Lab 3

FPGAs as Accelerators

Introduction

The goal of this Lab is to implement the LSAL algorithm on the x86, Arm and FPGA of the zedboard and to optimize it in every case using Valgrind, Intel advisor and Vitis HLS.

LSAL stands for local sequence alignment algorithm that is used in bioinformatics and works by giving an input of two input strings, a database D of length M, and a query Q of length N. The objective is to find regions of similarity between subsequences of all possible lengths. An $M \times N$ similarity matrix S is constructed to hold similarity scores for each subsequence comparison. A second matrix (called direction matrix) is formed to hold the direction path through matrix S to produce an alignment. The cell value of the direction matrix indicates the direction followed to reach that cell. The optimal alignment is produced by starting from the position of the maximum score in matrix S and following the directions found at the same index in the direction matrix until a zero in S is found.

In typical cases, the size M of the database string can be in the order of millions of symbols.

**File structure

Software (x86 & Arm)

Workflow

The general workflow for the development of the code which is meant to run on x86 and Arm environments is as follows:

- First we **implement** the LSAL algorithm without considering the CPU running time and only taking into account the functionality of the code.
- 2. Then we **profile** the code using **Valgrind** and **Intel Advisor** while identify the parts of the

- code that take the most amount of time to run and which of them can change.
- 3. Depending on the results of the previous step we change the necessary parts of the code but now aiming for **performance**.
- 4. Lastly we **compare** the running times of the optimized and unoptimized version both by CPU running times and **Roofline analysis** results.

In both the unoptimized and optimized code we have added a **debug** DEFINE that allows us to debug any possible problem by just using the command *make* debug of our MAKEFILE.

Unoptimized

The **unoptimized code** represents an implementation of the LSAL algorithm where the output matrix is being calculated row-wise.

In the code we have added a **second for loop** (compared to the lab input) in order for the algorithm to calculate the values of the **first row** because it meets a lot of edge cases which would be not efficient to place it in the main loop as all those edge cases would need to be checked for every value of the output arrays while this only needs to happen while the first row is being filled out.

In the main loop that was already there from the lab input we have added all the cases and the necessary calculations. At the end of the for loop we save the results both in the similarity matrix and the direction matrix while checking If the max index needs to be "dethroned".

The results for a varying number of array sizes (Query and Database) are shown in the table below.

	x86 vs ARM Unoptimized (in seconds)							
N M		М	ARM	x86	Difference			
	32	32	0.000098	0.000013	86.7347%			
	32	65536	0.175177	0.034103	80.5323%			

256	65536	1.402216	0.263528	81.2063%
256	300000	6.417753	1.196854	81.3509%

As we can see the x86 is **82% faster** on average than the ARM processor of the zedboard.

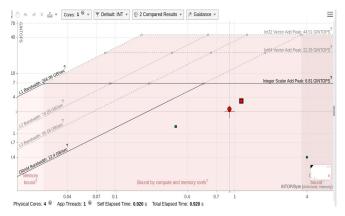
Code Profiling

Optimized

**valgrind

Comparison

Lastly we have run the **Roofline Analysis** that compares the optimized and unoptimized code (when run on x86) using the **Intel Advisor** as shown below:



<u>Image:</u> Diagram of Roofline Model Analysis using Intel Advisor

The **red circle** represents the unoptimized version whereas the **red square** represents the optimized version of the code.

As we can see the optimized version has achieved better parallelism (as it is placed higher) and is even less dependent on the memory bandwidth (as it is placed more to the right).

With these changes the running times have dropped significantly with an average decrease of 37% on the x86 and 56% in the ARM processor of the zedboard.

As a conclusion, the optimized performs better on all aspects and has reduced running time both on x86 and on Arm by 46.5% on average.

x86 (sec)						
N M	Unoptimized	Optimised	Optimisation			

32	32	0.000013	0.000012	7.6923%
32	65536	0.034103	0.018605	45.4447%
256	65536	0.263528	0.137813	47.7046%
256	300000	1.196854	0.628575	47.4811%

ARM (sec)							
N M		Unoptimised	Optimised	Optimisation			
32	32	0.000098	0.000045	54.0816%			
32	65536	0.175177	0.076079	56.5702%			
256	65536	1.402216	0.586488	58.1742%			
256	300000	6.417753	2.685104	58.1613%			

Hardware (FPGA)

During the last part of the lab we use **Vitis HLS** to implement the LSAL algorithm on FPGA hardware.

In order to have the optimum outcome we defined a streamlined **workflow**:

- First our team tries different **optimization methods** on Visual Studio Code IDE.
- Then functionality of the C code is tested using Vitis HLS's **C Simulation**.
- At this point synthesis and Synthesis Design Report of Vitis HLS is used to analyze the resources in-use and the time estimations.
- Next we use the provided makefile to emulate the kernel design using QEMU
- Lastly we test the design **natively** on the FPGA and **extract** the **timing** of our **implementation**

It is important to note that both C Simulation, which tests functionality of the code before it gets synthesised, and software emulation using QEMU are really important as a simple mistake can be detected and fixed long before the time it takes to have the kernel implemented into a bitstream.

Also Synthesis Design Report is a great tool to have in order to make sure the HLS optimizations you use have been implemented in the correct way. For example an easy mistake to make is placing a #pragma above a loop instead of inside it, which could result in vastly different implementations.

Algorithmic Optimizations

The main optimization introduced in the category of algorithmic optimizations is using *diagonals* to calculate the *similarity matrix*. As mentioned during the lecture in this way we *limit data dependencies* and "unlock" *parallelism*.

		Т	G	T	T	Α	С	G	G
	P								
	P								
	P								
	P								0
	P							0	0
	P						0	0	0
	P					0	0	0	0
	G	0	2	1	0	0	0	2	2
=	G T G A C	0	2	1	0	0	0	2	4
Database [M+2(N-1)]	Т	2	1	4	3	2	1	1	3
1+2	Т	2	4	3	6	5	4	3	2
≥	G	1		3	5	5	4	6	5
base	Α	0	3	3	4	7	6	5	5 7 7
ata	С	0	2	2	3	6	9	8	7
	Т	2	1	4	4	5	8	8	7
	Α	1	1	3	3	6	7	7	7
	P								
	P								
	P								
	P								
	P								
	P								
	Р								

Image: Showing diagonal parallelism, image provided during lecture.

This method requires that every diagonal is of the same size. Thus we need to enlarge the database by 2(N-1), where N is the size of query and M the size of database.

We realized during the calculation of a diagonal that there are data dependencies on the 2 diagonals above the one in calculation. That means once the diagonal is calculated it can be moved to the buffer of the above diagonal.

Also one thing noted to us is that at the beginning of each iteration of the loop we have a **write-after-read** on the *current diagonal*, *because* at the *end* of a *iteration* we write the diagonal we just calculated to main memory while at the *start* of the next we try to

write to it. That may be an **obstacle** to having a **pipelined** design with **low LL**.

ADD MORE ABOUT THE LOOPS AND IFs

HLS Optimizations

This section includes every optimization that is **RTL** specific using HLS.

Array buffers

A method of making memory access faster is by using memory blocks that are near the processing unit of the acceleration. The designer in this case has 2 main options:

- by using Block RAM (BRAM), that is a distinct memory block surrounded by Look-up Tables, and
- by using the Flip-Flops inside the Look-up Tables of the FGPA, which is faster but at the expense of making the rest of the LuT hard to utilize.

Thus for the best results a combination of the two is needed.

For our implementation the arrays has the following characteristics:

Array	Description	#pragma			
string1	Buffer of query	PARTITION	factor=2 cyclic		
string2	Buffer of database	PARTITION	factor=2 cyclic		
current_diag	Buffer of current diagonal	PARTITION	factor=2 block		
up_diag	Buffer of the above diagonal	PARTITION	factor=2 cyclic		
upper_diag	Buffer of 2 diagonals above the current one	PARTITION	factor=2 cyclic		
direction_diag	Buffer of current diagonal	PARTITION	factor=2 block		

Γιατί cyclic ή block

Arbitrary Elements

Another easy **optimization** to make is to reduce the **size** of the **bus** used on the design.

For example in the case of the **query** and **database** we know as a fact that they need to enumerate just the 4

nucleotides in existence plus one more undefined state we use in combination with the diagonals optimization. Thus we only need to 3-bits to enumerate 5 states, $(2^3 = 8 > 5 \text{ states})$.

In the exact same fashion the bits used to represent the *direction matrix* are reduced to *3-bits*.

To be noted other data structures such as the similarity matrix, it's diagonal buffers and max_index must not be represented by a smaller number of bits because the RTL designers cannot easily calculate the maximum value each structure is going to store.

Comparison

Results

FPGA vs CPU