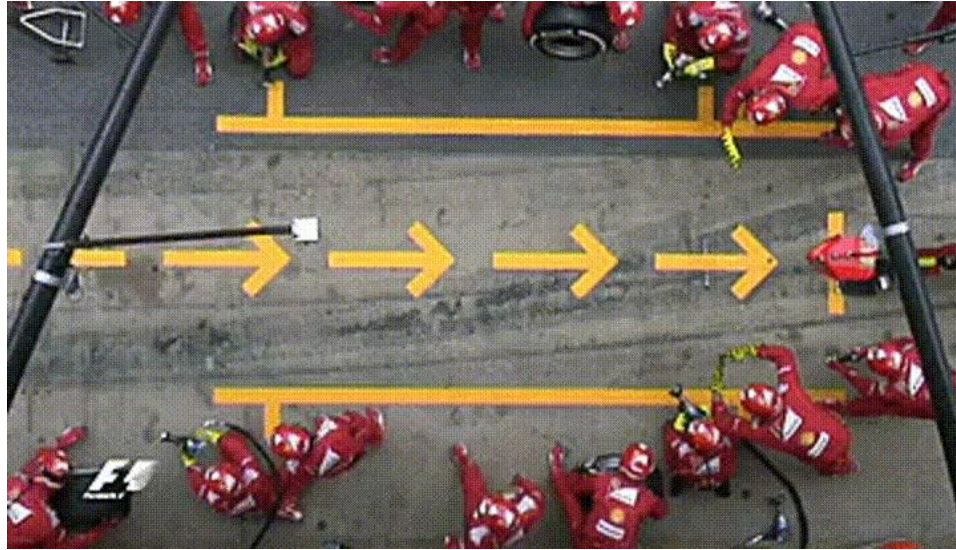



Futureverse: A Unifying Parallelization Framework in R for Everyone - Part 2



Henrik Bengtsson

University of California, San Francisco
R Foundation, R Consortium

  @HenrikBengtsson

 HenrikBengtsson

 jottr.org

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Parallelization should be simple

```
x <- 1:20
```

```
y <- lapply(x, slow)
```

Main R session:

```
1m: y[[1]] <- slow(x[1])
```

```
2m: y[[2]] <- slow(x[2])
```

...

```
20m: y[[20]] <- slow(x[20])
```

Time: 20 mins

```
x <- 1:20
```

```
y <- mclapply(x, slow, mc.cores=2)
```

Parallel worker #1:

```
1m: y[[1]] <- slow(x[1])
```

```
2m: y[[2]] <- slow(x[2])
```

...

```
10m: y[[10]] <- slow(x[10])
```

Parallel worker #2:

```
y[[11]] <- slow(x[11])
```

```
y[[12]] <- slow(x[12])
```

...

```
y[[20]] <- slow(x[20])
```

Time: 10 mins

Overwhelming to get started

- So many parallel API - which one should I choose?
 - `mclapply()`, `parLapply()`, `foreach()`, ...
- What operating systems should I support?
 - I use Linux. Will it work on Windows and macOS?
- Will it scale?
- Do I need to maintain two code bases - sequential and parallel?
- **Error in { : task 1 failed - "object 'data' not found"**

R package: future

- A simple, unifying solution for parallel APIs
- "Write once, run anywhere"
- 100% cross platform
- Easy to install (< 0.5 MiB total)
- Very well tested, lots of CPU mileage, used in production
- Things “just work”



Dan LaBar
@embiggenData

All we need are three building blocks

```
f <- future(expr)    # evaluate in parallel
r <- resolved(f)      # check if done
v <- value(f)         # wait & get result
```

This was invented in 1975

```
parallel_lapply <- function(X, FUN, ...) {
  fs <- lapply(X, function(x) future(FUN(x, ...)))
  lapply(fs, value)
}
```

Lab 2: Refresher and parallelize purrr

- Task 1: `purrr::map()` -> `parallel_map()`
- Task 2: `purrr::map_dbl()` -> `parallel_map_dbl()`
- Task 3-4: Things that are problematic

Building things using the core future blocks

```
f <- future(expr)    # create future  
r <- resolved(f)     # check if done  
v <- value(f)        # wait & get result
```



A parallel version of lapply()

```
#' @importFrom future future value
parallel_lapply <- function(X, FUN, ...) {
  # Create futures
  fs <- lapply(X, function(x) future(FUN(x, ...)))
  # Collect their values
  lapply(fs, value)
}
```

```
> library(DNAseq)
> plan(multisession)
> bam <- parallel_lapply(fq, align)
> bam
[1] "file1.bam" "file2.bam" "file3.bam"
```


Package: future.apply

- Futurized version of base R's `lapply()`, `vapply()`, `replicate()`, ...
- ... on all future-compatible backends
- Load balancing ("chunking")
- Proper parallel random number generation

```
bam <- lapply(fq, align)
```

```
bam <- future_lapply(fq, align)
```

```
plan(multisession)
```

```
plan(cluster, workers = c("n1", "n2", "n3"))
```

```
plan(batchtools_slurm)
```

```
...
```

A parallel version of purrr::map()

```
#' @importFrom purrr map
#' @importFrom future future value
parallel_map <- function(.x, .f, ...) {
  # Create futures
  fs <- map(.x, function(x) future(.f(x, ...)))
  # Collect their values
  map(fs, value)
}
```

```
> library(DNAseq)
> plan(multisession)
> bam <- parallel_map(fq, align)
> bam
[1] "file1.bam" "file2.bam" "file3.bam"
```

Package: furr (Davis Vaughan)

- Futurized version of **purrr**'s `map()`, `map2()`, `modify()`, ...
- ... on all future-compatible backends
- Load balancing ("chunking")
- Proper parallel random number generation

```
bam <-          map(fq, align)
```

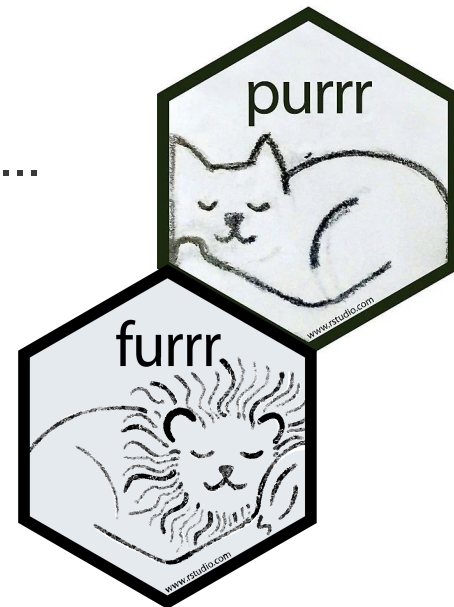
```
bam <- future_map(fq, align)
```

```
plan(multisession)
```

```
plan(cluster, workers = c("n1", "n2", "n3"))
```

```
plan(batchtools_slurm)
```

```
...
```



“Base R vs Tidyverse”

Base R style (R & future.apply)

```
bam <- lapply(fq, align)
```

```
bam <- future_lapply(fq, align)
```

Tidyverse style (purrr & furrr)

```
bam <- map(fq, align)
```

```
bam <- future_map(fq, align)
```

Seriously ...

It's not a war - use the style you prefer!

Both work equally well and are equally fast.

User chooses how to parallelize

- sequential
`plan(sequential)`
- parallelize on local machine
`plan(multisession)`
- multiple local or remote computers, or cloud compute services
`plan(cluster, workers=c("n1", "m2.uni.edu", "vm.cloud.org"))`
- High-performance compute (HPC) cluster
`plan(batchtools_slurm)`

Your future code remains the same!

Let's talk foreach



blasbenito.com

<https://blasbenito.com> › post · [Översätt den här sidan](#)

Parallelized loops with R | Blas M. Benito, PhD

1 apr. 2021 — To run tasks in **parallel**, foreach uses the operator `%dopar%`, that has to be supported by a **parallel** backend. If there is no **parallel** backend, % ...



Stack Overflow

<https://stackoverflow.com> › ru... · [Översätt den här sidan](#)

run a for loop in parallel in R

12 juli 2016 — Running things in **parallel** requires quite a bit of overhead. You will only get a substantial speed up if functionThatDoesSomething takes enough ...

1 svar · Bästa svaret: Thanks for your feedback. I did look up parallel after I posted this questio...

How can I run a for **loop** in **parallel** in **R** - Stack Overflow 29 okt. 2018

Parallel Computing for nested for **loop** in **R** - Stack Overflow 23 feb. 2022

How to **parallelize** a for **loop** that is looping over a vector in **R** 25 aug. 2022

How to **parallelize** for loops in **R** using multiple cores? 28 nov. 2021

Fler resultat från stackoverflow.com



Appilon

<https://www.appilon.com> › post · [Översätt den här sidan](#)

R doParallel: A Brain-Friendly Introduction to Parallelism in R

To run the **loop** in **parallel**, you need to use the `foreach()` function, followed by `%dopar%`. Everything after curly brackets (inside the **loop**) will be executed in ...



ScatterPlot.Bar

<https://scatterplot.bar> › blog › h... · [Översätt den här sidan](#)

How to parallelize for loops in R

5 feb. 2023 — 4) Perform **parallel for loop** calculation in **R** using “`foreach()`” function. Again, this code uses the objects and functions that were necessary ...



[Example with Duck Duck Go ...](#)

The name foreach() tricks us to believe it's a for-loop ...

```
fq <- fs::dir_ls(glob = "*.fq")  
bam <- list()  
for (ii in seq_along(fq)) {  
  bam[[ii]] <- align(fq[[ii]])  
}
```


... but we *must never* think of it as a for-loop

```
library(foreach)

fq <- fs::dir_ls(glob = "*.fq")
bam <- list()
foreach(ii = seq_along(fq)) %dopar% {
  bam[[ii]] <- align(fq[[ii]])
}
```

***This does not work because:
foreach() is not a for-loop!***

Repeat after me: foreach() is not a for-loop!

```
for (ii in 1:1000) {  
  message("foreach() is not a for-loop!")  
}
```

foreach() is not a for-loop!

foreach() is not a for-loop!

foreach() is not a for-loop!

foreach() is not a for-loop!

foreach() is not a for-loop!

foreach() is not a for-loop!

foreach() is just like lapply() ...

```
fq <- fs::dir_ls(glob = "*.fq")  
bam <- list()  
lapply(seq_along(fq), function(ii) {  
  bam[[ii]] <- align(fq[[ii]])  
})
```

This does not work, because the <- assignment is done inside a function

... and just like map() ...

```
fq <- fs::dir_ls(glob = "*.fq")  
bam <- list()  
purrr::map(seq_along(fq), function(ii) {  
  bam[[ii]] <- align(fq[[ii]])  
})
```

***This does not work, because the <-
assignment is done inside a function***

If foreach() had looked like ...

```
fq <- fs::dir_ls(glob = "*.fq")  
bam <- list()  
foreach(seq_along(fq), function(ii) {  
  bam[[ii]] <- align(fq[[ii]])  
})
```

It would be clear that the <- assignment is done inside a function

lapply(), map(), foreach() return values

```
fq <- fs::dir_ls(glob = "*.fq")
```

```
bam <- lapply(seq_along(fq), function(ii) {  
  align(fq[[ii]])  
})
```

```
bam <- purrr::map(seq_along(fq), function(ii) {  
  align(fq[[ii]])  
})
```

```
bam <- foreach(ii = seq_along(fq)) %dopar% {  
  align(fq[[ii]])  
}
```

lapply(), map(), foreach() return values

```
fq <- fs::dir_ls(glob = "*.fq")
```

```
bam <- lapply(fq, align)
```

```
bam <- purrr::map(fq, align)
```

```
bam <- foreach(x = fq) %dopar% align(x)
```

Package: doFuture

- **%dofuture%** - a futurized foreach adaptor
- ... on all future-compatible backends
- Load balancing ("chunking")
- Proper parallel random number generation

```
bam <- foreach(x = fq) %do%          align(x)
```

```
bam <- foreach(x = fq) %dofuture% align(x)
```

```
plan(multisession)
```

```
plan(cluster, workers = c("n1", "n2", "n3"))
```

```
plan(batchtools_slurm)
```

```
...
```


Stay with your favorite coding style 1/2

Base R style (R & future.apply)

```
bam <- lapply(fq, align)
```

```
bam <- future_lapply(fq, align)
```

Tidyverse style (purrr & furrr)

```
bam <- map(fq, align)
```

```
bam <- future_map(fq, align)
```

Foreach style (foreach & doFuture)

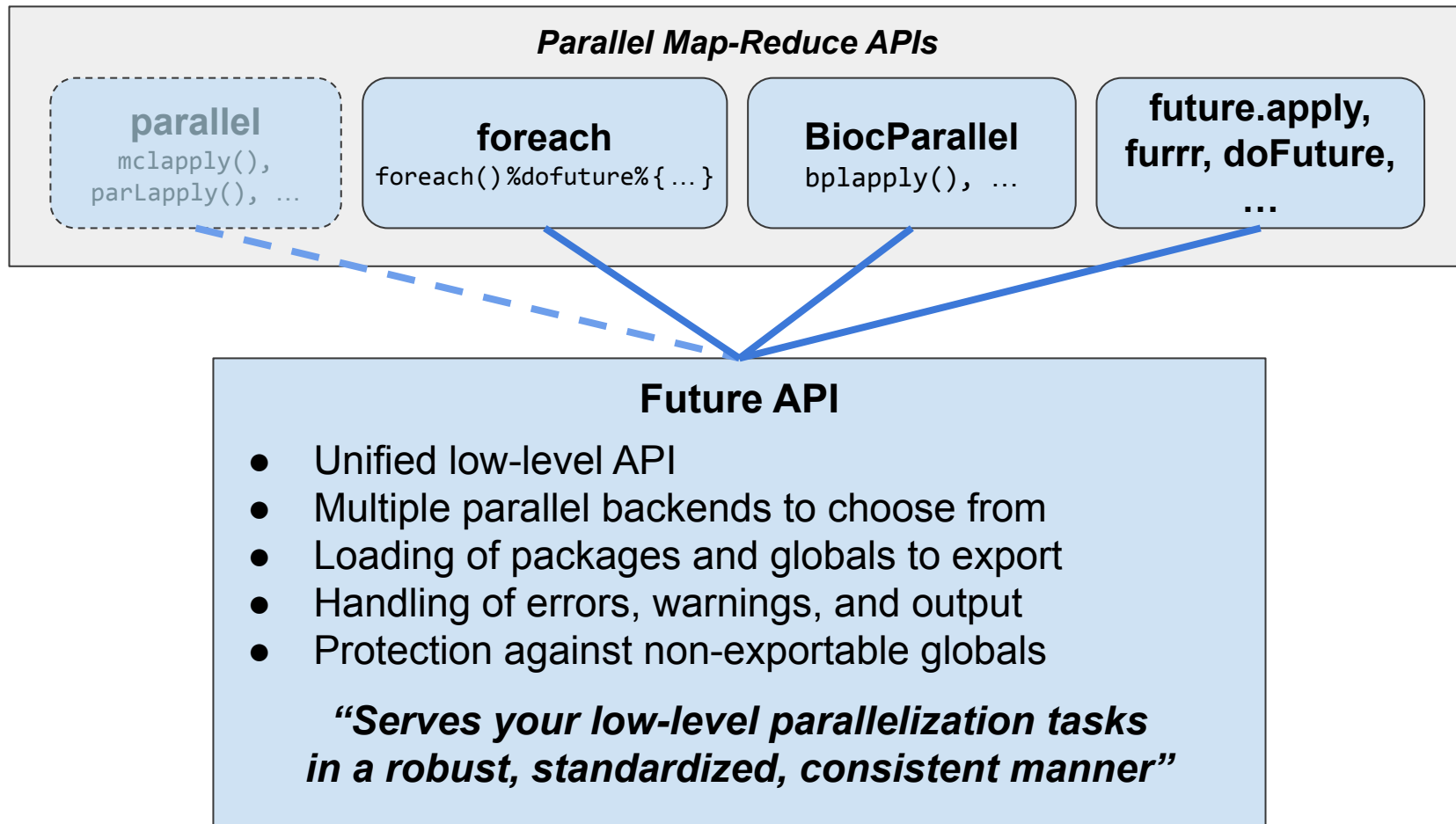
```
bam <- foreach(x = fq) %do% align(x)
```

```
bam <- foreach(x = fq) %dofuture% align(x)
```

Stay with your favorite coding style 2/2

```
# Bioconductor's BiocParallel  
register(DoparParam()) # BiocParallel to use %dopar%  
doFuture::registerDoFuture() # %dopar% to use futures  
bam <- bplapply(fq, align)
```

2024: Futureverse widely supported



Output, Warnings, and Errors

Lab 2: Errors and parallel processing

- Tasks 5-9: Errors
- Tasks 10-11: Warnings

Output and warnings behave consistently for all parallel backends

```
> x <- c(-1, 10, 30)
> y <- future_lapply(x, function(z) {
  message("z = ", z)
  log(z)
})
```

```
z = -1
```

```
z = 10
```

```
z = 30
```

Warning message:

In log(z) : NaNs produced

```
>
```

<= Output relayed from workers

<= Warnings are relayed too

Other frameworks: No output/warnings

```
> x <- c(-1, 10, 30)
> y <- mclapply(x, function(z) {
  message("z = ", z)
  log(z)
})
>
```

**<= Output and warnings
completely muffled!**

```
> cl <- makeCluster(2)
> y <- parLapply(cl, x, function(z) {
  message("z = ", z)
  log(z)
})
>
```

**<= Output and warnings
completely muffled!**

Same for foreach w/ doParallel etc.

```
> x <- c(-1, 10, 30)
> cl <- makeCluster(2)
> doParallel::registerDoParallel(cl)
> y <- foreach(z = x) %dopar% {
  message("z = ", z)
  log(z)
}
>
```

**<= Output and warnings
completely muffled!**

foreach w/ doFuture works

```
> x <- c(-1, 10, 30)
> y <- foreach(z = x) %dofuture% {
  message("z = ", z)
  log(z)
}
```

```
z = -1
```

```
z = 10
```

```
z = 30
```

Warning message:

In log(z) : NaNs produced

```
>
```

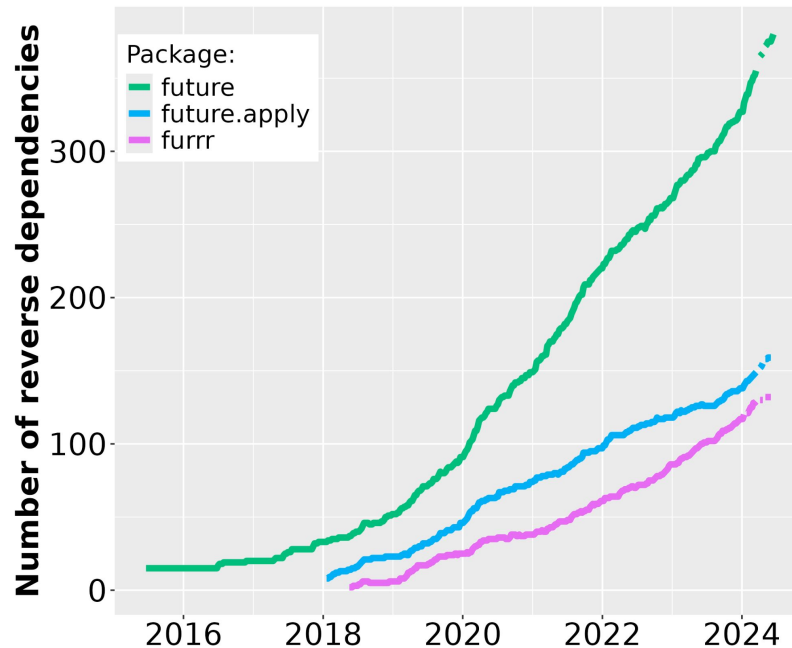
<= Output relayed from workers

<= Warnings are relayed too

Who's using Futureverse?

Many packages use Futureverse to parallelize

- **Seurat**: Large-Scale Single-Cell Genomics
 - Instructions: “set plan(multisession)” from [help\(“prepsctfindmarkers”\)](#)
- **mlr3**: Next-Generation Machine Learning
 - Instructions: “set plan(multisession)” from [mlr3 book](#)



downloads 217K/month

Load balancing (“chunking”)

Chunking: All in a single round (default)

<pre>x <- 1:20 y <- map_dbl(x, slow)</pre>	<pre>plan(multisession, workers = 2) x <- 1:20 y <- future_map_dbl(x, slow)</pre>
--	---

Main R session:

```
1m: y[1] <- slow(x[1])  
2m: y[2] <- slow(x[2])  
...  
...
```

```
20m: y[20] <- slow(x[20])
```

Time: 20 mins

Parallel worker #1: Parallel worker #2:

1m: y[1] <- slow(x[1])	y[11] <- slow(x[11])
2m: y[2] <- slow(x[2])	y[12] <- slow(x[12])
...	...
10m: y[10] <- slow(x[10])	y[20] <- slow(x[20])

Time: 10 mins

Chunking

```
plan(multisession, workers = 3)
```

```
x <- 1:20
```

```
y <- future_map_dbl(x, slow)
```

<i>Parallel worker #1:</i>	<i>Parallel worker #2:</i>	<i>Parallel worker #3:</i>
1m: y[1] <- slow(x[1])	y[8] <- slow(x[8])	y[15] <- slow(x[15])
2m: y[2] <- slow(x[2])	y[9] <- slow(x[9])	y[16] <- slow(x[16])
...
6m: y[6] <- slow(x[6])	y[13] <- slow(x[13])	y[20] <- slow(x[20])
7m: y[7] <- slow(x[7])	y[14] <- slow(x[14])	

Time: 7 mins

Chunking

```
plan(multisession, workers = 4)
```

```
x <- 1:20
```

```
y <- future_map_dbl(x, slow)
```

	<i>Parallel worker #1:</i>	<i>Parallel worker #2:</i>	<i>Parallel worker #3:</i>	<i>Parallel worker #4:</i>
1m:	y[1] <- slow(x[1])	y[6] <- slow(x[6])	y[11] <- slow(x[11])	y[16] <- slow(x[16])
2m:	y[2] <- slow(x[2])	y[7] <- slow(x[7])	y[12] <- slow(x[12])	y[17] <- slow(x[17])

5m:	y[5] <- slow(x[5])	y[10] <- slow(x[10])	y[15] <- slow(x[15])	y[20] <- slow(x[20])

Time: 5 mins

Uniform tasks with default chunking

10 tasks: ■ ■ ■ ■ ■ ■ ■ ■ ■ ■

```
y <- future_map_dbl(x, slow)
```

Worker #1: ■ ■ ■ ■ ■

Worker #2: ■ ■ ■ ■ ■

Worker #1: ■ ■ ■ ■

Worker #2: ■ ■ ■

Worker #3: ■ ■ ■

Worker #1: ■ ■ ■

Worker #2: ■ ■ ■

Worker #3: ■ ■

Worker #4: ■ ■

Variables tasks with default chunking

10 tasks: 

```
y <- future_map_dbl(x, slow)
```

Worker #1: 

Worker #2: 

Worker #1: 

Worker #2: 

Worker #3: 

Worker #1: 

Worker #2: 

Worker #3: 

Worker #4: 

Variables tasks with teeny chunks

10 tasks: 

```
y <- future_map_dbl(x, slow,  
                    .options=future_options(chunk.size=1))
```

Worker #1: 
Worker #2: 

Worker #1: 
Worker #2: 
Worker #3: 




Worker #1: 
Worker #2: 
Worker #3: 
Worker #4: 

Variables tasks with small chunks

10 tasks: 

```
y <- future_map_dbl(x, slow,  
                    .options=future_options(chunk.size=2))
```

Worker #1: 
Worker #2: 

Worker #1: 
Worker #2: 
Worker #3: 

Worker #1: 
Worker #2: 
Worker #3: 
Worker #4: 

High Performance Compute (HPC)

Backend package: future.batchtools

```
plan(future.batchtools::batchtools_slurm)
```

```
fq <- fs::dir_ls(glob = "*.fq")          ## 80 files; 200 GB each  
bam <- future_lapply(fq, align)         ## 1 hour each
```

```
{henrik: ~}$ squeue
```

Job ID	Name	User	Time Use	S
606411	xray	alice	46:22:22	R
606638	future_lapply-5	henrik	00:52:05	R
606641	python	bob	37:18:30	R
606643	future_lapply-6	henrik	00:51:55	R
...				

Progress Updates



progressr - Inclusive, Unifying API for Progress Updates

Works anywhere - including Futureverse, purrr, lapply, foreach, for/while loops, ...

API for Developers:

```
p <- progressor(along = x)
p(msg)
```

Developer decides:

where in the code progress updates should be signaled

API for Users:

```
handlers(global = TRUE)
handlers("cli")
```

User decides:

if, when, and how progress updates are presented

Developer focuses on providing updates

Package code

```
snail <- function(x) {
  p <- progressor(along = x)
  y <- map_dbl(x, function(z) {
    p(paste0("z=", z))
    slow(z)
  })
  sum(y)
}
```

User

```
> handlers$global = TRUE)
> x <- snail(x)
> y <- snail(x)
```

[====>=====] 10% z=10

User decides how progress is presented

```
# without progress updates
```

```
> x <- 1:50  
> y <- snail(x)
```

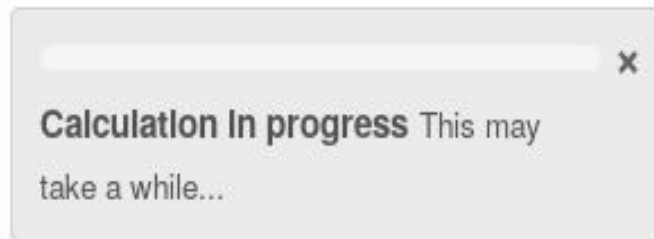
```
> handlers("beep")  
> y <- snail(x)
```

♪ ♪ ♪ ♪ ... ♪

```
> handlers("cli", "beep")  
> y <- snail(x)  
[=====>-----] 40% z=20
```

♪ ♪ ♪ ♪ ... ♪

Works also with Shiny
withProgressShiny()



future + progressr = ♥



Futureverse supports live progress updates

```
snail <- function(x) {  
  p <- progressor(along=x)  
  y <- future_map_dbl(x, function(z) {  
    p(paste0("z=", z, " by ", Sys.getpid()))  
    slow(z)  
  })  
  sum(y)  
}
```

```
> handlers(global = TRUE)  
> handlers("cli", "beep")  
> plan(multisession)  
> y <- snail(x)
```

```
[=>=>=>=>=>=>=>] 90% z=30 by 3002
```

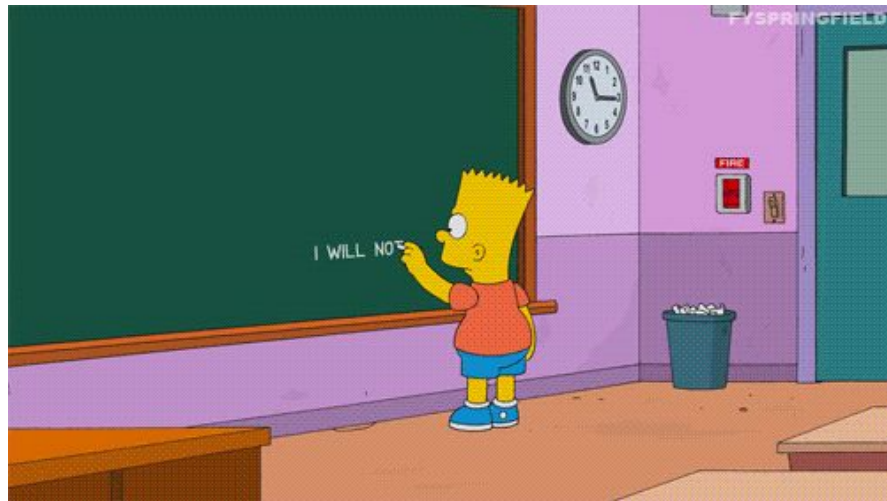
    ... 

Lab 2: Progress updates

- Task 12-17: Progress updates and customization
- Task 18: Progress updates in parallel





Take home: future = 99% worry-free parallelization

- Use Futureverse instead of mclapply(), parLapply(), doParallel(), ...
- Use future.apply, furrr, or foreach with doFuture - your choice
- "Write once, run anywhere" - compute clusters too
- Global variables - automatically taken care of
- Stdout, messages, warnings, *progress* - captured and relayed



It's easy to get started ❤️

- It's easy to get started - just try it
- Support: <https://github.com/HenrikBengtsson/future/discussions>
- Tutorials: <https://www.futureverse.org/tutorials.html>
- Blog posts: <https://www.futureverse.org/blog.html>
- More features on the roadmap
- I love feedback and ideas

  @HenrikBengtsson
 HenrikBengtsson
 jottr.org

