

# Package ‘bigparallelr’

February 2, 2021

**Title** Easy Parallel Tools

**Version** 0.3.1

**Description** Utility functions for easy parallelism in R. Include some reexports from other packages, utility functions for splitting and parallelizing over blocks, and choosing and setting the number of cores used.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**Imports** bigassertr (>= 0.1.1), doParallel, flock, parallel, parallelly, RhpcBLASctl

**Depends** foreach

**Suggests** testthat, covr

**URL** <https://github.com/privefl/bigparallelr>

**BugReports** <https://github.com/privefl/bigparallelr/issues>

**NeedsCompilation** no

**Author** Florian Privé [aut, cre]

**Maintainer** Florian Privé <florian.prive.21@gmail.com>

**Repository** CRAN

**Date/Publication** 2021-02-02 13:40:02 UTC

## R topics documented:

assert_cores . . . . .	2
get_blas_ncores . . . . .	3
nb_cores . . . . .	3
plus . . . . .	4
register_parallel . . . . .	4
split_costs . . . . .	5
split_len . . . . .	6
split_parapply . . . . .	6
split_vec . . . . .	8

---

assert_cores	<i>Check number of cores</i>
--------------	------------------------------

---

### Description

Check that you are not trying to use too many cores.

### Usage

```
assert_cores(ncores)
```

### Arguments

ncores	Number of cores to check. Make sure is not larger than <code>getOption("bigstatsr.ncores.max")</code> (number of logical cores by default). We advise you to use <code>nb_cores()</code> . If you really know what you are doing, you can change this default value with <code>options(bigstatsr.ncores.max = Inf)</code> .
--------	---

### Details

It also checks if two levels of parallelism are used, i.e. having `ncores` larger than 1, and having a parallel BLAS enabled by default. You could remove this check by setting `options(bigstatsr.check.parallel.blas = FALSE)`.

We instead recommend that you disable parallel BLAS by default by adding `try(bigparallelr::set_blas_ncores(1), silent = TRUE)` to your `.Rprofile` (**with an empty line at the end of this file**) so that this is set whenever you start a new R session. You can use `usethis::edit_r_profile()` to open your `.Rprofile`. For this to be effective, you should restart the R session or run `options(default.nproc.blas = NULL)` once in the current session.

Then, in a specific R session, you can set a different number of cores to use for matrix computations using `bigparallelr::set_blas_ncores()`, if you know there is no other level of parallelism involved in your code.

### Examples

```
## Not run:

assert_cores(2)

## End(Not run)
```

---

get_blas_ncores	<i>Number of cores used by BLAS (matrix computations)</i>
-----------------	---

---

**Description**

Number of cores used by BLAS (matrix computations)

**Usage**

```
get_blas_ncores()
```

```
set_blas_ncores(ncores)
```

**Arguments**

ncores            Number of cores to set for BLAS.

**Examples**

```
get_blas_ncores()
```

---

nb_cores	<i>Recommended number of cores to use</i>
----------	---

---

**Description**

This is base on the following rule: use only physical cores and if you have only physical cores, leave one core for the OS/UI.

**Usage**

```
nb_cores()
```

**Value**

The recommended number of cores to use.

**Examples**

```
nb_cores()
```

---

plus	<i>Add</i>
------	------------

---

**Description**

Wrapper around Reduce to add multiple arguments. Useful

**Usage**

```
plus(...)
```

**Arguments**

... Multiple arguments to be added together.

**Value**

```
Reduce('+', list(...))
```

**Examples**

```
plus(1:3, 4:6, 1:3)
```

---

register_parallel	<i>Register parallel</i>
-------------------	--------------------------

---

**Description**

Register parallel in functions. Do [makeCluster\(\)](#), [registerDoParallel\(\)](#) and [stopCluster\(\)](#) when the function returns.

**Usage**

```
register_parallel(ncores, ...)
```

**Arguments**

ncores Number of cores to use. If using only one, then this function uses [foreach::registerDoSEQ\(\)](#).  
 ... Arguments passed on to [makeCluster\(\)](#).

**Examples**

```
## Not run:

test <- function(ncores) {
  register_parallel(ncores)
  foreach(i = 1:2) %dopar% i
}

test(2) # only inside the function
foreach(i = 1:2) %dopar% i

## End(Not run)
```

---

`split_costs`*Split costs in blocks*

---

**Description**

Split costs in consecutive blocks using a greedy algorithm that tries to find blocks of even total cost.

**Usage**

```
split_costs(costs, nb_split)
```

**Arguments**

`costs`            Vector of costs (e.g. proportional to computation time).  
`nb_split`        Number of blocks.

**Value**

A matrix with 4 columns lower, upper, size and cost.

**Examples**

```
split_costs(costs = 150:1, nb_split = 3)
split_costs(costs = rep(1, 151), nb_split = 3)
split_costs(costs = 150:1, nb_split = 30)
```

---

split_len	<i>Split length in blocks</i>
-----------	-------------------------------

---

**Description**

Split length in blocks

**Usage**

```
split_len(total_len, block_len, nb_split = ceiling(total_len/block_len))
```

**Arguments**

total_len	Length to split.
block_len	Maximum length of each block.
nb_split	Number of blocks. Default uses the other 2 parameters.

**Value**

A matrix with 3 columns lower, upper and size.

**Examples**

```
split_len(10, block_len = 3)
split_len(10, nb_split = 3)
```

---

split_parapply	<i>Split-parApply-Combine</i>
----------------	-------------------------------

---

**Description**

A Split-Apply-Combine strategy to parallelize the evaluation of a function.

**Usage**

```
split_parapply(
  FUN,
  ind,
  ...,
  .combine = NULL,
  ncores = nb_cores(),
  nb_split = ncores,
  opts_cluster = list(),
  .costs = NULL
)
```

## Arguments

<code>FUN</code>	The function to be applied to each subset matrix.
<code>ind</code>	Initial vector of indices that will be splitted in <code>nb_split</code> .
<code>...</code>	Extra arguments to be passed to <code>FUN</code> .
<code>.combine</code>	Function to combine the results with <code>do.call</code> . This function should accept multiple arguments (using <code>...</code> ). For example, you can use <code>c</code> , <code>cbind</code> and <code>rbind</code> . This package also provides function <code>plus</code> to add multiple arguments together. The default is <code>NULL</code> , in which case the results are not combined and are returned as a list, each element being the result of a block.
<code>ncores</code>	Number of cores to use. Default uses <code>nb_cores()</code> .
<code>nb_split</code>	Number of blocks. Default uses <code>ncores</code> .
<code>opts_cluster</code>	Optional parameters for clusters passed as a named list. E.g., you can use <code>type = "FORK"</code> to use forks instead of clusters. You can also use <code>outfile = ""</code> to redirect printing to the console.
<code>.costs</code>	Vector of costs (e.g. proportional to computation time) associated with each element of <code>ind</code> . Default is <code>NULL</code> (same cost).

## Details

This function splits indices in parts, then apply a given function to each part and finally combine the results.

## Value

Return a list of `ncores` elements, each element being the result of one of the cores, computed on a block. The elements of this list are then combined with `do.call(.combine, .)` if `.combine` is not `NULL`.

## Examples

```
## Not run:

str(
  split_parapply(function(ind) {
    sqrt(ind)
  }, ind = 1:10000, ncores = 2)
)

## End(Not run)
```

---

`split_vec`*Split object in blocks*

---

**Description**

Split object in blocks

**Usage**

```
split_vec(x, block_len, nb_split = ceiling(length(x)/block_len))
```

```
split_df(df, block_len, nb_split = ceiling(nrow(df)/block_len))
```

**Arguments**

<code>x</code>	Vector to be divided into groups.
<code>block_len</code>	Maximum length (or number of rows) of each block.
<code>nb_split</code>	Number of blocks. Default uses the other 2 parameters.
<code>df</code>	Data frame to be divided into groups.

**Value**

A list with the splitted objects.

**Examples**

```
split_vec(1:10, block_len = 3)
str(split_df(iris, nb_split = 3))
```



# Index

`assert_cores`, 2  
`foreach::registerDoSEQ()`, 4  
`get_blas_ncores`, 3  
`makeCluster()`, 4  
`nb_cores`, 3  
`plus`, 4  
`register_parallel`, 4  
`registerDoParallel()`, 4  
`set_blas_ncores (get_blas_ncores)`, 3  
`split_costs`, 5  
`split_df (split_vec)`, 8  
`split_len`, 6  
`split_parapply`, 6  
`split_vec`, 8  
`stopCluster()`, 4