# High Performance Computing Project - A.A. 2022/2023

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## Chapter 1

# Benchmarking MKL, OpenBLAS, and BLIS

#### 1.1 Introduction

In this exercise we compare the performance of three High Performance Libraries (HPC): MKL, Open-BLAS, and BLIS. In particular, we focus on the level 3 BLAS function called gemm, which multiples an  $m \times k$  matrix A times a  $k \times n$  matrix B and stores the result in an  $m \times n$  matrix C.

This function comes in two types, one for single precision (float) and the other for double precision (double). Furthermore, it is capable of exploiting paralellism using OpenMP (OMP) to speed up the calculations, provided that we have the required computational resources.

Using squared matrices only, we perform a scalability study in two scenarios. In the first scenario, we fix the number of cores, and increase the size of the matrices from 2000 to 20000. In the second scenario, we fix the matrix size to 10000 and increase the number of cores that gemm can use by modifying the OMP\_NUM\_THREADS environment variable.

In both scenarios, we repeat the measurements for both single and double precision, for both THIN and EPYC nodes, using the maximum number of cores.

Furthermore, for the second scenario, we also modify the thread affinity policy of OMP in order to observe any differences.

## 1.2 Methodology

#### 1.2.1 Compiling BLIS and obtaining binaries

We begin by downloading the BLIS library by using the following commands:

```
$git clone https://github.com/flame/blis.git
$cd blis
$srun -p {NODE} -n1 ./configure --enable-cblas --enable-threading=openmp --prefix=/path/to/myblis
$srun -p {NODE} -n 1 --cpus-per-task={P} make -j {P}
$make install
```

Where NODE can be specified as either THIN or EPYC and P are the available cores for each node, 24 and 128 respectively.

With these commands, we have compiled the BLIS library for the desired architecture.

Next, we specify the flag in the Makefile to compile for float or double using DUSE\_FLOAT or -DUSE\_DOUBLE. Then, we run:

```
$salloc -n {P} -N1 -p {NODE} --time=1:0:0
$module load mkl/latest
$module load openBLAS/0.3.23-omp
$export LD_LIBRARY_PATH=/path/to/myblis/lib:$LD_LIBRARY_PATH
$srun -n1 make cpu
```

Which will generate the binaries for the desired architecture, with floar or double precision, depending on the flag we used.

To run, we use:

```
$srun -n1 --cpus-per-task=128    ./gemm_mkl.x {size_M} {size_K} {size_N}
$srun -n1 --cpus-per-task=128    ./gemm_oblas.x {size_M} {size_K} {size_N}
$srun -n1 --cpus-per-task=128    ./gemm_blis.x {size_M} {size_K} {size_N}
```

At the end of this procedure, we should have the appropriate binaries for each architecture, and for each type of precision, double or float.

We now detail the steps to obtain the measurements for both scenarios.

#### 1.2.2 Using a fixed number of cores

For this section, we use all the cores available in a THIN or an EPYC node: 24 and 128, respectively. Since we only use squared matrices, we can describe the dimensions of the matrices with a single number, which we call "size".

For both architectures, we start with a size of 2000 and end with a size of 20000, with jumps of 2000 for a total of 10 sizes. For each size, we repeat the measurement 10 times and report the average and standard deviation.

Finally, we repeat the measurements for both floating point precision and double point precision.

The scripts that were used can be found in the folder exercise2/scripts, under the name es2\_1\_thin.sh and es2\_1\_epyc.sh.

It is important to observe that in this section, since we are using the entire node, there is little possibility to play with combinations of thread affinity.

This will be done for the next section.

Furthermore, contrary to the guidelines for the exercise, we decided to use the entire node to benchmark its full capacity, and also to avoid wasting resources.

In fact, to obtain an accurate benchmark, we need to reserve the whole node, regardless of the number of cores we decide to use. This is because if other people began to use the other half of the node, this could introduce additional workloads which interfere with the benchmark.

#### 1.2.3 Using a fixed matrix size

For this section, we fix the size of the matrices to 10000. Then, we slowly increase the number of cores to be used, until we reach the maximum.

To set the number of cores, we change the environment variable OMP\_NUM\_THREADS to the desired value.

For THIN nodes, which have 24 cores, we start using 1 core, then 2 and then we increase by steps of 2, for a total of 13 points.

For EPYC nodes, which have 128 cores, we start from 1, then 10 and then we increase by steps of 10 until 120. We also use 128 cores, to see what happens at full capacity. We obtain a total of 14 points.

We repeat all measurements 10 times and report the average and standard deviation.

As usual, we repeat this process for both floating and double point precision.

In this section, we have the liberty to explore different thread allocation policies since we are not always using the whole node.

We decided to use following combinations:

- 1. OMP\_PLACES=cores and OMP\_PROC\_BIND=close
- 2. OMP\_PLACES=cores and OMP\_PROC\_BIND=spread

The scripts that were used can be found in the folder exercise2/scripts, under the names es2\_2\_close\_thin.sh, es2\_2\_close\_epyc.sh, es2\_2\_spread\_thin.sh, and es2\_2\_spread\_epyc.sh.

#### 1.3 Results and Discussion

Before we discuss the results of both exercises individually, we briefly introduce the equation to calculate the theoretical peak performance  $(T_{pp})$  of a machine:

$$T_{pp} = \text{Core Count} \times \text{clock freq.} \times \text{IPC}$$
 (1.1)

Where IPC is the instructions per cycle that the architecture is capable of executing.

This equation is very intuitive. The clock frequency tells us how many cycles per second a single core is able to achieve. The ipc factor tells us how many instructions per cycle the core can execute. This number is different for single precision (SP) and double precision (DP) operations. Finally, we need to multiple this by the number of cores that our machine has.

On orfeo, THIN and EPYC nodes are composed of:

- THIN: 24 Intel(R) Xeon(R) Gold 6126 CPU's at 2.60GHz Skylake
- EPYC: 128 EPYC AMD 7H12 CPU's at 2.60GHz Zen 2 (7002 a.k.a "Rome")

Skylake architecture is reported[1] to be able to execute 64 SP FLOP per cycle and 32 DP FLOP per cycle. On the other hand, Zen 2 is reported[1] to execute 32 SP FLOP per cycle and 16 DP FLOP per cycle.

Therefore, we obtain:

Node Type	Total Cores	IPC (SP)	IPC (DP)	$T_{pp}$ (SP)	$T_{pp}$ (DP)	
THIN	24	64	32	$\sim 4 \text{ TFLOPS}$	$\sim 2 \text{ TFLOPS}$	1
EPYC	128	32	16	$\sim 10.6 \text{ TFLOPS}$	$\sim 5.3 \text{ TFLOPS}$	

Table 1.1: Performance table of THIN and EPYC node architectures.

Now we can proceed to discuss the results of the exercise.

#### 1.3.1 Using a fixed number of cores

As mentioned above, in this section we keep the number of cores fixed to the maximum available in the node, namely 24 for THIN and 128 for EPYC, and we slowly increase the size of the matrices being multiplied from m = 2000 to m = 20000.

We first show the results for THIN and then for EPYC nodes.

#### **THIN Nodes**

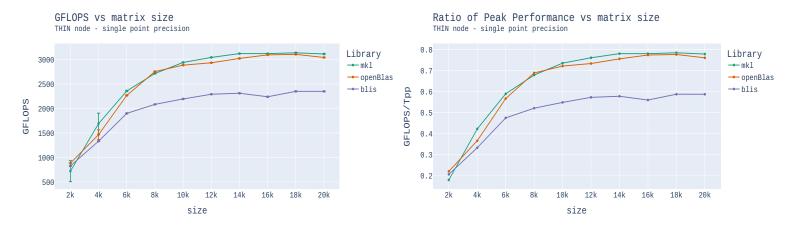


Figure 1.1: Results of SP matrix-matrix multiplication for THIN nodes. MKL and OpenBLAS perform similarly, outperforming BLIS for all matrix sizes.

We see that both MKL and OpenBLAS are able to reach  $\sim 3.2$  TFLOPS, which is around  $\sim 80\%$  of  $T_{pp}$ . On the other hand, the BLIS library is not able to exploit the full potential of the machine, arriving only to  $\sim 2.4$  TFLOPS, which is  $\sim 60\%$  of  $T_{pp}$ .

Furthermore, looking at the ratio of peak performance on the right, we observe that for small matrix sizes, none of the libraries are able to fully exploit the theoretical peak performance of the machine. This is most likely because the problem size is so small, that the majority of cores are starving for data rather than crunching numbers. In fact, we are able to reach the best performance when dealing with matrices of size 20000.

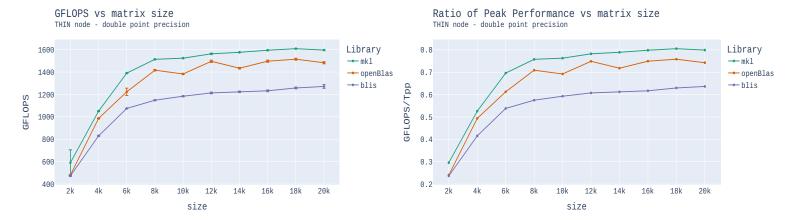


Figure 1.2: Results of DP matrix-matrix multiplication for THIN nodes. MKL performs the best, slightly above OpenBLAS. Both outperform BLIS for all matrix sizes.

We see that MKL reaches  $\sim 1.6$  TFLOPS, while OpenBLAS is slightly lower, at  $\sim 1.5$  TFLOPS, which is  $\sim 80\%$  and  $\sim 75\%$  of  $T_{pp}$ , respectively. On the other hand, BLIS arrives to  $\sim 1.3$  TFLOPS, which is  $\sim 65\%$  of  $T_{pp}$ .

Furthermore, since double precision is a heavier computation compared to single precision, we see that the libraries perform much better than the their single precision counterparts. For example, looking at the plot for single precision, for matrix size of 4000, we obtain on average around 40% of  $T_{pp}$ . On the other hand, for double precision, looking at the same size, we are already at 50% of  $T_{pp}$ .

For both SP and DP, and for all matrix size, we notice that MKL and OpenBLAS are better able to exploit the full potential of a THIN node compared to BLIS. Therefore, on THIN nodes, if we need to multiply two matrices, we should always use either MKL or OpenBLAS to get some more performance. To get the absolute best performance, it is preferable to use MKL.

These results shouldn't be surprising, considering that MKL is developed by Intel and THIN nodes are Intel-based. Therefore, it is natural to expect that this library is very fine-tuned to their own architecture and is able to exploit the performance of their machines.

Lastly, we observe the impressive results achieved by OpenBLAS which is based on the original implementation of Kazushige Goto, and is able to achieve a similar performance to MKL, which is maintained by an entire corporation.

#### **EPYC Nodes**

Now we show the results on EPYC nodes, which have a  $T_{pp}$  of 10.6 TFLOPS for SP and 5.3 TFLOPS for DP

We first show the results of matrix-matrix multiplication for single point precision.

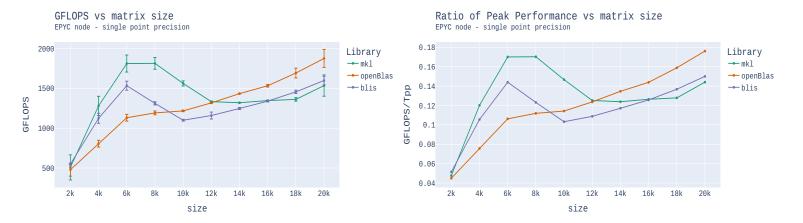


Figure 1.3: Results of SP matrix-matrix multiplication for EPYC nodes. We notice that asymptotically, OpenBLAS outperforms MKL and BLIS, while for small matrices, OpenBLAS performs the worst.

In this case, we obtain some results. None of the libraries are able to reach more than 20% of  $T_{pp}$ . Furthermore, for matrices of size  $\leq$  9000, MKL and BLIS outperform OpenBLAS. Between sizes 9000 and 12000, MKL performs best, and OpenBLAS begins to perform better than BLIS. For sizes  $\geq$  12000, OpenBLAS performs the best.

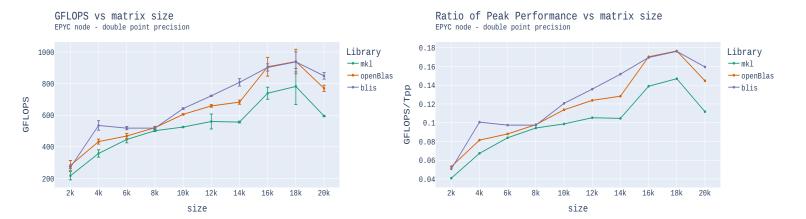


Figure 1.4: Results of DP matrix-matrix multiplication for EPYC nodes. BLIS outperforms MKL and OpenBLAS, for all matrix sizes.

Again, we notice that none of the libraries are able to achieve more than 20% of  $T_{pp}$ . However, in this case, BLIS outperforms the other two libraries for all matrix sizes. The next best performer is OpenBLAS, followed by MKL, which performs the worst.

In conclusion, on EPYC nodes, it seems that for DP matrix-matrix multiplication, it is better to use BLIS, while for SP, it is very dependant on the size of the matrices. However, for large matrices, we should use OpenBLAS while for smaller ones, we should use MKL.

#### 1.3.2 Using a fixed matrix size

In this section, we fix the matrix size to 10000 and we slowly increase the amount of cores that the libraries can exploit for multithrading, through OMP. For THIN nodes, we arrive to 24 cores, while for EPYC nodes, we arrive to 128 cores.

Furthermore, since we are slowly increasing the number of cores that the libraries can use for multithreading, we can study the effects of using different thread allocation policies.

As mentioned above, we chose to always use OMP\_PLACES=cores for these experiments. However, we used both OMP\_PROC\_BIND=close and OMP\_PROC\_BIND=spread. In the first case, the threads will occupy first one entire socket, and then, when it is full, the other socket. In the second case, the threads will be placed as spread as possible, on two sockets. In both cases, when we use the full node, we expect the results to be the same.

#### **THIN Nodes**



Figure 1.5: Results of SP matrix-matrix multiplication as the number of cores increase, using close policy.

MKL and OpenBLAS are able to maintain  $\sim 75\%$  of  $T_{pp}$  from 6 cores and onwards. On the other hand, BLIS is able to achieve  $\sim 60\%$  of  $T_{pp}$ , although with a lot of cores, this figure decreases to 55%. These numbers are consistent with the results that we obtained previously.

Interestingly, we notice that with 2 cores, there is a significant performance drop. This is most likely explained by the fact that both cores are mapped to the same socket and must share resources, such as the higher level caches.

In conclusion, once again, we notice that the best performing library is MKL which is Intel based, closely followed by OpenBLAS.

Using a spread policy, we obtain very similar results to the case where we use a close policy. The main difference is that we don't have the same performance drop at 2 cores. This is most likely due to the fact that with a spread policy, each core is mapped to its own socket and there is no contention for resources.

In fact, we notice that on average, the performance is slightly better than the close policy counterpart, and this is probably due to better resource sharing from the beginning.

This highlights the importance of using the correct mapping policy to obtain better performance. Now we briefly analyze the results obtained for double precision.

The analysis and discussion is very similar to the case of single point precision. As usual, MKL, which is Intel based, performs the best, closely followed by OpenBLAS, and finally, BLIS performs the worst.

The percentage of  $T_{pp}$  achieved is rather similar, with OpenBLAS performing slightly worse.

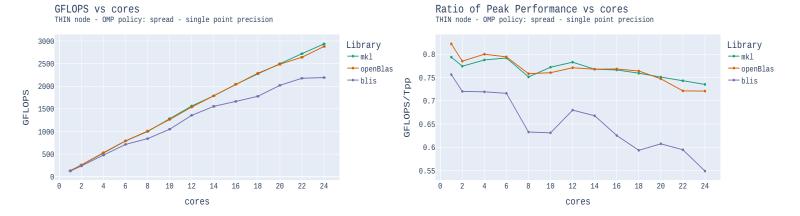


Figure 1.6: Results of SP matrix-matrix multiplication as the number of cores increase, using spread policy.



Figure 1.7: Results of DP matrix-matrix multiplication as the number of cores increase, using close policy.



Figure 1.8: Results of DP matrix-matrix multiplication as the number of cores increase, using spread policy.

#### **EPYC Nodes**

We discuss the situation on EPYC nodes. Considering the results of the first part of the exercise, we expect that MKL won't be the dominating library to perform matrix-matrix multiplication since we are using an AMD architecture. We also expect some more fluctuation in performance among the libraries.

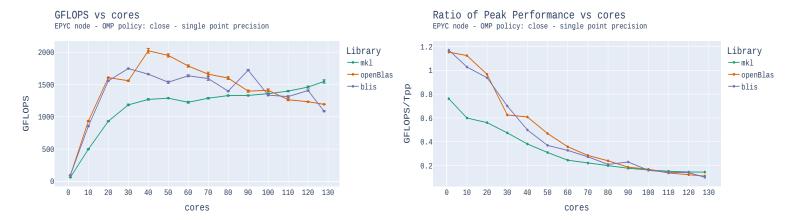


Figure 1.9: Results of SP matrix-matrix multiplication as the number of cores increase, using close policy.

For an EPYC node, we see that OpenBLAS obtains the best performance until 80 cores. In fact, this plot suggests that it is less convenient to use the entire epyc node to compute the matrix-matrix multiplication. This can be seen by the fact that the peak performance is obtained with 40 cores. Since this number is just shy of 32, which is the size of a NUMA region inside a single EPYC socket, this seems to suggest that for a matrices of size 10000, it is more convenient to use a single NUMA region, rather than the whole node.

However, it could be the case that for a much bigger matrix, using the whole node may be beneficial. We also notice that for all three libraries, as we increase the number of cores, they get worse and worse at exploiting the full peak performance of the machine. In fact, all three libraries are capable of performing  $\sim 20\%$  of  $T_{vv}$ .

We investigate this in the end.

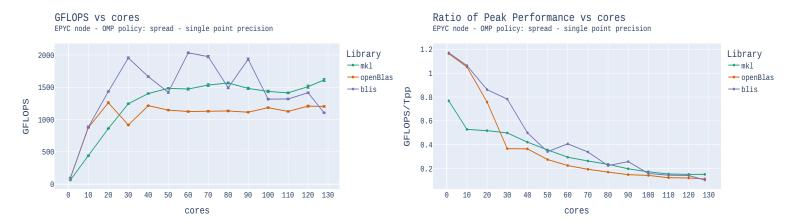


Figure 1.10: Results of SP matrix-matrix multiplication as the number of cores increase, using spread policy.

Using the spread policy, we observe that BLIS is the best choice, although it suffers from considerable fluctuations. Interestingly, all the fluctuations happen at 30, 60, and 90 cores. These are all values

that are close to full usage of a NUMA region. Once again, this seems to suggest that it is better to fully utilize a subset of NUMA regions, rather than use an intermediate value.

We also notice that using the spread policy causes both MKL and BLIS to improve and OpenBLAS to worsen. This is interesting because it seems to suggest that the latter library is better able to handle resource contention while the first two are better at fully exploiting resources.

Finally, we notice that also here, all three libraries are not able to fully exploit the theoretical peak performance of the machine, and progressively get worse, until  $\sim 15\%$  of  $T_{pp}$ .

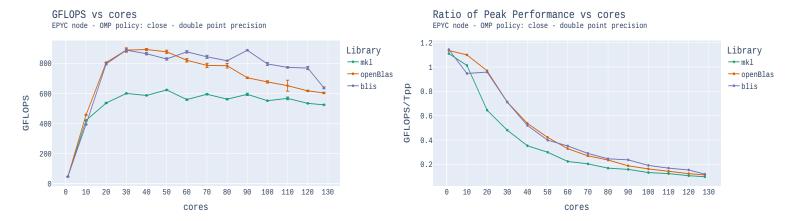


Figure 1.11: Results of DP matrix-matrix multiplication as the number of cores increase, using close policy.

For double precision, using a close policy, we observe that BLIS performs the best for many cores, while for the first 64 cores, it performs close to OpenBLAS. MKL performs the worst.

Also, we see that there are less

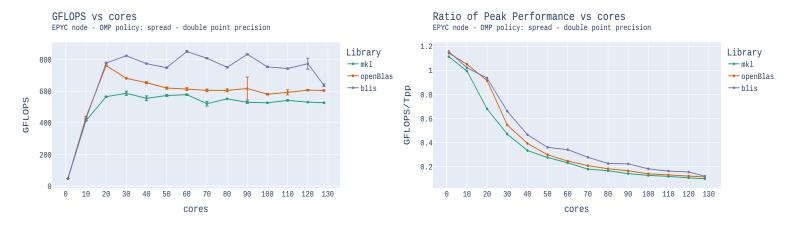


Figure 1.12: Results of DP matrix-matrix multiplication as the number of cores increase, using spread policy.

#### 1.4 Conclusion

## Chapter 2

# Conway's Game of Life

#### 2.1 Introduction

This exercise is devoted to implementing a scalable version of Conway's Game of life[2]. The game consists of a  $k \times k$  grid, where each cell can be "alive" or "dead".

The grid evolves over time by looking at a cell's C eight nearest neighbors and observing the following simple rules:

- A dead cell with exactly three live neighbors comes to live (birth).
- A live cell with two or three neighbors stays alive (survival).
- A dead or live cell less than two or more than three neighbors dies or stays dead by under or overpolulation, respectively (death).

These seemingly simple rules give rise to many interesting behaviors and patterns.

Depending on how we update the cells, there exist two methods to evolve the grid: static and ordered. In static evolution, we freeze the state of the grid  $\mathcal{G}_t$  at time step t, and compute  $\mathcal{G}_{t+1}$  separately, while looking at  $\mathcal{G}_t$ .

On the other hand, in ordered evolution, we start from a specific cell, usually in position (0,0) (top left), and update the elements inplace. In this scenario, the state of each cell depends on the evolution of all the cells before it.

Our implementation must satisfy the following requirements:

- 1. Randomly initialize a square grid ("playground") of size  $k \times k$  with  $k \ge 100$  and save it as a binary PGM file.
- 2. Load a binary PGM file and evolve for n steps.
- 3. Save a snapshot during the course of evolution with frequency s (s = 0 means save at the end).
- 4. Support both static and ordered evolution.

Lastly, it must use both MPI[3] and OpenMP[4] to paralellize the computations and be able to process grids of considerably high dimensions.

## 2.2 Methodology

Since programs in MPI need to be rewritten completely from their serial counterparts, we must begin to conceptualize the problem in an encapsulated manner from the start.

At a high abstract level, we must make two important choices:

- 1. How we will decompose the problem.
- 2. How we will perform the IO (this has important consequences on the organizational paradigm we will use).

We briefly discuss both of these topics more in depth in the following subsections.

#### 2.2.1 Problem decomposition

To exploit paralellism, we must first identify the concurrency in our application and then apply some form of decomposition. The two most important types of decomposition are domain and functional decomposition.

In domain decomposition, multiple workers are performing the same set of instructions on different portions of data (SIMD). In functional decomposition, workers are performing different instructions on possibly different data (MIMD).

In the case of static evolution, each cell can be updated independently from each other, as long as we have access to its neighbors. Therefore, one immediately obviously form of paralellism is for each MPI process to update their "part" of the whole grid.

For this, we need to decide how to split the grid since we can do both a 1D or 2D decomposition of our grid. It is known that a 2D decomposition is more efficient as it can exploit more bandwidth (more workers will send shorter messages at the same time). However, it is more complicated both from an implementation point of view, as well as it is worse for memory access.

Let's talk briefly about this second aspect. Although we will talk about our grid as a 2D array, internally, for efficiency, it will be represented as a 1D array. Therefore, each process will work on a strip of continuous data as shown in the figure below.

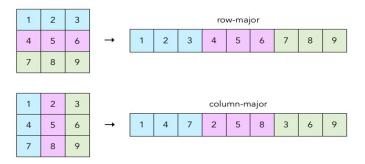


Figure 2.1: .

Fas one long array, in a 1D split, each process will need to work on a continuous "strip" of this memory.

### 2.3 Implementation

#### 2.4 Results and Discussion

#### 2.5 Conclusions

#### 2.5.1 How to add Tables

# **Bibliography**

- [1] wikichip. "Floating-point operations per second (flops)." (), [Online]. Available: https://en.wikichip.org/wiki/flops.
- [2] LifeWiki. "Conway's game of life." (), [Online]. Available: https://conwaylife.com/wiki/Conway%27s\_Game\_of\_Life.
- [3] OpenMPI. "Openmpi." (), [Online]. Available: https://www.open-mpi.org/.
- [4] OpenMP. "Openmp." (), [Online]. Available: https://www.openmp.org/.