

# Package ‘regioneReloaded’

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**Type** Package

**Title** RegioneReloaded: Multiple Association for Genomic Region Sets

**Version** 1.7.0

**URL** <https://github.com/RMalinverni/regioneReload>

**Description** RegioneReloaded is a package that allows simultaneous analysis of associations between genomic region sets, enabling clustering of data and the creation of ready-to-publish graphs. It takes over and expands on all the features of its predecessor regioneR. It also incorporates a strategy to improve p-value calculations and normalize z-scores coming from multiple analysis to allow for their direct comparison. RegioneReloaded builds upon regioneR by adding new plotting functions for obtaining publication-ready graphs.

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## Contents

AlienGenome . . . . .	3
AlienRSList_broad . . . . .	3
AlienRSList_narrow . . . . .	4
chooseHclustMet . . . . .	4
cleanCrosswiseMatrix . . . . .	5
createUniverse . . . . .	6
crosswiseMatrix . . . . .	7
crosswisePermTest . . . . .	7
cw_Alien . . . . .	9
cw_Alien_RaR . . . . .	9
cw_Alien_ReG . . . . .	10
cw_Alien_ReG_no_Square . . . . .	10
cw_Alien_ReR . . . . .	11
DFfromLZ . . . . .	11
genoMatrixeR-class . . . . .	12
getHClust . . . . .	12
getMatrix . . . . .	13
getMultiEvaluation . . . . .	14
getParameters . . . . .	15
gmxrMatrix . . . . .	15
gmxrMatrix<- . . . . .	16
gmxrMultiOverlaps . . . . .	16
gmxrParam . . . . .	17
makeCrosswiseMatrix . . . . .	17
makeLZMatrix . . . . .	19
mlzsMatrix . . . . .	20
mlzsMatrix<- . . . . .	20
mlzsMultiLocalZscores . . . . .	21
mlzsParam . . . . .	21
mlzsParam<- . . . . .	22
mLZ_regA_ReG . . . . .	22
mLZ_regA_ReG_br . . . . .	23
mLZ_regD_ReG . . . . .	23
multiLocalZscore . . . . .	24
multiLocalZScore-class . . . . .	25
multiPermTest . . . . .	26
plotCrosswiseDimRed . . . . .	27
plotCrosswiseMatrix . . . . .	29
plotLocalZScoreMatrix . . . . .	30

plotSingleLZ . . . . .	31
plotSinglePT . . . . .	32
print.genoMatriXeR-method . . . . .	33
randomizeRegionsPerc . . . . .	34
similarRegionSet . . . . .	35
subList . . . . .	36

<b>Index</b>	<b>37</b>
--------------	-----------

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AlienGenome	<i>AlienGenome</i>
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---

### Description

The Alien Genome is an artificial genomic coordinates system for the purposes of testing and demonstrating the functions of `regioneReload` with a low computing time.

### Usage

```
data(cw_Alien)
```

### Format

An objects of class [GRanges](#).

### Details

The Alien Genome consists of four chromosomes and is generated by the following code:

```
AlienGenome <-
toGRanges(data.frame(
  chr = c("A1Chr1", "A1Chr2", "A1Chr3", "A1Chr4"),
  start = c(rep(1, 4)),
  end = c(2e6, 1e6, 5e5, 1e5)
))
```

---

AlienRSList_broad	<i>AlienRSList_broad</i>
-------------------	--------------------------

---

### Description

List of region sets (as [GRanges](#)) on the [AlienGenome](#).

### Usage

```
data(cw_Alien)
```

**Format**

A list of [GRanges](#) objects.

**Details**

This region sets are generated for the purpose of demonstrating the functions of `RegionReloaded` with a low computing time and "predictable" associations. The regions are generated with by combining `createRandomRegions()` and `similarRegionSet()` so that there is a known overlap between certain region sets. To see a full description of this sample data and the code used to generate it, see the `RegionReloaded` vignette.

---

AlienRSList_narrow	<i>AlienRSList_narrow</i>
--------------------	---------------------------

---

**Description**

List of region sets (as [GRanges](#)) on the [AlienGenome](#).

**Usage**

```
data(cw_Alien)
```

**Format**

A list of [GRanges](#) objects.

**Details**

This region sets are generated for the purpose of demonstrating the functions of `RegionReloaded` with a low computing time and "predictable" associations. The regions are generated with by combining `createRandomRegions()` and `similarRegionSet()` so that there is a known overlap between certain region sets. To see a full description of this sample data and the code used to generate it, see the `RegionReloaded` vignette.

---

chooseHclustMet	<i>chooseHclustMet</i>
-----------------	------------------------

---

**Description**

Evaluate and choose the best method for clustering a matrix using the `hclust()` function.

**Usage**

```
chooseHclustMet(GM, scale = FALSE, vecMet = NULL, distHC = "euclidean")
```

**Arguments**

GM	matrix, numerical matrix.
scale	logical, if TRUE, the clustering will be performed using the scaled matrix. (default = FALSE)
vecMet	character, vector of methods that will be tested in the function. If NULL, the following methods will be tested: "complete", "average", "single", "ward.D2", "median", "centroid" and "mcquitty. (default = NULL)
distHC	character, the distance measure to be used from those available in <code>dist()</code> . (default = "euclidean")

**Value**

An object of class `hclust`

**See Also**

`hclust()`

**Examples**

```
M1 <- matrix(1:18, nrow = 6, ncol = 3)
set.seed(42)
M2 <- matrix(sample(100, 18), nrow = 6, ncol = 3)
GM <- cbind(M1, M2)

chooseHclustMet(GM)
```

---

cleanCrosswiseMatrix *cleanCrosswiseMatrix*

---

**Description**

Clean and scale a matrix from a `genoMatriXeR` object

**Usage**

```
cleanCrosswiseMatrix(GM, GM_pv, pvcut, scale, subEX)
```

**Arguments**

GM	matrix, numerical matrix of z-scores.
GM_pv	matrix, numerical matrix of pvalues.
pvcut	numeric, the z-score value is substituted by subEX (0 by default) for all the associations with an adj.pvalue (as calculated in <code>crosswisePermTest()</code> ) higher than pvcut. (default = 0.05)

scale	logical, if TRUE the matrix will be scaled. (default = FALSE)
subEX	numeric, value used to substitute the z-score values when the associated pvalue is higher than pvcut. (default = 0)

**Value**

a matrix filtered for a matrix of pvalue

**See Also**

[makeCrosswiseMatrix\(\)](#)

---

createUniverse	<i>createUniverse</i>
----------------	-----------------------

---

**Description**

Create the universe parameter for [regioneR::resampleRegions\(\)](#) using all unique regions present in Alist.

**Usage**

```
createUniverse(Alist, joinR = TRUE)
```

**Arguments**

Alist	list of regions set in a format accepted for <a href="#">regioneR</a>
joinR	logical, if TRUE all the regions will be joined using the function <a href="#">regioneR::joinRegions()</a> .(default == TRUE)

**Value**

A list of [GRanges](#) objects

**Examples**

```
data("cw_Alien")

universe <- createUniverse(AlienRSList_narrow)
```

---

crosswiseMatrix	<i>crosswiseMatrix</i>
-----------------	------------------------

---

**Description**

Create a matrix from a `genoMatrixeR` object.

**Usage**

```
crosswiseMatrix(mPT, zs.type='norm_zscore',...)
```

**Arguments**

mPT	an object of class <code>genoMatrixeR</code> .
zs.type	character, z-score type to use to generate the matrix, either raw z-score ("zscore") or normalized z-score ("norm_zscore"). (default = "norm_zscore")
...	further arguments to be passed to other methods.

**Value**

a numeric matrix

---

crosswisePermTest	<i>crosswisePermTest</i>
-------------------	--------------------------

---

**Description**

Perform multiple permutation tests between each element in two lists of region sets.

**Usage**

```
crosswisePermTest(Alist, Blist = NULL, sampling = FALSE, fraction = 0.15,
  min_sampling = 5000, ranFUN = "randomizeRegions", evFUN = "numOverlaps",
  ntimes = 100, universe = NULL, adj_pv_method = "BH",
  genome = "hg19", ...)
```

**Arguments**

Alist, Blist	<code>GRangesList</code> or list of region sets in any accepted formats by <code>regioneR</code> package ( <code>GRanges</code> , <code>data.frame</code> etc.).
sampling	logical, if TRUE the function will use only a sample of each element of Alist to perform the test as specified in fraction. (default = FALSE)
fraction	logical, if sampling=TRUE, defines the fraction of the region sets used to perform the test. (default = 0.15)

<code>min_sampling</code>	numeric, minimum number of regions accepted after sampling is performed with the specified fraction. If the number of sampled regions is less than <code>min_sampling</code> , the number specified by <code>min_sampling</code> will be used as number of regions sampled instead. (default = 5000)
<code>ranFUN</code>	character, the randomization strategy used for the test, see <code>regioneR</code> . (default = "randomizeRegions")
<code>evFUN</code>	character, the evaluation strategy used for the test, see <code>regioneR</code> . (default = "numOverlaps")
<code>ntimes</code>	numeric, number of permutations used in the test. (default = 100)
<code>universe</code>	region set to use as universe, used only when <code>regioneR::resampleRegions()</code> function is selected. (default = NULL)
<code>adj_pv_method</code>	character, the method used for the calculation of the adjusted p-value, to choose between the options of <code>p.adjust()</code> . (default = "BH")
<code>genome</code>	character or <code>GRanges</code> , genome used to compute the randomization. (default = "hg19")
<code>...</code>	further arguments to be passed to other methods.

## Details

This function performs multiple permutation tests for all pairwise combinations of the elements in two lists of region sets. Essentially, it uses the `regioneR::permTest()` function and its associated randomization and evaluation functions. It creates and returns a `genoMatriXeR` object with the result of the permutation tests stored in the `multiOverlaps` slot. In addition, all the parameters used for the test are stored in the `parameters` slot.

## Value

A object of class `genoMatriXeR` containing three slots

- `@parameters`
- `@multioverlaps`
- `@matrix`

## See Also

`genoMatriXeR`, `regioneR`, `regioneR::permTest()`, `regioneR::overlapPermTest()`

## Examples

```
fakeGenome <- regioneR::toGRanges("chrF", 1, 1000)
regA <- regioneR::createRandomRegions(nregions = 10, length.mean = 10,
length.sd = 2, genome = fakeGenome)
regB <- regioneR::createRandomRegions(nregions = 10, length.mean = 10,
length.sd = 2, genome = fakeGenome)
regAs <- similarRegionSet(GR = regA, genome = fakeGenome, name = "A",
vectorPerc = seq(0.1, 0.3, by = 0.1))
regBs <- similarRegionSet(GR = regB, genome = fakeGenome, name = "B",
```



```
vectorPerc = seq(0.1, 0.3, by = 0.1))
ABLlist <- c(regAs, regBs)
cw_ptAB <- crosswisePermTest(ABLlist, genome = fakeGenome, ntimes = 10)
print(cw_ptAB)
```

---

cw\_Alien

*cw\_Alien*


---

### Description

Alien Genome crosswise matrix using [regioneR::randomizeRegions](#), [regioneR::circularRandomizeRegions](#), [regioneR::resampleRegions](#), [regioneR::resampleGenome](#) functions as permutation strategies.

### Usage

```
data(cw_Alien)
```

### Format

An objects of class [genoMatriXeR](#); see [makeCrosswiseMatrix\(\)](#).

---

cw\_Alien\_RaR

*cw\_Alien\_RaR*


---

### Description

Alien Genome crosswise matrix using [regioneR::randomizeRegions\(\)](#) function a permutation strategy. Alist = AlienRSList\_narrow, Blist = AlienRSList\_narrow

### Usage

```
data(cw_Alien)
```

### Format

An objects of class [genoMatriXeR](#); see [makeCrosswiseMatrix\(\)](#).

---

<code>cw_Alien_ReG</code>	<code><i>cw_Alien_ReG</i></code>
---------------------------	----------------------------------

---

**Description**

Alien Genome crosswise matrix using `regioneR::resampleGenome()` function as permutations strategy. Alist = AlienRSList\_narrow, Blist = AlienRSList\_narrow

**Usage**

```
data(cw_Alien)
```

**Format**

An objects of class `genoMatriXeR`; see `makeCrosswiseMatrix()`.

---

<code>cw_Alien_ReG_no_Square</code>	<code><i>cw_Alien_ReG_no_Square</i></code>
-------------------------------------	--

---

**Description**

Alien Genome crosswise matrix using `regioneR::resampleGenome()` function as permutations strategy. Alist = AlienRSList\_narrow, Blist = AlienRSList\_broad

**Usage**

```
data(cw_Alien)
```

**Format**

An objects of class `genoMatriXeR`; see `makeCrosswiseMatrix()`.

---

cw_Alien_ReR	<i>cw_Alien_ReR</i>
--------------	---------------------

---

**Description**

Alien Genome crosswise matrix using `regioneR::resampleRegions()` function a permutation strategy. Alist = AlienRSList\_narrow, Blist = AlienRSList\_narrow

**Usage**

```
data(cw_Alien)
```

**Format**

An objects of class `genoMatriXeR`; see `makeCrosswiseMatrix()`.

---

DFfromLZ	<i>Dataframe from MultiLocalZScore object</i>
----------	---

---

**Description**

Dataframe from MultiLocalZScore object

**Usage**

```
DFfromLZ( mLZ, RS )
```

**Arguments**

mLZ	object class <code>MultilocalZScore</code>
RS	string name of single region set present in the mLZ object

**Value**

a data.frame from `multiLocalZScore`

---

genoMatriXeR-class      *genoMatriXeR Class*

---

### Description

An S4 class for "genoMatriXeR" object.

### Slots

parameters List of parameters used to create the object.

multiOverlaps Results of multiple pairwise permutation tests generated with `crosswisePermTest()`.

matrix List of numerical matrices containing z-score, pvalues and correlation values generated with `makeCrosswiseMatrix()`

### Examples

```
data("cw_Alien")

AlienRSList_narrow_small <- AlienRSList_narrow[c("regA","regB","regC")]

cw_test <- crosswisePermTest(Alist = AlienRSList_narrow_small,Blist = AlienRSList_narrow_small,
                             sampling = FALSE, genome = AlienGenome, per.chromosome = TRUE,
                             ranFUN = "resampleGenome", evFUN = "numOverlaps",
                             ntimes = 10, mc.cores = 2)

class(cw_test)
```

---

getHClust                      *getHClust*

---

### Description

get Object of class `hclust` from `genoMatriXeR` or `multiLocalZScore`

### Usage

```
getHClust( rR, hctype = "rows")
```

### Arguments

rR                      A `genoMatriXeR` or `multiLocalZScore` object.  
hctype                  character. Can be "rows" or "cols". (default= "cols")

**Value**

an object of class [hclust](#)

**See Also**

[genoMatriXeR](#), [multiLocalZScore](#), [hclust](#)

**Examples**

```
data("cw_Alien")

cw_Alien_ReG <- makeCrosswiseMatrix(cw_Alien_ReG)
hc <- getHClust(cw_Alien_ReG)

plot(hc)
```

---

getMatrix

*Get Matrix*

---

**Description**

Returns the matrix from an [genoMatriXeR](#) or [multiLocalZScore](#) object.

**Usage**

```
getMatrix(rR)
```

**Arguments**

rR                    [genoMatriXeR](#) or [multiLocalZScore](#) object

**Value**

a numerical matrix from a

**See Also**

[genoMatriXeR](#), [multiLocalZScore](#), [makeCrosswiseMatrix](#), [makeLZMatrix](#)

**Examples**

```
data("cw_Alien")

cw_Alien_ReG <- makeCrosswiseMatrix(cw_Alien_ReG)
mtx <- getMatrix(cw_Alien_ReG)

mtx
```

```
data("cw_Alien")

cw_Alien_RaR <- makeCrosswiseMatrix(cw_Alien_RaR)
GM <- getMatrix(cw_Alien_RaR)

GM
```

---

getMultiEvaluation     *getMultiEvaluation*

---

### Description

Get multiEvaluation slot from [genoMatrixeR](#) or [multiLocalZScore](#) class.

### Usage

```
getMultiEvaluation( rR, namesRS = NULL)
```

### Arguments

rR                    A [genoMatrixeR](#) or [multiLocalZScore](#) object.  
namesRS              a vector of names. (default = NA)

### Value

If rR is a [genoMatrixeR](#) object, a list of data frames resuming the associations results. If rR is a [multiLocalZScore](#) object, a list of two elements: "resumeTable" that is a data frame summarizing the associations and "shifts", a list of shifts computed from [multiLocalZscore\(\)](#) function for the elements indicated in the nameRS vector.

### See Also

[genoMatrixeR](#), [multiLocalZScore](#)

### Examples

```
data("cw_Alien")

mevs <- getMultiEvaluation(cw_Alien_ReG, names = "regA")

mevs
```

---

getParameters	<i>getParameters</i>
---------------	----------------------

---

**Description**

Get parameters from a `genoMatriXeR` or `multiLocalZScore` class object.

**Usage**

```
getParameters(rR, show_err = FALSE)
```

**Arguments**

<code>rR</code>	A <code>genoMatriXeR</code> or <code>multiLocalZScore</code> class object.
<code>show_err</code>	logical, if TRUE the function returns a list with two dataframes: one containing the parameter values and one with any error messages that have been generated during the permutation test iterations when running <a href="#">crosswisePermTest</a> .

**Value**

A dataframe with parameters and values, or a list with two dataframes with parameters and errors information.

**See Also**

[genoMatriXeR](#), [multiLocalZScore](#)

**Examples**

```
data("cw_Alien")  
  
prm <- getParameters(cw_Alien_ReG)  
  
prm
```

---

<code>gmxrMatrix</code>	<i>Export matrix slot from genoMatriXeR objects</i>
-------------------------	---

---

**Description**

Export matrix slot from `genoMatriXeR` objects

**Usage**

```
gmxrMatrix(x)
```

**Arguments**

x                    A genoMatriXeR object.

**Value**

matrix slot of a genoMatriXeR object.

**See Also**

[genoMatriXeR](#)

---

gmxrMatrix<-                    *Set matrix slot value of a genoMatriXeR object*

---

**Description**

Set matrix slot value of a genoMatriXeR object

**Usage**

```
gmxrMatrix(x) <- value
```

**Arguments**

x                    A genoMatriXeR object.  
value                Value to assign to the matrix slot.

**Value**

A genoMatriXeR object.

---

gmxrMultiOverlaps                *Export multiOverlaps slot from genoMatriXeR objects*

---

**Description**

Export multiOverlaps slot from genoMatriXeR objects

**Usage**

```
gmxrMultiOverlaps(x)
```

**Arguments**

x                    A genoMatriXeR object.



**Value**

multiOverlaps slot of a genoMatriXeR.

**See Also**

[genoMatriXeR](#)

---

gmxrParam

*Export parameters from genoMatriXeR objects*

---

**Description**

Export parameters from genoMatriXeR objects

**Usage**

```
gmxrParam(x)
```

**Arguments**

x                    A genoMatriXeR object.

**Value**

Parameters slot of a genoMatriXeR object.

**See Also**

[genoMatriXeR](#)

---

makeCrosswiseMatrix

*makeCrosswiseMatrix*

---

**Description**

Populate the matrix slot in a [genoMatriXeR](#) object.

**Usage**

```
makeCrosswiseMatrix(mPT, clusterize = TRUE, hc.method = NULL, dist.method = "euclidean",
transform = FALSE, scale = FALSE, zs.type = 'norm_zscore', symm_matrix = TRUE,
selectRow = NULL, selectCol = NULL, pvcut = 1, subEX = 0, GM_diag = TRUE, ...)
```

**Arguments**

mPT	an object of class <a href="#">genoMatriXeR</a> .
clusterize	logical, if TRUE the matrix will be clustered using the method specified by <code>hc.method</code> (default = TRUE)
hc.method	character, select the <a href="#">hclust()</a> method to use for clustering the matrix. If NULL, the clustering method will be automatically selected by the function <a href="#">chooseHclustMet()</a> . (default = NULL)
dist.method	character, the distance measure to be used from those available in <a href="#">dist()</a> . (default = "euclidean")
transform	logical, if TRUE the matrix will be transformed using the function <a href="#">t()</a> . (default = FALSE)
scale	logical, if TRUE the matrix will be scaled. (default = FALSE)
zs.type	character, z-score type to use to generate the matrix, either raw z-score ("zscore") or normalized z-score ("norm_zscore"). (default = "norm_zscore")
symm_matrix	logical, if TRUE the matrix will be treated as symmetrical (same clustering for rows and columns). (default = TRUE)
selectRow, selectCol	vector, the matrix will be reduced selecting the rows and/or columns in this vector. (default = NULL)
pvcut	numeric, the z-score value is substituted by subEX (0 by default) for all the associations with an adj.pvalue (as calculated in <a href="#">crosswisePermTest()</a> ) higher than pvcut. (default = 0.05)
subEX	numeric, value used to substitute the z-score values when the associated pvalue is higher than pvcut. (default = 0)
GM_diag	logic, if FALSE the values of the diagonal will be set to 0. (default = TRUE)
...	further arguments to be passed to other methods.

**Details**

This function will create a series of matrices of z-scores, adj.pvalues and pearson correlation values from all the pairwise permutation tests stored in the `multiOverlaps` slot of a [genoMatriXeR](#) as calculated with [multiPermTest\(\)](#). These matrices will then be stored in the `matrix` slot of the [genoMatriXeR](#) object. In addition, clustering will be performed on the association matrices using [hclust](#).

**Value**

An object of class [genoMatriXeR](#) containing three slots, with a populated `matrix` slot.

- @parameters
- @multioverlaps
- @matrix

**See Also**

[crosswisePermTest\(\)](#), [chooseHclustMet\(\)](#), [plotCrosswiseMatrix\(\)](#)

**Examples**

```
data("cw_Alien")

cw_Alien_ReG <- makeCrosswiseMatrix(cw_Alien_ReG)

summary(cw_Alien_ReG)
```

---

makeLZMatrix	<i>Make Local Z-Score Matrix</i>
--------------	----------------------------------

---

**Description**

Create a local z-score matrix from a [multiLocalZScore](#) object and save it in its matrix slot.

**Usage**

```
makeLZMatrix(mLZA, normalize = TRUE, clusterize = TRUE,
             centralize = NA, hc.method = NULL, dist.method = "euclidean",
             scale = FALSE, ...)
```

**Arguments**

mLZA	an object of class <a href="#">multiLocalZScore</a> or a numerical matrix.
normalize	logical, if TRUE the z-score values in the matrix will be normalized. (default = FALSE)
clusterize	logical, if TRUE the matrix will be clustered using the method specified by hc.method (default = TRUE)
centralize	numeric, only z-score values in a number of steps (defined by centralize) around the center of the local association will be used for clustering. If NA, all the values in the matrix will be used for clustering. (default = NA)
hc.method	character, select the <a href="#">hclust()</a> method to use for clustering the matrix. If NULL, the clustering method will be automatically selected by the function <a href="#">chooseHclustMet()</a> . (default = NULL)
dist.method	character, the distance measure to be used from those available in <a href="#">dist()</a> . (default = "euclidean")
scale	logical, if TRUE the matrix will be scaled. (default = FALSE)
...	further arguments to be passed to other methods.

**Value**

A object of class [multiLocalZScore](#) containing three slots, with a populated matrix slot.

- @parameters
- @multiLocalZscores
- @matrix

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

```
data("cw_Alien")
```

---

mlzsMatrix	<i>Export matrix from multiLocalZScore objects</i>
------------	--

---

**Description**

Export matrix from multiLocalZScore objects

**Usage**

```
mlzsMatrix(x)
```

**Arguments**

x                    A multiLocalZScore object.

**Value**

A printed output for multiLocalZScore matrix slot.

**See Also**[multiLocalZScore](#)

---

mlzsMatrix<-	<i>Set matrix slot value of a multiLocalZScore object.</i>
--------------	--

---

**Description**

Set matrix slot value of a multiLocalZScore object.

**Usage**

```
mlzsMatrix(x) <- value
```

**Arguments**

x                    A multiLocalZScore object.  
value                Value to assign to the multiLocalZScore slot.

**Value**

A multiLocalZScore object.

---

mlzsMultiLocalZscores    *Export multiLocalZscores slot from multiLocalZScore objects*

---

**Description**

Export multiLocalZscores slot from multiLocalZScore objects

**Usage**

```
mlzsMultiLocalZscores(x)
```

**Arguments**

x                    A multiLocalZScore object.

**Value**

multiLocalZscores slot of a multiLocalZScore object.

**See Also**

[multiLocalZScore](#)

---

mlzsParam                *Export parameters from multiLocalZScore objects*

---

**Description**

Export parameters from multiLocalZScore objects

**Usage**

```
mlzsParam(x)
```

**Arguments**

x                    A multiLocalZScore object.

**Value**

parameters slot of a multiLocalZScore object.

**See Also**

[multiLocalZScore](#)

---

mLzsParam<-	<i>Set parameters slot value of a multiLocalZScore object</i>
-------------	---

---

**Description**

Set parameters slot value of a multiLocalZScore object

**Usage**

```
mLzsParam(x) <- value
```

**Arguments**

x	A multiLocalZScore object.
value	Value to assign to the parameters slot.

**Value**

A multiLocalZScore object.

---

mLZ_regA_ReG	<i>mLZ_regA_ReG</i>
--------------	---------------------

---

**Description**

Alien Genome multiLocalZScore calculated for regA regionset from AlienRSList\_narrow using [regioneR::resampleGenome\(\)](#) function as permutation strategy.

**Usage**

```
data(cw_Alien)
```

**Format**

An objects of class [multiLocalZScore](#); see [makeLZMatrix\(\)](#).

---

*mLZ\_regA\_ReG\_br*      *mLZ\_regA\_ReG\_br*

---

**Description**

Alien Genome multiLocalZScore calculated for regA regionset from AlienRSList\_broad using [regioneR::resampleGenome\(\)](#) function as permutation s strategy.

**Usage**

`data(cw_Alien)`

**Format**

An object of class [multiLocalZScore](#)

---

*mLZ\_regD\_ReG*      *mLZ\_regD\_ReG*

---

**Description**

Alien Genome multiLocalZScore calculated for regD regionset from AlienRSList\_narrow using [regioneR::resampleGenome\(\)](#) function as permutation s strategy.

**Usage**

`data(cw_Alien)`

**Format**

An object of class [multiLocalZScore](#)

---

multiLocalZscore      *multiLocalZscore*

---

### Description

Perform multiple permutation tests between a region set and each element in a list of region sets using shifted positions to calculate a local z-score.

### Usage

```
multiLocalZscore(A, Blist = NULL, sampling = FALSE, fraction = 0.15,
  min_sampling = 5000, ranFUN = "randomizeRegions", evFUN = "numOverlaps",
  ntimes = 100, adj_pv_method = "BH", genome = "hg19", universe = NULL,
  window = 1000, step = 100, ...)
```

### Arguments

A	query region set for which to estimate local z-score values.
Blist	<a href="#">GRangesList</a> or list of region sets in any accepted formats by <a href="#">regioneR</a> package ( <a href="#">GRanges</a> , <a href="#">data.frame</a> etc.).
sampling	logical, if TRUE the function will use only a sample of each element of Alist to perform the test as specified in fraction. (default = FALSE)
fraction	logical, if sampling=TRUE, defines the fraction of the region sets used to perform the test. (default = 0.15)
min_sampling	numeric, minimum number of regions accepted after sampling is performed with the specified fraction. If the number of sampled regions is less than min_sampling, the number specified by min_sampling will be used as number of regions sampled instead. (default = 5000)
ranFUN	character, the randomization strategy used for the test, see <a href="#">regioneR</a> . (default = "randomizeRegions")
evFUN	character, the evaluation strategy used for the test, see <a href="#">regioneR</a> . (default = "numOverlaps")
ntimes	numeric, number of permutations used in the test. (default = 100)
adj_pv_method	character, the method used for the calculation of the adjusted p-value, to choose between the options of <a href="#">p.adjust()</a> . (default = "BH")
genome	character or <a href="#">GRanges</a> , genome used to compute the randomization. (default = "hg19")
universe	region set to use as universe, used only when <a href="#">regioneR::resampleRegions()</a> function is selected. (default = NULL)
window	numeric, window (number of base pairs) in which the local z-score will be calculated. (default = 1000)
step	numeric, step (number of base pairs) by which will be estimated the local Z-score. (default = 100)
...	further arguments to be passed to other methods.



## Details

This function performs multiple permutation tests between a single region set and each element in a list of region sets. For every pairwise combination, the evaluation step is repeated each time shifting the position of all the regions in the query region set by a fixed step inside a defined window (using `regioneR::localZScore()`). This produces a "local z-score" profile that can be indicative of the nature of the association between region sets. For example, an association can occur "centrally" if the z-score value drops sharply when sifting the region set. On the other hand, two region sets may have a peak of local z-score away from the central position if they happen to occur often at a regular distance, showing a "lateral" association.

## Value

A object of class `multiLocalZScore` containing three slots

- @parameters
- @multiLocalZscores
- @matrix

## See Also

`regioneR::localZScore()`

## Examples

```
fakeGenome<- regioneR::toGRanges("chrF",1,1000)
regA <- regioneR::createRandomRegions(nregions = 10, length.mean = 10,
length.sd = 2,genome = fakeGenome)
regB <- regioneR::createRandomRegions(nregions = 10,length.mean = 10,
length.sd = 2,genome = fakeGenome)
regAs <-similarRegionSet(GR = regA,genome = fakeGenome, name = "A",
vectorPerc = seq(0.1,0.3,by =0.1))
regBs <-similarRegionSet(GR = regB,genome = fakeGenome, name = "B",
vectorPerc = seq(0.1,0.3,by =0.1))
ABList <- c(regAs,regBs)

mlz_ptAB <- multiLocalZscore(A = regA, Blist = ABList,
genome = fakeGenome, ntimes = 10)
summary(mlz_ptAB)
```

---

multiLocalZScore-class

*multiLocalZScore Class*

---

## Description

An S4 class for "multiLocalZScore" object.

**Slots**

parameters List of parameters used to create the object

multiLocalZscores Results of multiple pairwise permutation tests on shifted region sets generated with `multiLocalZscore()`.

matrix List of numerical matrices containing local z-scores and correlation values generated with `makeLZMatrix()`.

**Examples**

```
data("cw_Alien")

AlienRSList_narrow_small <- AlienRSList_narrow[c("regA", "regB", "regC")]

mlz_test <- multiLocalZscore(A = AlienRSList_narrow_small$regA, Blist = AlienRSList_narrow_small,
                             sampling = FALSE, genome = AlienGenome, per.chromosome = TRUE,
                             ranFUN = "resampleGenome", evFUN = "numOverlaps",
                             ntimes = 10, mc.cores = 2)

class(mlz_test)
```

---

multiPermTest

*multiPermTest*


---

**Description**

multiPermTest

**Usage**

```
multiPermTest (A, Blist, ranFUN, evFUN, uni, genome, rFUN, ntimes, adj_pv_method, ...)
```

**Arguments**

A	Genomic Ranges or any accepted formats by <code>regioneR</code> package ( <code>GRanges</code> , <code>data.frame</code> etc.).
ranFUN	character, the randomization strategy used for the test, see <code>regioneR</code> . (default = "randomizeRegions")
evFUN	character, the evaluation strategy used for the test, see <code>regioneR</code> . (default = "numOverlaps")
uni	region set to use as universe, used only when <code>regioneR::resampleRegions()</code> function is selected. (default = NULL)
genome	character or <code>GRanges</code> , genome used to compute the randomization. (default = "hg19")
ntimes	numeric, number of permutations used in the test. (default = 100)
adj_pv_method	character, the method used for the calculation of the adjusted p-value, to choose between the options of <code>p.adjust()</code> . (default = "BH")
...	further arguments to be passed to other methods.

**Details**

Perform a multiple permutation test

**Value**

a data frame object computed starting from results of `regioneR::permTest()` function

**See Also**

`regioneR::permTest()`

---

plotCrosswiseDimRed    *plotCrosswiseDimRed*

---

**Description**

Plot a visualization of a `genoMatriXeR` object (or matrix) using different dimensional reduction algorithms (PCA, tSNE and UMAP).

**Usage**

```
plotCrosswiseDimRed(mPT, type = "PCA", GM_clust = NA, clust_met =
  "hclust", nc = 5, listRS = NULL, main = "", labSize = 2, emphasize = FALSE,
  labAll = FALSE, labMaxOverlap = 100, ellipse = TRUE, colPal = NULL,
  perplexity = 10, theta = 0.1, return_table = FALSE, return_plot = TRUE, ...)
```

**Arguments**

<code>mPT</code>	an object of class <code>genoMatriXeR</code> or a numerical matrix.
<code>type</code>	character, dimensional reduction algorithm to use ("PCA", "tSNE", "UMAP"). (default = "PCA")
<code>GM_clust</code>	numeric, vector of assigned clusters used to cluster the matrix. If NA, the matrix will be clustered using the method defined by <code>clust_met</code> . (default = NA)
<code>clust_met</code>	character, unsupervised cluster strategy used ( <code>hclust</code> , <code>kmeans</code> or <code>pam</code> ). (default = "hclust")
<code>nc</code>	numeric, number of clusters to define if using the default "kmeans" method. (default = 5)
<code>listRS</code>	list, a list of names of region sets of interest to be highlighted in the graph. (default = NULL)
<code>main</code>	character, title for the plot. (default = "")
<code>labSize</code>	numeric, size for point labels in the plot. If 0, no labels will be plotted. (default = 2)
<code>emphasize</code>	logical, if TRUE, only the cluster in which the elements of <code>listRS</code> are present will be highlighted. (default = FALSE)

<code>labAll</code>	logical, if TRUE all data points are labelled, even if not in <code>listRS</code> when <code>emphasize = TRUE</code> . (default = FALSE)
<code>labMaxOverlap</code>	numeric, max.overlaps for <code>geom_text_repel</code> . (default = 100)
<code>ellipse</code>	logical, if TRUE ellipses will be drawn around the clusters. (default = FALSE)
<code>colPal</code>	character, colors to use as palette for the plot. If NULL, default colors will be used. (default = NULL)
<code>perplexity, theta</code>	numeric, if <code>type = "tSNE"</code> values of perplexity and theta for the function <code>Rtsne()</code> . (default = 10)
<code>return_table</code>	logical, if TRUE a table with the cluster assigned to each region is returned. (default = FALSE)
<code>return_plot</code>	logical, if TRUE a plot is returned. (default = TRUE)
<code>...</code>	further arguments to be passed on to other methods

**Details**

This function generates a plot with a two-dimensional representation of the association data stored in a `genoMatriXeR` object by using either PCA, tSNE or UMAP transformations of the data. This function incorporates a clustering step and allows to highlight specific region sets of interest and the clusters they belong to. In addition to generating a plot, a table with the cluster assignments can be retrieved.

**Value**

A ggplot object or a table with cluster assignments is returned.

**See Also**

`crosswisePermTest()`

**Examples**

```
data("cw_Alien")

cw_Alien_ReG <- makeCrosswiseMatrix(cw_Alien_ReG)

plotCrosswiseDimRed(cw_Alien_ReG, type = "PCA")

CDR_clust <- plotCrosswiseDimRed(cw_Alien_ReG, type = "UMAP", return_table = TRUE)

print(CDR_clust)
```

---

plotCrosswiseMatrix *plotCrosswiseMatrix*

---

### Description

Plot matrix of associations/correlations stored in a [genoMatriXeR](#) object.

### Usage

```
plotCrosswiseMatrix(mPT, lineColor = NA, interpolate = FALSE, colMatrix =
"default", matrix_type = "association", cor = "row",
maxVal = NA, main = "", ord_mat = NULL)
```

### Arguments

mPT	an object of class <a href="#">genoMatriXeR</a> or a numerical matrix.
lineColor	logical, color for the line grid delineating the tiles of the matrix plot. If NA, no line will be drawn. (default = NA)
interpolate	logical, if TRUE the image will be interpolated using the function <a href="#">geom_raster()</a> . (default = FALSE)
colMatrix	character or vector of colors, if "default" will be used a default selection see..
matrix_type	character, type of matrix to be plotted, either "association" or "correlation". (default = "association")
cor	character, if matrix_type is "correlation", choose if the function <a href="#">cor()</a> will be executed on each "row" or "col" of the matrix. (default = "row")
maxVal	numeric, maximum absolute value displayed by the plot. If "max", the maximum values in the matrix are used. If NA, the 0.95 quantile of all absolute values is used. (default = NA)
main	character, title of the plot. (default = "")
ord_mat	numeric, list with two numeric vectors that represent the ordering of rows and column of the matrix to be used in the plot. If NULL, the order of the matrix is preserved as is. (default = NULL)

### Details

This functions creates a graphical representation of the matrix of associations stored in a [genoMatriXeR](#) object. The values plotted and clustering options can be controlled when creating the matrix with the function [makeCrosswiseMatrix](#).

### Value

Returns a ggplot object.

### See Also

[crosswisePermTest](#) [makeCrosswiseMatrix](#)

**Examples**

```

data("cw_Alien")

cw_Alien_ReG <- makeCrosswiseMatrix( cw_Alien_ReG)

plotCrosswiseMatrix(cw_Alien_ReG, matrix_type = "association")

plotCrosswiseMatrix(cw_Alien_ReG, matrix_type = "correlation")

```

---

plotLocalZScoreMatrix *Plot Local Z-Score Matrix*

---

**Description**

Plot Local Z-Score Matrix of associations/correlations stored in a [multiLocalZScore](#) object.

**Usage**

```

plotLocalZScoreMatrix (mLZ, lineColor = NA, colMatrix = "default",
matrix_type = "association", maxVal = "max", main = "", labSize = 6,
revert = FALSE, highlight = NULL, highlight_size = 2.5, highlight_max = FALSE,
smoothing = FALSE, ...)

```

**Arguments**

mLZ	an object of class <a href="#">multiLocalZScore</a> or a matrix
lineColor	logical, color for the line grid delineating the tiles of the matrix plot. If NA, no line will be drawn. (default = NA)
colMatrix	character or vector of colors, if "default" will be used a default selection see..
matrix_type	character, type of matrix to be plotted, either "association" or "correlation". (default = "association")
maxVal	numeric, maximum absolute value displayed by the plot. If "max", the maximum values in the matrix are used. If NA, the 0.95 quantile of all absolute values is used. (default = NA)
main	character, title of the plot. (default = "")
labSize	numeric, size for the plot labels. (default = 6)
revert	logical, if TRUE reverts the order of the plotted elements. (default = FALSE)
highlight	character, vector indicating the region set names to highlight by adding labels pointing to the 0 shift position (default = NULL)
highlight_size	numeric, size of the highlight labels. (default = 2.5)
highlight_max	logical, if TRUE the highlight labels are placed at the maximum local z-score value instead of the 0 shift position. (default = FALSE)
smoothing	logical, if TRUE the <a href="#">stats::smooth.spline</a> function will be applied to the local z-score profile. (default = FALSE)
...	further arguments to be passed to other methods.

**Value**

Returns a ggplot object.

**See Also**

[multiLocalZscore](#) [makeLZMatrix](#) [multiLocalZScore](#)

**Examples**

```
data("cw_Alien")
```

---

plotSingleLZ

*plotSingleLZ*

---

**Description**

Plot the result of specific local Z-Score tests from a [multiLocalZScore](#) object in the form of line plot profiles.

**Usage**

```
plotSingleLZ(mLZ, RS, xlab = "", normZS = TRUE, ylim = NULL, main = NA,
  colPal = NULL, labValues = TRUE, labSize = 2.5, labMax = FALSE, smoothing = FALSE, ...)
```

**Arguments**

mLZ	an object of class <a href="#">multiLocalZScore</a> .
RS	character, vector of region set names for which to plot the local Z-score results.
xlab	character, label for the x axis. (default = NA)
normZS	logical, indicates whether the normalized Z-score values should be plotted. If FALSE, the raw Z-score is used. (default = TRUE)
ylim	numeric, vector with two elements: minimum and maximum Y values of the plot. If NULL, the plot limits are set by default so all data points can be plotted. (default = NULL)
main	character, title for the plot. If NA, the name of the query region set in the multi-LocalZScore object will be used. (default = NA)
colPal	character, colors to use as palette for the plot. If NULL, default colors will be used. (default = NULL)
labValues	logical, if TRUE each local Z-score profile is labelled at position 0 with the name of the region set and its Z-score value at the central position. (default = TRUE)
labSize	numerical, size of the labels from labValues in the plot. (default = 2.5)

labMax	logical, if TRUE the labels are placed at the maximum value of each local Z-score profile instead of the center. (default = FALSE)
smoothing	logical, if TRUE the <code>smooth.spline()</code> function will be applied to the localZ-score profile. (default = FALSE)
...	further arguments to be passed to other methods.

### Details

This function generates a line plot with the local Z-score profiles of selected region sets from a `multiLocalZScore` object. This type of plot complements the local Z-score matrix (generated by `plotLocalZScoreMatrix`, since it allows to visualize in detail the local Z-score profile of just the region sets of interest.

This plot is well suited for a single or a few region sets, but will get busy if attempting to plot many different profiles. For the latter, the full matrix generated by `plotLocalZScoreMatrix` is usually a better visualization option.

### Value

Returns a ggplot object.

### See Also

`multiLocalZscore()`, `makeLZMatrix()`

### Examples

```
data("cw_Alien")

plotSingleLZ(mLZ_regA_ReG, RS = c("regD", "regD_02", "regA", "regAB_04"),
labMax = TRUE, smoothing = TRUE)
```

---

plotSinglePT

*plotSinglePT*

---

### Description

Plot the result of a single pairwise permutation test from a `genoMatriXeR` object.

### Usage

```
plotSinglePT(mPT, RS1, RS2, xlab = NA, main = NA)
```



**Arguments**

mPT	an object of class <a href="#">genoMatriXeR</a> .
RS1, RS2	character, names of region sets in a genoMatriXeR object for which to represent the pairwise permutation test results.
xlab	character, label for x axis. (default = NA)
main	title for the plot, if NA the name of the genoMatriXeR object is used (default = NA)

**Details**

This function generates a plot representing the result of a single permutation test stored in a [genoMatriXeR](#) object. This includes a plot of the density distribution of the randomized evaluations and a vertical line showing the observed evaluation in the original region set. The values of the mean randomized evaluations and the value of the observed evaluation are shown, in addition to the calculated Z-score, normalized Z-score and adjusted p-value.

**Value**

Returns a ggplot object.

**See Also**

[crosswisePermTest](#) [makeCrosswiseMatrix](#)

**Examples**

```
data("cw_Alien")
plotSinglePT(cw_Alien_ReG, RS1 = "regA", RS2 = "regA_05")
plotSinglePT(cw_Alien_ReG, RS1 = "regA", RS2 = "regC")
```

---

print,genoMatriXeR-method

*Print method for genoMatriXeR class*

---

**Description**

Print method for genoMatriXeR class

**Usage**

```
## S4 method for signature 'genoMatriXeR'
print(x)
```

**Arguments**

x                    A genoMatriXeR object.

**Value**

A printed output for genoMatriXeR objects.

**See Also**

[genoMatriXeR](#)

---

randomizeRegionsPerc    *randomizeRegionsPerc*

---

**Description**

Create a random region set similar to a reference region set.

**Usage**

```
randomizeRegionsPerc(GR, genome = "hg19", frac = 0.2, ...)
```

**Arguments**

GR	a <a href="#">GRanges</a> object with the input region set.
genome	genome of reference to generate the similar region sets. (default = "hg19")
frac	fraction of the original region set to randomize. (default = 0.2)
...	further arguments to be passed to other methods.

**Details**

This function takes an input region set and generates a region set where a fraction of the regions has been randomized.

**Value**

a [GRanges](#) object

**See Also**

[similarRegionSet\(\)](#)

**Examples**

```
data("cw_Alien")

nreg <- 100

regA <-
  createRandomRegions(
    nregions = nreg,
```

```
length.mean = 100,  
length.sd = 10,  
non.overlapping = TRUE,  
genome = AlienGenome  
)  
  
regA_02 <- randomizeRegionsPerc(GR = regA, genome = AlienGenome, frac = 0.2)
```

---

similarRegionSet      *similar RegionSets*

---

## Description

Create a list of similar region sets to a reference region set.

## Usage

```
similarRegionSet(GR, name, genome, vectorPerc)
```

## Arguments

GR	a <a href="#">GRanges</a> object with the input region set.
name	character, name for the output region sets. The names will be generated by adding an underscore and the fraction of similarity after the name of each region set generated. (default = "A")
genome	genome of reference to generate the similar region sets. (default = "hg19")
vectorPerc	numeric, vector of desired randomized fractions. (default = seq(.1,.9,.1))

## Details

This function takes a region set as an input and a vector of desired randomized fractions. For each fraction value, a new region set will be generated where that fraction of the original regions in the input region set has been randomized. In effect, this creates region sets that are "similar" to a controlled degree to the original region set. This tool can be useful for validation purposes and its use in the demonstration of the usage of this package can be seen in the [RegionReloaded](#) vignette.

## Value

A list of [GRanges](#) objects.

## See Also

[GRanges](#)

**Examples**

```

data("cw_Alien")

A<-createRandomRegions(nregions = 20, length.mean = 1000, length.sd = 100,
genome = AlienGenome)

similAList <- similarRegionSet(GR = A, genome = AlienGenome,
vectorPerc = seq(0.1,0.9,0.2), name = "test")

summary (similAList)

data("cw_Alien")

regA <- createRandomRegions(
  nregions = 100,
  length.mean = 10,
  length.sd = 5,
  genome = AlienGenome
)

listRegA <- similarRegionSet(GR = regA, genome = AlienGenome)
summary(listRegA)

```

---

<code>subList</code>	<i>Sub List from region set list</i>
----------------------	--------------------------------------

---

**Description**

create a samples sublist starting from a list of Region Set

**Usage**

```
subList(Alist, min_sampling, fraction)
```

**Arguments**

<code>Alist</code>	GRangesList or list of Region Set of any accepted formats by <code>regioneR</code> package
<code>min_sampling</code>	numeric, minimum number of regions for each element of the list, if the number of regions is less than <code>min_samplnig</code> as subsempilng will be take the entire regionset
<code>fraction</code>	numeric, percentage of regions selected for the subsampling

**Value**

a sublist of GenomicRanges from an original GenomicRanges list

# Index

## \* datasets

AlienGenome, 3  
AlienRSList\_broad, 3  
AlienRSList\_narrow, 4  
cw\_Alien, 9  
cw\_Alien\_RaR, 9  
cw\_Alien\_ReG, 10  
cw\_Alien\_ReG\_no\_Square, 10  
cw\_Alien\_ReR, 11  
mLZ\_regA\_ReG, 22

## \* function

multiPermTest, 26

## \* internal

cleanCrosswiseMatrix, 5  
crosswiseMatrix, 7  
DFfromLZ, 11  
gmxrMatrix, 15  
gmxrMatrix<-, 16  
gmxrMultiOverlaps, 16  
gmxrParam, 17  
mlzsMatrix, 20  
mlzsMatrix<-, 20  
mlzsMultiLocalZscores, 21  
mlzsParam, 21  
mlzsParam<-, 22  
multiPermTest, 26  
print, genoMatriXeR-method, 33  
subList, 36

AlienGenome, 3, 3, 4  
AlienRSList\_broad, 3  
AlienRSList\_narrow, 4

chooseHclustMet, 4  
chooseHclustMet(), 18, 19  
cleanCrosswiseMatrix, 5  
cor(), 29  
createRandomRegions(), 4  
createUniverse, 6  
crosswiseMatrix, 7

crosswisePermTest, 7, 15, 29, 33  
crosswisePermTest(), 5, 12, 18, 28  
cw\_Alien, 9  
cw\_Alien\_RaR, 9  
cw\_Alien\_ReG, 10  
cw\_Alien\_ReG\_no\_Square, 10  
cw\_Alien\_ReR, 11

data.frame, 7, 24, 26  
DFfromLZ, 11  
dist(), 5, 18, 19

genoMatriXeR, 7–18, 27–29, 33, 34  
genoMatriXeR-class, 12  
geom\_raster(), 29  
geom\_text\_repel, 28  
getHclust, 12  
getMatrix, 13  
getMultiEvaluation, 14  
getParameters, 15  
gMXR (genoMatriXeR-class), 12  
gmxrMatrix, 15  
gmxrMatrix<-, 16  
gmxrMultiOverlaps, 16  
gmxrParam, 17  
GRanges, 3, 4, 6–8, 24, 26, 34, 35  
GRangesList, 7, 24

hclust, 5, 12, 13, 18, 27  
hclust(), 4, 5, 18, 19

kmeans, 27

localZScore, 20

makeCrosswiseMatrix, 13, 17, 29, 33  
makeCrosswiseMatrix(), 6, 9–12  
makeLZMatrix, 13, 19, 31  
makeLZMatrix(), 22, 26, 32  
mLZ\_regA\_ReG, 22  
mLZ\_regA\_ReG\_br, 23

mLZ\_regD\_ReG, 23  
mLZS (multiLocalZScore-class), 25  
mlzsMatrix, 20  
mlzsMatrix<-, 20  
mlzsMultiLocalZscores, 21  
mlzsParam, 21  
mlzsParam<-, 22  
multiLocalZScore, 11–15, 19–23, 25, 30–32  
multiLocalZscore, 24, 31  
multiLocalZscore(), 14, 26, 32  
multiLocalZScore-class, 25  
multiPermTest, 26  
multiPermTest(), 18

p.adjust(), 8, 24, 26  
pam, 27  
plotCrosswiseDimRed, 27  
plotCrosswiseMatrix, 29  
plotCrosswiseMatrix(), 18  
plotLocalZScoreMatrix, 30, 32  
plotSingleLZ, 31  
plotSinglePT, 32  
print,genoMatrixeR-method, 33

randomizeRegionsPerc, 34  
regioneR::circularRandomizeRegions, 9  
regioneR::joinRegions(), 6  
regioneR::localZScore(), 25  
regioneR::overlapPermTest(), 8  
regioneR::permTest(), 8, 27  
regioneR::randomizeRegions, 9  
regioneR::randomizeRegions(), 9  
regioneR::resampleGenome, 9  
regioneR::resampleGenome(), 10, 22, 23  
regioneR::resampleRegions, 9  
regioneR::resampleRegions(), 6, 8, 11, 24,  
26  
Rtsne(), 28

similarRegionSet, 35  
similarRegionSet(), 4, 34  
smooth.spline(), 32  
stats::smooth.spline, 30  
subList, 36

t(), 18