9, sizeTo = NULL, clockwise = FALSE,
  silent = FALSE, callFrom = NULL)
```

Arguments

dat	(character or numeric vector) main input where number of unique (and redundant) should be determined
frL	(logical) optional (re-)introducing results from duplicated to shorten time of execution
plotDispl	(logical) decide if pie-type plot should be produced
tit	(character) optional title in plot
col	(character) custom colors in pie
radius	(numeric) radius passed to pie
sizeTo	(numeric or character) optional reference group for size-population relative adjusting overall surface of pie
clockwise	(logical) argument passed to pie
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

Value

vector with counts of n (total), nUnique (wo any repeated), nHasRepeated (first of repeated), nRedundant), optional figure

See Also

[correctToUnique](#), [unique](#)

Examples

```
layout(1:2)
uniqCountReport(rep(1:7,1:7),plot=TRUE)
uniqCountReport(rep(1:3,1:3),plot=TRUE,sizeTo=rep(1:7,1:7))
```

upperMaCoord	<i>(upper) pairwise x,y combinations</i>
--------------	--

Description

upperMaCoord gets pairwise combinations for 'n' elements; return matrix with x & y coordinates to form all pairwise groups for n elements. But no distinction of 'upper' or 'lower' possible like in [triCoord](#)

Usage

```
upperMaCoord(n)
```

Arguments

n (integer) number of elements for making all pair-wise combinations

Value

2-column matrix with indexes for all pairwise combinations of 1:n

See Also

[lower.tri](#), more evolved version [triCoord](#)

Examples

```
upperMaCoord(4)
```

withinRefRange	<i>Check for values within range of reference</i>
----------------	---

Description

withinRefRange checks which values of numeric vector 'x' are within range +/- 'fa' x 'ref' (ie within range of reference).

Usage

```
withinRefRange(x, fa, ref = NULL, absRef = TRUE, asInd = FALSE)
```

Arguments

x	matrix or data.frame
fa	(numeric) absolute or relative tolerance value (numeric, length=1), interpreted according to 'absRef' as absolute or relative to 'x' (ie fa*ref)
ref	(numeric) (center) reference value for comparison (numeric, length=1), if not given mean of 'x' (excluding NA or non-finite values) will be used
absRef	(logical) return result as absolute or relative to 'x' (ie fa*ref)
asInd	(logical) if TRUE return index of which values of 'x' are within range, otherwise return values if 'x' within range

Value

numeric vector (containing only the values within range of reference)

Examples

```
## within 2.5 +/- 0.7
withinRefRange(-5:6, fa=0.7, ref=2.5)
## within 2.5 +/- (0.7*2.5)
withinRefRange(-5:6, fa=0.7, ref=2.5, absRef=FALSE)
```

writeCsv

Write (and convert) csv files

Description

This functions allows to write data into csv-files (and/or tabulated txt files) from given vector or read from file 'input' and (re-)write using specified conversions. An optional filter to select columns (column-name specified via 'filterCol') is available. The output may be simultaneously written to multiple formats, as specified in 'expTy', tabulation characters may be converted to avoid accidentally split/shift text to multiple columns. Note: Mixing '.' and ',' as comma separators via text-columns or fused text&data may cause problems lateron, though.

Usage

```
writeCsv(input, inPutFi = NULL, expTy = c("Eur", "US"),
  imporTy = "Eur", filename = NULL, quote = FALSE,
  filterCol = NULL, replMatr = NULL, returnOut = FALSE,
  SYLKprevent = TRUE, digits = 22, silent = FALSE, debug = FALSE,
  callFrom = NULL)
```

Arguments

input	either matrix or data.frame
inPutFi	(character or NULL) file-name to be read (format as US or Euro-type may specified via argument imporTy)
expTy	(character) 'US' and/or 'Eur' for sparator and decimal type in output
imporTy	(character) default 'Eur' (otherwise set to 'US')
filename	(character) optional new file name(s)
quote	(logical) will be passed to write.csv
filterCol	(integer or character) optionally, to export only the columns specified here
replMatr	optional, matrix (1st line:search, 2nd li:use for replacing) indicating which characters need to be replaced)
returnOut	(logical) return output as object
SYLKprevent	(logical) prevent difficulty when opening file via Excel. In some cases Excel presumes (by error) the SYLK format and produces an error when trying to open files : To prevent this, if necessary, the 1st column-name will be changed from 'ID' to 'Id'.
digits	(interger) limit number of signif digits in output (ie file)
silent	(logical) suppress messages
debug	(logical) for bug-tracking: more/enhanced messages
callFrom	(character) allow easier tracking of message(s) produced

Value

writes file to disk and returns NULL unless returnOut=TRUE

See Also

write.csv in [write.table](#), batch reading using this package [readCsvBatch](#)

Examples

```
dat1 <- data.frame(ini=letters[1:5],x1=1:5,x2=11:15,t1=c("10,10","20.20","11,11","21,21","33.33"),
  t2=c("10,11","20.21","k1;k1","az,az","ze.ze"))
fiNa <- file.path(tempdir(),paste("test",1:2,".csv",sep=""))
writeCsv(dat1,filename=fiNa[1])
dir(path=tempdir(),pattern="cs")
(writeCsv(dat1,replM=rbind(bad=c(";",",",""),replBy="__"),expTy=c("Eur"),
  returnOut=TRUE,filename=fiNa[2]))
```

`XYToDiffPpm`*Express difference as ppm*

Description

XYToDiffPpm transforms offset (pariwise-difference) between 'x' & 'y' to ppm (as normalized difference ppm, parts per million, ie $(x-y)/y$). This type of expressing differences is used eg in mass-spectrometry.

Usage

```
XYToDiffPpm(x, y, nSign = NULL, silent = FALSE, callFrom = NULL)
```

Arguments

<code>x</code>	(numeric) typically for measured variable
<code>y</code>	(numeric) typically for theoretical/expected value (vector must be of same length as 'x')
<code>nSign</code>	(integer) number of significant digits in output
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

Value

numeric vector of (ratio-) ppm values

See Also

[ratioToPpm](#) for classical ppm

Examples

```
set.seed(2017); aa <- runif(10,50,900)
cbind(x=aa,y=aa+1e-3,ppm=XYToDiffPpm(aa,aa+1e-3,nSign=4))
```

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