High Performance Computing Assignment 2022/2023

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1 Exercise 1

1.1 Introduction

1.1.1 Rules of the Game of Life (GOL)

Each cell can be either "alive" or "dead" depending on the conditions of the neighbouring cells:

- a cell becomes, or remains, alive if 2 to 3 cells in its neighbourhood are alive;
- a cell dies, or does not generate new life, if either less than 2 cells or more than 3 cells in its neighbourhood are alive (under-population or over-population conditions, respectively). In this way, the evolution of the system is completely determined by the initial conditions and by the rules adopted to decide the update of the cells' status.

1.1.2 Notations

This report aims to describe the algorithms chosen for running the Game of Life and their performances, according to the "size" of the problem. Firstly, we define precisely what are the inputs of the problem and what are the outputs.

The main inputs are:

- matrix size, that is a rectangular grid `isize` $\times$ `jsize` (in the experiments we will focus just on square matrices);
- number n of steps to be calculated;
- the type of evolution: static or ordered;
- the frequency s of screenshots requested during the run.

Considering the hardware point of view, there are other important inputs such as the number of MPI processes (`nMPI`) and OMP threads (`nOMP`).

The outputs are the final snapshot after n steps and the time measured during the run of the algorithm which is crucial for the scalability analysis (we will focus on it later).

1.1.3 Methodology

The general setting of this work is organised into the `main.c`, and two source files: `write_pgm_images.c` and `game_functions.c`. The main actually records all the inputs and chooses to run the static or the ordered algorithm. In `write_pgm_images.c` there are the read and write functions for *pgm* images (this is taken from GitHub repository assignment). Finally, `game_functions.c` contains all we need to run the game. In particular, there are:

- `void initialize_game(int isize, int jsize, const char *image_name, double prob)` just creates a `isize` $\times$ `jsize` matrix with every cell alive with probability `prob` and it saves it in a file with name `image_name`.
- `void run_game(int isize, int jsize, const char *image_name, int total_steps, int step_for_snap, int evolution_type)` gets the initial matrix from `image_name`, then run the static (or ordered if `evolution_type` $==$ 0) for `total_steps` number of steps.
- `unsigned char upgrade_cell(unsigned char **pixels, int i, int j, int isize, int jsize)` is the nucleus of the algorithm: it returns a char value ('0' if alive, '255' if dead) that represents the new status of the cell (i, j), given the 2d array `pixels`. This function follows the rule of the game, and note that it just needs "local" information of the neighbourhood of (i, j) to give an output, not all matrix.

The key part of `run_game` algorithm is the nested 'for' loop with the `upgrade_cell` function. This for loop can be parallelized using OMP pragmas, and this is the main and unique point in which we used openMP tools. The entire `run_game` function is built in order to exploit a possible increasing number of MPI processes in the following way:

- We split the starting 2d array into `nMPI` slices with horizontal cuts (so the slices are of `k` $\times$ `jsize`, where `k` is to be determined). If `isize` is a multiple of `nMPI`, all the slices will be equal of dimension: $\frac{\texttt{isize}}{\texttt{nMPI}} \cdot \texttt{jsize}$. Otherwise if the euclidean division gives us $\texttt{isize} = q \cdot \texttt{nMPI} + r$, then the slices will have vertical length of:

$$q+1, q+1, \ldots, q+1, q, \ldots, q$$

with exactly r times the number $q+1$. Hence every MPI process performs its task only on its own slice. It is now obvious that at the beginning of every iteration, we need an `MPI_Scatterv` call to distribute the slices, and at the end of the iteration, an `MPI_Gatherv` to rebuild the entire image (see **Conclusions** section from improvements on this part).

1.2 Implementation

1.2.1 `upgrade_cell` function

We start from the simple function `upgrade_cell`. It doesn't exploit any OMP threadization nor MPI processes, because the operations done are very simple and fast. The only possible problem is the presence of boundaries, but it is easily overcome by using some basic modular arithmetic. Firstly, we store the coordinates of the neighbours, in the following way:

```
int i_mod[3] = {(isize + i - 1) % isize, i % isize, (isize + i + 1) % isize};
int j_mod[3] = {(jsize + j - 1) % jsize, j % jsize, (jsize + j + 1) % jsize};
```

Then we evaluate the sum of the number stored in the neighbours and check if it is equal to $255 \cdot 5$ or $255 \cdot 6$ (in this case the cell (i, j) becomes alive, that is '0').

1.2.2 `run_game` function

The codes of this function are logically divided into two parts, the first concerning the ordered evolution, the other the static evolution.

Ordered evolution The core of this function is the following:

```
for ( int i = 0; i < isize; i++ ){
    for ( int j = 0; j < jsize; j++ ){
        pixels[i][j] = upgrade_cell(isize,jsize,pixels,i,j);
    }
}
```

The previous nested 'for' cycle is inside a big 'for' cycle that iterates on the number of steps (`time_steps` is the variable that counts the steps). Inside there is also:

```
if ( time_steps % step_for_snap == 0){
    sprintf(snapshot_string, "snapshot_O_%05d", time_steps);
    write_pgm_image(pixels, MAXVAL, isize, jsize, snapshot_string);
}
```

Static evolution In the static evolution we exploit MPI and OMP features, as generally explained in the section before. After the call `MPI_Comm_rank(MPI_COMM_WORLD, &rank)`, we split the 2d array `pixels` into `nMPI` "slices":

```
MPI_Comm_rank(MPI_COMM_WORLD, &rank);
MPI_Comm_size(MPI_COMM_WORLD, &size);

// Here we split the image along the y axis
int sub_isize = isize / size;
int rest =  isize % size;

// In the following way we can share part of the image in pieces of sub_isize and sub_isize
    +1
int rank_minor_rest = (rank < rest);
int start = rank * sub_isize + (rank)*(rank_minor_rest);
int end = (rank + 1) * sub_isize + (rank+1)*(rank_minor_rest);

//we need this because the previous assignment from a certain point adds only zeros
if (!rank_minor_rest){
        start += rest;
        end   += rest;
}
```

Then, we need to create two arrays of integers for the calls of MPI_Scatterv and MPI_Gatherv, which are respectively `senddispls` and `recvdispls`. The entry i of such arrays specifies the displacement (relative to sendbuf or recvbuffer) from which to take the outgoing data to process i.

The other two necessary arrays, one for MPI_Scatterv one for MPI_Gatherv, are `sendcounts` and `recvcounts`. Their scope is to specify the number of elements to send (or receive) to (from) each processor. Here there is the code and then an explanation:

```
int sum = 0;
int double_jsize = 2 * jsize;
for (int i = 0; i < size; i++){
    recvcounts[i] = (sub_isize + (i < rest) ) * jsize;
    sendcounts[i] = recvcounts[i]+ double_jsize;
    recvdispls[i] = sum;
    senddispls[i] = sum-jsize;
    sum += recvcounts[i];
}
```

Concerning the MPI_Gatherv call (so, `recvcounts` and `recvdispls`) we just need to create the slices as explained in the **Methodology** section, that is $q\times$ `jsize` or $(q+1)\times$ `jsize` depending on the rest.

For the MPI_Scatterv call, we want to update a slice of dimensions $k\times$`jsize` that begins at row i. So, we need at least a slice of $(k+2)\times$ `jsize` that begins at row $i-1$ (then the function `upgrade_cell` works). This is what exactly we are doing in the previous code for `senddispls` and `sendcounts`. However, the reasoning do not work with the first and the last slices because we would use rows indexes of -1 and `isize`, that are not defined. So, we fix this problem by sending each time all the 2d array, which is the aim of the following code.

```
senddispls[0] = 0;
senddispls[size-1] = 0;
sendcounts[0] = isize * jsize;
sendcounts[size-1] = isize * jsize;
```

Clearly, this is an unoptimized version because we send each time all "central" data of the array, which are pointless for the first and the last slices. In any case, all other slices receive just the information they need, so there are no obvious optimizations in this sense. Now, the core of the static evolution function is almost straightforward. After the allocations of the arrays `data_image` and `sub_image`, the following code is inside a 'for' loop that iterates over the number of steps.

```
MPI_Barrier(MPI_COMM_WORLD);
MPI_Scatterv(pixels, sendcounts, senddispls, MPI_UNSIGNED_CHAR, data_image,
    end_minus_start * jsize, MPI_UNSIGNED_CHAR, 0, MPI_COMM_WORLD);

#pragma omp parallel for shared(temp_init,xsize,jsize,pixels,sub_image) collapse(2)
for(int temp = temp_init; temp < end-start+temp_init; temp++){
    for(int k = 0; k < jsize; k++){
        sub_image[temp-temp_init][k] = upgrade_cell(isize,jsize,data_image,temp,k);
    }
}

MPI_Barrier(MPI_COMM_WORLD);
MPI_Gatherv(sub_image, (end-start) * jsize, MPI_UNSIGNED_CHAR, pixels, recvcounts,
    recvdispls, MPI_UNSIGNED_CHAR, 0, MPI_COMM_WORLD);
```

The variable `end_minus_start` is an integer (different for each MPI process) that represents the number of rows contained in `data_image`. Also `temp_init` is a variable defined outside the global 'for' loop, and represents the row index of `data_image` that corresponds to the cell (i, j) that has to be updated. The method for snapshots is the same as the ordered case.

As we can read from the previous analysis, what we have done is a domain decomposition among MPI tasks, and threads are used only with the nested for loop. What follows is a scalability analysis for both OMP and MPI features.

1.3 Results & discussion

Recall that Amdahl's law states that "the overall performance improvement gained by optimizing a single part of a system is limited by the fraction of time that the improved part is actually used". This is the key point we wish to underline of experiments: the improvable part is not always the slowest part of the code.

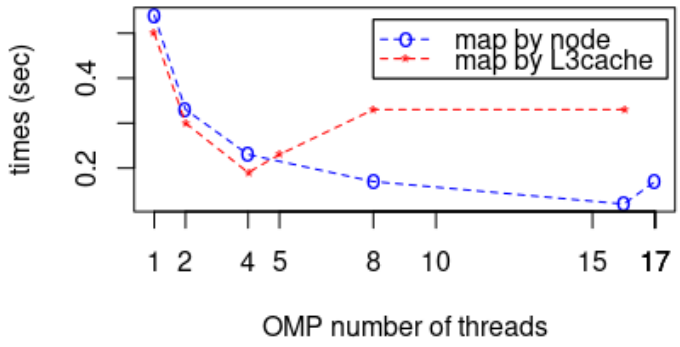
The section is divided into an OMP and MPI scalability analysis, for each case we provide some meaningful examples and relative comments. When we talk about "the time of the nested 'for' loops" we refer to the time measured to execute lines 5 to 10 of the previous code. All datasets are present in the GitHub repository, in the 'statistics' folder.

1.3.1 OpenMP scalability

Example 1: Here are reported the inputs data of our first experiment

> Size: 1000×1000, $n = 100$, $s = 50$, nodes: 3 EPYC, MPI processes = 8, OMP_PLACES=cores, OMP_PROC_BIND=close

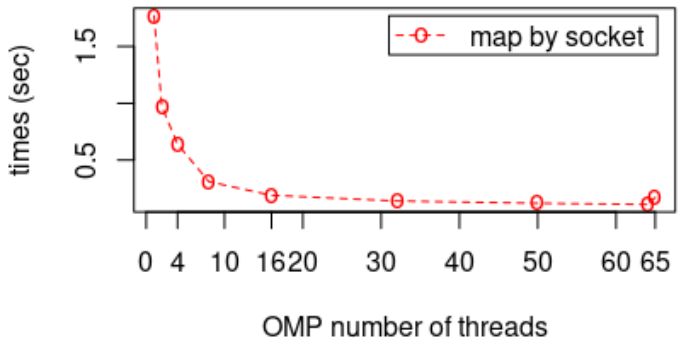
The results are shown in the following plot:



Note that mapping by L3cache increases performance until the number of threads is 4, then it increases the time needed. This is simply explained by the fact that an L3cache is divided among 4 cores and then at most 4 threads (since SMT = 1 in this case) can be exploited for each MPI process. The same reasoning holds for the map by node option: indeed, when we consider 8 MPI processes and 16 threads for each process, then 128 cores are sufficient. However, by the option -map-by node all MPI processes are spread among the 3 nodes we have requested.

Something strange happens if we try to use the –map-by socket option with $nMPI = 8$ (not shown in the figure): the time taken is approximately independent with respect to OMP threads and it is 12.6 ± 0.5 seconds. Note that we have requested 3 EPYC nodes, so we have theoretically at most 6 sockets (with 64 cores each), hence when we use more than 6 sockets the slurm has some issues finding the appropriate location for each MPI process. Usually, I know how many sockets I can use, so I will ask for less: let us decrease $nMPI$ for testing properly the -map-by socket option.

> Same as before but with MPI processes = 2.



Note that in the datasets (in GitHub) the time measured for an MPI_Scatterv (idem for MPI_Gatherv) starts from the call of MPI_Barrier to the end of MPI_Scatterv. Every MPI call takes a time of the order of 10^{-4} seconds, which is really fast compared to the updating for loop which takes, for every single iteration with just one thread, approximately 10^{-2} seconds. By Amdahl's law, we can make the process faster, increasing the number of OMP threads (also increasing the number of MPI processes, but we will see later).

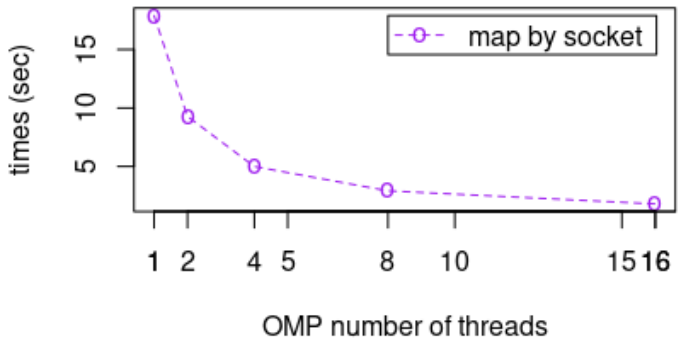
Note that when we consider 65 threads for both MPI processes, then we have to consider 2 distinct nodes because one node contains 128 cores (less than $65 \cdot 2 = 130$). This fact makes the MPI calls a little slower and it is the reason for the strange red right tail of the plot.

We also repeated Example 1 with a fixed $nMPI = 8$ with a map-by-numa option: what we got (consul the GitHub repository) is a very smooth scalability when we increase $nOMP$.

Finally, we have tried to change binding policies (between 'spread' and 'close') and also places (choosing 'threads'). The times measured are identical, however when we have chosen 'threads' as places and 'close' as binding, the time is 2% less, we think because the shared memory among threads is the nearest possible, and this reduces time when threads search for `data_image`.

Example 2: We try now to increase the size of the matrix. We use 2 MPI processes, with a map-by-socket option (from experiments I've seen that the discussion above about the number and location of MPI processes is still valid).

Size: 10000×10000, $n = 10$, $s = 5$, nodes: 3 EPYC, MPI processes = 2, OMP_PLACES=cores, OMP_PROC_BIND=close



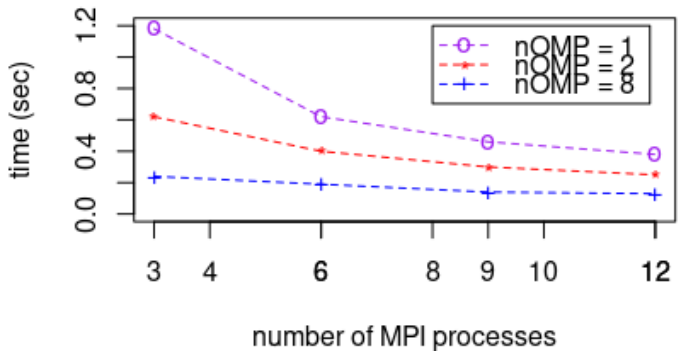
We can see from the plot above that if we double the number of threads, then the time almost halves. This is possible because `MPI_Scatterv` and `MPI_Gatherv` calls take about 0.02 seconds, while the two nested 'for' loops take 0.8 seconds. In this case, by Amdahl's law, increasing the number of OMP threads is the right choice because the improvable time is a large fraction of the total.

If we change threads policy, for instance, we set OMP_PROC_BIND as 'spread', then the times we measure are very similar to the 'close' case, `MPI_Gatherv` call is slightly slower, 'for' loops and `MPI_Scatterv` remain constant. we have also tried to set OMP_PLACES as 'threads' with both 'close' and 'spread' policies, and the results are similar. Only with 'spread' the times are slightly increased because of the 'for' loops are slower in accessing shared memory as they are far from each other within the same socket (with 'cores' as places this effect was not measurable).

1.3.2 Strong MPI scalability

Example 1:

Size: 1000×1000, $n = 100$, $s = 50$, nodes: 3 EPYC, map by numa, OMP_PLACES=cores, OMP_PROC_BIND=close

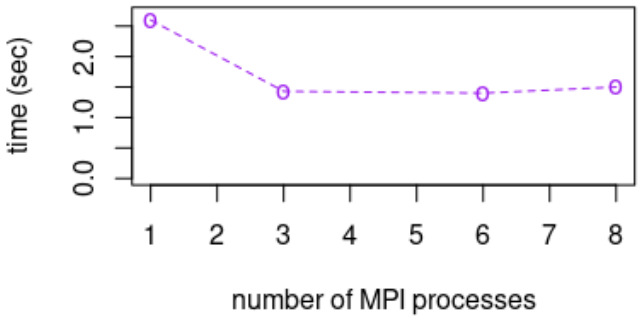


The description of the plot above starts from the times recorded with one single MPI process with one single thread: an overall time of 3.55 seconds (with $\texttt{nMPI} = 1, \texttt{nOMP} = 1$, not shown in the figure), with $3 \cdot 10^{-5}$ for every MPI calls and $3.5 \cdot 10^{-2}$ seconds the nested 'for' loop. The improvable part is a fraction of 99.8%, so we can increase both the number of MPI processes and threads for each process. The results are pretty

clear, and we also know when to stop increasing `nMPI` or `nOMP`. Indeed, when we increase `nMPI` also MPI calls are a bit slower, however, what we reach when we choose `nMPI` $= 12$ and `nOMP` $= 8$ is that 'for' loops take $3 \cdot 10^{-4}$ seconds each, and also MPI calls $4 \cdot 10^{-4} \pm 2 \cdot 10^{-4}$ seconds. Amdahl's law tells us that at this point it's difficult to obtain better performance because the improvable part now is not the largest one.

Example 2:

Size: 10000×10000, $n = 10$, $s = 5$, nodes: 3 EPYC, map by numa, OMP_PLACES=cores, OMP_PROC_BIND=close, OMP_NUM_THREADS=16

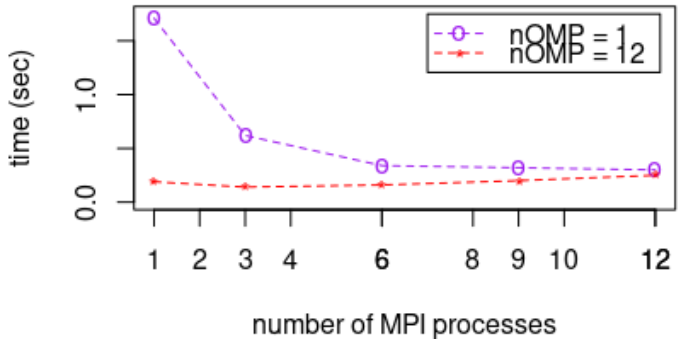


This experiment shows that a high number of MPI processes could be of low utility. Indeed, when `nMPI` $= 1$ a single nested 'for' loop takes approximately 0.2 seconds, while an MPI calls 0.015 seconds. However, even with `nMPI` $= 8$ the time of the 'for' decreases to 0.04 seconds and MPI calls increase to 0.04 seconds each. In this situation the improvable time is half of the total, however, the gain in time due to the increase of `nMPI` is balanced by the loss caused by slower MPI calls.

We did the experiment with a map-by-socket and $nOMP = 64$, $nMPI = 2$, on the same image. It takes a total of 1.1 seconds, which is better than 1.5 seconds with the same amount of cores (i.e. -map-by numa, $nOMP = 16$ and $nMPI = 8$). This is a natural consequence of a decrease in the number of MPI calls, and it's the best way of doing the experiment.

Example 3:

Size: 100×100, $n = 5000$, $s = 2500$, nodes: 3 EPYC, map by numa, OMP_PLACES=cores, OMP_PROC_BIND=close



This time the 2d array is very tiny but it is updated for a long time. With a single MPI process, the nested 'for' loops take 10^{-4} seconds for every iteration. So, increasing `nMPI` gives us better performance until 'for' loops take the same time as MPI calls. The stationary time is 0.34 seconds (with `nMPI` $= 9$). Hence, we can scale with respect to MPI processes.

With `nOMP` $= 12$ we see nice performances, however, we come across a danger when we try to increase `nMPI`. The reason is simple: the nested 'for' loops are so fast that if we increase `nMPI` the delay due to slower MPI calls is not recovered by a faster 'for' loop.

1.3.3 Weak MPI scalability

The goal now is: given an initial size, show to run-time behaviour when you scale up from 1 socket (saturated with OpenMP threads) up to as many sockets you can keeping fixed the workload per MPI task.

In order to maintain fixed the MPI workload, we use several increasing input images of dimensions $\{(500, 500), (500, 1000), (1000, 1000), (1000, 1500)\}$ with respectively
`nMPI` $= 1, 2, 4, 6$. The places for MPI processes are socket (of three different EPYC nodes), so we are going to use `nOMP` $= 64$.

All the statistics for the experiment are precisely stated in `Weak_MPI_scalability.csv` in the `statistics` folder. However, the significant conclusion is that even if all MPI processes have the same amount of work, the overall time increases principally because of the increased number of messages that we need to send. Indeed, every MPI_Gatherv and MPI_Scatterv become a bit slower when we increase the size of the input images (and also `nMPI`).

Given the previous image dimensions and `nMPI` size, we set $n = 500$ and $s = 250$. The overall times vary from 0.14 sec of the $(500, 500)$ case up to 1 sec of the $(1000, 1500)$ case. If we also take a look at the specific time, we note that the 'for' loop time remains more or less constant for every test, while MPI calls become up to 10 times slower as we increase the size of the input array.

1.4 Conclusions

This report concludes that increasing the number of MPI processes is not always the right choice: as often happens, the bottleneck is due to communication processes. Indeed, you have to consider that increasing `nMPI` usually slows the calls of MPI_Scatterv and MPI_Gatherv, and sometimes, especially when the 2d array is very big (time depends mainly on the bandwidth) or very tiny (message latency becomes a bottleneck), could nullify the gain in time for the 'for' loops. In addition, increasing `nMPI` is useful when the improvable part is a consistent fraction of the total work (as Amdahl's law suggests). We have not seen a significant disadvantage in increasing `nOMP`.

1.4.1 Further improvement

The code we implemented could be optimized, in particular, the MPI calls. Indeed, the first and the last slices receive every time the whole 2darray, and this could slow down a little bit the communications. Some possible improvements are the following:

- We can use better MPI calls just for adjacent slices, instead of building the image after every iteration.
- In principle, it should also be possible to decrease the memory occupied by the image, encoding it with bool values Indeed we have only two states (alive or dead), all operations should use the bool values and the translation from bools to pgm file should be effective only if snapshots are required.
- we can compress-decompress the sparse matrix for the communication messages if bandwidth is "too low" with respect to matrix sizes.

2 Exercise 2

2.1 Introduction

This assignment aims to understand, test and show the performance of dense matrix product (provided by `MKL` and `OBLAS` libraries) running over some nodes of *ORFEO*. In particular, the benchmark includes an analysis of the scalability in two ways:

- Measuring time and Gflops of executions increasing the size of the matrices at a fixed number of cores (64 for EPYC and 12 for THIN) for single and double precision. Different threads allocation policies were also tested.
- Measuring time and Gflops of executions increasing the number of cores at a fixed matrix size for both single and double precision.

The algorithm used is called `gemm` (general matrix multiplication) and is tested only with squared matrices with both float (32 bits) and double (64 bits) precision.

2.2 EPYC and THIN node details

The scalability studies are performed for *THIN* and *EPYC* nodes. We share below the technical information obtained through the command `lscpu`:

- `EPYC-01`: it has two sockets, each equipped with an AMD Epyc 7h12 (a 64-core CPU). Each socket is divided into 4 numa regions. CPUs max MHz is 2600 and min MHz is 1500. The sum of all cache memory (both sockets) is the following: L1d is 4MiB; L1i is 4MiB, L2 is 64MiB and L3 is 512 MiB (only 32 instances instead of 128). Simultaneous multi-thread is disabled.
- `THIN-007`: it has 2 sockets, each equipped with an Intel Xeon Gold 6126 (a 12-core CPU). Each socket contains just one numa region. CPUs have max 3700 MHz and min 1000 MHz. The sum of all cache memory (both sockets) is the following: L1d is 768 KiB, L1i is 768 KiB, L2 is 24 MiB and L3 is 38.5 MiB (2 instances instead of 24). Simultaneous multi-thread is disabled.

We want to point out that on `/sys/devices/system/cpu/smt` of the THIN node there was the file control with 'on' written. It means that SMT is supported by the CPU and enabled. All logical CPUs can be onlined and offlined without restrictions.

The theoretical peak performance is given by:

$$\text{Number of cores} \times \text{Frequency} \times \text{Floating operations per clock cycle.}$$

There exist different values to evaluate the cpu frequency, for the purpose of theoretical peak performance, we decided to use the maximum value since we want to estimate an upper bound. We also found some discrepancies between web data[1] and those reported with `lscpu`. In particular, for the EPYC node case, the direct inspection provides 2.6GHz as max and 1.5GHz as min frequency while on web we have founded 2.6GHz as base with a boost up to 3.3GHz.

The number of floating operations per clock cycle is hard to evaluate since depends on different factors. We estimated it based on web research. The peak performance amounts to:

- EPYC: $64 \times 3.3\text{GHz} \times 16(\text{float}) = 3379\,\text{Gflops}$.
- THIN: $12 \times 3.7\text{GHz} \times 64(\text{float}) = 2841\,\text{Gflops}$.

We'll see later that the peak performance of the EPYC node is almost reached while the peak performance of the THIN nodes is way above, probably caused by an overestimation of the upper bound.

2.3 Slurm job

In the following, we report an example of a slurm job file that we used to submit on Orfeo.

[1] https://www.intel.it/content/www/it/it/products/sku/120483/intel-xeon-gold-6126-processor-19-25m-cache-2-60-ghz/specifications.html
https://www.amd.com/en/products/cpu/amd-epyc-7h12

```
#!/bin/bash
#SBATCH --no-requeue
#SBATCH --job-name="Curaba_test"
#SBATCH --partition=EPYC
#SBATCH --nodes=1
#SBATCH --exclusive
#SBATCH --time=45:00

module load architecture/AMD
module load mkl
module load openBLAS/0.3.21-omp

export code=/u/dssc/ccurab00/scratch/Foundations_of_HPC_2022/Assignment/exercise2
export OMP_NUM_THREADS=64

cd $code
make clean
make cpu

gcc -fopenmp 00_where_I_am.c -o 00_where_I_am.x
rm where_I_am.csv
./00_where_I_am.x >> where_I_am.csv

for i in {0..20}
do      let size=$((2000+2000*$i))
        for j in {1..3}
        do
                echo $size
                ./gemm_mkl.x $size $size $size >> 1_double_mkl_EPYC.csv
                ./gemm_oblas.x $size $size $size >> 1_double_oblas_EPYC.csv
        done
done
```

The executable `00\_where\_I\_am.x` is a simple code that writes on the `where\_I\_am.csv` file where (which core) each thread is executed: it's just for checking purposes.

We also highlight that, for each matrix dimension, we executed 3 test and calculate the mean so we can get a more robust estimate of time and gflop scalability.

2.4 Results

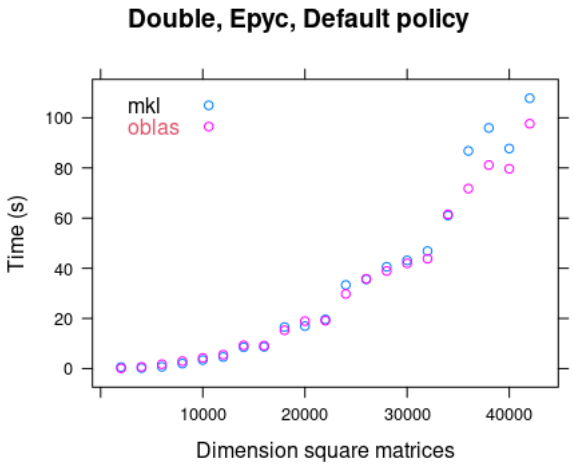
It follows some considerations we provided looking at the graphs:

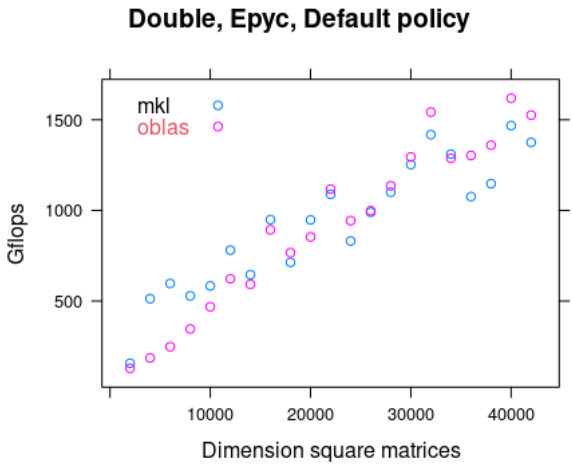
- There's a huge difference in the performance of the two libraries for *THIN* node cases. We discarded various hypotheses to explain such a difference: most of them were based on the fact that the node could contain non-homogeneous CPUs (some faster than others) but we have observed the same difference also when all the *THIN* node is used. Even if, as stated before, the `mkl` library can take advantage of SMT, this doesn't seem to be enough to explain such difference, especially on intensive and optimized computational task, such as matrix multiplication. The only hypothesis we formulated (that we haven't discarded) to explain such behaviour is the following: somehow the `mkl` library code produces a favourable vectorization of data that exploits all the computational capacity of the CPUs. It's like performing twice the operations per clock.

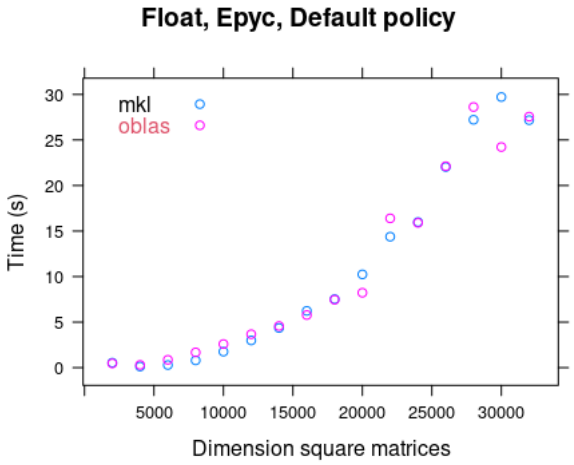
- The number of `float` operations per second is approximately twice the `double` operations per second as expected. This rule doesn't seem to fit rigorously on *EPYC* node: in fact `float` operations per second could be $\frac{3}{2}$ or even less than `double` operations per second. This may be caused by several factors. First of all, instructions are composed by different parts and performing the operation (execution) is just one of them: we think that fetching, decoding and write-back aren't performed at half of the time for `float` data with respect to `double` data. Also, we aspect that the overhead time is partially proportional to the number of operations executed and so is a bit higher for the `float` case.

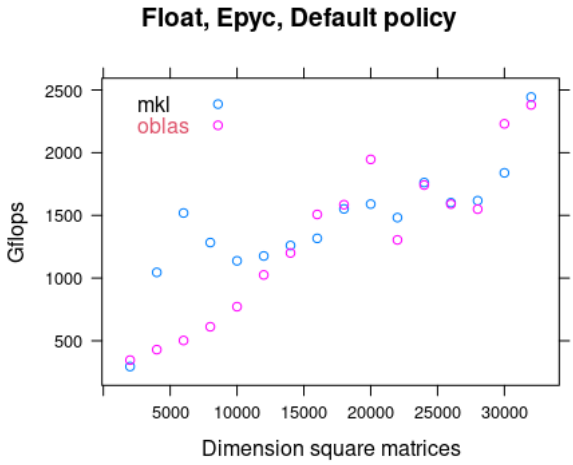
- Since for *EPYC* node the number of gflops tends to increase linearly with respect to the square dimension (we remember that the number of operations required by the task increases approximately as

a cubic function with respect to the matrices dimension) we observe that time increases approximately as a quadratic function. On the other hand, the *THIN* node reaches the plateau[2] quickly and his time seems to grow up approximately as a cubic function as expected.

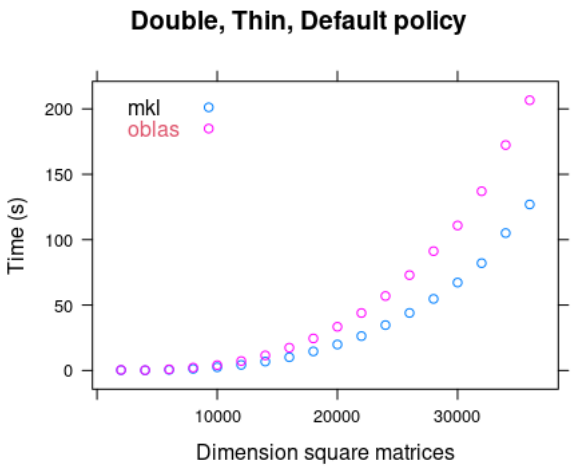


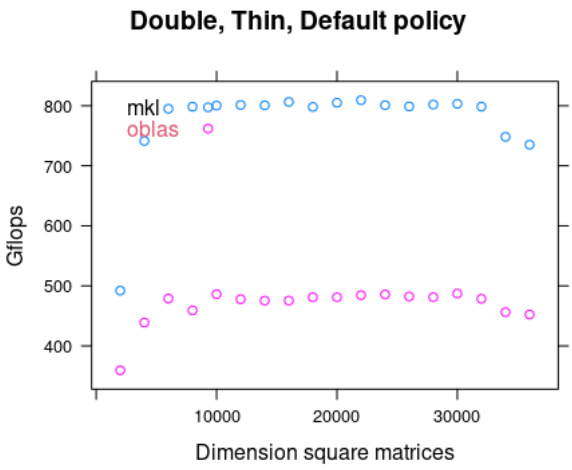


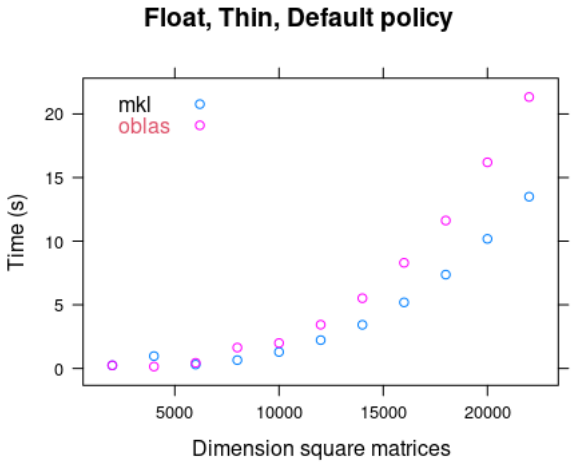


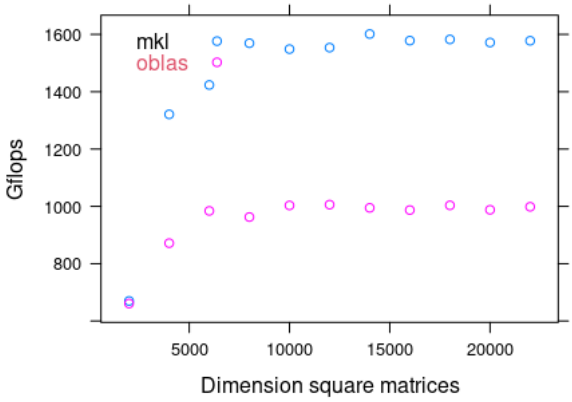


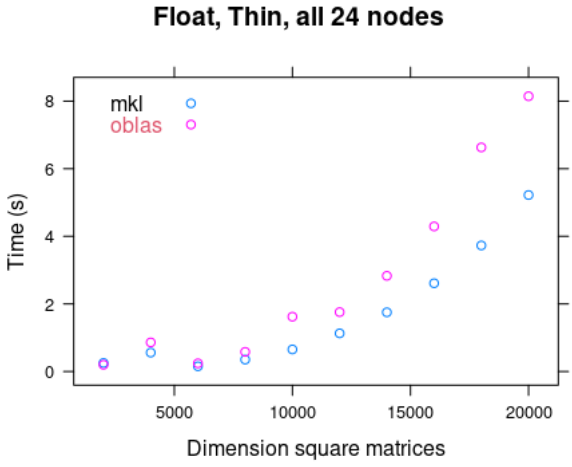
[2]maximum number of floating operation per second

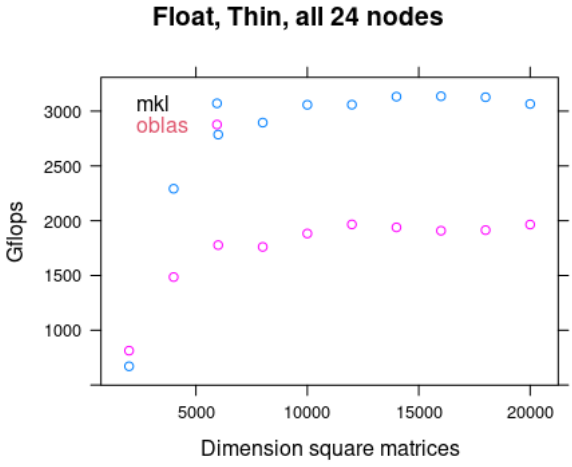

Double, Thin, Default policy
mkl
oblas
Time (s)
0
50
100
150
200
10000
20000
30000
Dimension square matrices

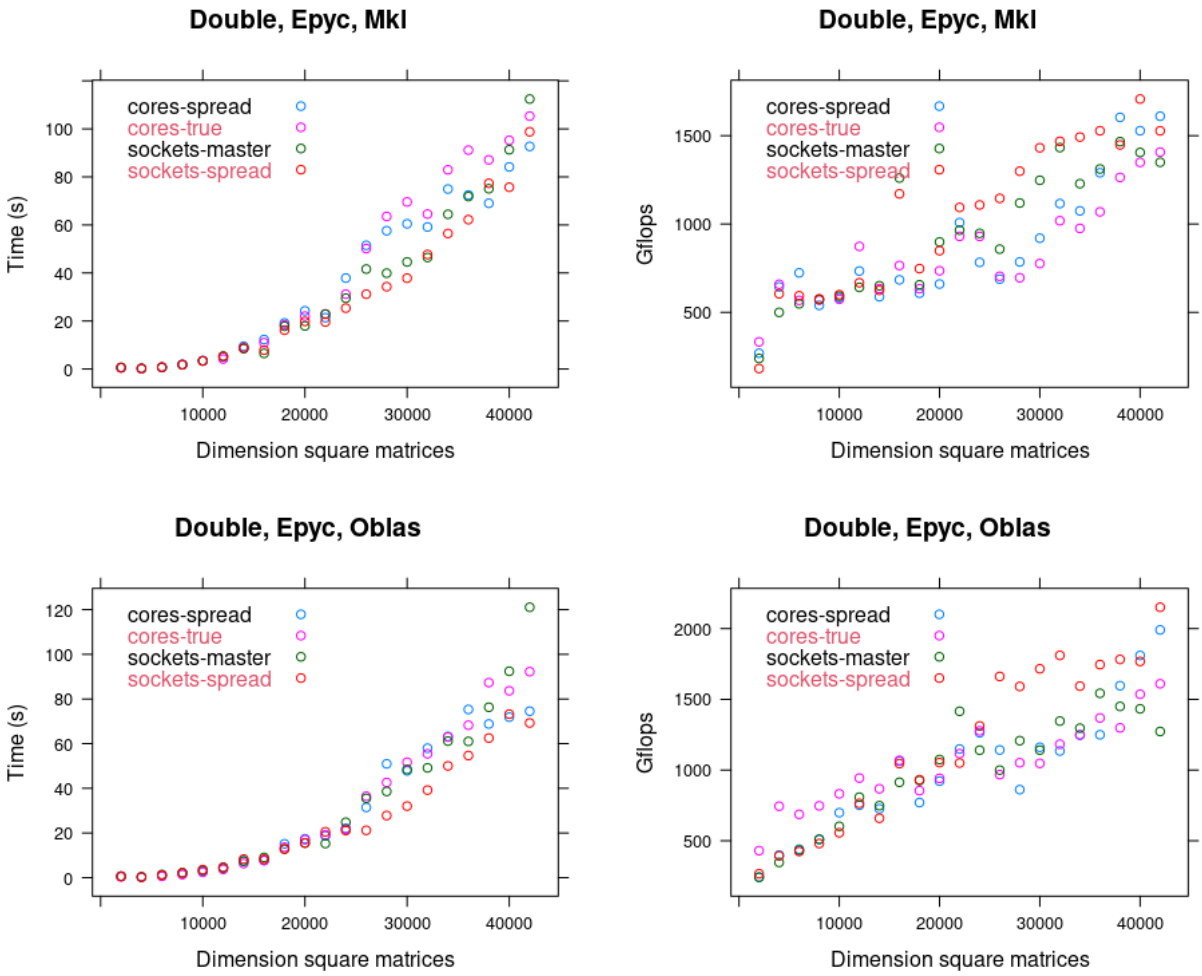

Double, Thin, Default policy
mkl
oblas
Gflops
400
500
600
700
800
10000
20000
30000
Dimension square matrices


Float, Thin, Default policy
mkl
oblas
Time (s)
0
5
10
15
20
5000
10000
15000
20000
Dimension square matrices


Float, Thin, Default policy
mkl
oblas
Gflops
800
1000
1200
1400
1600
5000
10000
15000
20000
Dimension square matrices

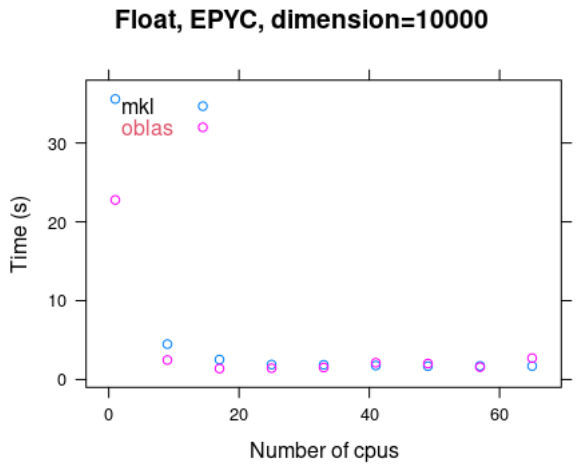

Float, Thin, all 24 nodes
mkl
oblas
Time (s)
0
2
4
6
8
5000
10000
15000
20000
Dimension square matrices

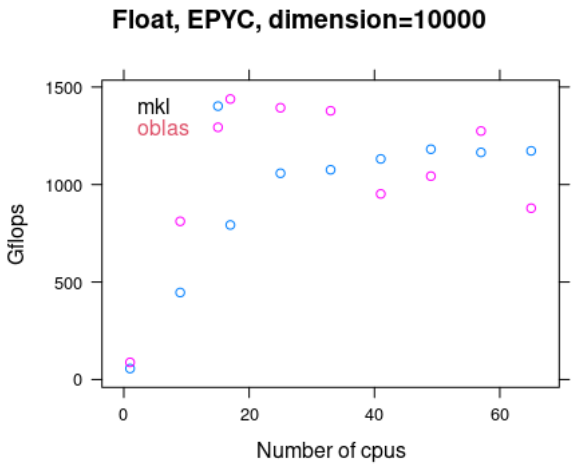

Float, Thin, all 24 nodes
mkl
oblas
Gflops
1000
1500
2000
2500
3000
5000
10000
15000
20000
Dimension square matrices



Looking at the different thread affinity policies chosen we can deduce that:

- All policies assign each of the 64 threads at a different core (there aren't constrained policies like cores-master) and the task is computationally intensive without moving much memory, therefore they perform nearly the same.
- The policy sockets-master constrains the threads to use just one node, so it's using less L3 cache memory and less dram (only 4/8 *NUMA* regions used). This produces a bit worse performance on average.
- The policy cores-true forbids the migration of threads: this constraint doesn't allow the operative system to optimize the computation and results in a bit worse performance.
- The spread policies (cores-spread and sockets-spread) are nearly the same: they both use all *NUMA* regions available hence they perform nearly the same.





Looking at the last figures (in particular the gflops graph) we can see that the strong scalability propriety is greatly satisfied until it reaches about 16 CPUs (this plateau is case dependent: higher the matrices dimension - the higher the maximum number of CPUs that we can use to minimize the computational time). This may be caused by the fact that operations aren't completely independent from each other and so some CPUs are just starving, waiting for the end of other computations.