# Package: BiocParallel.FutureParam (via r-universe)

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**Version** 0.2.1-9001

**Depends** R (>= 3.3.0), future (>= 1.21.0), BiocParallel (>= 1.6.0)

**Imports** methods

**Suggests** markdown, R.rsp

**VignetteBuilder** R.rsp

**Title** Use Futures with BiocParallel

**Description** A 'BiocParallelParam' class for using futures with the BiocParallel framework, e.g. BiocParallel::register(FutureParam()).

**License** LGPL (>= 2.1)

**LazyLoad** TRUE

**URL** https://BiocParallel.FutureParam.futureverse.org, https://github.com/HenrikBengtsson/BiocParallel.FutureParam

**BugReports** https://github.com/HenrikBengtsson/BiocParallel.FutureParam/issues

**RoxygenNote** 7.3.3

**Roxygen** list(markdown = TRUE)

**Repository** https://futureverse-devel.r-universe.dev

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**RemoteUrl** https://github.com/futureverse/BiocParallel.FutureParam

**RemoteRef** develop

**RemoteSha** 689aa00b8f5d8508b07475b6e982529af1c365e6

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`BiocParallel.FutureParam` *BiocParallel.FutureParam: A BiocParallelParam class using Futures*

## Description

The **BiocParallel.FutureParam** package provides FutureParam, a BiocParallel::BiocParallelParam class, for the **BiocParallel** package that works with *any* type of future. (that is supported by Future API of the **future** package) can be used for asynchronous (parallel/distributed) or synchronous (sequential) processing.

## Details

Futures themselves are provided by the **future** package, e.g. multicore, multisession, ad hoc cluster, and MPI cluster futures. Additional futures are provided by other packages. For example, batchtools futures are implemented by the **future.batchtools** package, which expands the support for asynchronous processing to anything that the **batchtools** package supports.

To use futures with the **BiocParallel** package, load **BiocParallel.FutureParam**, call `register(FutureParam())`, select the type of future you wish to use via `future:plan()`.

## Author(s)

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- Ryan Thompson [contributor]

## See Also

Useful links:

- https://BiocParallel.FutureParam.futureverse.org
- https://github.com/HenrikBengtsson/BiocParallel.FutureParam
- Report bugs at https://github.com/HenrikBengtsson/BiocParallel.FutureParam/issues

## Examples

```
library("BiocParallel.FutureParam")
register(FutureParam())
plan(multisession)

mu <- 1.0
sigma <- 2.0
x <- bplapply(1:3, mu = mu, sigma = sigma, function(i, mu, sigma) {
  rnorm(i, mean = mu, sd = sigma)
})
print(x)
```

```
## WORKAROUND: For some reason, 'R CMD check' on Windows will give an
## error when running this example with plan(multisession), unless we
## reset the future plan at the end.
plan(sequential)
```

---

FutureParam *Creates a FutureParam object*

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## Description

Creates a FutureParam object

## Usage

```
FutureParam(...)
```

## Arguments

| | |
|---|---|
| ... | Arguments passed to the initialization method of BiocParallel::BiocParallelParam. |

## Value

A BiocParallel::BiocParallelParam object of class FutureParam.

## Examples

```
library("BiocParallel.FutureParam")
register(FutureParam())
plan(multisession)

mu <- 1.0
sigma <- 2.0
x <- bplapply(1:3, mu = mu, sigma = sigma, function(i, mu, sigma) {
  rnorm(i, mean = mu, sd = sigma)
})
print(x)

## WORKAROUND: For some reason, 'R CMD check' on Windows will give an
## error when running this example with plan(multisession), unless we
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plan(sequential)
```

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