

# Package: easy.utils (via r-universe)

September 15, 2024

**Type** Package

**Title** Frequently Used Functions for Easy R Programming

**Version** 0.0.4

**Description** Some utility functions for validation, data manipulation or color palettes. These functions can be helpful to reduce internal codes everywhere in package development.

**Depends** R (>= 4.1.0), methods

**Imports** dplyr, fastmatch, Polychrome, rlang, scales

**Suggests** randomcoloR

**License** MIT + file LICENSE

**Encoding** UTF-8

**URL** <https://github.com/ycli1995/easy.utils>

**BugReports** <https://github.com/ycli1995/easy.utils/issues>

**LazyData** true

**RoxygenNote** 7.2.3

**Repository** <https://ycli1995.r-universe.dev>

**RemoteUrl** <https://github.com/ycli1995/easy.utils>

**RemoteRef** HEAD

**RemoteSha** cc8ea784a4fde483be840650a9cbb1003b65a7ec

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checkAlignedDims	<i>Check whether some dimensions of two arrays are aligned</i>
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## Description

Check whether some dimensions of two arrays are aligned

## Usage

```
checkAlignedDims(
  incoming,
  reference,
  align.dims,
  in.name = NULL,
  ref.name = NULL,
  withDimnames = FALSE
)
```

## Arguments

incoming	The array-like object to check
reference	The array-like object to be aligned with
align.dims	A integer vector indicating which dimensions of reference should be used for alignment. The length must be equal to the dimension numbers of incoming
in.name	The name of incoming. Only use for verbose.
ref.name	The name of reference. Only use for verbose.
withDimnames	Logical. Whether to also align the dimension names.

## Details

Some examples for align.dims:

- c(1, 1): The dim[1] of incoming must align with the dim[1] of reference, and the dim[2] of incoming must align with the dim[1] of reference.
- c(2, 1): The dim[1] of incoming must align with the dim[2] of reference, and the dim[2] of incoming must align with the dim[1] of reference.
- c(NA, 1): The dim[1] of incoming doesn't need to align with any dimension of reference, but the dim[2] of incoming must align with the dim[1] of reference.
- c(2, NA): The dim[1] of incoming must align with the dim[2] of reference, but the dim[2] of incoming doesn't need to align with any dimension of reference.

**Value**

If any dimension is not aligned, raise an error.

**Examples**

```
# Get some expression matrices ----
exp1 <- matrix(0, 10, 20)
colnames(exp1) <- paste0("cell_", 1:ncol(exp1))
rownames(exp1) <- paste0("gene_", 1:nrow(exp1))

exp2 <- matrix(0, 10, 15)
colnames(exp2) <- paste0("cell_", 1:ncol(exp2))
rownames(exp2) <- paste0("gene_", 1:nrow(exp2))

exp3 <- matrix(0, 10, 20)
colnames(exp3) <- paste0("c_", 1:ncol(exp3))
rownames(exp3) <- paste0("g_", 1:nrow(exp3))

# Get some PCA embedding matrices ----
pca1 <- matrix(0, 10, 5)
rownames(pca1) <- paste0("cell_", 1:nrow(pca1))
colnames(pca1) <- paste0("PC_", 1:ncol(pca1))

pca2 <- matrix(0, 20, 5)
rownames(pca2) <- paste0("cell_", 1:nrow(pca2))
colnames(pca2) <- paste0("PC_", 1:ncol(pca2))

pca3 <- matrix(0, 20, 5)
rownames(pca3) <- paste0("c_", 1:nrow(pca3))
colnames(pca3) <- paste0("PC_", 1:ncol(pca3))

# Error: The Dim 2 of exp1 is not aligned with the Dim 2 of exp2!
try(checkAlignedDims(exp2, exp1, c(1, 2)))

checkAlignedDims(exp3, exp1, c(1, 2))

# Error: The Dim 1 of exp3 is not aligned with the Dim 1 of exp1!
try(checkAlignedDims(exp3, exp1, c(1, 2), withDimnames = TRUE))

checkAlignedDims(exp3, exp1, c(NA, 2)) # Don't check the rows of exp3

# Error: The Dim 2 of exp3 is not aligned with the Dim 2 of exp1!
try(checkAlignedDims(exp3, exp1, c(NA, 2), withDimnames = TRUE))

# Error: The Dim 1 of pca1 is not aligned with the Dim 2 of exp1!
# Don't check the columns of pca1
try(checkAlignedDims(pca1, exp1, c(2, NA)))

checkAlignedDims(pca2, exp1, c(2, NA))
checkAlignedDims(pca2, exp1, c(2, NA), withDimnames = TRUE)
checkAlignedDims(pca3, exp1, c(2, NA))
```

```
# Error: The Dim 1 of pca3 is not aligned with the Dim 2 of exp1!
try(checkAlignedDims(pca3, exp1, c(2, NA), withDimnames = TRUE))
```

---

checkColorMap	<i>Check color map for a factor</i>
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### Description

Function to make sure that all levels of a factor map to distinct colors.

### Usage

```
checkColorMap(x, colors = NULL, ...)
```

```
## Default S3 method:
checkColorMap(x, colors = NULL, ...)
```

### Arguments

x	An R object contains the factor vector to be checked.
colors	A named vector, whose names are factor levels and values are colors. If is NULL, just generate colors with setColor. Otherwise, it first generates colors for each level, then replaces those with names mapping to colors.
...	Arguments passed to other methods.

### Value

An updated colors vector, whose names are identical to the levels.

### Examples

```
## Assign colors for a character or factor vector.
xx <- sample(LETTERS, 10)
cols <- setColor(xx)

## Ensure each level in 'xx' get a color
checkColorMap(xx, cols)
```

---

checkSameLength	<i>Check whether the lengths of input objects are equal</i>
-----------------	---

---

**Description**

Check whether the lengths of input objects are equal

**Usage**

```
checkSameLength(...)
```

**Arguments**

... R objects to be compared

**Value**

TRUE or FALSE

---

chunkPoints	<i>Generate chunk points</i>
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**Description**

Unexported helper function `ChunkPoints` from **Seurat**. This can be quite useful when user needs to chunk some operations.

**Usage**

```
chunkPoints(dsize, csize)
```

**Arguments**

dsize How big is the data being chunked  
csize How big should each chunk be

**Value**

A 2 x N `matrix` where each column is a chunk. The first row contains start points, and the second row contains end points.

**References**

<https://github.com/satijalab/seurat/blob/763259d05991d40721dee99c9919ec6d4491d15e/R/utilities.R#L1699>

## Examples

```
### Split an index vector with 15273 elements into chunks, each of which has
### 3000 elements.
chunkPoints(15273, 3000)
```

---

fastIntersect	<i>A fast version of base::intersect()</i>
---------------	--

---

## Description

A fast version of base::intersect()

## Usage

```
fastIntersect(x, y, keep.duplicated = FALSE)
```

## Arguments

x, y	Vectors to be compared.
keep.duplicated	Whether or not to keep duplicated elements in x

## Value

A vector of a common mode.

## References

<https://stackoverflow.com/questions/72631297/speed-up-setdiff-intersect-union-operations-on-vectors>

## See Also

[intersect](#)

## Examples

```
x <- sample(LETTERS, 12)
y <- sample(LETTERS, 12)
fastIntersect(x, y)
```

---

fetchColnames	<i>Fetch column names exists in the data object</i>
---------------	---

---

**Description**

Fetch column names exists in the data object

**Usage**

```
fetchColnames(object, query)
```

**Arguments**

object	Any object that has implemented colnames(object).
query	Column names to check.

**Value**

An update query where only entries existing in colnames(object) are kept. If no any query was found, raise an error.

---

getDiscreteColors	<i>Generate palettes of distinct colors</i>
-------------------	---

---

**Description**

Generate palettes of distinct colors

**Usage**

```
getDiscreteColors(  
  n,  
  pal = NULL,  
  is.extend = TRUE,  
  random = c("no", "randomColor", "distinctColorPalette", "Polychrome"),  
  seed = 1234,  
  verbose = FALSE,  
  ...  
)  
  
setColor(x, pal = NULL, ...)
```

**Arguments**

n	How many colors do we need?
pal	Name of the palette to use. Use names(pal_discrete) to get all palette names
is.extend	When $n > \text{length}(\text{pal\_discrete}[[\text{pal}]])$ , whether or not to extend the colors with <a href="#">colorRampPalette</a> .
random	Choose a method to generate random colors. Default is "no".
seed	Seed for random colors.
verbose	Show progress messages.
...	Extra parameters passed to other functions depending on random: <ul style="list-style-type: none"> <li>• <a href="#">randomColor()</a> or <a href="#">distinctColorPalette()</a>. This requires manual installation of <b>randomcoloR</b></li> <li>• <a href="#">createPalette</a> from <b>Polychrome</b></li> </ul>
x	A factor to use colors.

**Value**

A vector with n colors. For setColor, also set names as factor levels.

**Examples**

```
getDiscreteColors(10)
getDiscreteColors(
  10,
  random = "Polychrome",
  seedcolors = scales::hue_pal()(4)
)

## Assign colors for a character or factor vector.
xx <- sample(LETTERS, 10)
cols <- setColor(xx)
```

---

isValidCharacters      *Check valid characters*

---

**Description**

Check if input characters are valid (neither NA nor "")

**Usage**

```
isValidCharacters(x)
```

**Arguments**

x	A vector, matrix or list
---	--------------------------



**Value**

A logical vector

**Examples**

```
isValidCharacters(c("a", "", "b"))  
isValidCharacters(c("a", NA, "b"))
```

---

pal_discrete	<i>A palette list for distinct colors.</i>
--------------	--

---

**Description**

A palette list for distinct colors.

**Usage**

```
pal_discrete
```

**Format**

An object of class list of length 20.

---

pasteFactors	<i>Paste two factor vectors</i>
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---

**Description**

Paste two factors and re-assign the levels

**Usage**

```
pasteFactors(x, y, collapse = "_")
```

**Arguments**

x, y	Factor vectors
collapse	A character string to separate the x and y.

**Value**

A new factor vector

**Examples**

```
x <- factor(c(rep("A", 10), rep("B", 10)), levels = c("A", "B"))
y <- factor(c(rep("a", 5), rep("b", 15)), levels = c("a", "b"))
pasteFactors(x, y)
```

---

replaceEntries

*Replace entries according to a mapping list*


---

**Description**

Replace entries according to a mapping list

**Usage**

```
replaceEntries(x, map, ...)

## S4 method for signature 'vector,list'
replaceEntries(x, map, ...)
```

**Arguments**

x	An R vector
map	A named list representing one-to-one or one-to-many mappings. Normally, each name represents a new value, and each element contain the old value(s) to be replaced.
...	Arguments passed to other methods.

**Value**

A updated x

**Examples**

```
set.seed(1234)
fact <- factor(c("A", "A", "B", "A", "B", "C", "D", "E", "D"))
map <- list("a" = c("B", "e")) ## Turn all "B" and "E" into "a"
replaceEntries(fact, map)
```

---

`unlistMap`*Unlist a mapping list into a named vector*

---

**Description**

Function to unlist a one-to-one or one-to-many 'key-value' list into a named vector. Useful for batched replacement of vector elements.

**Usage**

```
unlistMap(map, keep.unique = TRUE)
```

**Arguments**

<code>map</code>	A named list. Each element must be a vector.
<code>keep.unique</code>	Whether or not to remove elements with duplicated names from the output vector.

**Value**

A named vector whose names are original values in `map`, and elements are keys of `map`

**Examples**

```
map <- list(X = c("a", "b"), Y = c("c", "d"))
unlistMap(map)

map <- list(X = c("a", "b", "c"), Y = c("c", "d"))
unlistMap(map)
unlistMap(map, keep.unique = FALSE)
```

---

`verboseMsg`*Simple verbose message wrapper*

---

**Description**

Simple verbose message wrapper

**Usage**

```
verboseMsg(..., verbose = NULL)
```

**Arguments**

... Pass to [message](#)  
verbose Whether or not to show the message. If is NULL, will search verbose variable in [parent.frame](#).

**Value**

Print the progress to console when verbose is TRUE.

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