

# Package ‘BiocParallel’

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**Type** Package

**Title** Bioconductor facilities for parallel evaluation

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**Description** This package provides modified versions and novel implementation of functions for parallel evaluation, tailored to use with Bioconductor objects.

**biocViews** Infrastructure

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RNAseqData.HNRNPC.bam.chr14, Rsamtools, GenomicAlignments,  
ShortRead, RUnit, BiocStyle, knitr

**Collate.unix** AllGenerics.R BiocParallelParam-class.R ErrorHandling.R  
bpbackend-methods.R bpisup-methods.R bplapply-methods.R  
bpmapplly-methods.R bpiterate-methods.R bpschedule-methods.R  
bpstart-methods.R bpstop-methods.R bpvec-methods.R  
bpvectorize-methods.R bpworkers-methods.R bpaggregate-methods.R  
DoparParam-class.R MulticoreParam-class.R register.R  
SerialParam-class.R SnowParam-class.R BatchJobsParam-class.R  
utilities.R unix/mclapply.R unix/pvec.R unix/bpiterate.R  
unix/zzz.R

**Collate.windows** AllGenerics.R BiocParallelParam-class.R  
ErrorHandling.R bpbackend-methods.R bpisup-methods.R  
bplapply-methods.R bpmapplly-methods.R bpiterate-methods.R  
bpschedule-methods.R bpstart-methods.R bpstop-methods.R  
bpvec-methods.R bpvectorize-methods.R bpworkers-methods.R  
bpaggregate-methods.R DoparParam-class.R MulticoreParam-class.R  
register.R SerialParam-class.R SnowParam-class.R  
BatchJobsParam-class.R utilities.R windows/zzz.R

**VignetteBuilder** knitr

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BiocParallel-package *Bioconductor facilities for parallel evaluation*

---

## Description

This package provides modified versions and novel implementation of functions for parallel evaluation, tailored to use with Bioconductor objects.

## Details

This package uses code from the [parallel](#) package,

## Author(s)

Author: Bioconductor Package Maintainer [cre], Martin Morgan [aut], Michel Lang [aut], Ryan Thompson [aut]

Maintainer: Bioconductor Package Maintainer <maintainer@bioconductor.org>

---

BatchJobsParam-class *Enable parallelization on batch systems*

---

## Description

This class is used to parameterize scheduler options on managed high-performance computing clusters.

## Usage

```
BatchJobsParam(workers, catch.errors = TRUE, cleanup = TRUE,
  work.dir = getwd(), stop.on.error = FALSE, seed = NULL,
  resources = NULL, conffile = NULL, cluster.functions = NULL,
  progressbar = TRUE, ...)
```

## Arguments

workers	integer(1)Number of workers to divide tasks (e.g., elements in the first argument of <code>bplapply</code> ) between. On Multicore and SSH backends, this defaults to all available nodes. On managed (e.g., slurm, SGE) clusters workers defaults to NA, meaning that the number of workers equals the number of tasks. See argument <code>n.chunks</code> in <code>chunk</code> and <code>submitJobs</code> for more information.
catch.errors	logical(1)Flag to determine in apply-like functions (see e.g. <code>bplapply</code> ) whether to quit with an error as soon as one application fails or encapsulation of function calls in <code>try</code> blocks which triggers a resume mechanism (see <code>bpresume</code> ). Defaults to TRUE.
cleanup	logical(1)BatchJobs creates temporary directories in the <code>work.dir</code> . If <code>cleanup</code> is set to TRUE (default), the directories are removed from the file systems automatically. Set this to FALSE whenever it might become necessary to utilize any special functionality provided by BatchJobs. To retrieve the registry, call <code>loadRegistry</code> on the temporary directory.
work.dir	character(1)Directory to store temporary files. Note that this must be shared across computational nodes if you use a distributed computing backend. Default is the current working directory of R, see <code>getwd</code> .
stop.on.error	logical(1)Stop all jobs as soon as one jobs fails ( <code>stop.on.error == TRUE</code> ) or wait for all jobs to terminate. Default is FALSE.
seed	integer(1L)Set an initial seed for the RNG. See <code>makeRegistry</code> for more information. Default is NULL where a random seed is chosen upon initialization.
resources	list()List of job specific resources passed to <code>submitJobs</code> . Default is NULL where the resources defined in the configuration are used.
conffile	character(1)URI to a custom BatchJobs configuration file used for execution. Default is NULL which relies on BatchJobs to handle configuration files.
cluster.functions	ClusterFunctionsSpecify a specific cluster backend using on of the constructors provided by BatchJobs, see <code>ClusterFunctions</code> . Default is NULL where the default cluster functions defined in the configuration are used.

progressbar      logical(1) Suppress the progress bar used in BatchJobs and be less verbose. Default is FALSE.  
 ...              Addition arguments, currently not handled.

### BatchJobsParam constructor

Return an object with specified values. The object may be saved to disk or reused within a session.

### Methods

The following generics are implemented and perform as documented on the corresponding help page: [bpworkers](#), [bpstart](#), [bpstop](#), [bpisup](#), [bpbackend](#), [bpbackend<-](#)

### Author(s)

Michel Lang, <mailto:michellang@gmail.com>

### See Also

`getClass("BiocParallelParam")` for additional parameter classes.  
`register` for registering parameter classes for use in parallel evaluation.

### Examples

```
p <- BatchJobsParam(progressbar=FALSE)
bplapply(1:10, sqrt, BPPARAM=p)

## Not run:
## see vignette for additional explanation
funs <- makeClusterFunctionsSLURM("~/slurm.tmpl")
param <- BatchJobsParam(4, cluster.functions=funs)
register(param)
bplapply(1:10, function(i) sqrt)

## End(Not run)
```

---

BiocParallelParam-class

*Virtual classes (for developer reference)*

---

### Description

These classes are primarily relevant to developers.  
 BiocParallelParam is a virtual class on which all parameter classes extend. It has no slots.

### Author(s)

Martin Morgan <mailto:mtmorgan@fhcrc.org>

**Examples**

```
getClass("BiocParallelParam")
```

---

bpaggregate

*Apply a function on subsets of data frames*


---

**Description**

This is a parallel version of [aggregate](#).

**Usage**

```
## S4 method for signature formula,BiocParallelParam
bpaggregate(x, data, FUN, ..., BPPARAM=bpparam())

## S4 method for signature data.frame,BiocParallelParam
bpaggregate(x, by, FUN, ..., simplify=TRUE, BPPARAM=bpparam())

## S4 method for signature matrix,BiocParallelParam
bpaggregate(x, by, FUN, ..., simplify=TRUE, BPPARAM=bpparam())

## S4 method for signature ANY,missing
bpaggregate(x, ..., BPPARAM=bpparam())
```

**Arguments**

x	A data.frame, matrix or a formula.
by	A list of factors by which x is split; applicable when x is data.frame or matrix.
data	A data.frame; applicable when x is a formula.
FUN	Function to apply.
...	Additional arguments for FUN.
simplify	If set to TRUE, the return values of FUN will be simplified using <a href="#">simplify2array</a> .
BPPARAM	An optional <a href="#">BiocParallelParam</a> instance determining the parallel back-end to be used during evaluation.

**Details**

bpaggregate is a generic with methods for data.frame matrix and formula objects. x is divided into subsets according to factors in by. Data chunks are sent to the workers, FUN is applied and results are returned as a data.frame.

The function is similar in spirit to [aggregate](#) from the stats package but [aggregate](#) is not explicitly called. The bpaggregate formula method reformulates the call and dispatches to the data.frame method which in turn distributes data chunks to workers with bplapply.

**Value**

See [aggregate](#).

**Author(s)**

Martin Morgan <mailto:mtmorgan@fhcrc.org>.

**Examples**

```
if (all(require(Rsamtools) &&
         require(GenomicAlignments))) {

  fl <- system.file("extdata", "ex1.bam", package="Rsamtools")
  param <- ScanBamParam(what = c("flag", "mapq"))
  gal <- readGAlignments(fl, param=param)

  ## Report the mean map quality by range cutoff:
  cutoff <- rep(0, length(gal))
  cutoff[start(gal) > 1000 & start(gal) < 1500] <- 1
  cutoff[start(gal) > 1500] <- 2
  bpaggregate(as.data.frame(mcols(gal)$mapq), list(cutoff = cutoff), mean)

}
```

---

bpcontrols

*Control (start, stop, query) back-end Params*

---

**Description**

Use functions on this page to start, stop, and query the ‘back-ends’ that perform a parallel evaluation.

**Usage**

```
bpworkers(x, ...)
```

  

```
bpstart(x, ...)
```

```
bpstop(x, ...)
```

```
bpisup(x, ...)
```

  

```
bpbackend(x, ...)
```

```
bpbackend(x, ...) <- value
```

**Arguments**

x	An instance of a BiocParallelParam class, e.g., <a href="#">MulticoreParam</a> , <a href="#">SnowParam</a> , <a href="#">DoparParam</a> . x can be missing, in which case the default back-end (see <a href="#">register</a> ) is used.
...	Additional arguments, perhaps used by methods.
value	Replace value for back-end.

**Details**

bpworkers reports the number of workers in the back-end as a scalar integer with value  $\geq 0$ .

bpstart starts the back-end, if necessary. For instance, [MulticoreParam](#) back-ends do not need to be started, but [SnowParam](#) back-ends do. bp\* functions like [bplapply](#) will automatically start the back-end if necessary.

bpstop stops the back-end, if necessary and possible.

bpi sup tests whether the back-end is available for processing, returning a scalar logical value.

bpbackend retrieves an object representing the back end, if possible. Not all back-ends can be retrieved; see `showMethods("backend")`.

bpbackend<- updates the back end, and is only meant for developer use.

**Value**

bpworkers returns a scalar integer  $\geq 0$ .

bpi sup returns a scalar logical.

bpstart, bpstop return an updated x, invisibly.

bpbackend, bpbackend<- return or accept back end-specific objects.

**Author(s)**

Martin Morgan <mailto:mtmorgan@fhcrc.org>.

**See Also**

[BiocParallelParam](#) for possible values of x.

**Examples**

```
bpworkers(SerialParam())

## Not run:
p <- SnowParam(2L)
bpworkers(p)          # 2 local nodes, communicating via sockets
bpstart(p)           # start cluster
bplapply(1:10, sqrt, BPPARAM=p)
bpstop(p)            # stop cluster

p <- SnowParam(4L)
bplapply(1:10, sqrt, BPPARAM=p) # automatically start / stop cluster
```

```
## End(Not run)
```

---

bpiterate *Parallel iteration over an indeterminate number of data chunks*

---

### Description

bpiterate iterates over an indeterminate number of data chunks (e.g., records in a file). Each chunk is processed by parallel workers in an asynchronous fashion; as each worker finishes it receives a new chunk. Data are traversed a single time.

### Usage

```
bpiterate(ITER, FUN, ..., BPPARAM=bpparam())

## S4 method for signature ANY,ANY,missing
bpiterate(ITER, FUN, ..., BPPARAM=bpparam())

## S4 method for signature ANY,ANY,BiocParallelParam
bpiterate(ITER, FUN, ..., BPPARAM=bpparam())
```

### Arguments

ITER	A function with no arguments that returns an object to process, generally a chunk of data from a file. When no objects are left (i.e., end of file) it should return NULL and continue to return NULL regardless of the number of times it is invoked after reaching the end of file. This function is run on the master.
FUN	A function to process the object returned by ITER; run on parallel workers separate from the master. When BPPARAM is a MulticoreParam, FUN is ‘decorated’ with additional arguments and therefore must have ... in the signature.
BPPARAM	An optional <a href="#">BiocParallelParam</a> instance determining the parallel back-end to be used during evaluation, or a list of <a href="#">BiocParallelParam</a> instances, to be applied in sequence for nested calls to bpiterate. Currently only <a href="#">MulticoreParam</a> is supported for bpiterate.
...	Arguments to other methods, specifically named arguments for FUN, or REDUCE or init. <ul style="list-style-type: none"> <li>• REDUCE: Optional function that combines (reduces) output from FUN. As each worker returns, the data are combined with the REDUCE function. REDUCE takes 2 arguments; one is the current result and the other is the output of FUN from a worker that just finished. Currently not supported on Windows.</li> <li>• init: Optional initial value for REDUCE; must be of the same type as the object returned from FUN. When supplied, reduce.in.order is set to TRUE.</li> <li>• reduce.in.order: Logical. When TRUE, REDUCE is applied to the results from the workers in the same order the tasks were sent out.</li> </ul>

## Details

Currently only `MulticoreParam` and `SerialParam` are supported.

`bpiterate` iterates through an unknown number of data chunks, dispatching chunks to parallel workers as they become available. In contrast, other `bp*apply` functions such as `codebplapply` or `bpmapply` require the number of data chunks to be specified ahead of time. This quality makes `bpiterate` useful for iterating through files of unknown length.

`ITER` serves up chunks of data until the end of the file is reached at which point it returns `NULL`. Note that `ITER` should continue to return `NULL` regardless of the number of times it is invoked after reaching the end of the file. `FUN` is applied to each object (data chunk) returned by `ITER`.

## Value

A list of output type specified by `FUN`. When `REDUCE` is supplied the list is of length 1.

## Author(s)

Valerie Obenchain <mailto:vobencha@fhcrc.org>.

The multi-core implementation is a modification of the `sclapply` in `HTSeqGeni` by Gregorie Pau.

## See Also

- [bpvec](#) for parallel, vectorized calculations.
- [bplapply](#) for parallel, lapply-like calculations.
- [BiocParallelParam](#) for details of `BPPARAM`.

## Examples

```
if (all(require(Rsamtools) &&
        require(RNAseqData.HNRNPC.bam.chr14) &&
        require(GenomicAlignments) &&
        require(ShortRead) &&
        .Platform$OS.type != "windows")) {

  ## -----
  ## Iterating through a BAM file
  ## -----

  ## Select a single file and set yieldSize in the BamFile object.
  fl <- RNAseqData.HNRNPC.bam.chr14_BAMFILES[[1]]
  bf <- BamFile(fl, yieldSize = 300000)

  ## bamIterator() is initialized with a BAM file and returns a function.
  ## The return function requires no arguments and iterates through the
  ## file returning data chunks the size of yieldSize.
  bamIterator <- function(bf) {
    done <- FALSE
    if (!isOpen( bf))
      open(bf)
```

```

function() {
  if (done)
    return(NULL)
  yld <- readGAlignments(bf)
  if (length(yld) == 0L) {
    close(bf)
    done <<- TRUE
    NULL
  } else yld
}
}

## Initialize the iterator.
ITER <- bamIterator(bf)

## Create a FUN that counts reads in a region of interest.
roi <- GRanges("chr14", IRanges(seq(19e6, 107e6, by = 10e6), width = 10e6))
counter <- function(reads, roi, ...) {
  countOverlaps(query = roi, subject = reads)
}
## Create a MulticoreParam and call bpiterate().
bpparam <- MulticoreParam(workers = 2)
res <- bpiterate(ITER, counter, BPPARAM = bpparam, roi = roi)

## The result length is the same as the number of data chunks.
length(res)
colSums(do.call(rbind, res))

## -----
## Iterating through a FASTA file
## -----

## Set data chunk size with n in the FastqStreamer object.
sp <- SolexaPath(system.file(extdata, package = ShortRead))
fl <- file.path(analysisPath(sp), "s_1_sequence.txt")
fqs <- FastqStreamer(fl, n = 100)

## Create an iterator that returns data chunks the size of n.
fastqIterator <- function(fqs) {
  done <- FALSE
  if (!isOpen(fqs))
    open(fqs)

  function() {
    if (done)
      return(NULL)
    yld <- yield(fqs)
    if (length(yld) == 0L) {
      close(fqs)
      done <<- TRUE
      NULL
    } else yld
  }
}

```

```

    }
  }

  ## Initialize the iterator.
  ITER <- fastqIterator(fqs)

  ## The processor summarizes the number of times each sequence occurs.
  summary <- function(reads, ...) {
    tables(reads, n = 0)$distribution
  }

  bpparam <- MulticoreParam(workers = 2)
  bpiterate(ITER, summary, BPPARAM = bpparam)

  ## Results from the workers are combined on the fly when a
  ## REDUCE function is provided. Collapsing the data in this
  ## way can substantially reduce memory requirements.
  fqs <- FastqStreamer(fl, n = 100)
  ITER <- fastqIterator(fqs)
  bpiterate(ITER, summary, BPPARAM = bpparam, REDUCE = merge, all = TRUE)

  ## -----
  ## Multiple files
  ## -----
  ## Currently bpiterate() is only implemented for the multi-core
  ## environment (i.e., MulticoreParam). A single machine may not
  ## have enough memory to process multiple files. In this case the
  ## files can be distributed over a snow cluster with bplapply()
  ## then processed with bpiterate() on each cluster node.

  ## Select a subset of files, create a BamFileList.
  fls <- RNAseqData.HNRNPC.bam.chr14_BAMFILES[1:3]
  bfl <- BamFileList(fls, yieldSize = 200000)

  ## Cluster size is defined by the number of files.
  snowp <- SnowParam(workers = length(bfl))

  ## Currently bpiterate() is only supported in the multi-core environment
  ## and must use MulticoreParam.
  myFUN <- function(file, bamIterator, counter, ...) {
    library(BiocParallel) ## for bpiterate
    library(Rsamtools)   ## for Bam file manipulation
    library(GenomicAlignments) ## for readGAlignments
    ITER <- bamIterator(file)
    bpiterate(ITER, counter, BPPARAM = MulticoreParam(workers=2), roi = roi)
  }

  ## Distribute the files across the snow cluster workers with bplapply().
  ## Each cluster node acts as a master and spawns 2 children.
  res <- bplapply(bfl, myFUN, BPPARM = snowp, bamIterator = bamIterator,
    counter = counter, roi = roi)

  ## The result is of length 3 (# of files).

```

```

## > length(res)
## [1] 3

## Each list element is of length 5 (# of iterations of size yieldSize).
## > elementLengths(res)
## ERR127306 ERR127307 ERR127308
##          5          5          5
}

```

---

bplapply

*Parallel lapply-like functionality*


---

### Description

bplapply applies FUN to each element of X. Any type of object X is allowed, provided length, [, and [[ methods are available. The return value is a list of length equal to X, as with [lapply](#).

### Usage

```
bplapply(X, FUN, ..., BPRESUME = getOption("BiocParallel.BPRESUME", FALSE),
         BPPARAM=bpparam())
```

```
## S4 method for signature ANY,ANY
```

```
bplapply(X, FUN, ..., BPRESUME = getOption("BiocParallel.BPRESUME", FALSE),
         BPPARAM=bpparam())
```

```
## S4 method for signature ANY,missing
```

```
bplapply(X, FUN, ..., BPRESUME = getOption("BiocParallel.BPRESUME", FALSE),
         BPPARAM=bpparam())
```

```
## S4 method for signature ANY,BiocParallelParam
```

```
bplapply(X, FUN, ..., BPRESUME = getOption("BiocParallel.BPRESUME", FALSE),
         BPPARAM=bpparam())
```

### Arguments

X	Any object for which methods length, [, and [[ are implemented.
FUN	The function to be applied to each element of X.
...	Additional arguments for FUN, as in <a href="#">lapply</a>
BPRESUME	Flag to determine if a previous partially successful run should be resumed. See <a href="#">bpresume</a> for details.
BPPARAM	An optional <a href="#">BiocParallelParam</a> instance determining the parallel back-end to be used during evaluation, or a list of <a href="#">BiocParallelParam</a> instances, to be applied in sequence for nested calls to bplapply.

**Details**

See `showMethods{bplapply}` for additional methods, e.g., `method?bplapply("MulticoreParam")`.

**Value**

See [lapply](#).

**Author(s)**

Martin Morgan <mailto:mtmorgan@fhcrc.org>. Original code as attributed in [mclapply](#).

**See Also**

[bpvec](#) for parallel, vectorized calculations.

[BiocParallelParam](#) for possible values of BPPARAM.

**Examples**

```
showMethods("bplapply")

## ten tasks (1:10) so ten calls to FUN default registered parallel
## back-end. Compare with bpvec.
system.time(result <- bplapply(1:10, function(v) {
  message("working") ## 10 tasks
  sqrt(v)
}))
result
```

---

bpmapply

*Parallel mapply-like functionality*


---

**Description**

`bpmapply` applies `FUN` to first elements of `...`, the second elements and so on. Any type of object in `...` is allowed, provided `length`, `[]`, and `[[` methods are available. The return value is a list of length equal to the length of all objects provided, as with [mapply](#).

**Usage**

```
bpmapply(FUN, ..., MoreArgs=NULL, SIMPLIFY=TRUE, USE.NAMES=TRUE,
         BPRESUME=getOption("BiocParallel.BPRESUME", FALSE), BPPARAM=bpparam())

## S4 method for signature ANY,ANY
bpmapply(FUN, ..., MoreArgs=NULL, SIMPLIFY=TRUE, USE.NAMES=TRUE,
         BPRESUME=getOption("BiocParallel.BPRESUME", FALSE), BPPARAM=bpparam())

## S4 method for signature ANY,missing
```

```

bpmapply(FUN, ..., MoreArgs=NULL, SIMPLIFY=TRUE, USE.NAMES=TRUE,
         BPRESUME=getOption("BiocParallel.BPRESUME", FALSE), BPPARAM=bpparam())

## S4 method for signature ANY,BiocParallelParam
bpmapply(FUN, ..., MoreArgs=NULL, SIMPLIFY=TRUE, USE.NAMES=TRUE,
         BPRESUME=getOption("BiocParallel.BPRESUME", FALSE), BPPARAM=bpparam())

```

## Arguments

FUN	The function to be applied to each element passed via . . . .
. . .	Objects for which methods <code>length</code> , <code>[]</code> , and <code>[[</code> are implemented. All objects must have the same length or shorter objects will be replicated to have length equal to the longest.
MoreArgs	List of additional arguments to FUN.
SIMPLIFY	If TRUE the result will be simplified using <a href="#">simplify2array</a> .
USE.NAMES	If TRUE the result will be named.
BPRESUME	Flag to determine if a previous partially successful run should be resumed. See <a href="#">bpresume</a> for details.
BPPARAM	An optional <a href="#">BiocParallelParam</a> instance determining the parallel back-end to be used during evaluation.

## Details

See `showMethods{bplapply}` for additional methods, e.g., `method?bplapply("MulticoreParam")`.

## Value

See [lapply](#).

## Author(s)

Michel Lang . Original code as attributed in [mclapply](#).

## See Also

[bpvec](#) for parallel, vectorized calculations.

[BiocParallelParam](#) for possible values of BPPARAM.

## Examples

```

showMethods("bpmapply")

## ten tasks (1:10) so ten calls to FUN default registered parallel
## back-end. Compare with bpvec.
result <- bpmapply(function(greet, who) {
  paste(Sys.getpid(), greet, who)
}, c("morning", "night"), c("sun", "moon"))
cat(paste(result, collapse="\n"), "\n")

```

---

bpresume	<i>Resume computation with partial results</i>
----------	--

---

### Description

Resume partial successful calls to `bplapply` or `bpmapply`

### Usage

```
bplasterror()  
bpresume(expr)
```

### Arguments

`expr` expression A expression which calls either `bplapply` or `bpmapply`.

### Usage

The resume mechanism is triggered if the argument `catch.errors` of the `BiocParallelParam` class is set to `TRUE`. The methods `bplapply` and `bpmapply` then store the current state of computation. Recalling the call directory with argument `BPRESUME` set to `TRUE` will then only compute the missing parts of the previous call and merge the results.

Alternatively, if the call to `bplapply` and `bpmapply` is inside a function not accessible directly by the user, the last call can be embedded into `bpresume` which sets an option accordingly to enable the resume feature down in the call stack.

The function `bplasterror` returns a `LastError` object containing the partial results and errors to investigate.

Note that nested calls of the apply functions can cause troubles in some scenarios.

### Author(s)

Martin Morgan <mailto:mtmorgan@fhcrc.org>

### Examples

```
## -----  
## Catch errors:  
## -----  
  
## By default catch.errors is TRUE in BiocParallelParam objects.  
SnowParam(workers = 2)  
  
## If catch.errors is FALSE an ill-fated bplapply() simply stops  
## displaying the error message.  
snowp <- SnowParam(workers = 2, catch.errors = FALSE)  
## Not run:  
> res <- bplapply(list(1, "two", 3), sqrt, BPPARAM = snowp)
```

```

Error in checkForRemoteErrors(val) :
  one node produced an error: non-numeric argument to mathematical function

## End(Not run)

## When catch.errors is TRUE the same call provides traceback
## information (truncated here) and suggests use of bplastererror() and
## bpresume().
snowp <- SnowParam(workers = 2)
## Not run:
> res <- bplapply(list(1, "two", 3), sqrt, BPPARAM = snowp)
Error: 1 errors; first error:
  Error in FUN(...): non-numeric argument to mathematical function

For more information, use bplastererror(). To resume calculation, re-call
the function and set the argument BPRESUME to TRUE or wrap the
previous call in bpresume().

First traceback:
  19: parallel:::slaveRSOCK()
  18: slaveLoop(makeSOCKmaster(master, port, timeout, useXDR))
  ...

## End(Not run)

## bplastererror() reports the number of successful results and error message.
## Not run:
> bplastererror()
2 / 3 partial results stored. First 1 error messages:
[2]: Error in FUN(...): non-numeric argument to mathematical function

## End(Not run)

## -----
## Resume calculations:
## -----

## The resume mechanism attempts to re-run the data element that failed.
## In our example the character "two" list element will never succeed. In
## the runs below we replace the character with a numeric and compute the
## result.

## There are two methods for resuming a suspended calculation, one
## approach is to wrap the original call in bpresume().
## Not run:
> bpresume(res <- bplapply(list(1, 2, 3), sqrt, BPPARAM = snowp))
Resuming previous calculation...
> res
[[1]]
[1] 1

[[2]]
[1] 1.414214

```

```
[[3]]
[1] 1.732051

## End(Not run)

## An equivalent approach is to set BPRESUME = TRUE in bplapply().
## Not run:
res <- bplapply(list(1, 2, 3), sqrt, BPPARAM = snowp, BPRESUME = TRUE)

## End(Not run)
```

---

bpschedule

*Schedule back-end Params*

---

## Description

Use functions on this page to influence scheduling of parallel processing.

## Usage

```
bpschedule(x, ...)
```

## Arguments

x	An instance of a BiocParallelParam class, e.g., <a href="#">MulticoreParam</a> , <a href="#">SnowParam</a> , <a href="#">DoparParam</a> . x can be missing, in which case the default back-end (see <a href="#">register</a> ) is used.
...	Additional arguments, perhaps used by methods.

## Details

bpschedule returns a logical(1) indicating whether the parallel evaluation should occur at this point.

## Value

bpschedule returns a scalar logical.

## Author(s)

Martin Morgan <mailto:mtmorgan@fhcrc.org>.

## See Also

[BiocParallelParam](#) for possible values of x.

**Examples**

```

bpschedule(SnowParam()) # TRUE
bpschedule(MulticoreParam(2)) # FALSE on windows

p <- MulticoreParam(recursive=FALSE)
bpschedule(p) # TRUE
bplapply(1:2, function(i, p) {
  bpschedule(p) # FALSE
}, p = p, BPPARAM=p)

```

bpvec

*Parallel, vectorized evaluation***Description**

bpvec applies FUN to subsets of X. Any type of object X is allowed, provided length, [, and c methods are available. The return value is a vector of length equal to X, as with FUN(X).

**Usage**

```

bpvec(X, FUN, ..., AGGREGATE=c, BPPARAM=bpparam())

## S4 method for signature ANY,ANY
bpvec(X, FUN, ..., AGGREGATE=c, BPPARAM=bpparam())

## S4 method for signature ANY,BiocParallelParam
bpvec(X, FUN, ..., AGGREGATE=c, BPPARAM=bpparam())

## S4 method for signature ANY,missing
bpvec(X, FUN, ..., AGGREGATE=c, BPPARAM=bpparam())

```

**Arguments**

X	Any object for which methods length, [, and c are implemented.
FUN	The function to be applied to subsets of X.
...	Additional arguments for FUN.
AGGREGATE	A function taking any number of arguments ... called to reduce results (elements of the ... argument of AGGREGATE from parallel jobs. The default, c, concatenates objects and is appropriate for vectors; rbind might be appropriate for data frames.
BPPARAM	A optional <a href="#">BiocParallelParam</a> instance determining the parallel back-end to be used during evaluation.

## Details

When BPPARAM is an instance of a class derived from BiocParallelParam for which no other method applies, this method creates a vector of indexes and uses these in conjunction with bplapply to arrange for parallel evaluation.

When BPPARAM is a class for which no method is defined (e.g., [SerialParam](#)), FUN(X) is used.

See showMethods{bpvec} for additional methods, e.g., method?bpvec("MulticoreParam").

## Value

The result should be identical to FUN(X, ...) (assuming that AGGREGATE is set appropriately).

## Author(s)

Martin Morgan <mailto:mtmorgan@fhcrc.org>. Original code as attributed in [pvec](#).

## See Also

[bplapply](#) for parallel lapply.

[BiocParallelParam](#) for possible values of BPPARAM.

## Examples

```
showMethods("bpvec")

## ten tasks (1:10), called with as many back-end elements are specified
## by BPPARAM. Compare with bplapply
system.time(result <- bpvec(1:10, function(v) {
  message("working") ## 10 tasks
  sqrt(v)
}))
result
```

---

bpvectorize

*Transform vectorized functions into parallelized, vectorized function*

---

## Description

This transforms a vectorized function into a parallel, vectorized function. Any function FUN can be used, provided its parallelized argument (by default, the first argument) has a length and [ method defined, and the return value of FUN can be concatenated with c.

## Usage

```
bpvectorize(FUN, ..., BPPARAM=bpparam())
```

```
## S4 method for signature ANY,ANY  
bpvectorize(FUN, ..., BPPARAM=bpparam())
```

```
## S4 method for signature ANY,missing  
bpvectorize(FUN, ..., BPPARAM=bpparam())
```

## Arguments

FUN	A function whose first argument has a length and can be subset <code>[]</code> , and whose evaluation would benefit by splitting the argument into subsets, each one of which is independently transformed by FUN. The return value of FUN must support concatenation with <code>c</code> .
...	Additional arguments to parallization, unused.
BPPARAM	An optional <a href="#">BiocParallelParam</a> instance determining the parallel back-end to be used during evaluation.

## Details

The result of `bpvectorize` is a function with signature `...;` arguments to the returned function are the original arguments FUN. BPPARAM is used for parallel evaluation.

When BPPARAM is a class for which no method is defined (e.g., [SerialParam](#)), FUN(X) is used.

See `showMethods{bpvectorize}` for additional methods, if any.

## Value

A function taking the same arguments as FUN, but evaluated using [bpvec](#) for parallel evaluation across available cores.

## Author(s)

Ryan Thompson <mailto:rct@thompsonclan.org>

## See Also

[bpvec](#)

## Examples

```
psqrt <- bpvectorize(sqrt) ## default parallelization  
psqrt(1:10)
```

---

DoparParam-class	<i>Enable parallel evaluation using registered dopar backend</i>
------------------	--

---

## Description

This class is used to dispatch parallel operations to the dopar backend registered with the foreach package.

## Usage

```
DoparParam(catch.errors = TRUE)
```

## Arguments

`catch.errors` `logical(1)` Flag to determine in apply-like functions (see e.g. [bplapply](#)) whether to quit with an error as soon as one application fails or encapsulation of function calls in `try` blocks which triggers a resume mechanism (see [bpresume](#)). Defaults to TRUE.

## DoparParam constructor

Return a proxy object that dispatches parallel evaluation to the registered foreach parallel backend.

There are no options to the constructor. All configuration should be done through the normal interface to the foreach parallel backends.

## Methods

The following generics are implemented and perform as documented on the corresponding help page (e.g., `?bpisup`): [bpworkers](#), [bpstart](#), [bpstop](#), [bpisup](#), [bpbackend](#), [bpbackend<-](#), [bpvec](#).

## Author(s)

Martin Morgan <mailto:mtmorgan@fhcrc.org>

## See Also

`getClass("BiocParallelParam")` for additional parameter classes.

`register` for registering parameter classes for use in parallel evaluation.

[foreach-package](#) for the parallel backend infrastructure used by this param class.

## Examples

```
# First register a parallel backend with foreach
library(doParallel)
cl <- makeCluster(2)
registerDoParallel(cl)
```

```

p <- DoparParam()
bplapply(1:10, sqrt, BPPARAM=p)
bpvec(1:10, sqrt, BPPARAM=p)

stopCluster(c1)
## Not run:
register(DoparParam(), default=TRUE)

## End(Not run)

```

---

MulticoreParam-class *Enable multi-core parallel evaluation*

---

## Description

This class is used to parameterize single computer multicore parallel evaluation on non-Windows computers. `multicoreWorkers()` chooses the number of workers based on operating system (Windows only supports 1 core), global user preference (`options(mc.cores=...)`), or the minimum of 8 and the number of detected cores (`detectCores()`).

## Usage

```

MulticoreParam(workers = multicoreWorkers(), catch.errors = TRUE,
  setSeed = TRUE, recursive = TRUE, cleanup = TRUE,
  cleanupSignal = tools::SIGTERM, verbose = FALSE, ...)
multicoreWorkers()

```

## Arguments

<code>workers</code>	<code>integer(1)</code> Number of workers on with Multicore and SSH backend which defaults here to all workers available. On managed HPC workers defaults to NA but can be set to control chunking of jobs. See argument <code>n.chunks</code> in <a href="#">chunk</a> and <a href="#">submitJobs</a> for more information.
<code>catch.errors</code>	<code>logical(1)</code> Flag to determine in apply-like functions (see e.g. <a href="#">bplapply</a> ) whether to quit with an error as soon as one application fails or encapsulation of function calls in <code>try</code> blocks which triggers a resume mechanism (see <a href="#">bpresume</a> ). Defaults to TRUE.
<code>setSeed</code>	<code>logical(1)</code> , as described in <code>parallel::mcpipeline</code> argument <code>mc.set.seed</code> .
<code>recursive</code>	<code>logical(1)</code> indicating whether recursive calls are evaluated in parallel; see <code>parallel::mclapply</code> argument <code>mc.allow.recursive</code> .
<code>cleanup</code>	<code>logical(1)</code> indicating whether forked children will be terminated before <code>bplapply</code> returns, as for <code>parallel::mclapply</code> argument <code>cleanup</code> . If TRUE, then the signal sent to the child is <code>cleanupSignal</code> .
<code>cleanupSignal</code>	<code>integer(1)</code> the signal sent to forked processes when <code>cleanup=TRUE</code> .
<code>verbose</code>	<code>logical(1)</code> when TRUE echo stdout of forked processes. This is the complement of <code>parallel::mclapply</code> 's argument <code>mc.silent</code> .
<code>...</code>	Additional arguments passed to <a href="#">mclapply</a>

### **MulticoreParam constructor**

Return an object with specified values. The object may be saved to disk or reused within a session.

### **Methods**

The following generics are implemented and perform as documented on the corresponding help page (e.g., `?bpisup`): [bpworkers](#), [bpstart](#), [bpstop](#), [bpisup](#), [bpschedule](#), [bpbackend](#).

### **Author(s)**

Martin Morgan <mailto:mtmorgan@fhcrc.org>

### **See Also**

`getClass("BiocParallelParam")` for additional parameter classes.  
`register` for registering parameter classes for use in parallel evaluation.

### **Examples**

```
multicoreWorkers()
p <- MulticoreParam()
bplapply(1:10, sqrt, BPPARAM=p)
bpvec(1:10, sqrt, BPPARAM=p)

## Not run:
register(MulticoreParam(), default=TRUE)

## End(Not run)
```

---

register

*Maintain a global registry of available back-end Params*

---

### **Description**

Use functions on this page to add to or query a registry of back-ends, including the default for use when no BPPARAM object is provided to functions.

### **Usage**

```
register(BPPARAM, default=TRUE)
registered(bpparamClass)
bpparam(bpparamClass)
```

**Arguments**

BPPARAM	An instance of a <code>BiocParallelParam</code> class, e.g., <code>MulticoreParam</code> , <code>SnowParam</code> , <code>DoparParam</code> .
default	Make this the default <code>BiocParallelParam</code> for subsequent evaluations? If FALSE, the argument is placed at the lowest priority position.
bpparamClass	When present, the text name of the <code>BiocParallelParam</code> class (e.g., “Multi-coreParam”) to be retrieved from the registry. When absent, a list of all registered instances is returned.

**Details**

The registry is a list of back-ends with configuration parameters for parallel evaluation. The first list entry is the default and is used by `BiocParallel` functions when no `BPPARAM` argument is supplied.

By default, the registry includes `MulticoreParam`, `SnowParam`, `BatchJobsParam` and `SerialParam`. The objects are constructed from global options of the corresponding name, or from the default constructor (e.g., `SnowParam()`) if no option is specified. The user can set customizations during start-up (e.g., in an `.Rprofile` file) with, for instance, `options(MulticoreParam=quote(MulticoreParam(workers=8)))`.

The act of “registering” a back-end modifies the existing `BiocParallelParam` in the list; only one param of each type can be present in the registry. When `default=TRUE`, the newly registered param is moved to the top of the list thereby making it the default. When `default=FALSE`, the param is modified ‘in place’ vs being moved to the top.

`bpparam()`, invoked with no arguments, returns the default `BiocParallelParam` instance from the registry. When called with the text name of a `bpparamClass`, the global options are consulted first, e.g., `options(MulticoreParam=MulticoreParam())` and then the value of `registered(bpparamClass)`.

**Value**

`register` returns, invisibly, a list of registered back-ends.

`registered` returns the back-end of type `bpparamClass` or, if `bpparamClass` is missing, a list of all registered back-ends.

`bpparam` returns the back-end of type `bpparamClass` or,

**Author(s)**

Martin Morgan <mailto:mtmorgan@fhcrc.org>.

**See Also**

`BiocParallelParam` for possible values of `BPPARAM`.

**Examples**

```
## -----
## The registry
## -----
```

```

## The full registry.
registered()

## When default = TRUE the last param registered becomes the new default.
snowparam <- SnowParam(workers = 3, type = "PSOCK")
register(snowparam, default = TRUE)
registered()

## Retrieve the default back-end,
bpparam()

## or a specific BiocParallelParam.
bpparam("MulticoreParam")

## -----
## Specifying a back-end for evaluation
## -----

## The back-end of choice is specified in the BPPARAM argument to
## the BiocParallel functions. None, one, or multiple back-ends can be
## provided.

## BPPARAM not specified:
## The default back-end from the registry is used.
bplapply(1:6, sqrt)

## BPPARAM as a single param:
bplapply(1:6, sqrt, BPPARAM = MulticoreParam(3))

## BPPARAM as a list of params:
## Useful for multiple levels of parallel evaluation. The 1:6 are divided
## among Snow workers, each of which dispatch to Multicore workers.
myfun <- function(x, BPPARAM, ...) {
  library(BiocParallel)
  res <- bplapply(x, sqrt, BPPARAM = BPPARAM)
  do.call(mean, res)
}
params <- list(bpparam("SnowParam"), bpparam("MulticoreParam"))
bplapply(list(1:2, 3:4, 5:6), myfun, BPPARAM = params)

```

---

SerialParam-class      *Enable serial evaluation*

---

## Description

This class is used to parameterize serial evaluation, primarily to facilitate easy transition from parallel to serial code.

## Usage

```
SerialParam(catch.errors = TRUE)
```

**Arguments**

`catch.errors` `logical(1)` Flag to determine in apply-like functions (see e.g. [bplapply](#)) whether to quit with an error as soon as one application fails or encapsulation of function calls in `try` blocks which triggers a resume mechanism (see [bpresume](#)). Defaults to TRUE.

**SerialParam constructor**

Return an object to be used for serial evaluation of otherwise parallel functions such as [bplapply](#), [bpvec](#).

**Methods**

The following generics are implemented and perform as documented on the corresponding help page (e.g., `?bpworkers`): [bpworkers](#), [bpisup](#), [bpstart](#), [bpstop](#), are implemented, but do not have any side-effects.

**Author(s)**

Martin Morgan <mailto:mtmorgan@fhcrc.org>

**See Also**

`getClass("BiocParallelParam")` for additional parameter classes.  
`register` for registering parameter classes for use in parallel evaluation.

**Examples**

```
p <- SerialParam()
simplify2array(bplapply(1:10, sqrt, BPPARAM=p))
bpvec(1:10, sqrt, BPPARAM=p)

## Not run:
register(SerialParam(), default=TRUE)

## End(Not run)
```

---

SnowParam-class	<i>Enable simple network of workstations (SNOW)-style parallel evaluation</i>
-----------------	---

---

**Description**

This class is used to parameterize simple network of workstations (SNOW) parallel evaluation on one or several physical computers. `snowWorkers()` chooses the number of workers based on global user preference (`options(mc.cores=...)`), or the minimum of 8 and the number of detected cores (`detectCores()`).

**Usage**

```

SnowParam(workers = snowWorkers(), type=c("SOCK", "PSOCK", "FORK", "MPI"),
  catch.errors = TRUE, ...)

## invoke as(cl, "SnowParam")
## S4 method for signature SOCKcluster,SnowParam
coerce(from, to)
## S4 method for signature spawnedMPIcluster,SnowParam
coerce(from, to)

snowWorkers()

```

**Arguments**

workers	integer(1) Number of workers on with Multicore and SSH backend which defaults here to all workers available. On managed HPC workers defaults to NA but can be set to control chunking of jobs. See argument n.chunks in <a href="#">chunk</a> and <a href="#">submitJobs</a> for more information.
type	character(1) type of cluster to use, as described in <a href="#">clusterMap</a> argument type. Use MulticoreParam instead of type=FORK.
catch.errors	logical(1) Flag to determine in apply-like functions (see e.g. <a href="#">bplapply</a> ) whether to quit with an error as soon as one application fails or encapsulation of function calls in <a href="#">try</a> blocks which triggers a resume mechanism (see <a href="#">bpresume</a> ). Defaults to TRUE.
...	Additional arguments passed to <a href="#">makeCluster</a>
from, to	(N.B. Use <code>as(from, "SnowParam")</code> to coerce from a cluster created with, e.g., <code>parallel::makeCluster</code> ). <code>from</code> is a <code>SOCKcluster</code> or derived instance (e.g., <code>from parallel::makeCluster</code> ), to be coerced to a <code>SnowParam</code> instance.

**SnowParam constructor**

Return an object representing a SNOW cluster. The cluster is not created until `bpstart` is called.

`bpstart` creates the cluster by invoking `makeCluster` with arguments `spec=workers`, `type`, and other arguments passed to `...` in `SnowParam`.

Use `as(cl, "SnowParam")` to coerce a cluster created directly by `parallel::param` to a `SnowParam` instance. Instances created in this way cannot be started or stopped.

**Methods**

The following generics are implemented and perform as documented on the corresponding help page (e.g., `?bpisup`): [bpworkers](#), [bpstart](#), [bpstop](#), [bpisup](#), [bpbackend](#), [bpbackend<-](#), [bpvec](#).

**Author(s)**

Martin Morgan <mailto:mtmorgan@fhcrc.org>

**See Also**

`getClass("BiocParallelParam")` for additional parameter classes.  
`register` for registering parameter classes for use in parallel evaluation.

**Examples**

```
snowWorkers()  
p <- SnowParam(2L)  
bplapply(1:10, sqrt, BPPARAM=p)  
bpvec(1:10, sqrt, BPPARAM=p)  
  
## Not run:  
register(SnowParam(2L), default=TRUE)  
  
## End(Not run)
```

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