Introduction to parallel R

Course: Parallel computing in R

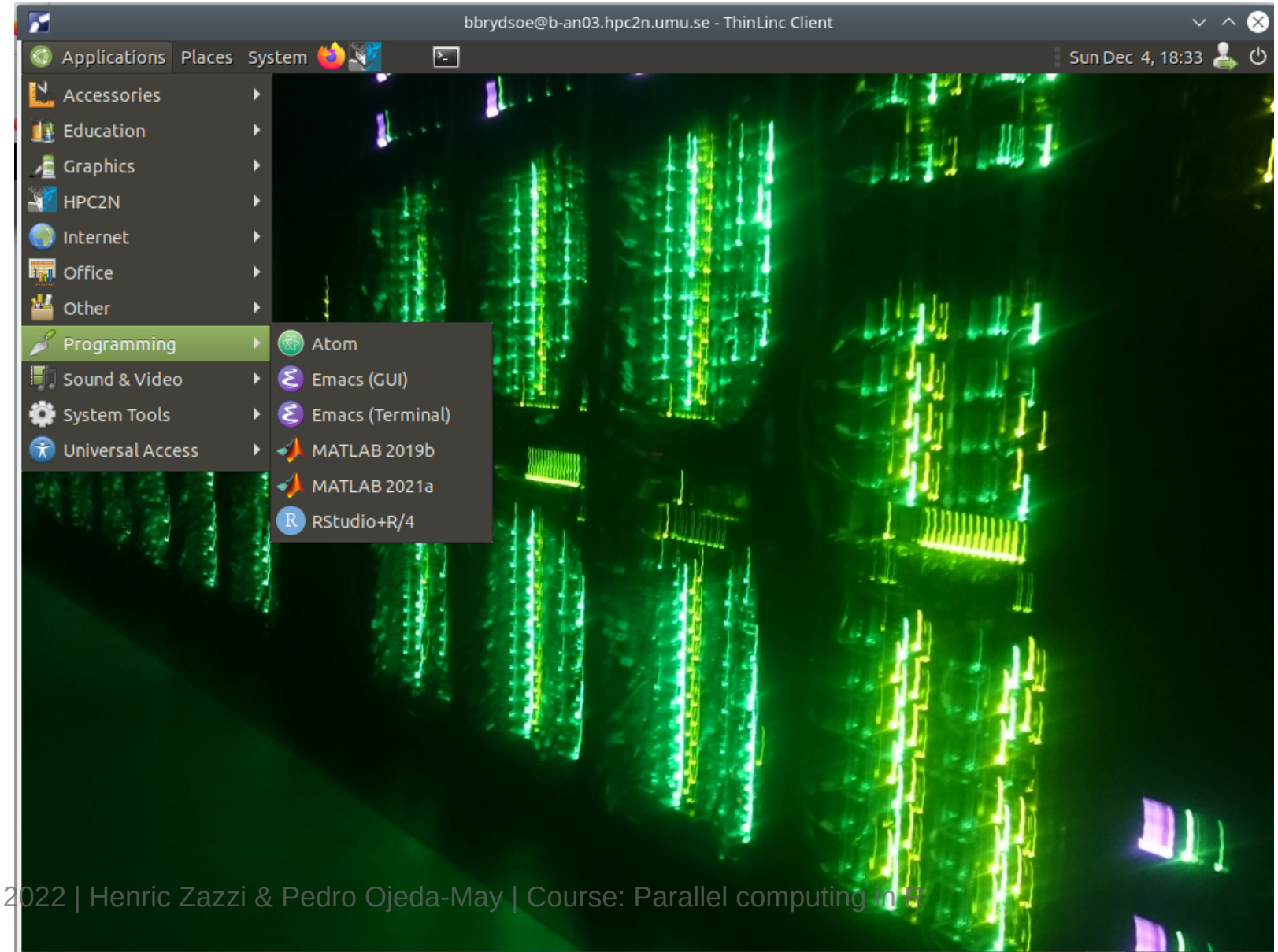
Overview

1. Client software
2. Installing packages
3. How to run R in parallel
4. Functions in R for speeding up execution

Client software

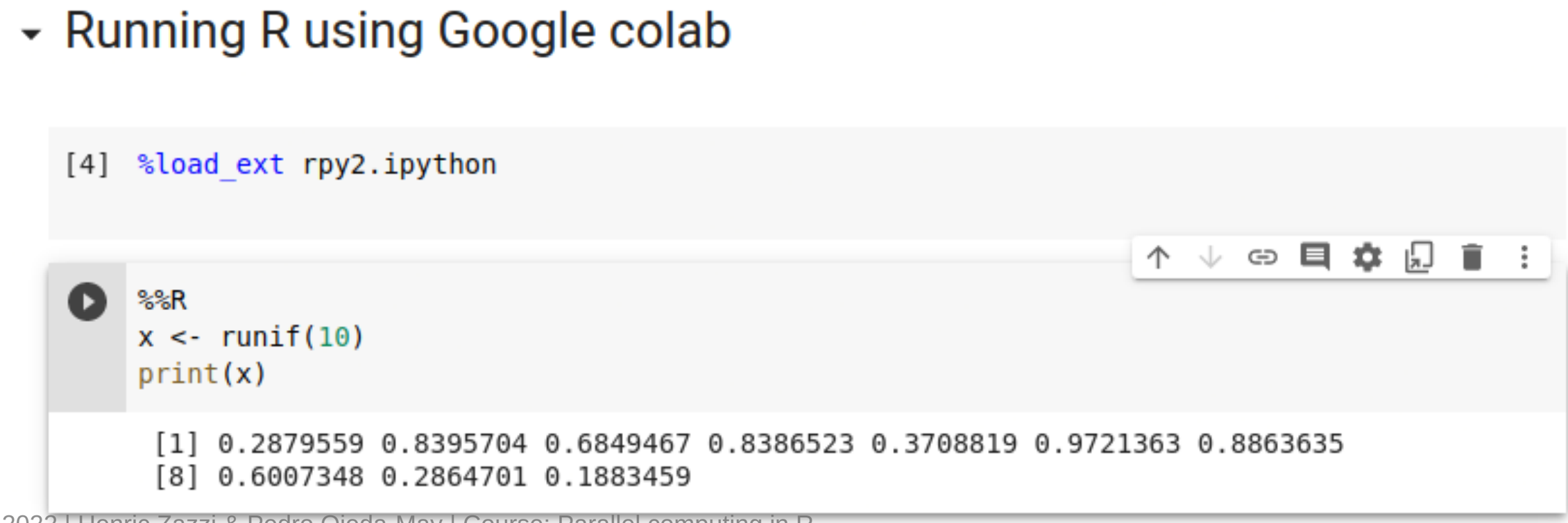
How to install R/RStudio on Linux

https://posit.co/download/rstudio-desktop/



Running R using Jupyter-notebook

1. Create a new google colab notebook
   https://colab.research.google.com/#create=true
2. You can run both R and Python
3. You can install R packages (within limits)



Installing R packages

How to install packages in R

List of packages

```
> installed.packages()
          Package
Matrix    "Matrix"
Rmpi      "Rmpi"
base      "base"
```

Where are they installed

```
> .libPaths()
[1] "/home/hzazzi/R/3.6"
[2] "/usr/local/lib/R/site-library"
```

Install packages

```
> install.packages("<NAME>",
    lib=.libPaths()[1])
```

How to install R packages on cluster

1. Create folder for your R library

```
mkdir ~/myR/library
export R_LIBS_USER=~/myR/library
```

2. Install the package you need in your local folder

```
> .libPaths()
[1] "/home/hzazzi/myR/library"
[2] "/usr/local/lib/R/site-library"
> install.packages("<NAME>",lib=.libPaths()[1])
```

How to run R on cluster

How to run interactively

1. Request a SLURM job allocation

```
salloc -A <ALLOCATION> -p shared -N 1 -t 10
```

2. Add the necessary modules

```
ml R/<VERSION>
```

How to run interactively (2)

1. Run!

```
srun -n 1 R --no-save < [myscript]
```

Prints all output (code, results)

```
srun -n 1 Rscript [myscript]
```

Prints only results

2. Exit the job allocation

```
exit
```

How to send in jobs

1. Create an SBATCH script file
2. Send in the job

```
sbatch [myscript]
```

3. Monitor the job

```
squeue -u [username]
```

4. Kill the job (if needed)

```
scancel [jobID]
```

```
#!/bin/bash -l
# Set the job allocation
#SBATCH -A <allocation>
# Run on a shared partition
#SBATCH -p shared
# The name of the script is myjob
#SBATCH -J myjob
# Only 1 minute wall-clock time
#SBATCH -t 1:00
# Number of nodes
#SBATCH --nodes=1
#SBATCH -e error_file.e
#SBATCH -o output_file.o
# Load the modules
module add R/<VERSION>
srun -n 1 R --no-save < [R file]
```

Functions in R for speeding up execution

Calculate how fast your code is

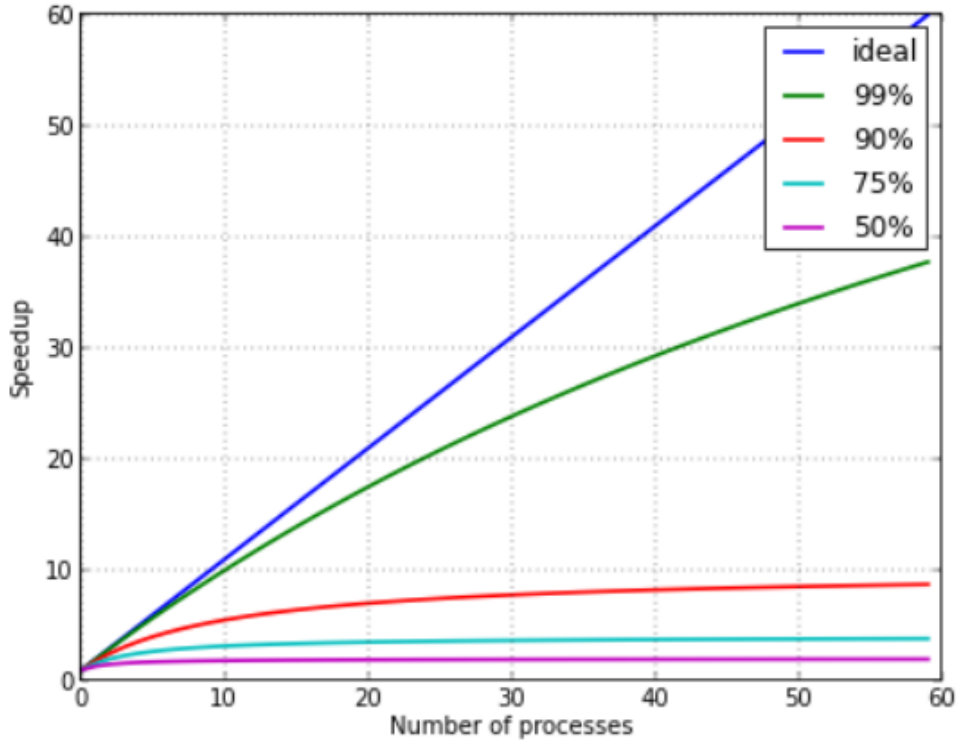
- Compare parallel execution with increasing number of processes

1. Method 1

```
start_time <- Sys.time()
<ALL THE CODE>
print(Sys.time() - start_time)
```

2. Method 2

```
print(system.time({
<ALL THE CODE>
}))
```



Microbenchmark

- Library to provide more accurate timing of your functions
- By default runs your code a 100 times
    - You can set the flag *times=N* to change that
- Outputs statistics of your code

```
library(microbenchmark)
res <- microbenchmark({
  <ALL THE CODE>
  })
```

To get only the average of the computing time

```
summary(res)$mean
```

apply function collection

1. Executes functions **FUN** to elements of variable **X**
2. Compiled optimization as we do not have to do a *for* loop
3. Works on internal and user defined functions

Example of lapply

- We have a list of vectors (Default dataset of co2 concentrations in ppm 1959 to 1997)

```
x <- split(co2, ceiling(seq_along(co2)/12))
names(x) <- c(1959:1997)
```

- Using **for** loop to calculate yearly mean of *x*

```
for (i in x)
  print(mean(i))
```

- Using **lapply** to calculate mean of *x*

```
print(lapply(x, mean))
```

Table of functions

Function	Arguments	Objective	Input	Output
apply	apply (x, M, FUN)	Apply to rows (M=1), columns (M=2), both (M=c(1,2())	Data frame, vector	Vector, list, array
lapply	lapply(x, FUN)	Apply to all elements of the input	List, vector, data frame	list
sapply	sapply(x, FUN)	apply to all the elements	List, vector, data frame	Vector, matrix

Example: replicate

Easy method to multiply your data for additional analysis

```
y <- replicate(n = 10, expr = co2, simplify = F)
```

Replicate is a wrapper for sapply

Simplify	Return type
T (True)	Array
F (False)	List