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CAMPUS BRUGGE

Using an MPSoC to implement DNA sequence alignment

Implementation and acceleration of the Smith-Waterman algorithm

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Summary

Tijdens de laatste decennia hebben biologen grote stappen gezet in het begrijpen van het leven; dieren, mensen en planten. Sinds het opkomen van DNA sequencing technieken is genetica een onderdeel geworden van de biologie. Maar, door de hoeveelheid DNA sequencing data die verwerkt moet worden, is het analyseren van genetische toepassingen erg rekenintensief voor computers, bijvoorbeeld bij analyse van het menselijk genoom, wat bestaat uit 3 miljard baseparen.

Een grote fundamentele applicatie binnen de genetica is het ”short read genome mapping” of het ”short read alignment”, wat probeert de locatie van een kort stukje DNA terug te vinden in het volledige genoom. Als er genoeg van deze ”reads” gealigneerd kunnen worden, kan hier veel interessante info uit worden afgeleid. Bijvoorbeeld, bij voldoende aligneringen kunnen we het volledige genoom afleiden uit ons bemonsterd DNA. Zo kan men op basis van het aantal reads die aligneren op 1 genomische regio (wat men ook wel de ”reading depth” noemt) te weten komen of er een trisomy van chromosoom-21 (Down syndroom) aanwezig is bij een foetus.

Typisch wordt een ”read” vergeleken met het volledige genoom via het Smith-Waterman algoritme. Als resultaat krijgen we dan de positie van deze read terug in het genoom.

Een volledige genoomsequentie in 1 keer bepalen kan niet, vanwege de technieken die de sequencing machines gebruiken. Deze machines kunnen enkel reads van een korte lengte aan, met een maximum van een paar honderd baseparen ineens. Tegenwoordig wordt er meer en meer DNA gesequenced, en dit groeit exponentieel. Gezien er meer vraag is naar goede aligneringstechnieken, moeten deze ook worden verbeterd om bij te blijven met de stijgende vraag naar DNA sequencing. Maar, meestal worden deze nieuwe technieken enkel geprogrammeerd op de standaard processoren van een computer.

In deze thesis zullen we het Smith-Waterman algoritme bestuderen, en uit deze studie leren we dat een implementatie op een ”gewone” processor niet de beste optie is. Er bestaan andere elektronische technologieën om dit algoritme op uit te voeren, zoals bijvoorbeeld een FPGA. We zullen een MPSoC gebruiken, die beide een stuk ARM (de ”gewone” processor) en FPGA (de gespecialiseerde hardware) aan boord heeft.

In de meeste klinische toepassingen waar dit soort alignering gebruikt wordt, is het aantal reads die gealigneerd moeten worden in de miljoenen. Als ultiem resultaat willen we de ”time-to-result” van een klinische test verkleinen, zodat de rekenkracht van de computers niet de bottleneck wordt van de tests.

Eerst werd een softwareversie van het algoritme geïmplementeerd op de ARM processor. Deze

hebben we getest met een sequencing van het SARS-CoV-2 (coronavirus) als een dataset, en vergeleken met resultaten bekomen via een gekend bio-informatische software (Galaxy). Nadat we de resultaten van beide de eigen implementatie en via Galaxy vergelijken met elkaar, kunnen we dezelfde conclusies trekken. Verder zijn we ook in staat om mutaties te ontdekken in het gemonsterde genoom in vergelijking met onze referentie.

Nadat we dit ook geïmplementeerd hebben op de FPGA gespecialiseerde hardware, hebben we een implementatie die dezelfde resultaten betoonde als onze softwareversie, maar deze resultaten 4 keer sneller kan bereiken.

Abstract

Short read genome mapping is an important application in genomics. It is an algorithm to locate a short read of DNA on the full genome. If enough of such short reads are mapped, some interesting results can be achieved. For example, if enough reads are mapped, we can extrapolate the full genome of the organism and all DNA mutations can be detected. Moreover, the amount of reads in one place (referred to as the reading depth) can give useful information, e.g. the presence of extra DNA like a trisomy of chromosome-21 in Down syndrome patients.

Typically, each read is compared with the whole genome in a local alignment, for example with the Smith-Waterman algorithm (S-W). As an output, we get the position in the human genome and alignment with its score (how well the sequence fits in that spot). This practice is commonly referred to as *Mapping to reference genome*.

A full genome cannot be determined immediately, because the machines that determine this sequence can only handle short reads consisting of a few hundred bases. DNA sequencing machines are currently capable of producing millions of reads per day, and their throughput is growing at an exponential rate. This exponential growth should be accompanied by an improvement in genome mapping techniques, to keep up with the throughput of these machines. However, most of the current software tools used for genome mapping are run on traditional CPUs.

If we analyze the S-W algorithm, we can see that the value of each cell in the matrix only depends on the left-upmost 3 cells. Therefore, it leads us to believe that this algorithm can be accelerated on other hardware solutions such as an FPGA since the S-W algorithm is heavily parallelizable.

In most clinical applications where mapping to a human reference genome is used, the number of reads to be compared with the genome is in the millions, which further increases the demand to speedup the process of mapping the reads in the genome, to decrease the time-to-result.

In literature accelerating short read alignment on FPGAs was described to be 28 times faster in respect to CPUs and 9 times to GPU [15]. showed a speedup of 5.6x to 71.3x dependent on the accuracy of the alignment [17]).

The idea of this thesis was to implement the Smith-Waterman alignment algorithm on an MPSoC, which contains both programmable FPGA hardware and an ARM processor in 1 chip. As a target board, the ZCU 104 evaluation kit was chosen.

As a starting point, a software implementation was implemented on the ARM processor. After running the software implementation with the unmapped sequences from the SARS-CoV-2 (coro-

navirus) as a sample set, we obtained a dataset of mapped reads. The reads were also mapped by using the Galaxy (Bowtie 2) online tool. We observed that our implementation is working correctly since the reading depth graphs are approximately the same. Furthermore, we were able to detect and identify several DNA mutations in the coronavirus DNA sequenced by the University of Washington in respect to the reference sequence from Wuhan (China).

Some reads showed different results in comparison with the Galaxy online tool, but this will probably be because the parameters used are a bit different. However, the important part is that the reading depths are the same, as well as the consistently mutated bases marked in the genome that were detected.

After implementing the Smith-waterman matrix fill-in in the FPGA hardware, we achieved speedup of 4.41 in comparison with an implementation running fully on the ARM processor.

Keywords: Smith-Waterman algorithm, short read genome mapping, accelerator, MPSoC, FPGA, HLS

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List of abbreviations

A - *Adenine* - One of the 4 nitrogen bases present in DNA
ASIC - *Application Specific Integrated Circuit* - An integrated circuit especially designed for a specific application
BAM - *Binary Alignment Map* - The file format used for storing mapped reads, binary
BLAST - *Basic Local Alignment Search Tool* - A heurisitic algorithm for finding local alignments
bp - *base pairs* - 2 nitrogen bases that are connected with hydrogen bonds in DNA. Adenine is connected with Thymine, Guanine with Cytosine
C - *Cytosine* - One of the 4 nitrogen bases present in DNA
cfDNA - *cell-free DNA* - cell free DNA, which is found in the blood plasma
CIGAR - *Concise Idiosyncratic Gapped Alignment Report* - A string that indicates where matches, insertions and deletions occur in a mapped sequence
CLB - *Complex Logic Block* - The basic element in an FPGA
CPU - *Central Processing Unit* - The integrated circuit present in every computer which is easily reprogrammable.
DNA - *DesoxyriboNucleic Acid* - A molecule present in the nucleus of a cell that stores the genetic information for all living organisms
FAT - *File Allocation Table* - A technology for organizing file systems
FPGA - *Field Programmable Gate Array* - An integrated circuit consisting of programmable logic components
G - *Guanine* - One of the 4 nitrogen bases present in DNA
GPU - *Graphical Processing Unit* - A semiconductor technology that is specialized in video encoding and decoding
HDL - *Hardware Description Language* - A set of commands that can be used to describe how the hardware in an FPGA should be programmed
hg - *human genome* - A reference for the full DNA sequence found in the nucleus of the cells from every human
HLS - *High Level Synthesis* - A compiler used to translate C code into HDL code
IDE - *Integrated development environment* - A software application that provides utilities to a programmer when programming an application
Indel - *Insertion or Deletion* - A single term to describe an insertion or deletion in DNA
MPSoC - *Multi-Processor System on Chip* - An integrated circuit that containts multiple microprocessors and/or programmable hardware

NGS - *Next Generation Sequencing* - The technique used most often to determine the sequence DNA

NIPT - *Non-Invasive Prenatal Testing* - a test for detecting genetic defects in a foetus

N-W - *Needleman-Wunch algorithm* - An algorithm used for global alignment, which is similar to Smith-Waterman

SAM - *Sequence Alignment Map* - The file format used for storing mapped reads, text-based

SIMD - *Single Instruction Multiple Data* - A technology in CPUs that can manipulate more than 1 attribute with a single instruction

S-W - *Smith-Waterman algorithm* - A variation of the N-W algorithm, adapted for local alignment. It is a dynamic programming technique

sWGS - *shallow Whole-Genome Sequencing* - an experiment to detect gains and losses in DNA material

T - *Thymine* - One of the 4 nitrogen bases present in DNA

USB - *Universial Serial Bus* - An industry standard for connections between a computer and peripherals

Chapter 1

Introduction

//TODO introduce BUT

1.1 Introduction

Over the last few decades, biologists have made major steps in trying to understand life; animals, humans, and plants. Since the rise of DNA sequencing techniques, genomics has become an emerging field within biology. However, genomic applications are often very computationally demanding, due to the size of the involved datasets, for example when analyzing the 3 billion base pairs of the human genome.

One fundamental application in genomics is short read genome mapping, which attempts to locate a short read of DNA on the full genome. If enough of such short reads are mapped, some interesting results can be achieved. For example, if enough reads are mapped, we can extrapolate the full genome of the organism. Even the amount of reads in one place (referred to as the reading depth) can give useful information, e.g. the presence of a trisomy of chromosome-21 in Down syndrome patients.

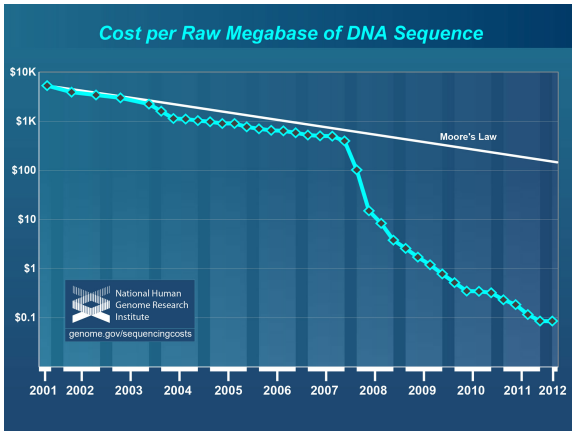


Figure 1.1: Megabase means 1 million nucleotide bases. In this graph we can see that the cost of sequencing decreases significantly overtime, hence the demand of sequencing increases. This increases is more than Moore's law, which is the reason we that mapping techniques should improve to keep up with the demand [16].

A full genome cannot be determined immediately, because the machines that determine this sequence can only handle short reads consisting of a few hundred bases. These sequencing machines are currently capable of producing millions of reads per day, and their throughput is growing at an exponential rate [16]. This exponential growth should be accompanied by an improvement in genome mapping techniques, to keep up with the throughput of these machines. However, most of the current software tools used for genome mapping are run on traditional CPUs.

This thesis will implement genome mapping on an MPSoC (Multi-Processor System on Chip), which has an amount of programmable logic available to accelerate some aspects of the currently used algorithms. As a sample set, DNA sequencing reads of the PhiX and SARS-CoV-2 viruses will be explored. However, the algorithms discussed in this thesis can be expanded to the full human genome, where there is a high need for accelerating the algorithm and thus reducing the time-to-result of clinical tests.

1.2 Organization of the chapters

The further chapters of this thesis are organized as follows:

Chapter 2: The theoretical background in genetics, molecular biology, and DNA, as well as the sequencing technology.

Chapter 3: The theoretical background regarding alignment, existing alignment algorithms, as well as the problem statement with some example clinical applications.

Chapter 4: The theoretical background on existing implementations of the Smith-Waterman algorithm on different kinds of hardware, as well as the hardware selection process.

Chapter 5: A chapter which covers the difficulties I had when learning the required programming techniques, covering High-Level Synthesis and SDSoC.

Chapter 6: A detailed description of the developed software implementation, as well as the results achieved with this implementation.

Chapter 7: The analysis of the software implementation and where to accelerate using FPGA hardware. Also, the comparison between the accelerated version and the software version.

Chapter 8: Conclusion and future work.

Chapter 2

Background information on DNA and DNA sequencing

2.1 Biology and DNA

2.1.1 History of genetics and DNA

Genetics For thousands of years, humans have observed the effects of heredity and implemented their knowledge to domesticate plants and animals. However, the science behind heredity was only started to be understood since 1859 with the publication of *on the origin of species* by Charles Darwin.

Around 1865, an Austrian monk and botanist Gregor Mendel, who studied at the university in Brno in the current Czech Republic, published his results on the hybridization studies of pea plants. He is often credited as being the father of modern genetics. In his findings, he implemented the role of *factors* that influence the expression of traits. These factors later became known as *genes*.

Gregor Mendel

DNA In 1869, Swiss physician Friedrich Miescher discovered a microscopic substance in the pus of discarded surgical bandages. Later, in 1909, Phoebus Levene named this substance DeoxyriboNucleic Acid (DNA) since it is found in the nucleus of a cell and has acidic properties.

The full structure of DNA was discovered by Francis Crick and James Watson at the Cavendish Laboratory at the University of Cambridge.

2.1.2 Structure of DNA

DNA, or Deoxyribonucleic Acid, is the molecule that stores the genetic information of all living organisms. It is the information that programs all of the activities in a cell.

Structurally, DNA is a polymer, which means each molecule is built up out of small repeating molecular units. In DNA, these units are called *nucleotides*.

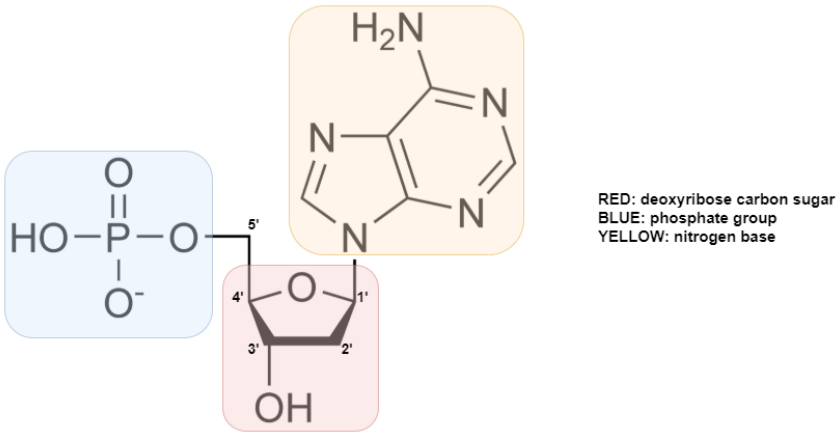


Figure 2.1: The structure of one nucleotide

Each nucleotide consists of 3 parts:

1. A carbon sugar molecule called *Deoxyribose*.
2. A phosphate group to connect the Deoxyribose molecules.
3. One of four possible nitrogen bases: Adenine (A), Thymine (T), Cytosine (C) or Guanine (G).

It is important to note that in most living organisms DNA does not exist as a single polymer, but rather a pair of molecules that are held tightly together. This is the famous *double helix*.

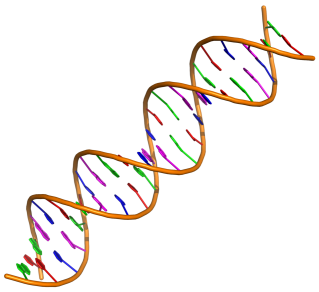


Figure 2.2: The famous double helix [6].

Like in any good structure, there is a need for the main support. In DNA, the sugars and phosphates bond together to form twin backbones. These sugar-phosphate bonds run down each side of the helix, but chemically in opposite directions.

The first phosphate group, at the start of the molecule, connects to the sugar group's 5th carbon ($5'$). At the end of the structure, the 3rd carbon ($3'$) of the sugar group is unconnected. This makes

a pattern typically noted as $[5' \rightarrow 3']$. Now, since the other molecule in the helix goes in the opposite direction, the pattern of the other backbone is typically noted as $[3' \rightarrow 5']$.

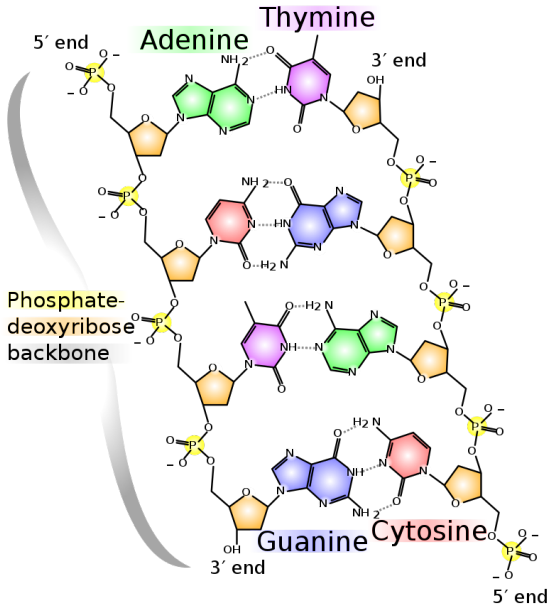


Figure 2.3: A short part of a DNA molecule containing a $[5' - ACTG - 3']$ (left) and a complementary strand of $[3' - TGAC - 5']$ (right). These 2 strands are interconnected by hydrogen bonds [5].

These two long chains are linked together by the nitrogen bases via their relatively weak hydrogen bonds, but there can't just be any pair of nitrogen bases. Adenine can only make hydrogen bonds with Thymine. Likewise, Guanine can only bond with Cytosine. These bonded nitrogen bases are called *base paires*.

It is the order of these bases, which is also called the *sequence*, that allows this DNA to store useful information. In this way, e.g. $AGGTCCATG$ means something completely different as a base sequence than e.g. $TTCCAGATC$.

Since each of the bases in the sequence has only one possible counterpart, you can predict what its matching counterpart will be in the opposite string. For example:

If the following sequence is known

$$[5' - AGGTCCG - 3']$$

we can deduce the sequence in the other direction as

$$[3' - TCCAGGC - 5']$$

2.1.3 DNA in the human body

In human cells, DNA molecules can be found in the nucleus of all cells in the body. It consists of 46 very long molecules, which during cell division condense in what we call *chromosomes*.

The only exception is in reproductive cells (the egg cell and the sperm cell), which only have 23 chromosomes.

The 23 chromosomes, which make up our whole DNA, are always present in pairs in the cells, making a total of 46 chromosomes. Each time, the pair consists of one chromosome from the father and the other one from the mother.

The 23 chromosome pairs are classified in:

- 22 pairs of autosomal chromosomes, marked 1 to 22 according to the length of the sequence. The longest chromosome (chromosome number-1) is 248,956,422 bases long. The shortest (chromosome number-22) is 50,818,468 bases long.
- In each cell, there is also an X chromosome plus an X or Y chromosome, dependent on the gender (XY for male, XX for female).

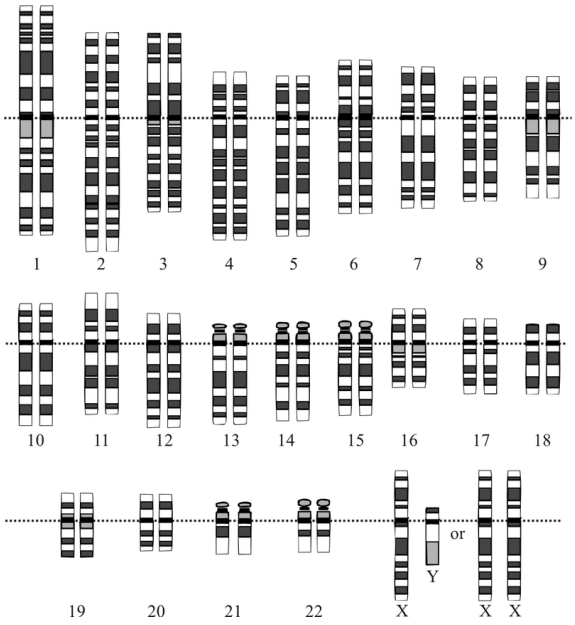


Figure 2.4: the 46 human chromosomes [8].

These chromosomes are packed tightly together in the nucleus of the cell. If all of these 46 chromosomes are put together, this makes about two times 3 billion base pairs. These 3 billion base pairs provide the assembly instructions for pretty much everything inside the cell.

2.2 The Human Genome Project

In the field of Bioinformatics, an important dataset is the *Human Genome*. This is the full DNA sequence found in the Nucleus, ordered from chromosome 1 to 22, followed by the X and Y chromosome.

In October 1990, biologists in the relatively new field of molecular biology started the Human Genome Project. The goal of this project was to determine the sequence of the 3 billion base pairs that make up human DNA. This project was completed and published in 2003. So, nowadays we have a good idea of how the human genome is built up.

The Human Genome is easily found on the internet since it is publically available. One of the most often used assembly is *hg19*, which was published in 2009. Since DNA has only 4 possible bases (A, T, C or G), this can be encoded in a 2-bit representation. If this encoding is used, ideally the Human Genome is approximately 750 megabytes.

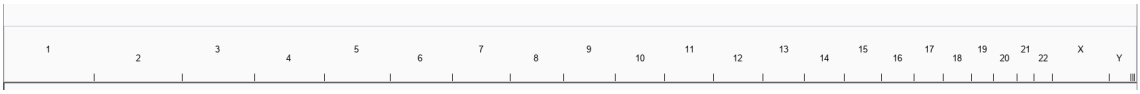


Figure 2.5: The order and the sizes of the chromosomes of the human genome as depicted in the IGV software

2.3 Sequencing

2.3.1 The sequencing technology

The term *Sequencing* is used for all techniques to read and decipher the DNA code from a given snippet of DNA. During the last years, the techniques that sequence human DNA has changed quite a lot. For about 15 years the *Next Generation Sequencing (NGS)* is the technique most often used. The biggest advantage of NGS, in comparison with other techniques, is the speed of the sequencing since it can sequence billions of short DNA molecules in parallel. In practice, this sequencing is most often done by the instruments of the company Illumina, which dominates the market (around 90% market share).

How whole-genome NGS works

1. The DNA to sequence is isolated from the cells. Most often this is the whole genome.
2. In some cases, The isolated DNA can now be copied enzymatically. This step is repeated until there are enough copies of the same DNA. Usually, this is in the millions or billions of copies.

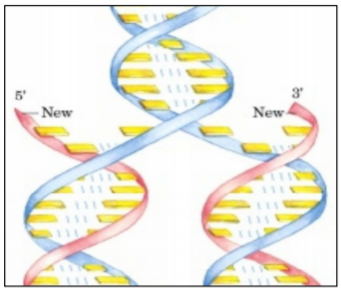


Figure 2.6: the enzymatic copying of a string of DNA. The original is unzipped, thus allowing new nucleotide bases to attach to the exposed bases [].

3. the full DNA sequence is now broken apart into small DNA molecules (100 to 1000 bases long). This is done using enzymes or high-frequency sound waves.

4. Now the sequencing can start: a *flow cell* is used where these small DNA molecules can bind to a glass surface.

5. Different enzymatic and chemical reactions can now be done on this flow cell through an automatic flow of reagents. The following steps are iterated until the full read has been filled in:

   (a) The entire flowcell is filled with nucleotides, all with different nitrogen bases. Important is that at each of these nucleotides there is a fluorescent group attached. This also makes sure no other nucleotide can bind.

   (b) The fluorescent groups have a different color, dependent on the nitrogen base attached (A, G, T of C). At this time a camera picture of the flowcell is taken and stored.

   (c) After the flowcell is emptied of the loose nucleotides, another reagent flows in this flowcell. This reagent splits the fluorescent group so that in the next iteration a new nucleotide group can bind with the read.

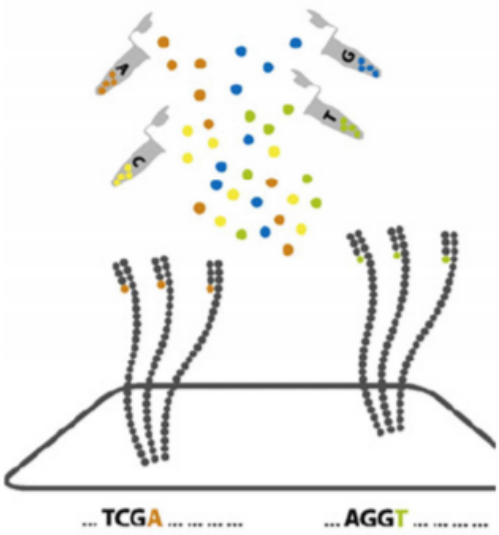


Figure 2.7: Sequencing technology used by Illumina attaches a nucleotide with a fluorescent tag to the next base in the read, then it captures a picture to determine the base, and removes the fluorescent tag so a new nucleotide group can bind in the next iteration [].

6. After the whole DNA snippets have been filled in, the machine deduces the sequence in the DNA snippet. The pictures that were taken in order during the operation show the colors released in a specific spot, and by extent the attached nitrogen base. By the means of some image processing techniques, it is quite easy to get all the sequences from all the molecules bound on the flowcell. This is called the *Primary processing*.

Figure 2.8: From left to right is the pictures taken at each iteration in the flowcell. The sequence determined in the picture is from the lower circled nucleotide sequence. The color at that specific spot marks which nucleotide has been bound. With the use of some image processing techniques the exact sequence in that spot can be identified [18].

7. In the *secundary processing*, the sequence is trimmed by quality, etc. The operations that are done on the read in this step are outside the scope of this thesis.

As a result of the NGS, we get a (large) file in the FASTQ format.

2.3.2 The FASTQ file format

Since the color of each spot observed in the camera pictures in the primary processing can have a light shift, there is a specific ”uncertainty” about the correct base is in that spot. This is called the *quality* of the base.

The *FASTQ* file format has become the de-facto standard as output from sequencing instruments. It is a text-based format for storing both the bases in the sequence and their corresponding quality.

A FASTQ file uses four lines per sequenced DNA fragment:

1. a ’@’ character followed by a sequence ID, plus an optional description. This description mostly contains the coordinate of the spot on the flowcell.
2. The sequence of DNA bases identified by the machine. This is either A, G, C, T, or n when the base cannot be identified with a specific threshold certainty.
3. a ’$+$’ character, optionally followed by the sequence ID (again) and an optional description.
4. the quality values for each respective base in line 2. The length of this line must be the same as the number of bases in line 2

The quality score in memory is a value in the range $0x21$ (lowest quality) to $0x7e$ (highest quality). Since this value is represented in ASCII in the file format, this ranges from the ’!’ character to the ’$\sim$’ character. Hereunder is a complete list of the possible values of the quality score:

```
!"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ
[\]^_`abcdefghijklmnopqrstuvwxyz{|}~
```

Important to note is that this quality score is logarithmic. Also, the ’@’ and ’$+$’ character is a possible value for the quality, so this will be something to look out for when implementing the interpreter for this file.

A FASTQ file containing a single sequence of a DNA fragment of 60 bases might look like this:

```
        FIX
```

Keep in mind that a FASTQ file consists of multiple of these sequences, all stacked under each other.

Chapter 3

Methods for DNA sequence alignment

3.1 DNA sequence aligning

The human genome (e.g. $hg19$) is used as a reference genome for all sequenced human DNA. However, the genetic code of all humans is slightly different, which also holds true for all other organisms. Genetic sequence alignment is the science where you try to align 2 sequences with each other so that the amount of differences is minimal. In this chapter, the most frequently used algorithms are discussed.

3.1.1 Alignment in general

In genetic codes, there are 3 types of differences between the given sequence and the reference:

- Insertion: one or more bases have been added in the genetic code in a specific spot.
- Deletion: one or more bases have been removed from the genetic code in a specific spot.
- Substitution: one or more bases have been substituted by other bases.

Inserts and deletions are often described by a single term, *indel*.

For example: if we want to align the following sequences:

```
Seq1: ATATCGGC
Seq2: ATCG
```

The alignment itself can now be done in different ways. Possible alignments are:

```
Alignment 1
Seq1: AtaTCgGc
Seq2: A--TC-G-
Alignment 2
Seq1: atATCGgc
Seq2: --ATCG--
```

Which alignment that is the actual output, depends on the algorithm and the given parameters (penalty and similarity scores). The '-' character represents a base that is not present.

Keep in mind, there is no one "correct" alignment. The core of the alignment algorithms is the same each time, but the parameters of these algorithms are changed depending on the application.

3.2 Local versus global alignment

To explain the difference between local and global alignment, we can take a look at the following example:

```
The 2 DNA sequences:
Seq1: TCCCAGTTTGTGTCAGGGGACACGAG
Seq2: CGCCTCGTTTTCAGCAGTTATGTGCAGATC

Alignment 1 :
Seq1: -----------tccCAGTT-TGTGTCAGgggacacgag
Seq2: cgcctcgttttcagCAGTTATGTG-CAGatc-------

Alignment 2 :
Seq1 : tcCCa-GTTTgt-GtCAGggg-acaC-GA-g
Seq2 : cgCCtcGTTTtcaG-CAGttatgtgCaGAtc
```

Both alignments are valid but different. The first alignment is *locally aligned*. This means that the similarities are prioritized in the same region, with the similarity as high as possible. On the other hand, the second alignment is *globally aligned*. Here the similarities over the full length of the sequences are used for the alignment.

In practice, the local alignment is used most often, since it can give you information of 2 sequences that do not have (approximately) the same length.

3.3 Commonly used algorithms

In this section, we will take a look at some algorithms that are used most often for DNA sequence alignment.

The most used algorithms are often categorized in 2 ways:

- local alignment versus global alignments (see Section 3.2)
- dynamic algorithms versus heuristic algorithms: dynamic algorithms are exact but slow and computationally demanding, whereas heuristic algorithms are faster but are approximations and the best alignment is not guaranteed.

Hereunder is a schematic view of some algorithms that are used in practice:

	Dynamic programming	**Heuristic programming**
Local alignment	Smith-waterman	FASTA, BLAST
Global alignment	Needleman-Wunsch	X

Table 3.1 Classification of DNA alignment algorithms

Keep in mind, a lot of other claimed ”algorithms” (for example BFAST, ...), are accelerated versions of the Smith-Waterman algorithm.

3.3.1 Needleman-Wunsch

Needleman and Wunch proposed a new algorithm for genetic sequence alignment in 1970, now known as the *Needleman-Wunsch* (N-W) algorithm. Since this algorithm is meant for global alignment, which is seldomly used in practice, further discussion of the algorithm will not be done. However, N-W has a lot of similarities with the Smith-Waterman algorithm, discussed in the next section.

3.3.2 Smith-Waterman

The *Smith-Waterman* (S-W) algorithm was first proposed by Temple F. Smith and Michael S. Waterman in 1981[22]. It is a variation on the N-W algorithm, adapted for local alignment. It is a dynamic programming technique, so an optimal local alignment is guaranteed.

The core of the algorithm is a matrix fillup, with data dependencies on the previous cells. Hereunder an analysis of the algorithm:

1. Symbols used in the analysis:

   Let sequences $A = a_1a_2a_3\ldots a_n$ and $B = b_1b_2b_3\ldots b_m$ be the sequences that need to be locally aligned. Here n and m are the lengths of the sequences A and B

2. Define the parameters:

   - Define $s(a,b)$ be the *similarity matrix* (sometimes also called the *substitution matrix*) for the two sequences. It is used for ”rewarding” when $a_i = b_j$ and ”punishing” when $a_i \neq b_j$.

     In the most general way, we define the similarity score as a matrix of values, e.g.:

	A	**C**	**G**	**T**
A	3	-3	-3	-3
C	-3	3	-3	-3
G	-3	-3	3	-3
T	-3	-3	-3	3

Table 3.2 Similarity matrix example

Often, there are only 2 scores used (equal or not equal). In this case, the similarity matrix can be condensed as follows:

$$s(a_i, b_j) = \begin{cases} +3, & a_i = b_j \\ -3, & a_i \neq b_j \end{cases}$$

- Define d as the *gap penalty* which regulates the score for an insertion or a deletion. This parameter can be:
  - *Linear*: The penalty is constant. So, in this case, it doesn't matter if the previous was also a gap or not.
  - *Affine*: An affine gap penalty considers gap opening and extension separately. For the sake of simplicity, my further implementation will not include this refinement of the algorithm. The algorithm can be extended to include this affine gap penalty, but this would make the algorithm more complex and we would limit our ability to develop possible accelerations. It is also expected to affect the DNA mapping on a reference genome. However, if we assume the size of the gaps as small, there won't be much difference in result in comparison with the linear penalty score.

3. The initialization: We construct a scoring matrix H with dimensions $(n+1) \times (m+1)$. The first column and first row we initialize with 0.

   For example: if we want to align the sequences A = $TGTTACGG$ and B = $GGTTGACTA$:

		T	G	T	T	A	C	G	G
	0	0	0	0	0	0	0	0	0
G	0								
G	0								
T	0								
T	0								
G	0								
A	0								
C	0								
T	0								
A	0								

Table 3.3 Example of the initialization of the scoring matrix

4. Matrix fill in: We fill in the matrix using the following formula:

$$H_{ij} = max \begin{cases} H_{i-1,j-1} + s(a_i, b_j), \\ H_{i-1,j} - d, \\ H_{i,j-1} - d, \\ 0 \end{cases}$$

If we keep in mind that the value of a cell may never be lower than 0, we can represent the data dependencies in the following schematic:

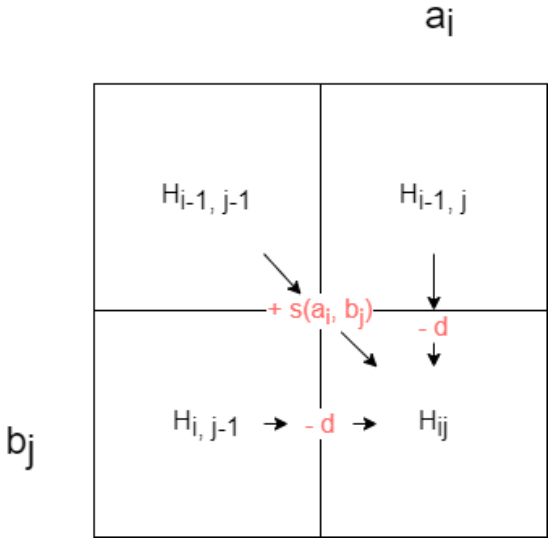


Figure 3.1: Data dependencies in the H matrix

Where $s(a,b)$ and d are the parameters of the algorithm. If we use the following values as an example:

$$s(a_i, b_j) = \begin{cases} +3, & a_i = b_j \\ -3, & a_i \neq b_j \end{cases} \qquad \text{and} \qquad d = 2$$

We can now fill up the scoring matrix H:

		T	G	T	T	A	C	G	G
	0	0	0	0	0	0	0	0	0
G	0	0	3	1	0	0	0	3	3
G	0	0	3	1	0	0	0	3	6
T	0	3	1	6	4	2	0	1	4
T	0	3	1	4	9	7	5	3	2
G	0	1	6	4	7	6	4	8	6
A	0	0	4	3	5	10	8	6	5
C	0	0	2	1	3	8	13	11	9
T	0	3	1	5	4	6	11	10	8
A	0	1	0	3	2	7	9	8	7

Table 3.4 Example of a populated scoring matrix

5. Traceback: We start at the cell with the highest score in the matrix H. Starting here we only move left, up or diagonally (left-up) to the cell on which the value in the cell was based until we hit a cell with value 0.

		T	G	T	T	A	C	G	G
	0	0	0	0	0	0	0	0	0
G	0	0	3	1	0	0	0	3	3
G	0	0	3	1	0	0	0	3	6
T	0	3	1	6	4	2	0	1	4
T	0	3	1	4	9	7	5	3	2
G	0	1	6	4	7	6	4	8	6
A	0	0	4	3	5	10	8	6	5
C	0	0	2	1	3	8	13	11	9
T	0	3	1	5	4	6	11	10	8
A	0	1	0	3	2	7	9	8	7

Table 3.5 Example of a traceback in S-W

From this traceback we can now deduce the following alignment:

```
GTT-AC
||||||
GTTGAC
```

This alignment is the output of our algorithm.

3.4 Problem definition

3.4.1 Mapping to a reference genome

From the DNA sequencing machines, we get a big amount of reads in the FASTQ format. We should note that all these reads are worthless without a proper interpretation.

In most cases, the first step in the analysis of the reads is knowing from which part of the genome it's derived. Typically, the read is compared with the whole genome in a local alignment, for example with the Smith-Waterman algorithm. As an output, we would get the position in the human genome and an alignment with its score (how well the sequence fits in that spot). This practice is commonly referred to as *Mapping to reference genome*.

Since the reads from DNA sequencing machines are 75 to 300 bases long, and the whole human genome is approximately 3 billion bases, this comparison is computationally a very intensive task. If we analyze the S-W algorithm (as we have done in Subsection 3.3.2), we can see that the value of each cell in the matrix is only dependent on the left-upmost 3 cells. Therefore, It leads us to believe that this algorithm can be accelerated on other hardware solutions such as an FPGA (which will be discussed in Chapter 4) since S-W is heavily parallelizable.

In most clinical applications where mapping to a human reference genome is used, the number of reads to be compared with the genome is in the millions.

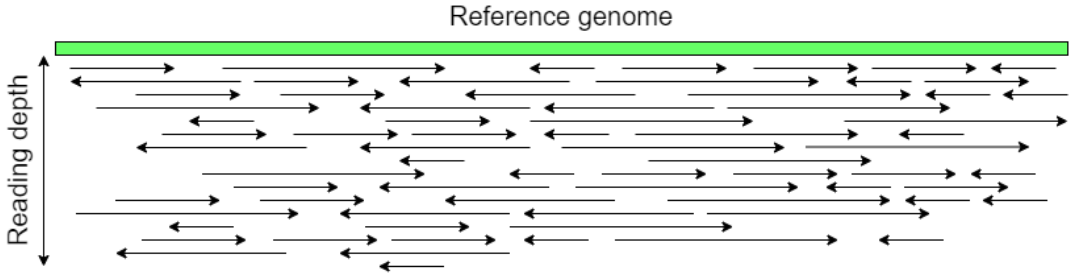


Figure 3.2: Mapping to a reference genome. The direction of the read is represented by arrows

Since the read can be from the complementary DNA molecule in the double helix, the sequences can be in forward $[5' \rightarrow 3']$ direction, or in complementary $[3' \rightarrow 5']$ direction. To transform that read to the used reference genome direction we need to perform the following changes to the read to make its reverse complementary:

1. The bases should be changed to their corresponding base in the base pair;
2. The sequence should be reversed.

We have no way of knowing in which direction the read is taken, both the forward and the backward possibility should be compared with the reference and the best-aligned version of these two should be chosen.

Please note, in most normal cases we can assume the distribution of reads is practically uniform. Therefore, each base in the human genome will be covered by a statistically expected amount of reads. This amount is referred to as the *reading depth*.

3.4.2 The sam and bam file format

As a convention, the output of mapping algorithms is in a *SAM* (Sequence Alignment Map) or *BAM* (Binary Alignment Map) file format. The BAM file format is just a compressed version of the SAM format, but the SAM format is more readable, which makes it easier for troubleshooting. There exist a lot of tools to transform a SAM to BAM file already, so in this thesis, we will focus on the SAM format. A SAM file consists of two sections: a header and an alignment section [13].

3.4.2.1 Header

The header is used for information that is independent of the alignments, such as the name of the used algorithm, reference genome, used commands during generation, etc. The header must be at the beginning of the file, before the alignment section. Each line of the header field must start with an '@' character, so these lines are easily distinguished from lines the alignment section.

3.4.2.2 Alignment Section

Each line in the alignment section represents one mapped sequence and consists of 11 mandatory and some optional fields, which are separated with a tab.

The 11 mandatory fields are:

1. **Qname**: this is the name of the query (the sequence to match) and can be found on the first line of the FASTQ file, which is the input to the mapping algorithm.
2. **FLAG**: a combination of bitwise flags where each bit has a specific interpretation. It consists of 11 bits, but for basic alignments only 2 fields are important:
   - bit 2 (binary: $00000000X00$, integer value 4) is set to 1 if the sequence is unmapped or the map is not found
   - bit 4 (binary: $000000X0000$, integer value 16) is set to 1 if the sequence has been mapped as its reverse complement.
3. **Rname**: the name of the reference genome. This can be found on the first line of the FASTA file, where the reference genome is stored. If the read is unmapped, this field contains a '*' character
4. **Pos**: the position of the leftmost base in the alignment. Keep in mind that the indexing of the reference starts with 1 for the first base.

5. **MapQ**: the mapping quality, which indicates how good the sequence fits in the specific position. This can be any value between 0 and 254. Value 255 is a reserved value to represent an unavailable quality.

6. **CIGAR**, which stands for *Concise Idiosyncratic Gapped Alignment Report*. It is a string that indicates where the matches (M), insertions (I), and deletions (D) occur. For example, if the CIGAR states $3M1I6M2D10M$ this means from left to right: 3 matches, then an insertion, followed by 6 matches, 2 deletions, and finally 10 matches. In case the sequence is unmapped, this field should be filled with a '*' character

7. **Rnext**: reference sequence name of the primary alignment of the text read in the template. For this thesis, we will fill this field with a '*' character.

8. **Pnext**: the position of the primary alignment of the next read in the template. For this thesis, we will fill this field with a '0' character.

9. **Tlen**: the observed template length, from the first till last mapped base. For this thesis, we will fill this field with a '0' character.

10. **Seq**: the full sequence. This can be found in the FASTQ file on the second line.

11. **Qual**: the qualities of the sequence, also given by the FASTQ file on the fourth line.

An example of one line in a SAM file:

```
SRR11   0   MN98   25   254   7M   *   0   0   GTTAAAG   BBBBBCB
```

In this example:

- The name of the sequence is $SRR11$
- The read is matched in the $[5' -> 3']$ direction
- The match is found at the 25th base of the reference genome
- The mapping quality is 254
- CIGAR = $7M$, so a perfect match
- The sequence is $GTTAAAG$ with quality $BBBBBCB$

3.4.3 Clinical application

In virtually all sequencing applications DNA alignment and reference mapping is needed. Applications which involve whole genome sequencing are particullarly hampered by a long computational analysis time.

We will discuss as examples two clinical applications of mapping to a reference genome.

1. ***NIPT* (non-invasive prenatal testing), a test for detecting genetic defects in a foetus.** During or after conception, DNA can be lost or gained in the fertilized egg cell. This can result in a severe syndrome of the child. For example, Down syndrome is caused by a trisomy of chromosome 21. Normally all chromosomes are present twice in each cell, one from the mother and the other from the father. In Down syndrome patients something went wrong during cell division at the very early stage of development, and the fetus has in its cells three times chromosome 21. Because chromosome 21 is quite small and does not contain that many genes, the child can survive, though with typical mental and clinical problems.

Figure 3.3: Trisomy 21 karyotype. The trisomy of chromosome-21 is indicated by an arrow [11].

Before high throughput DNA sequencing technologies were available like they are today, testing if a fetus has a trisomy-21 could only be done by taking a small amount of amniotic fluid (fluid around the fetus). However, to obtain this fluid there was a need for a risky invasive procedure (called *amniocentesis*) leading sometimes to termination of the pregnancy.

It is known that small amounts of DNA of the fetus are present in the blood of the mother, in the cell-free DNA (*cfDNA*) which we find in the blood plasma (the clear, aqueous part of the blood). The blood plasma is used by our body to transport 'waste', including DNA from cells that were broken down. When fetal cells die, which is a normal process, the building blocks of these cells are transported in the plasma of the blood from the mother, included small DNA fragments from the fetus.

NIPT (non-invasive prenatal testing) is used to analyze DNA derived from the mother's blood. A large number of short cfDNA fragments are sequenced at random. Then, each sequence is mapped to the whole human genome to find out where it comes from. Finally, the distribution of these reads is calculated. If we observe a higher frequency of reads as compared to normal individuals coming from chromosome-21, it is almost certain that the fetus has Down's syndrome.

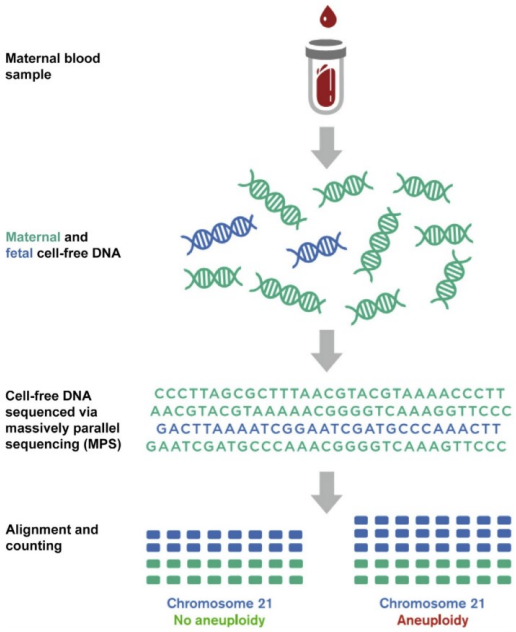


Figure 3.4: A schematic overview of the NIPT test [21].

Using the same method, we can also find other defects in the number of chromosomes. For example trisomy 18 (Edwards syndrome), trisomy 13 (Patau syndrome), or even in the sex chromosomes, such as XXY (Klinefelter syndrome) or lack of a second X or a Y chromosome (Turner syndrome).

2. **Shallow whole-genome sequencing of tumor DNA.**
   It is a known fact that damaged DNA can lead to tumor development. This damage can be single bases changes but can also be loss or gain of large DNA sequences where important genes are located. When someone is diagnosed with cancer, the knowledge of which DNA regions are lost or gained can be important to decide on treatment.

   A relatively new technique to detect all gains and losses of DNA material in one single experiment is shallow whole-genome sequencing. The technique is performed as follows: DNA from the tumor is fragmented (it is broken in small pieces, eg. by a fragmentase enzyme or by high-frequency sound). These pieces are sequenced randomly, and with a mapping algorithm to the reference genome, the over- or underrepresentation of reads (as compared with a normal sample) indicates if regions of the DNA have changed, and which regions these are.

Chapter 4

Platforms for accelerating the Smith-Waterman algorithm

As we have discussed in Subsection 3.3.2 (analysis of the Smith-Waterman algorithm) the value of each cell in the matrix is only dependent on the left-upmost 3 cells. Therefore, It leads us to believe that this algorithm can be accelerated on other hardware solutions that are better equipped for parallelism than a normal CPU.

4.1 Overview of possible hardware

When designing a processing unit based on the semiconductor technology, it is always a tradeoff between efficiency and flexibility. For example, the CPU in a PC is highly flexible so that it can run any set of instructions without a lot of intervention between context changes. On the other hand, if a certain algorithm or instruction set should be executed as fast as possible, the FPGA's and ASICs are the best choices. At the extreme, an ASIC or *Application Specific Integrated Circuit* can be chosen, but this means a complete chip should be designed from the ground up just for this specific application. However, an ASIC is extremely expensive to design and build, especially for small production quantities. In figure 4.1 an overview of the different options can be found.

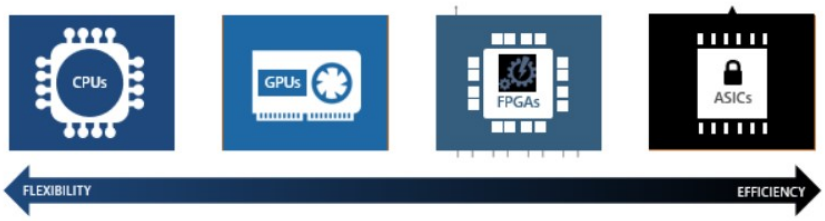


Figure 4.1: An overview of the different semiconductor technologies [1].

4.1.1 CPU

The power of the CPU lies in its flexibility: it can be very easily programmed with new instructions in a short time. However, if the CPU would only run one specific algorithm for its whole lifetime, it would be terribly inefficient. Also, CPUs work sequentially, which is less suitable for algorithms that demand a large number of computations which could be done in parallel.

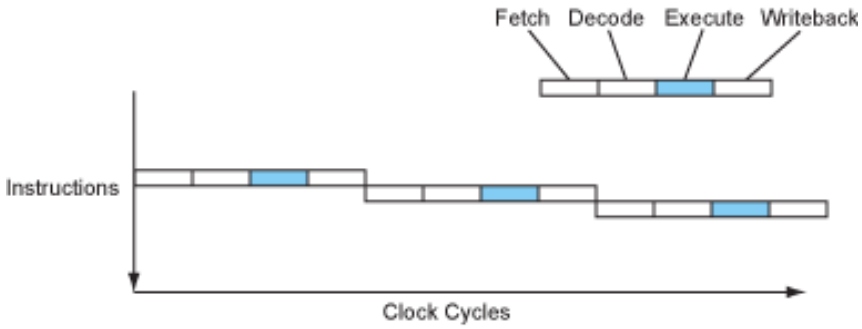


Figure 4.2: A cpu processes instructions sequentially. It could be accelerated using pipelining, but the maximum stays 1 instruction per clock cycle [10].

Since the original implementations of the S-W algorithm on CPU, it became clear that a CPU was not the most suitable platform since it consists of a lot of operations that can be done in parallel. However, since the rise of SIMD, CPU's speed for parallel operations have improved substantially. *SIMD* stands for *Single Instruction Multiple Data* and makes it possible to manipulate more than 1 attribute of data with a single instruction, although be it the same instruction on all the data. CLC bio, a Danish company specialized in bioinformatics, has been able to achieve impressive speedups with a software implementation using SIMD, closing in on 200x [2].

Nowadays, MIT has published *diagonalsw*, which is an implementation of S-W using the SIMD instruction set and is licensed under the open-source MIT license.

4.1.2 GPU

A GPU or *Graphical Processing Unit* is a semiconductor technology which is specialized in video encoding and decoding. Since video encoding and decoding are actually glorified matrix manipulations, a GPU could also be used to manipulate all kinds of matrices. Since the Smith-Waterman algorithm is a big matrix fill in, it leads researchers to believe that it could be accelerated on a GPU. In 1997, an implementation of S-W on a GPU was published which achieved a speedup of 2x over all previous software implementations [14].

At the time of writing, 11 different implementations for Smith-Waterman have been reported, 3 of which reporting a speedup over 30 times.

4.1.3 FPGA

An FPGA, or *Field Programmable Gate Array*, is an integrated circuit consisting of programmable logic components. These logic components can be programmed as any logic function, such as an AND, XOR, etc. In most FPGA other elements are also found, such as memory blocks, DSP blocks, etc.

In the most basic FPGA's, the following items are present:

1. CLB's, or *Complex Logic Blocks*, consisting of a *LookUp Table* (LUT) and a flipflop. A LUT can be programmable so that it contains any type of logic function.
2. Programmable Interconnects have to connect the CLB's into a bigger circuit, which is also called *routing*. This routing has the most influence on delays, and are also responsible for most errors.
3. I/O blocks, which connect the internal logic inside with the outside pins of the FPGA. Most can be configured as input, output, or bidirectional.

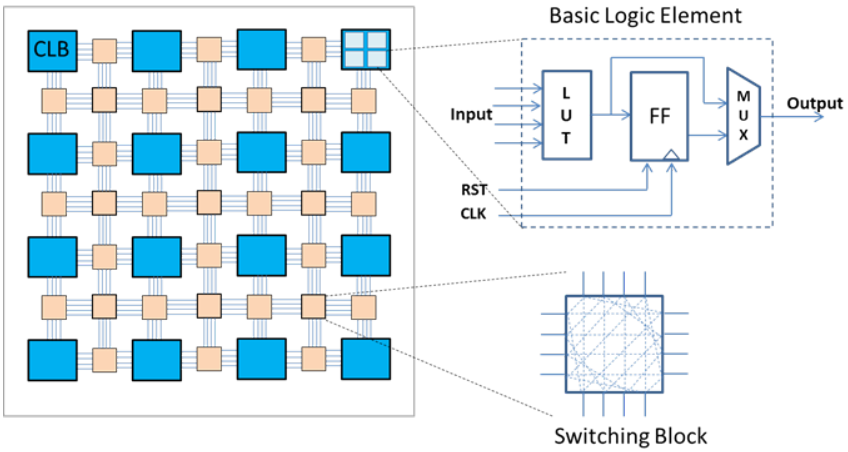


Figure 4.3: The basic layout of an FPGA [7].

For an implementation or design of a circuit which should be loaded in an FPGA, a *Hardware Description Language* (HDL) is often the only practical choice to implement such a system, since drawing the circuits with a CAD program or by hand would take a very long time.

In a paper from 2007, an implementation of S-W with an FPGA (Virtex-4) achieved a speedup of up to 100x in comparison with a 2.2GHz Opteron processor [20].A few companies have also made some implementations on FPGA in the past, e.g. Cray Inc. [3], TimeLogics [4], ...

A master's thesis from 2011 by Vermij E. [24] has a detailed analysis of an FPGA based Smith-Waterman implementation. In other papers, it was found that the performance per Watt level for an FPGA implementation is better than a GPU or CPU by a factor of 12-21 times.

4.2 Hardware selection

As the hardware the ZCU 104 evaluation kit was selected, which has an MPSoC onboard. An MPSoC (or *Multi-Processor System on Chip*) is an integrated circuit that contains multiple microprocessors. This means that both a processor and programmable hardware is available.

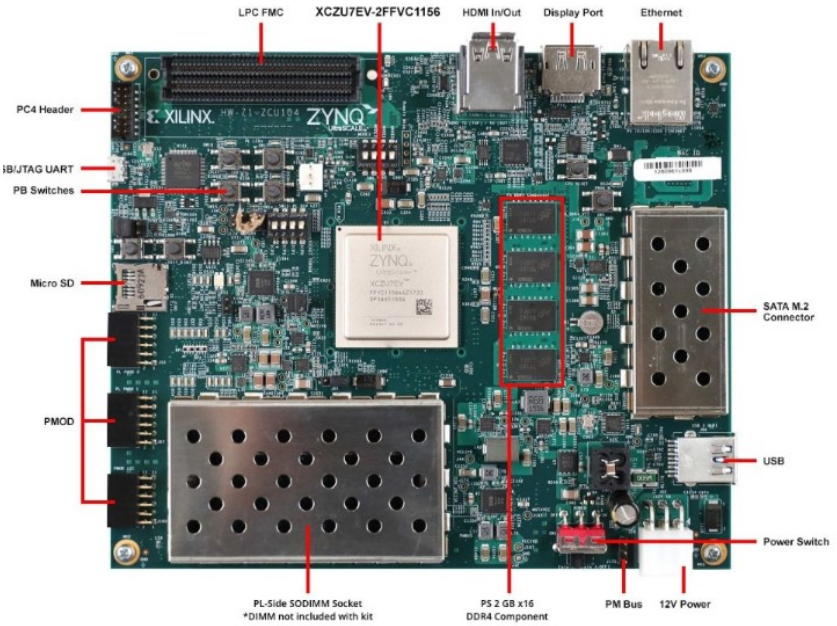


Figure 4.4: An overview of the hardware available on the ZCU 104 MPSoC evaluation kit

Reasons for choosing the ZCU 104 evaluation kit:

1. An MPSoC is present, which will be used the host to application;
2. Both a USB and Ethernet interface is available, which makes it easy to communicate with the target board;
3. An operating system can be run on the board (a Red Hat Linux distribution). This means we won't have to worry about implementing FAT or Ethernet stacks;
4. 16 times 2 gigabytes of RAM is available, which can come in handy when implementing big structures, like the alignment matrix;
5. It was available at the Brno University of Technology.

4.2.1 Recent advances in High-Level Synthesis

When programming an FPGA, an HDL is often used. However, if a specific implementation already exists in a programming language, it often has to be reimplemented from scratch in HDL to load it on the FPGA. Therefore people have been trying to make a compiler that compiles normal C code

into HDL. This ”compiler” is called HLS, or *High-Level Synthesis*. In recent years, HLS became popular as an alternative for designing and implementing a complex system that should be run on an FPGA.

When researching in the known literature, no implementation using HLS for the Smith-Waterman algorithm was found. This leads us to believe that this is still an unexplored area.

4.2.2 Platform communication

Initially, it seemed important that there is good communication between the board and the host to load and unload sequences since we didn't want the communication to become the bottleneck. However, when using S-W for genome mapping, this won't be an issue since the time it takes to map a read takes a lot longer than to transfer it.

In the end, no direct communication with the board was implemented. It seemed sufficient to just load the reads with the genome on an SD card, and insert this in the board. After the mapping process, the mapped reads are available on the same SD card. However, if this program would be used in practice, it doesn't seem practical to constantly change out the SD card. Therefore, another solution should be found. A possible solution could be by using the Ethernet stack available as part of the OS, so we could easily use FTP for on and offloading from and to the board.

Chapter 5

HLS and SDSoC learning tools

Disclaimer: The purpose of this chapter is to show the learning tools I used to achieve a suitable implementation for the genome mapping problem. New programming techniques such as HLS, SDSoC . . . were familiarized. This chapter might be less applicable if the reader is interested in the science and implementation approach of the genome mapping problem, but can be of interest if the reader is also new to the mentioned programming techniques.

5.1 Using Vivado HLS and Xilinx SDK

5.1.1 Learning HLS in examples

To learn HLS, I used learning materials from Mr. Martinek, who teaches HLS at the Brno University of Technology. It contains a theory part, and also hands-on lab examples. These labs were worth exploring in this thesis since they contain most concepts of HLS.

Lab1: BASIC WORKFLOW

- How to start a new project;
- What the difference is between a source and a test bench;
- The properties of the available IDE when designing in HLS;
- How to simulate the sources using the test benches;
- Generate Gantt charts and how to analyze them;
- Where to fiend the resulting VHDL code;
- What the co-simulation is and why it is used;
- Where to view the resulting simulation waveforms;

- How to export your design as an IP;
- It is possible to compare multiple solutions for a problem;
- How to set a directive (such as unrolling a loop).

lab2: EXPLORING DATA TYPES using an FIR filter

- When to use the floating point or fixed point representation;
- How to enable saturation when using fixed point;
- How to do calculations that normally would result in an overflow using a fixed point. This can be done by lowering the resolution (dropping LSBs) so the result can still be stored in the same bit width.

lab3: INTERFACES

- The basic argument-level interfaces and their differences, such as ap_vld, ap_none, and ap_hs;
- A block-level interface of a pipelined component (pipeline in the top function).

lab4: ARRAYS

- Sequential running of a design;
- How to pipeline an internal loop;
- What a rewind parameter is;
- How to do top-function pipelining;
- The array-map technique;
- How to partition arrays (cyclic and complete);
- How to reshape arrays

5.1.2 Learning how to program target board

At first, the Xilinx SDK was used to program the board. However, it was found to be unpractical to use, because after programming a ”Hello World” application it became clear that it would be bare-metal. This would mean there would be a need to implement a FAT or Ethernet stack ourselves. Therefore the SDSoC IDE was used for programming the target board, which structures the application on top of an operating system. This operating system takes care of the Ethernet and FAT stacks.

5.2 SDSoC

SDSoC is an IDE developed by Xilinx which is specialized in programming MPSoCs. It is based on the Eclipse IDE, so most of its features are familiar to most programmers.

The power of SDSoC lays in the ability to transfer functions from software to programmable logic easily. It can be done with just the click of a button. Then, the functions marked for hardware (written in C) will be fitted in the programmable logic using the HLS compiler. However, the syntax is not always accepted since HLS cannot implement every possible programming technique in C yet.

As mentioned earlier, in this implementation we will work on a Linux distribution.

5.2.1 Learning process on matrix multiplication example in SDSoC

To learn MPSoC and the SDSoC IDE, Xilinx' online available materials were used available at their GitHub page, which includes some hands-on assignments. The assignments use a matrix multiplication example, preinstalled with SDSoC. A weblink to this GitHub page can be found in the references [23].

lab1: INTRODUCTION

- Basic workflow: how to create a project, select platform, configure bare-metal or using an operating system, loading the examples;
- Working with hardware accelerators: mark a function for hardware, data motion network report;
- How to run the project

lab2: PERFORMANCE ESTIMATION

- Analyse the software solutions;
- How to view rescource utilization after comilation;
- Comparing software and hardware implementations

lab3: DMA

- There are directives to configure the way data is transferred between the software processor and the programmable logic:
    1. ACP: Hardware functions have cache-coherent access to DDR via the PS L2 cache.
    2. AFI (HP): Hardware functions have fast non-cache coherent access to DDR via the PS memory controller.

3. GP: The processor directly writes/reads data to/from hardware function. This would be inefficient for large data transfers.

This lab also covers how to set these directives.

- How to find more info on errors by using the log files
- the difference between the malloc() and sds_alloc() functions. The hardware functions can only access the physical address space and not the virtual one used by the software. Therefore, the sds_alloc() function was created to skip this virtual memory translation in software.

lab4: DIRECTIVES This lab covers how to set directives to speed up the hardware functions. Which directives to set and what they do, was already covered in the HLS labs at 5.1.1.

lab5: TASK-LEVEL PIPELINING By using task-level pipelining I was able to achieve a speedup of 3 times with a 32x32 matrix multiplication.

lab6: DEBUG In this lab the onboard debugging is covered.

lab7: HARDWARE DEBUG Using the trace feature in the SDSoC, it is possible to analyze what the application is doing? (software, hardware, transfer, or receive).

Chapter 6

Software implementation of the Smith-Waterman algorithm

This chapter will cover an approach to genome mapping using the Smith-Waterman algorithm. This is a computationally very demanding task, but is more precise than heuristic methods such as FASTA and BLAST.

6.1 The concept

For genome mapping a sequence of 75 to 300 bases in length should be mapped to the reference genome. The idea behind this mapping and the applications is thoroughly described in chapter 3.

In this implementation, a mapping with ”pure” Smith-Waterman was chosen. For sequencing applications where only a small part of the genome is sequenced, the read should only be mapped to these small candidate locations. The most computationally demanding task is when the alignment should be done with the whole genome. In this thesis, the alignment of the sequence is done with the whole genome. However, the concept is also applicable for read alignment to a selected region of a genome or a set of genomes from different organisms.

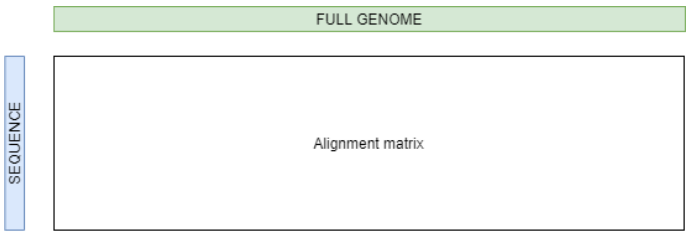


Figure 6.1: The concept of the implementation: the sequences is mapped to the whole genome

6.2 General overview of the implementation

6.2.1 Parameters and Types

Nucleotide base First of all, it seemed important to define the nucleotide bases. There are only 4 possible bases (A, C, G and T), so 2 bits are enough. The following coding was chosen:

Base	A	C	G	T
Code	00	01	10	11

Table 6.1 Encoding for the nucleotide bases

To store these bases the uint8_t type from the stdint library was used. It is 1 byte in size which is the smallest available type in the C language. If more time would have been available, and an implementation with the full human genome would have been made, it might be a good idea to define a specific type consisting of only 2 bits, which would be a lot more memory efficient.

DNA sequence type To easily keep track of a sequence in the program, a type was created which can hold a sequence of DNA. It consists of 2 parts: the length of the sequence and a pointer to the first base in memory. Since the genome can have a length of more than 3 billion bases, and the sequence is only a maximum of 300 bases in length, it made sense to use a separate type for the reference and the sequence.

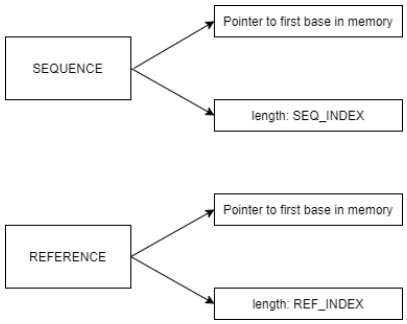


Figure 6.2: The created types to store the sequence and the reference

To index these ”arrays” of bases, a new type was created for both the sequence indexing (*SEQ_INDEX*) and the reference indexing (*REF_INDEX*). Since an index to the sequence can be as high as the $length - 1$, it made sense to make the length attribute out of these newly created index types.

6.2.2 The code structure

1. Allocate some memory for the following data:

   (a) The reference genome, which can be quite large;

   (b) current read;
   (c) reverse complementary of current read;
   (d) matrix for during the alignment. The amount of memory that should be allocated to this matrix is equal to the size of the sequence times the size of the reference.

2. Initialize the first row and first column of the matrix on 0, to prevent edge cases when performing the Smith-Waterman Algorithm;
3. Load the reference genome from the fasta file;
4. Open the FASTQ file for loading unmapped reads, and the SAM file to store the reads once they are mapped;
5. For every read in the FASTQ file, we perform the following operations:
   (a) Load the next read from FASTQ file;
   (b) Perform the alignment. (see Subsection 6.3.3);
   (c) write the mapped read to the SAM file;
6. Close the FASTQ and SAM files;
7. free the reserved memory again

6.3 Details of the implementation

As in most implementations in software, it was decided to split up the functionality of the program in multiple blocks. We have 3 big blocks:

1. Interfacing with the memory: reserving memory for the reference, the sequence, and the alignment matrix.
2. Interfacing with the files and the filesystem: Since the FASTA, FASTQ and SAM files are in a specific format, it made sense to build interpreters from and to these formats.
3. The alignment itself, which is the core of the program.

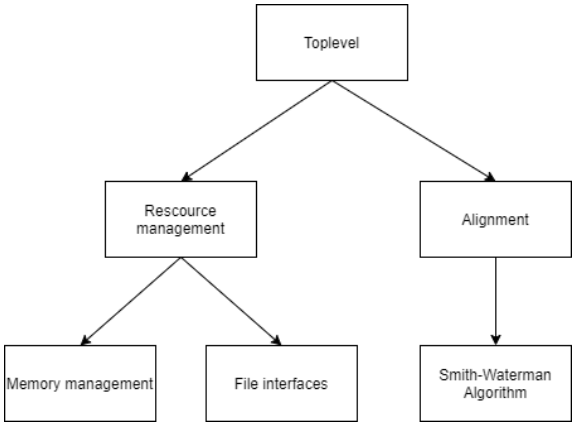


Figure 6.3: An organisation chart of the split up functionalities

6.3.1 File interfaces

6.3.1.1 Parameters and types

Since we need to interface FASTA, FASTQ, and SAM files, it seemed appropriate to create 3 custom types. For the FASTA file, which stores the genome, the type *GENOME* was created. In the case of the FASTQ file and the SAM file, the respective types *READ* and *MAPPED_READ* were created. Notice that the attributes of the types match the information to interface the files.

The information stored in the *GENOME* type is the name of the genome (*Rname*) and the reference.

GENOME
Rname Reference

Figure 6.4: The type created to store the genome information.

In the *READ* type, the current sequence is stored together with its quality string and its name.

READ
Qname Sequence Qualities

Figure 6.5: The type created to store the read information

The *MAPPED_READ* type contains all the information needed to write a full line in the SAM file, which is the output of the program. Mark, the read itself is also stored in this type since all the information in the read will also be written to the SAM file.

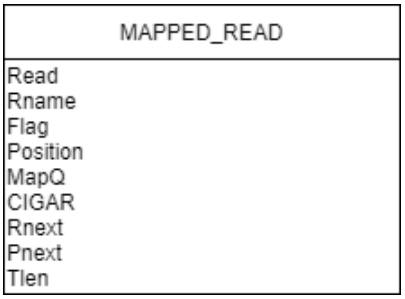


Figure 6.6: The type created to store the mapping information, together with the read

6.3.1.2 Code structure

First of all, the representation of the bases in the files (which is in the ASCII character format) should be transformable to the BASE type in the program. Because of this, conversion functions were created to change the character to base or vice versa.

FASTA interface The function of this part is to load the genome from the FASTA file into the created *GENOME* type. The FASTA file format is a simple text-based way of storing a genome. On the first line is a '¿' character followed by the name of the genome (*Rname*). Starting from the second line to the end of the file the genome is stored. Often, this genome is split up using spaces or in multiple lines, so when coding the interpreter we need to make sure to skip these whitespace characters.

For better code readability, the genome loading is split into 2 functions that are executed in order:

1. loading the genome info
2. loading the genome into the REFERENCE type.

FASTQ interface this part of the program is responsible for loading the next read as a stream. The buildup of a FASTQ file is thoroughly described in Subsection 2.3.2.

In this case, the code was also split up into functions for better readability:

1. Loading the QName, which is found on the first line for every read, behind a '@' character
2. Loading the sequence, which is stored in a text-based format in the FASTQ file, so it should be transformed to the SEQUENCE type. In a sequence, a base may be suddenly marked with an 'N' character, which means after the primary processing the process was unable to identify the base. Because of the way the sequencing machines work, this mostly happens at the end of the sequence. So, it was decided to only cut the sequence short at the moment an 'N' character is registered.

   For example, if the sequence were $ACGGCGCATTACNNAN$, the interface will only store $ACGGCGCATTAC$. This is justified by the fact that we are statistically certain that this

sequence will be matched correctly from the moment the read is more than 15-20 bases long. The statistical proof itself will not be covered in this thesis.

3. loading the qualities. Found on the fourth line for each read, the qualities for each base are stored. The information is stored in an array with the same length as the sequence.

SAM interface The SAM interface will write the current mapped read to a SAM file, one line for one read. The buildup of a SAM file is thoroughly described in Subsection 3.4.2.

For this implementation, some values of the SAM format are not important and should be set to a default value. So it came naturally to create an ”init” function, in which these default values are assigned.

- RNext should be set to the '*' character;
- Pnext should be set to 0;
- TLen should be set to 0;

Then, to write the line in the output SAM file, a function was created which accepts an attribute of the *MAPPED_READ* format and writes it as a line in the file.

6.3.2 Memory management

6.3.2.1 malloc and sds_alloc

The allocation of memory in a C program is usually done using the ”malloc” function. However, on the used SoC, a distribution of Linux is running. Like in most operating systems, this Linux distribution uses a virtual address space to enlarge the available RAM virtually.

The original idea for the project was to be able to accelerate certain functions using the programmable hardware available in the SoC chip. Since this hardware should be able to access the data in the memory, there two options:

1. Build a copy of the address translator on the hardware. This would require a lot of work and would slow the whole process of looking things up in memory down.
2. Let the software interface the physical memory so that we don't use the virtual addresses. This solution was used in the final implementation

Luckily, Xilinx has published a library with an *sds_alloc* function. This does the same as the malloc function in the C language but in physical memory instead of the virtual memory.

6.3.2.2 Allocating memory

To allocate memory, the following formula was used:

```
memory_pointer = (TYPE*) sds_alloc( length * sizeof(TYPE) );
```

The sds_alloc function returns a pointer to the first address in memory that has been reserved. It turns out that this pointer should be cast explicitly to the type used.

- In case of reserving space for the sequence and the reference, the ”TYPE” part in the formula should be filled in by the BASE type. For the length part of the formula, parameters were created named seqMax and refMax respectively.
- When space for the alignment matrix will be reserved, the ”TYPE” part in the formula should be filled in by the CELL type (for more explanation on the CELL-type, see Subsection 6.3.3.1). As for the length of the space to reserve, this should be equal to refMax times seqMax.

6.3.3 The alignment

6.3.3.1 Parameters and types

A naive approach to implementing the S-W algorithm might be to have the alignment matrix filled in by the values only. If we would use this approach, it would quickly become clear that the back-tracking is impossible, since we also need to know where the value originates from. Also, when generating the CIGAR-string, it is good to know which direction it originates from, as it implies a match (M), insertion (I), or a deletion (D). Since all this information should be stored in the alignment matrix, it seemed a good idea to create a new type. This type was called *CELL*.

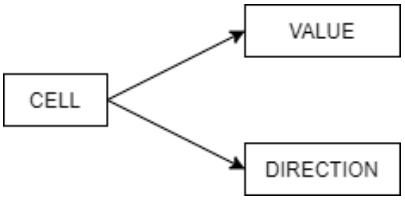


Figure 6.7: The type created to store the information for every cell in the alignment matrix

The cell stores the place it originates from, using a *DIRECTION* attribute. There are 4 possible directions a value can originate from: zero (coded as 0), diagonal (1), up (2), left (3).

Furthermore, it stores the value using a special type *CELL_VALUE*. The size of values this type can store should be greater than the length of the sequence times the similarity score. Keep in mind that to calculate the maximum, this value-type should be able to go negative.

6.3.3.2 Code structure

The alignment layer The alignment layer does everything in the alignment of the sequence that has nothing to do with the matrix fill in. That functionality is outsourced to a separate function.

Also, for the CIGAR string, a certain threshold was programmed in. The CIGAR string of a matched read consists of multiple parts. For example: $6M1I7M$ consists of 3 parts; $6M$, $1I$ and $7M$. By limiting the number of parts that are allowed we can define a threshold by which a sequence is considered as ”aligned”. If both the forward and reverse sequences go over this limit, the sequence will be marked as ”unmatched”.

1. Fill in the matrix using the forward direction of the sequence.
2. Store the maximum value of the matrix.
3. Generate the CIGAR string for this forward direction. We have to do this so early because you need the full matrix for the CIGAR generation, and we want to reuse the memory for the matrix according to the reverse sequence.
4. Check if the CIGAR limit has been exceeded. If not, then store the position of the map.
5. Reverse the sequence
6. Repeat for the reverse sequence.
7. Check for the limit of the CIGAR. If it was exceeded in both forward and reverse sequence, mark it as unmatched.
8. Check which read fit best (the forward or reverse one) by comparing the maximum values in the mapping. Assign the best one to the MAPPED_READ type.

The fill in layer This is probably the easiest layer of them all, but will also be one of the most computationally demanding ones. It skims over every cell in the matrix, except for the first row and first column, and uses the cell generation layer to generate the cell on that specific spot. Also, while having an iteration that goes over every cell, it is a good idea to use this iteration to find the maximum cell in the matrix, which is the starting point for the backtracking.

The cell generation layer This layer consists of 3 parts:

1. Generate the 3 values originating from diagonal, up, and left cells, using the formulas described by the S-W algorithm. For this step, the parameters s (for the similarity score) and gp (for the gap penalty) were created. For testing, These were mostly kept on $s = 3$ and $gp = 2$, but can be easily changed according to one’s needs.
2. Determine which of these three values is the greatest. If all negative, choose 0.
3. Assign the correct value and direction of the newly generated cell.

This layer must be efficiently coded, and since it runs for every cell (and there are a lot of cells), it can be expected to be the core of the program.

6.4 Implementation results

6.4.1 The IGV software

The free and easy to download program IGV[**?**] (or Integrative Genomics Viewer) is a visualization tool for exploring genomic datasets. In practice, it is used to examine the results from mapped reads.

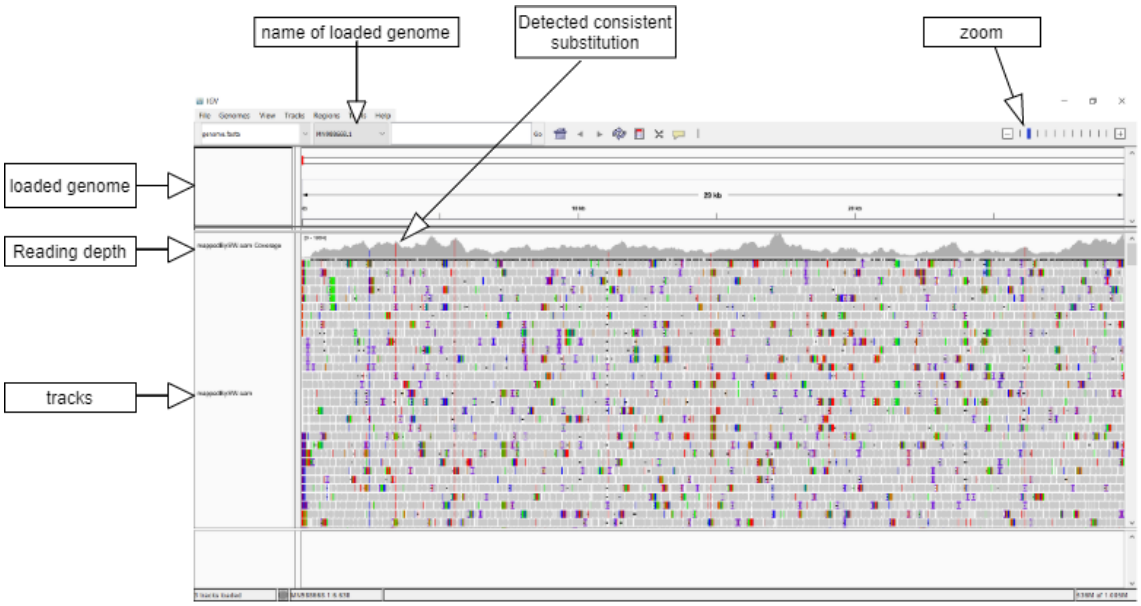


Figure 6.8: The layout of the IGV analysing software

The most important functions in IGV for this thesis are:

- It color-codes insertion, deletions or substitutions, so it is easy to see ”from a distance”;
- It can display the read depth for every base in the genome;
- If the read depth is sufficient, it can also determine if an indel or substitution is part of the read, or is consistent enough throughout all the reads to show it in the full genome;
- The sequence direction is indicated by an arrow when examining a specific read.

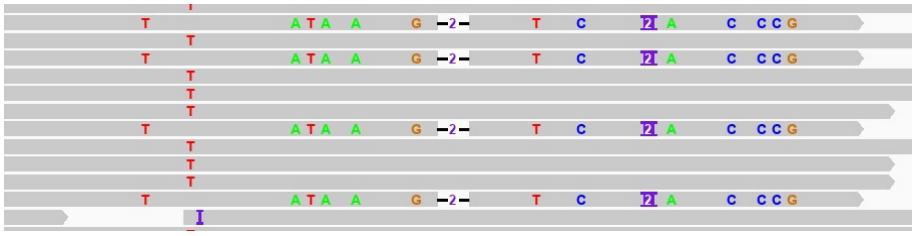


Figure 6.9: Close-up of a few reads in the IGV analysing software. Notice how the color coded bases are substitutions, whereas the matched bases are not shown. Moreover, a gap and insertion is also visible

6.4.2 Sample data

To try the implementation on the human genome directly seemed way too ambitious. Therefore, it seemed appropriate to try the implementation first on an organism that has a genome of only a few thousand bases in length. Since this thesis is performed around the spring of 2020, the ”coronavirus” (or SARS-CoV-2) seemed like an appropriate candidate. After a quick google search, it turned out that this virus had a genome consisting of merely 29 thousand bases.

The genome of the coronavirus was found easily online with reference number MN988668.1 in the genome bank of NCBI [8].

The FASTQ files obtained from a DNA sequence for the coronavirus used in this thesis were found in the SRA (sequence read archive) of the NCBI, submitted by the University of Washington.[**?**]

Of course, when fitting these fastQ files through the implementation from this thesis, we have to be able to compare it with an implementation which is considered as correct. Therefore, an online tool (galaxy) was used where a lot of existing bioinformatical algorithms and programs can be performed on given sample data using cloud computing [9]. By converting the fastQ files (given by the SRA of the NCBI) using one of these available applications, we can get a pretty good reference to match our results against. As the application to compare to, the Bowtie 2 algorithm was chosen, which is based on the S-W algorithm.

6.4.3 Results

We will compare the results from the sample data using the online Bowtie application and the implementation described in this chapter.

After running the software implementation overnight with the unmapped sequences from the coronavirus, we obtained a dataset of mapped reads. Both these mapped reads and the dataset obtained by using the Galaxy online tool were imported into IGV for comparison, which can be seen in figure 6.10

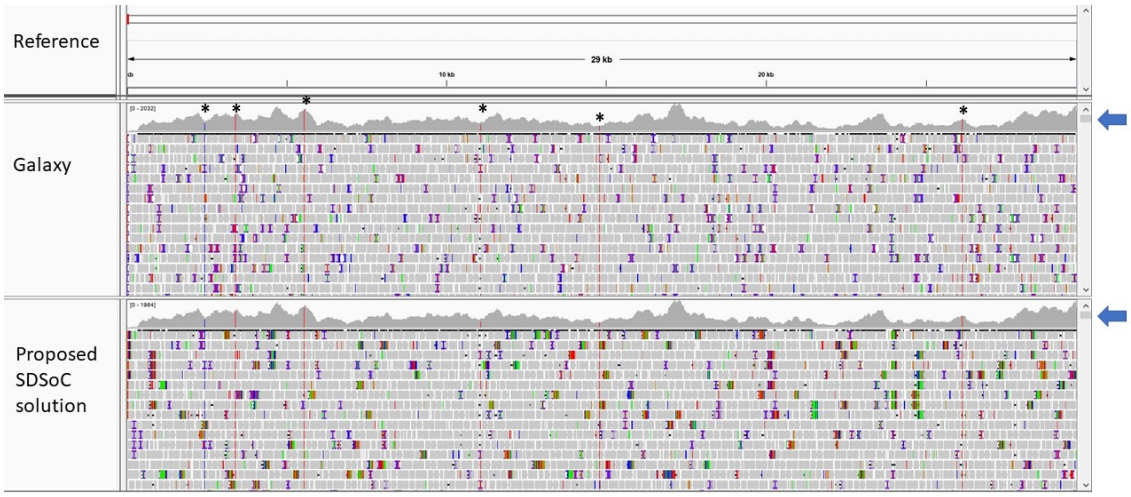


Figure 6.10: A comparison of the data obtained by Galaxy (top) and the data obtained by the implementation discussed in this chapter (bottom)

It can be observed that the implementation is working correctly since the reading depth graphs are approximately the same (indicated by an arrow). Furthermore, IGV was able to detect and identify consistent substitutions or indels in the reads.

If you look closely to figure 6.10, some small differences between the exact reads are visible. This will probably be because both the algorithm and the parameters were a bit different. However, the important part is that the reading depths are the same, as well as the consistently mutated bases marked in the genome (indicated by an asterisk).

The implications for the coronavirus data The coronavirus is constantly changing because of the mutations of some bases in the genome over time, just like the flu. In this way, it is possible to trace where infections originate. For example, the corona in China can have slightly different bases than from Italy or Spain. We can identify these changes by sequencing the whole genome and looking for consistent substitutions or indels over the whole dataset.

From these results shown by IGV 6.10, some mutations are shown, so we can assume that the coronavirus which was sequenced in Washington (taken from a US patient, the FASTQ file used) has some slight differences with the original Chinese sequenced genome (the reference sequence).

Chapter 7

Accelerating the software implementation using HLS

7.1 Analysing software performance

In the SDSoC environment, it is possible to analyze the software running on the SoC chip using a TCF profiler. After running this analysis, the TCF profiler returns an overview of the functions, sorted on the amount of time spent when running. The analysis is shown in figure 7.1

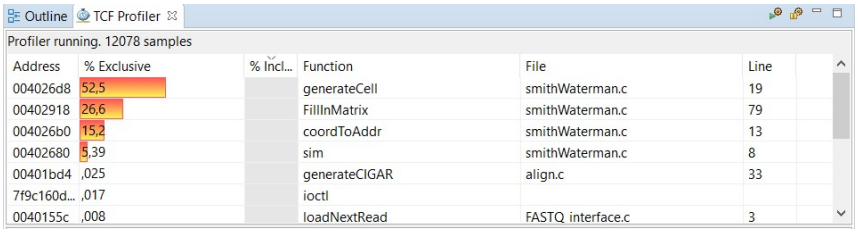


Figure 7.1: a TCF profile of the software implementation

When examining this analysis, we should keep in mind that the generateCell, coordToAddr, and sim functions are inline functions used in the FillInMatrix method. Just as suspected the software spends almost all of its time in these methods, so it's worth it to try to accelerate these functions.

7.2 Recoding parts of the software to be more hardware friendly

7.2.1 Recoding the Cell generation layer

In 2011, Vermij E. (Delft University of Technology, The Netherlands) studied RVE (recursive variable expansion) [24]. He discusses the most efficient ways to program a processing element to generate one value in the alignment matrix. His results can be found in figure 7.2.

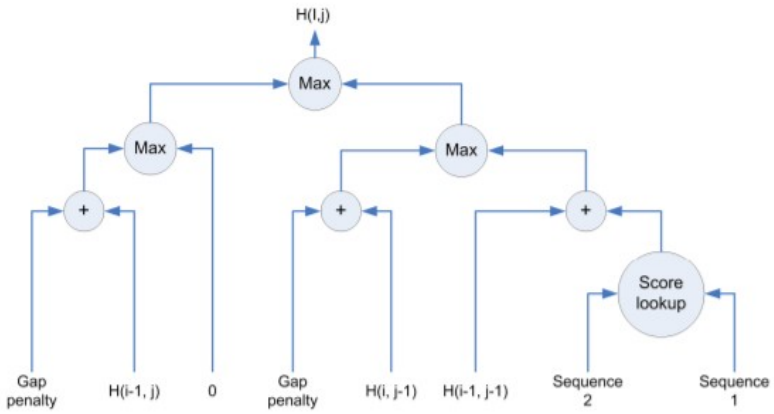


Figure 7.2: The optimal processing found by Vermij E. [24]

It seemed like a good idea to reimplement the generatecell function, using this newly found scheme. However, it is also important to keep track of where the value comes from. Therefore, the following (new) code was adopted for generating a cell:

```
//calculate the possible  values
CELL diagonalCELL = { diagonal.value + sim(refVal, seqVal), 1 };
CELL leftCELL = { left.value - gp, 2 };
CELL upCELL = { up.value - gp, 3 };
CELL zeroCELL = { 0, 0 };

CELL upstreamA = (leftCELL.value > upCELL.value) ? leftCELL : upCELL;
CELL upstreamB = (diagonalCELL.value > zeroCELL.value) ?
diagonalCELL : zeroCELL;

CELL newCell = (upstreamA.value > upstreamB.value) ? upstreamA : upstreamB;

//Return the cell:
return newCell;
```

Where the second attribute in the CELL type is the direction.

7.2.2 Recoding the FillIn layer

HLS does not support input and output from the same memory locations in hardware. Therefore, the Fillin layer also has to be recoded. We will take a look at the data dependencies again:

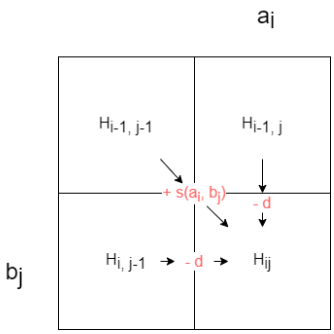


Figure 7.3: Data dependencies for generating a cell in the alignment matrix

Since the current cell only depends on the left-up 3 cells, we can compute every cell on the diagonal in parallel. Therefore, 3 arrays where created: one contains the current diagonal being generated, one contains the previous diagonal for the cell above and the cell to the left of the current generated cell, and one for the diagonal before that. This last array will house the left-up cell also needed for the new cell generation. A schematic of the data structures used can be found in table 7.1

	ref	T	G	T	T	A	C	G	G
seq	0	0	0	0	0	0	0	0	0
G	0	0	3	1	0	0	?		
G	0	0	3	1	0	?			
T	0	3	1	6	?				
T	0	3	1	?					
G	0	1	?						

=>

ppD	pD	cD
0	0	0
0	0	?
1	0	?
1	6	?
3	1	?
0	1	?

Table 7.1 The 3 newly created arrays to house the data needed for generating the next diagonal of cells. The '?' in the cD array (red) represents cells currently being generated. Notice that all the information needed to generate the new cell is present in the other 2 arrays

Also, keep note that the FillIn layer should keep track of the maximum location in the matrix. Having gained this new information, we can recode the FillInlayer as follows:

1. Create the arrays ppD, pD and cD. They should be the length of the sequence. All are initialized on zeros.
2. Start the current diagonal at the second column.
3. For every cell at the diagonal, do the following:
   (a) Check for edge cases. The row has to be smaller than the length of the sequence, the column can't be 0 or smaller and the column can't be bigger than the length of the reference.
   (b) Generate the new cell using the data in the ppD and pD arrays.
   (c) Write this new cell to memory, and its value to the cD array.

(d) Check if it is bigger than the current maximum. If so, the current maximum should be this new cell.

4. Set current diagonal to the next one.

5. Shift the values ($cD \rightarrow pD$ and $pD \rightarrow ppD$) and repeat from step 3, until the full matrix is filled.

6. Return the position of the maximum to the alignment level.

Note that by programming the Fill in Layer this way, there is no need to read cells from memory, since they can be generated using the arrays. Only the reference and read sequences should be read from memory.

7.3 Hardware acceleration

When accelerating the application, it was chosen to implement the FillIn and cell generation layer in hardware, since they are the functions where most computational time is spent (see Section 7.1). Therefore, they were merged into 1 convenient function, which will be transferred to the programmable hardware.

7.3.1 DMA

DMA or Direct Memory Access allows certain hardware systems in the computer to access the main system memory independent of the CPU. This can be of importance to the performance since the hardware system requires a lot of data movement between to and from the memory. The arrays (ref, seq, and matrix) are available in the memory, which means the programmable hardware should be able to access these arrays using DMA.

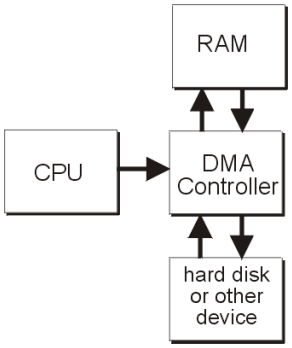


Figure 7.4: Schematic of a system using DMA

The following pragmas were used for the DMA:

```
#pragma SDS data access_pattern(ref:SEQUENTIAL, seq:SEQUENTIAL,
        matrix:SEQUENTIAL)
#pragma SDS data sys_port(ref:AFI, seq:AFI, matrix:AFI)
#pragma SDS data mem_attribute(ref:PHYSICAL_CONTIGUOUS,
        seq:PHYSICAL_CONTIGUOUS, matrix:PHYSICAL_CONTIGUOUS)
#pragma SDS data zero_copy(ref[0:refMax], seq[0:seqMax],
        matrix[0:refMax*seqMax])
```

- **access_pattern** can be either SEQUENTIAL or RANDOM. It specifies the data access pattern by the hardware to the memory. If SEQUENTIAL is used, the interface will be a stream (e.g. ap_fifo). On the other hand, when RANDOM is used, a RAM interface will be generated.
- **sys_port** can be ACP, AFI, GP or MIG. It specifies on which level the memory is interfaces.
  - ACP: Lets hardware functions have cache-coherent access to DDR using the PS L2 cache.
  - AFI: Hardware functions have fast non-cache coherent access to DDR via the PS memory controller.
  - GP: The processor directly writes/reads data to/from hardware function. This would be inefficient for large data transfers.
  - MIG: Hardware functions access DDR from PL via a MIG IP memory controller.

  We have quite a large amount of data, so GP doesn't seem like a good option. Likewise, the memory will be accessed uniform, we have no use for a cache as this would just slow it down. Therefore the AFI was selected.
- **mem_attribute** can be either PHYSICAL_CONTIGUOUS or NON_PHYSICAL_CONTIGUOUS. The default value is NON_PHYSICAL_CONTIGUOUS. PHYSICAL_CONTIGUOUS is used for memory allocated with sds_alloc. Likewise, NON_PHYSICAL_CONTIGUOUS is used with memory allocated using malloc.
- **zero_copy** means that the hardware function accesses the data directly from shared memory through an AXI master bus interface.

The data_pack pragma The data_pack pragma is used on the matrix since it is an array of structs (CELL type). This packs the data fields of a struct into a single scalar. The bitwidth of the packed struct is the sum of its attributes.

The bitwidth of (packed) data on the AXI but must be a power of 2, to interface with the memory. Therefore, it was chosen to change the CELL_VALUE type to an int16_t and the direction to uint16_t. This is however quite wasteful towards memory usage. It can be optimized by remodeling some of the code, but due to time constraints, this was not implemented.

7.3.2 Unrolling pragmas

Which loops are unrolled and how, is best described in pseudocode, which is found hereunder:

```
Create the current maximum (=0) and the position of the maximum;
Create the 3 arrays (pD, ppD, and cD) of size seqMax;

for i from 0 to seqMax: //initializing the arrays
   #pragma HLS UNROLL
   pD[i] = ppD[i] = cD[i] = 0;

for currentColumn from 2 to (refLength + seqLength): //The fillIn loop
   #pragma HLS loop_tripcount min=5000 avg=5150 max=5700
   #pragma HLS PIPELINE

   for i from 0 to seqMax: //the diagonal loop
      #pragma HLS UNROLL
      row = i;
      col = currentColumn - i;

      //edge cases
      if (i < seqLength && col != 0 && col <= refLength):
         generateCell(  //cell generation layer
                 diagonal value = ppD[i-1],
                 left value = pD[i],
                 up value = pD[i-1],
                 reference value = ref[col],
                 sequence value = seq[row]
         );
         store the current cell at cD[i];
         store the current cell in memory;
         if (value of cell bigger than maximum):
            replace current max position with this cell;


   for i from 0 to seqMax: //the shifting loop
      #pragma HLS UNROLL
      ppD[i] = pD[i];
      pD[i] = cD[i];

return the position of the maximum;
```

The unroll pragma transforms the loop to multiples copies of the loop body in the FPGA hardware, which allows the loop iterations to be executed in parallel. Since no parameters are given to this pragma, the loops will be unrolled fully, so the whole loop will be executed in parallel. Note that the number of iterations of the loop should be known at compile time.

In the code, all loops are unrolled fully, except for the loop that runs over every diagonal (the fill-in loop). Unrolling this loop would not affect execution speed since all elements in the loop are dependent on the previous iteration of this loop.

The loop_tripcount pragma is applied to a loop to manually specify the total number of iterations performed by a loop. In our code, this is applied to the fill-in loop since the number of iterations is not known at compile time (refLength and seqLength are variables).

The pipeline pragma will try to transform the body of the loop to a pipeline, where every iteration of the loop has a given II or *Initialization Interval*. If no II is given, the default is 1. This means it will try to run one iteration of the loop body for every clock cycle.

7.3.3 Comparison with the software

If we examine execution time (using the built-in latency analyzers in SDSoC), we can see we achieved a speedup of 4.41. This means the hardware variant of the implementation runs 4.41 times faster than the software variant.

Performance estimates for 'FillInHW in align.c:250' funct ...

SW-only (Measured cycles)	94414155
Hardware accelerated (Estimated cycles)	21410374
Estimated speedup	4,41

Performance estimates for 'FillInHW in align.c:272' funct ...

SW-only (Measured cycles)	94414155
Hardware accelerated (Estimated cycles)	21410374
Estimated speedup	4,41

Resource utilization estimates for Hardware functions

Resource	Used	Total	% Utilization
DSP	0	1728	0
BRAM	4	312	1,28
LUT	125724	230400	54,57
FF	53266	460800	11,56

Figure 7.5: Latency analyzer in SDSoC. We can see the number of clock cycles spent in the software and the hardware variant of the implementation, as well as the speedup. The speedup is calculated 2 times, since we run the fillIn function twice, once for the forward and once for the reverse sequence. The resource utilization of the FPGA hardware is also visible in this picture

Chapter 8

Conclusion and future research

Problem definition The best way to analyse DNA in detail is to sequence it. This will determine which bases and in which order they are occuring in the DNA. However, the most commonly used technology of DNA sequencing machines limit us to reads of 75-300 bases long. If we want to make assumptions about the whole genome, we will need to input a lot of these reads.

Typically, each read is compared with the whole genome in a local alignment, for example with the Smith-Waterman algorithm. As an output, we would get the position in the human genome and an alignment with its score (how well the sequence fits in that spot). This practice is commonly referred to as *Mapping to a reference genome*.

Sequencing maching produce millions of the reads in a sequencing experiment. Since each read from DNA sequencing machines are 75 to 300 bases long, and the whole human genome is approximately 3 billion bases, this mapping is computationally a very intensive task. If we analyze the S-W algorithm (as we have done in Subsection 3.3.2), we can see that the value of each cell in the matrix is only dependent on the left-upmost 3 cells. Therefore, it leads us to believe that this algorithm can be accelerated on hardware solutions such as an FPGA (as discussed in Chapter 4) since the S-W algorithm is heavily parallelizable.

In most clinical applications where mapping to a human reference genome is used, the number of reads to be compared with the genome is in the millions, which further increases the demand to speedup the process of mapping the reads in the genome, to decrease the time-to-result.

The idea of this thesis was to implement the Smith-Waterman alignment algorithm on an MPSoC, which contains both programmable FPGA hardware and an ARM processor in 1 chip. As a target board, the ZCU 104 evaluation kit was chosen.

Proposed solution and implementation As a starting point, a software implementation was implemented on the ARM processor. After running the software implementation overnight with the unmapped sequences from the coronavirus as a sample set, we obtained a dataset of mapped reads. The reads were also mapped by using the Galaxy online tool [] and both were imported into the IGV analyzing software for visualisation and comparison, which can be seen in figure 8.1

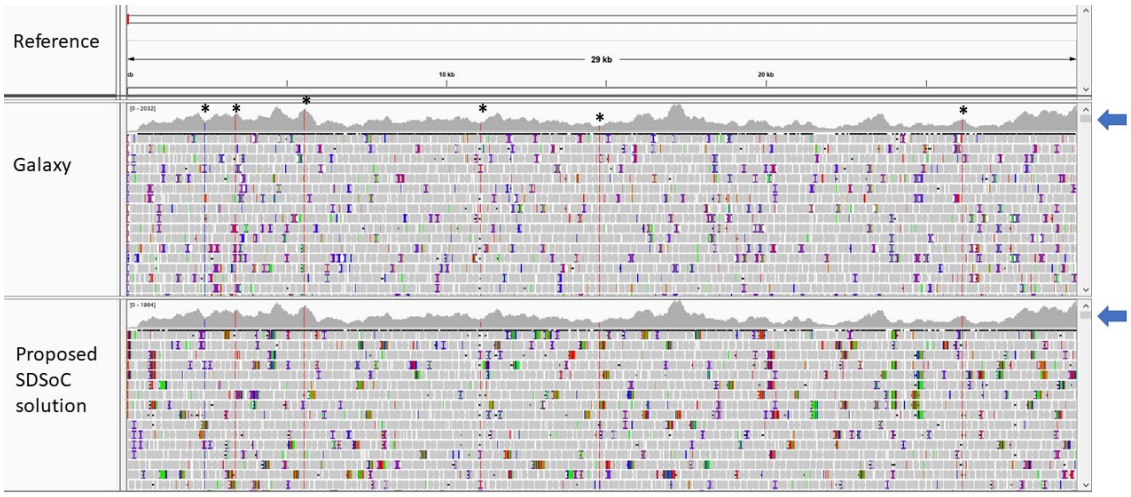
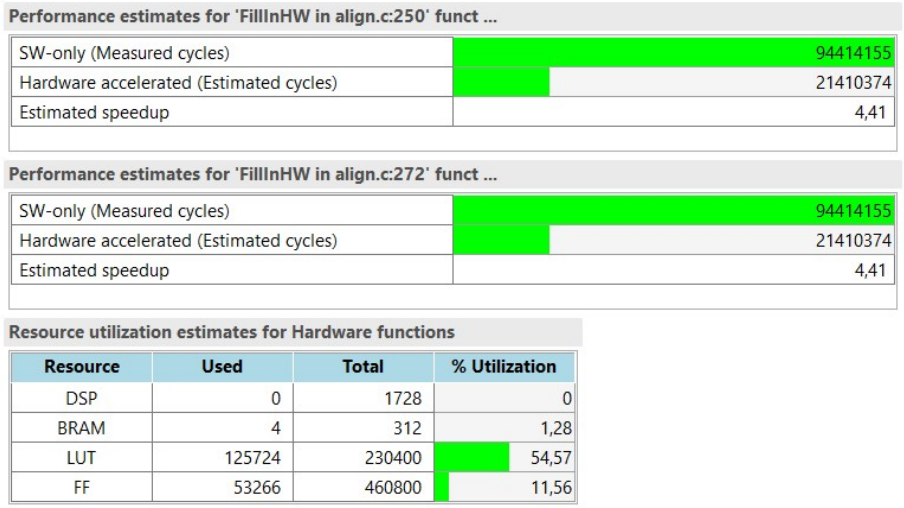


Figure 8.1: A comparison of the data obtained by Galaxy (top) and the data obtained by the implementation discussed in this chapter (bottom)

It can be observed that the implementation is working correctly since the reading depth graphs are approximately the same (indicated by an arrow). If we look closely to figure 8.1, some small differences between the exact reads are visible. This will probably be because both the algorithm and the parameters were a bit different. However, the important part is that the reading depths are the same, as well as the consistently mutated bases marked in the genome (indicated by an asterisk).

Hardware speedup After implementing the matrix fillIn in the FPGA hardware, we can examine execution time (using the built-in latency analyzers in SDSoC). The estimated achieved speedup was 4.41x. This means the hardware variant of the implementation runs 4.41 times faster than the software variant.



Performance estimates for 'FillInHW in align.c:250' funct ...

SW-only (Measured cycles)	94414155
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Performance estimates for 'FillInHW in align.c:272' funct ...

SW-only (Measured cycles)	94414155
Hardware accelerated (Estimated cycles)	21410374
Estimated speedup	4,41

Resource utilization estimates for Hardware functions

Resource	Used	Total	% Utilization
DSP	0	1728	0
BRAM	4	312	1,28
LUT	125724	230400	54,57
FF	53266	460800	11,56

Figure 8.2: The latency analyzer in SDSoC. We can see the number of clock cycles spent in the software and the hardware variant of the implementation, as well as the speedup. The speedup is calculated 2 times, since we run the fillIn function twice, once for the forward and once for the reverse sequence. The resource utilization of the FPGA hardware is also visible in this picture

Future work - recommendations for improving the current implementation the following optimizations could improve the proposed implementation:

- Treat the alignement gap opening and extension separately. In the current implementation, the gap penalty is treated linearly. However, the S-W algorithm could be refined to include an affine gap penalty. More info on the gap penalty can be found at Subsection 3.3.2.
- In a sequence, a base position may be suddenly marked with an 'N' character, which represents a base that was unidentified in the primary processing. In this thesis, it was decided to cut the sequence short at the moment an 'N' character is registered. However, a possible improvement might be to keep these unidentified bases in the alignment as a "generic" base and in this way improve the accuracy of the alignment. More info on the current implementation can be found at Subsection 6.3.1.2.
- Make some types more memory efficient, such as the BASE and the SEQ_INDEX type. Firstly, the BASE type only has 4 possible values (the 4 nucleotide bases). However, it is defined as 1 byte in the current implementation, since it is the smallest type that C supports. However, storing a base in 1 byte is memory inefficient. Improvements could be made by defining an own type, by stacking 4 bases in 1 byte. Secondly, the SEQ_INDEX type is stored as 2 bytes in the current implementation, even though it only contains values up to 300, which makes it memory inefficient. This could also be improved.
- If this implementation would be used in practice, there would be a need to find an easier way to on and offload data to board. Currently, this is accomplished by changing out the SD card, which could easily be improved using FTP since an Ethernet stack is, which are

already implemented by the operating system. The speed the data would be transferred at, is not important since we can assume the time it takes to map the sequence takes far longer.

Future work - recommendations for re-evaluating the alignment method In the field of alignment algorithms, a few alternatives exist to S-W since it takes a lot of computing power. In most cases, these algorithms will use a transformation or a lookup table to determine possible candidate locations, where a small regional S-W will be performed on a part of the genome. For example, The BFAST algorithm uses a hash table where candidate locations are stored for every sequence [19]. As a second example, in the Bowtie application, the candidate locations are determined using the Burrows-Wheeler Transform.

As future work, one of these more sophisticated algorithms can be selected. Some candidate locations can then be determined in a way defined by the algorithm. These candidate locations can then be mapped using the implementation of this thesis.

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