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Abstract

Due to advancements in DNA sequencing technologies the amount of genetic data has exploded over the last decade. Traditional models for representing said data can not account for the observed variation and more advanced representations are necessary to more accurately depict the true nature of genetical information. However, more complex models calls for more complex techniques for interacting with the data. In this thesis we present an efficient, non-heuristical approach for finding optimal alignments of genetic sequences against graph-based reference genomes.

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Preface

Chapter 1

Introduction

Chapter 2

Background

This chapter is divided into three sections. The first is concerned with the biological entities involved throughout the thesis. Because genetics is a huge discipline this chapter will only briefly describe the most critical areas, readers interested in a more thorough introduction are referred to the book "Introduction to genomics"[14]. The second section is directly aimed at the progress in the field of graph-based genomes through discussing relevant articles. Lastly some more general topics of computer science and bioinformatics which play a vital role in the proposed algorithm is presented.

2.1 Genetics

Deoxyribonucleic acid (DNA) is a molecule in which living organisms store genetic information. The information is encoded by *nucleotides* bound together by a sugar-phosphate backbone into strands. The nucleotides are smaller molecules which contain one of the nitrogenous bases *Adenine* (A), *Cytosine* (C), *Guanine* (G) or *Thymine* (T). Due to the chemical structure of the nucleotides, a DNA strand can be said to have a direction: Upstream towards the 5' end or downstream towards the 3' end. In the DNA molecule two reverse complementary strands are connected in a *double helix* structure. The two strands will have opposing directions, and every base in one of the strands will be connected to its *complementary base*, A with T and C with G. The paired nucleotides are called *base pairs*. Because either of the strands are easily deduced from the other, DNA is usually represented by only of them. DNA can be seen as a linear sequence of discrete units and can thus be represented by text strings, containing the four leading letters representing nucleotides. The text strings representations often also contain the letter N, referencing *aNy base*. The genetic sequence of an individual is called the *genotype*. All other observable traits of the individual is called the *phenotype*.

2.1.1 The central dogma

The process of transforming the genetic information into large functional biomolecules is called *the central dogma* of molecular biology. The central dogma states that DNA is transcribed into *messenger RNA* (mRNA) which in turn is translated into proteins. mRNA is, like DNA, a sequence of nucleotides consisting of same three bases A, C and G as well as *Uracil* (U). The mRNA can be divided into *codons* which are triplets of nucleotides encoding *amino acids*, which are the building blocks of proteins. The relationship between codons and amino acids can be looked up in a table called *The standard genetic code*[14, Chapter 1, p. 6]. Only a portion of the nucleotides in DNA act as *coding regions* which make it through the transcription process and code for actual protein sequences. These are also called *exons*. The remaining *non-coding regions* of the genetic sequence are known as *introns*. In humans about 1.3% of the genome is coding regions[14, Chapter 4], the rest is often referred to as *junk DNA*.

2.1.2 Variation

Genetic information is prone to mutations, either as a result of environmental influence or as a consequence of imperfections in reproduction. The simplest mutations are *point mutations* which affect a single nucleotide base. Point mutations can either be *Single-nucleotide polymorphisms* (SNPs) where a single base is substituted for another, or *insertions* or *deletions* (indels) where a single nucleotide is removed or inserted into the genetic sequence. Mutations can also occur over larger areas of the genome, where longer subsequences can be deleted, inserted, moved or reversed. A final type of mutations is *Copy number variations*, or *repeats*, where a longer sequence of DNA, typically at least 1 kb [6], is repeated a variable number of times.

As mutations happen randomly to individuals in a population, a diversity of genotypes emerges to form a *gene pool*. These different genotypes give rise to a variety of phenotypes. A subset of these phenotypes, and their associated individuals, can be better suited for survival and reproduction than others. Given enough time and enough scarcity in resources the best suited individuals will survive and pass on their genes to the next generation. This is the process of *natural selection* which is the main driving force behind evolution. Another mechanism in play is *genetic drift* which affects gene frequencies in a gene pool through non-selective, random processes.

Because there are more possible combinations of codons than there are amino acids in the standard genetic code there exists some overlap between the nucleotide triplets and the resulting amino acid. For instance the DNA triplets “CGA”, “CGC”, “CGG”, “CGT”, “AGA” and “AGG” all encode for the amino acid Arginine. In this cases point mutations can occur without affecting the resulting protein. These mutations are called *synonymous*, the opposing case which alters the amino acid sequence are called *non-synonymous*.

2.1.3 Reference genomes

A *reference genome* is a data structure which contains genetic information for a population, typically for a given species. The reference genome has a set of continuous nucleotide sequences, called *contigs*, combined into larger *scaffolds* which again are combined to form the *genome* for a species. The first reference genomes collapsed samples from several individuals into a linear *consensus sequence* which was representable for the species as a whole. Later reference genomes have been built more flexibly to allow positions on the genome, called *loci*, to have several variants, termed *alternate loci*. A specific variant of a gene is called an *allele*. A *haplotype* is a set of alleles which tend to be inherited together. Reference genomes form what can be seen as a dictionary for the genome of a species and can be used in sequencing (Section 2.1.5).

2.1.4 The human genome

The human genome consists of roughly 3 billion base pairs (bp). These base pairs are spread over 22 paired chromosomes and is assumed to contain about 23 000 genes [14]. The current human reference genome is GRCh38[grch38], developed and maintained by the *Genome Reference Consortium* [genome_reference_consortium]. GRCh38 contains 261 alternate loci, spread over 178 out of a total of 238 regions. An average human is estimated to deviate from the reference genome in 10.000-11.000 synonymous sites and 10.000-12.000 non-synonymous sites [4].

Major Histocompatibility Complex

The *Major Histocompatibility Complex* (MHC) is a genetic region spanning approximately 4 million base pairs (mb) NEEDS CITATION. In humans it is located on chromosome 6 and contains about 200 genes. MHC is a region known to contain genes which affect the functionality of the immune system [22]. Even more so MHC is known to be a highly variable region, containing variants that are directly associated with disease [7].

2.1.5 Sequencing

During *sequencing* a *sequencing machine* is used on a physical DNA fragment to find the underlying nucleotide sequence. The machines produce short *reads*, typically in the order of a hundred bp[sequencing_platforms], which are combined into longer sequences through a process called *assembly*. When the sequenced individual belongs to a specie with a reference genome, reads are typically mapped to positions in the reference to determine their underlying order in what is called *mapping assembly*. In the opposing case overlap techniques[20] or de Bruijn graphs (Section 2.2.1) are often used in what is known as *de novo assembly*[14, Chapter 1, p. 19].

The different sequencing technologies have varying degrees of errors introduced in their reads, often closely related to the sequencing

`cost[sequencing_platforms]`. The errors can take the form of both point mutations and larger structural variations. Reads produced by sequencing machines are typically prone to contain more errors in their peripherals. There exists efficient strategies for both estimating error rates [estimation_of_sequencing_error_rates_in_short_reads] and correct the reads[error_correction_of_datasets_with_non_uniform_coverage] Can probably provide more citations.

2.1.6 Alignment

Sequence alignment is the process of determining correspondence between text strings, in this case representing DNA, by mapping the elements from one to the elements of the other according to a *substitution matrix* (Fig. ??).

Definition 1 (Mapping score)

A *score* retrieved by mapping to characters c_1, c_2 against a substitution matrix. Referenced by $\text{mappingScore}(c_1, c_2)$

The alignment procedure is never allowed to change the order of the elements in the two strings, but can introduce *gaps*. A gap occurs when one element in one string does not have a counterpart in the opposing string (Fig. 2.1). When a gap occurs the resulting is penalized according to the length of the gap, by a *gap penalty*.

Definition 2 (Gap penalty)

The penalty received for a gap of a given length l . Referenced by $\text{gapPenalty}(l)$.

Gap penalties come in different shapes, often according to the origin of the data involved. A *linear gap penalty* gives linear penalties related to the gap length. An *affine gap penalty* distinguishes between opening and continuing a gap. A *logarithmic gap penalty* lets the increase in penalty fade as the gap expands. A schema which provides functionality for mapping bases and penalizing gaps is called a *scoring schema*.

Definition 3 (Scoring schema)

A structure which provides a $\text{mappingScore}(c_1, c_2)$ -function and a $\text{gapPenalty}(distance)$ -function. The alphabet Σ of a scoring schema is defined by the characters present in the scoring schema.

A gap refers to an element in one of the strings which has no counterpart in the other string when aligned (Fig. 2.1). The scoring schemas can be based around simple match/mismatch scores, which corresponds to the mathematical *Edit distance problem*, or more complex scores (Fig. 2.1). These complex models typically try to model the probabilities behind the physical processes responsible for change. The computational sequence alignment problem consists of finding the highest scoring alignment for any two strings. There exists two main variants of the problem: Finding *global alignments*, where two entire strings are aligned against each other, and finding *local alignments*, where a string is aligned against a substring of another. The two are traditionally solved respectively by the Needleman-Wunsch and Smith-Waterman algorithms which both are based on *dynamic*

programming (Section 2.3.1).

ACGGGCCTA
ACGGACCTA

(a) An alignment with no gaps, but one mismatch

ACGGGCCTA
ACGG--CTA

(b) An alignment with a single gap of length 2

If more than two sequences are aligned the result is a *Multiple sequence alignment* (MSA). This is typically done on sequences which is expected to share a common ancestor to determine which traits in the individuals arised from the same origins and how the involved species have diverged genetically over time. A final variant of the alignment problem is one involving large databases of sequences, where the algorithms does not only need to find the best alignment between two sequences, but also determine which sequence should be chosen in order to maximize the result. Both of the preceding techniques typically utilize heuristical methods in order to decrease the computational complexity.

Figure 2.1: Examples of aligned text strings

	A	C	G	T
A	91	-114	-31	-123
C	-114	100	-125	-31
G	-31	-125	100	-114
T	-123	-31	-114	91

Table 2.1: The HOXD70 substitution matrix

2.2 Graph-based genome representations

Representing genetic information as graphs instead of the traditional linear representations have some major advantages. Graphs are far more expressive structures compared to text strings, able to represent more complex relationships between the elements involved. Secondly, if biological questions can be rephrased to graph theoretical settings, the extensive mathematical field of graph theory can present more feasible approaches to previously hard problems. There is however a major problem: A more complex structure calls for more sophisticated variants of existing methods. Graph-based approaches have been used for some time in the assembly process, and more recently in relation to reference genomes. This section will present both of these approaches alongside some of the remaining unsolved problems. No graph theoretical foreknowledge is needed as all the involved elements will be defined before they are used, but for interested readers there exists good sources in the bibliography [21, Chapter 0] [24, Chapter 9] [1, Chapter 11]. Complexity in regards to the graphs and their operations is discussed using *big-O* notation [24, Chapter 2][1, Section 3.1]

2.2.1 Representation

Deciding upon the representation of the graph consists of defining the structure of the elements involved, namely the vertices and edges. As the graphs are built from genetic information the basic building blocks, the nucleotides, should obviously be represented. If the input data are more complex than single nucleotides, we must represent the relationships. Because the input data has variation, the structure needs to tolerate flexibility. There is however a risk of making the structures so flexible they present no consistency, and a flexibility/rigidness-tradeoff becomes apparent (Fig. 2.2). How the structures are defined in detailed should be determined through the operations which are desirable to perform on them.

de Bruijn graphs

In the article “An Eulerian path approach to DNA fragment assembly”[20], Pevzner, Tang and Waterman proposes *de Bruijn* graphs as a solution to find the correct assembly of repeats during fragment assembly. A de Bruijn graph is a structure where vertices represent *k-mers* from an alphabet and edges represent relationships between the k-mers of two vertices (Fig. 2.3). Pevzner et al. lets the vertices contain strings of length $l - 1$ and connects vertices with an edge wherever there exists a read of length l containing the two substrings. Formulating the problem in this fashion lets the problem be formulated as a *Eulerian path* problem, solvable in polynomial time, rather than the traditional “overlap-layout-consensus” method which is equivalent to the NP-complete problem of finding a *Hamiltonian path*[1, Section 11.1]. A great benefit with de Bruijn graphs is that there is no

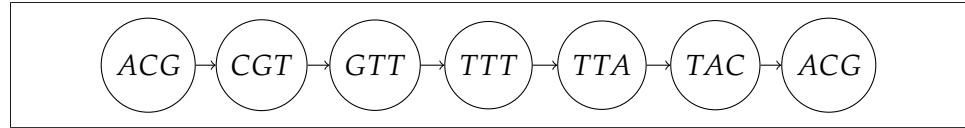
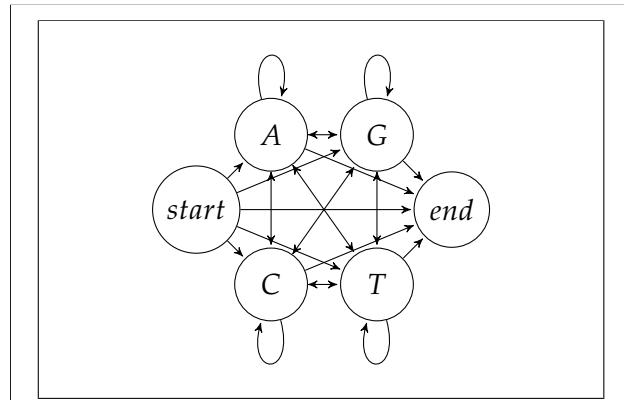
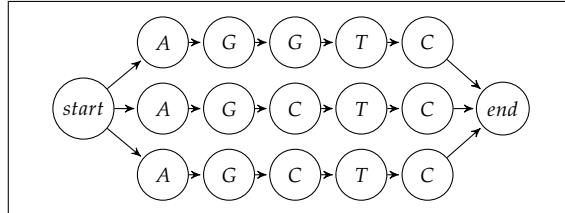


Figure 2.3: A de Bruijn graph with $k = 3$ corresponding to the sequence AC GTT TAC G

disambiguity: Any legal k -mer has at no point more than one vertex representing it.



(a) A graph with paths corresponding to every possible DNA string



(b) A graph which is built through alignments without allowing variation

Figure 2.2: Two sequence graphs displaying too much flexibility (a) and (arguably) too much rigidity (b)

A more detailed type of de Bruijn graphs is the colored variant where the origins of edges and vertices are stored as colors. The entire sequence originating from a single individual sample can be seen by following a path with a given color. Similarities between samples can be seen as multicolored stretches, variation take the form of bubbles. Colored de Bruijn graphs can be used for de novo assembly as a more powerful method for detecting variation, compared to traditional assembly techniques[8].

Cactus graphs

Cactus graphs for genome comparisons

Sequence graphs

WRONG: POMSA. The term *sequence graph* stems from the article “Mapping to a Reference Genome

structure”[19] and describes a graph structure which is possibly more intuitively pleasing. Every vertex in the graph corresponds to a single nucleotide from one or more genetic sequences used in building the graph. An edge represents two nucleotides which are consecutive in one of the

original sequences. Paths symbolize subsequences of the originating input sequences. To handle the arising problem that the contents of nodes are no longer unique each vertice can be given an index which is exclusive for their associated graph. Whenever a graph is referenced without being specifically classified the following definitions are assumed:

2.2.2 Mapping

Although the two terms are often used isomorphically we will in this thesis define mapping and alignment as two separate concepts. Mapping is the process of finding relationships between single characters of a string and single elements of a reference genome. Alignment is concerned with finding relationships between consecutive elements of an input string and substructures in the reference genome. For linear strings mapping is easy. Every string has the same underlying coordinate system, represented by the positions of the characters, and two elements from two separate sequences are either in the same position or they are not. If they are not the difference in position can be derived from the difference between the indexes. Because the indexes of a graph has only one property, uniqueness, they do not hold the intrinsic value of describing relationships between vertices. Any mapping system which uses fixed coordinates would face problems when dealing with a fluent graph able to merge in new information, as the internal relations are bound to change. In de Bruijn graphs the problem is solved by moving the mappable quality away from positions and into the data: For any possible k-mer there either is a corresponding vertice or there is not. In sequence graphs, where nucleotides are the most basic information, there exists an equal number of identically scoring positions for every base as there are vertices containing that vertice in the graph.

Paten et al.[19] introduce the concept of *context-based mapping* as a solution to the mapping problem when the reference is modeled as a graph. Context-based mapping is an approach where a vertice is identified by the surrounding environment in the graph. More technically a vertice has a set of *contexts* which are paths that pass through the vertice. Because these paths are linear and passes through vertices containing characters, the contexts can be treated as text strings. There are two concrete examples of approaches presented in the article: The *general left-right exact match mapping scheme* and the *central exact match mapping scheme*. The key words left-right and central refer to how a vertice defines it's contexts based on the surroundings. The former defines separate contexts for incoming and outgoing paths whereas the latter defines the vertice as a center of a path where the differences of the lengths of the two contexts are minimized. A *balanced central exact match mapping scheme* is a special case of the latter where both contexts are the same length, and the vertice thus is the center of a k-mer. This is a concept closely related to de Bruijn graphs.

Both of the examples use the word *exact* in their definitions. The term refers

to the fact that every context is *unique* to a single vertex which means every possible context either maps unambiguously to a single vertex or does not map at all. Because the graphs have the possibility of branching a vertex can have several contexts contained in *context sets*. Because every context is unique a collection of such will also be unique, which means context-based mapping leads to a two-way unique mapping schema. This is an even strong notion of mappability than positions in strings, as a character of a string does not necessarily map uniquely back to its position. This strong notion has a drawback: There exists situations where a vertex does not have a unique context which yields it unmappable.

2.2.3 Alignment

Intro

Dynamic programming on graphs

PO-MSA

Context-based alignment

Canonical, Stable, General Mapping using Context Schemes

2.3 Techniques and tools

2.3.1 Dynamic programming

Dynamic programming (DP) is a problem-solving technique where a problem instance is solved by combining the results of smaller subproblems. DP is similar to recursion in that every instance is solved by a *recurrence relation* (Equation 2.1) which recurses on smaller and smaller problems until a *base case* is found. A base case represent the bottom of the recursion and is a value which can easily be computed without further lookups. The main difference between recursion and DP is that the latter usually stores its intermediate results to allow for fast lookups for reoccurring instances. DP is often used as an approach for optimization problems in order to minimize computational complexity while giving a guarantee for optimal results [1, Chapter 9].

A problem which is typically solved by dynamic programming is the previously mentioned edit distance problem which utilizes a 2-dimensional array to store the computed values (Fig. 2.2). For two strings S and P , every index $[i, j]$ in the edit distance table represents the problem instance of the strings $S[0 : i], P[0 : j]$. The base cases can be seen in the first row and column. There are often dropped from the table itself due to the simple nature of their computations. The remainder of the table is filled out with the following recurrence relation:

	a	l	g	o	r	i	t	h	m
a	0	1	2	3	4	5	6	7	8
l	1	1	1	2	3	4	5	6	7
o	2	2	2	2	2	3	4	5	6
g	3	3	3	2	3	4	5	6	7
r	4	3	4	3	3	4	5	6	7
i	5	4	4	4	4	3	4	5	6
t	6	5	5	5	5	4	3	4	5
h	7	6	6	6	6	5	4	3	4
m	8	7	7	7	7	6	5	4	3
m	9	8	8	8	8	7	6	5	4

Table 2.2: The 2-dimensional array used for solving the edit distance problem for the strings S=“algorithm” and P=“logarithm” (Note: This follows regular ED scoring where every operation is penalized +1)

$$D[i, j] = \min \begin{cases} D[i - 1, j] + 1 \\ D[i, j - 1] + 1 \\ D[i - 1, j - 1] + \text{score}(S[i], P[j]) \end{cases} \quad (2.1)$$

where $\text{score}(x, y)$ is an inverse equality function. The score for the entire

problem instance can be found in the cell with the highest indexes in the bottom right corner.

There are two separate ways of using Dynamic Programming. A *bottom-up* approach starts at the smallest cases and computes everything until it reaches the actual given problem instances. This corresponds to starting in the top left corner of the edit distance array and computing the cells iteratively moving downwards to the right. A *top-down* procedure starts at the given problem instance and recursively computes every subproblem that is needed. This means starting in the bottom right corner of the 2-dimensional array and recursing upwards to the right. For the edit distance problem the choice of approach bears no big significance as every cell has to be computed either way, but there are problems where using top-down can avoid some computations which are irrelevant to the final result. The latter can also be efficient for heuristical methods where an area of the search space can be overlooked.

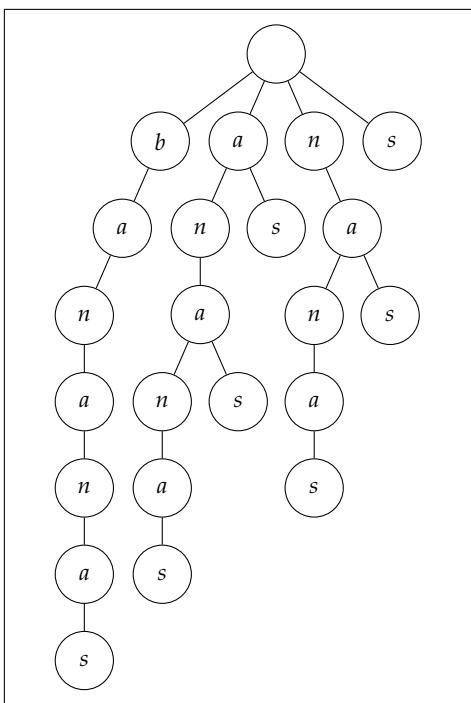
2.3.2 Implementing graphs

2.3.3 Suffix trees

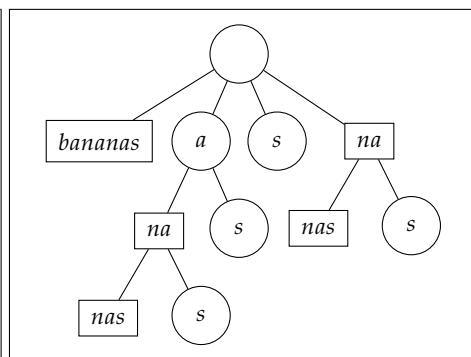
A *suffix trie* is a special tree constructed for specifically for strings of text, containing vertices representing characters (Fig. 2.4a). Every suffix of a string has a corresponding leaf vertex, where the vertices along path from the root to the vertex contains the characters in the suffix. From this it follows that every substring has a matching path starting in the root node. A *suffix tree*, or *compressed suffix trie*, is a suffix trie in which every linear path is compressed into a single vertex (Fig. 2.4b). Suffix trees can easily be extended to hold collections of strings[1, Chapter 20]. An elementary solution has a space complexity of $O(s)$, where s is the length of the string (or the total length of all strings if the tree is built from a collection), and a string of length m can be looked up in $O(km)$ time for an alphabet of size k [1, Section 20.6.1]

A Block-sorting Lossless Data Compression Algorithm

2.3.4 Visualization of graphs: The dot-format



(a)



(b)

Figure 2.4: The suffix tree (a) and suffix trie (b) of the string “bananas”

Chapter 3

The algorithm “Fuzzy context-based search”

The main concern of this chapter is to introduce the algorithm “Fuzzy context-based search” as a solution to the problem of aligning text strings against graph-based reference genomes. In order to do this we will first present formal definitions of the elements and structures involved as well as the problem itself. The following description of the algorithm will be a conceptual overview where the motivation behind the steps taken are also described. A more detailed introduction to an implementation of the algorithm will follow in the succeeding chapter, in which space and time complexity will also be discussed. Due to the abstract nature of this chapter the reader is advised to use the coming chapter as a reference whenever needed. The two have corresponding sections, and the latter contain exact details and concrete examples.

In order to avoid ambiguity when dealing with already existing concepts, the terms which are defined are given problem-specific names. For several of the terms there also follows a shorthand notation behind the original name in the definition title. Whenever these shorthand names are used in the subsequent explanatory sections we refer exclusively to the definitions done in this thesis.

3.1 The graphs

The graphs used as reference genome graphs will be built iteratively by starting out with an empty graph and sequentially merging in input sequences aligned against the existing structure. How the sequences are merged, and thus what the graphs look like, are decided entirely through the alignment procedure, which in part relies on the scoring schema. This first section is dedicated to precisely defining the involved graphs.

Definition 4 (Graph-based reference genome (Graph))

A pair $G = \{V, E\}$ where V is a set of vertices and E is a set of edges. $|G|$ denotes the number of vertices in G .

The involved graphs will be sequence graphs (Section 2.2.1) where every vertex correspond to a single nucleotide from a one or more input sequences used in building the graph. Whether the vertice originates from a single or several sequences is based on whether any new bases has been mapped, and consecutively merged into the vertice. In addition to the nucleobase the vertices will contain an index which is unique to the graph. Every graph G will have two special vertices $s_G = \{s, 0\}$ and $t_G = \{e, -1\}$ which represents unique start and end vertices.

Definition 5 (Graph genome vertex (Vertice))

A pair $v = \{b, i\}$ where $b \in \{A, C, T, G\}$ and i is a unique index. The vertice at index i is denoted v_i . The notation $b(v_i)$ references the first element in the pair (the nucleotide).

The edges model the relationships between the vertices and thus the relationships between the elements of the input sequences. Every edge has its origin from a consecutive pair of nucleotides in one or more input sequences.

Definition 6 (Graph genome edge (Edge))

An ordered pair $e = \{i_s, i_e\}$ where both elements are indexes for vertices.

There exists no information storing the origin of an edge, or whether an edge originates from one or more input sequences, and all edges are thus seen as equally probable when aligning a sequence. A sequence of vertices where there exists an edge for every pair of consecutive vertices is called a *path*. Paths is a way of capturing the combination of several individual characters into text strings in the domain of our graphs.

Definition 7 (Graph genome path (Path))

A list P of indexes such that for all consecutive pairs $p_x, p_{x+1} \in P$, where p_n denotes the n -th element of the list, there exists an edge $e = \{p_x, p_{x+1}\}$. The notation p_{-1} denotes the last element in the list. The length of P , $l(P)$, is equal to the number of indexes in the list. The distance $d(P)$ between p_0 and p_{-1} is $l(P) - 2$.

Corollary 1

Every edge e is also a path P with $l(P) = 2$ and $d(P) = 0$.

Paths spanning the entire length of a graph G , from s_G to t_G are named full paths. Every input sequence used to build the graph has a corresponding full path.

Definition 8 (Full path)

A path P through a graph G where $p_0 = 0$ and $p_{-1} = -1$

There is no correspondence the other way, meaning there can exist full paths which does not originate from a single input sequence (Fig. 3.1). When aligning regular text strings against eachother the introduction of gaps is a key element. The concept of strings with gaps are translated to graphs through *incomplete paths*.

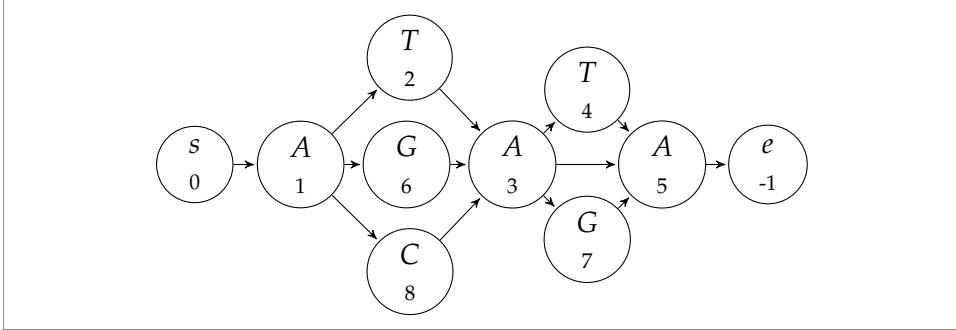


Figure 3.1: An example reference graph G made from the three sequences “ATATA”, “AGAGA” and “ACAA”. Although the graph is made from 3 sequences, 9 full paths can be found

Definition 9 (Incomplete path)

An list $P*$ of indexes such that for all consecutive pairs $\{p*_x, p*_x+1\} \in P*$ there exists a path P such that $p_0 = p*_x$ and $p_{-1} = p*_x+1$.

Conceptually incomplete paths can be seen as regular paths where some of the vertices are removed to reflect gaps. We can score an incomplete path by looking solely at the gaps present and avoiding the nucleobases contained in the vertices to produce a *path score*.

Definition 10 (Path score)

The total score of all gaps present in an incomplete path $P*$ according to a scoring schema

In an incomplete path there exists two possible relationships between consecutive elements: Either they are neighbours and there exists an edge between them, or they are not neighbours and are at the beginning and end of a path. Because the edges have distance 0 and are thus not penalized, the path score of an incomplete path can be found by summing up the gap penalties for a gap with the distance of the shortest path between every two consecutive vertices.

Corollary 2

$\text{pathScore}(P*) = \sum (|P*| - 2)_{i=0} \text{gapPenalty}(\text{distance}(p*_i, p*_i+1))$ where $\text{distance}(x, y)$ denotes the distance of the shortest path P where $P_0 = x$ and $P_{-1} = y$.

3.2 The alignment problem

Because the alignment problem is concerned with aligning text strings against graphs we need to define a second component alongside the graphs: The input sequences.

Definition 11 (Input sequence)

A string s over the alphabet $\{A, C, T, G\}$. The length of the string is given by $|s|$. The individual character on position $0 \leq x < |s|$ is referenced by s_x .

Once we have a clear definition of a graph G and an input sequence s we can try to find an *alignment* between the two, which model the relationship between the two. In order to do this, the alignments should provide relations between the smallest constituents of the two input structures, the vertices of the graph and the characters of the string, in a way such that the internal structures of the two are reflected against each other. We can model an alignment as a special variant of an incomplete path, which allows for *unmapped elements*. These elements are recognized as elements of $|s|$ which is mapped to 0, the index of the start-vertex and thus always an invalid mapping. The remaining elements of s is mapped to indexes of valid vertices of G which form an incomplete path P_* . Moving forward through the individual positions s_x which are mapped corresponds to traversing P_* .

Definition 12 (Alignment)

Given a graph G and a string s , an alignment A is an ordered list of length $|s|$ such that every element $a_x \in A$ is either 0 or the index for a valid vertex of G such that for every consecutive pair of valid indexes a_n, a_m there exists a path P where $p_0 = a_n$ and $p_{-1} = a_m$. A 0 represents an unmapped character in s .

When we have defined the alignments we can start scoring them. The scoring happens according to a scoring schema and should be the sum of three different scores:

1. The mapping scores of the mapped elements
2. The gap penalties for gaps in the graph, represented by the distance of the shortest path between consecutive pairs of mapped elements
3. The gap penalties for gaps in the string, represented by unmapped positions

We already know how to find the first two. The last can be found by summing up the gap penalties for all the gaps in the input sequence. A gap in the input sequence can be identified by a continuous subsequence $A_{x:y} \in A$ spanning the indexes x to $y - 1$ where every element is unmapped. An important aspect here is that every unmapped element should only be considered part of exactly one gap. We cover this aspect by only considering *maximal unmapped subsequences*

Definition 13

A subsequence $A_{x:y} \in A$, such that every $a^* = 0$ for every $a^* \in A^*$ and x is either 0 or $a_{x-1} \neq 0$ and y is either $|s| - 1$ or $a_{y+1} \neq 0$.

The gap penalties for gaps in the string is then defined as $\sum_{A^* \in A} \text{gapPenalty}(|A^*|)$ where A^* is the maximal unmapped subsequences of A .

Definition 14 (Alignment score)

Given a sequence s , a graph G and an alignment A , the score produced by combining mapping scores for the pairs $\{b(v_{a_x}), s_x\}$ for $0 \leq x < |s|$ with the path score for the incomplete path provided by consecutive mapped indexes of A and the gap penalties for the string gaps in A . We reference this score by $\text{alignmentScore}(A)$.

We can then easily define the alignment problem itself:

Definition 15 (The optimal alignment score problem)

For any pair $\{G, s\}$, where G is a graph and s is an input sequence, find one of the alignments A which produces the highest possible alignment score.

Notice that the definition only calls for finding one of the alignments which produce a highest possible score. This is done in order to simplify the abstract explanations of the algorithm. Implementation-wise this can trivially be changed to find all optimal alignments. The necessary adjustments is discussed as a part of the succeeding chapter in section 4.1.3. Additionally we have defined a bounded version of the problem, called *The bounded optimal alignment score problem*. This second version also considers a score threshold value T and deems a string s *unalignable* if the optimal alignment produces a score lower than T .

Definition 16 (The bounded optimal alignment score problem)

Given a triplet $\{G, s, T\}$ where G and s are as before and T is a numeric value, find the alignment A which produces the highest alignment score, if and only if the alignment score for A is higher than T . If no such alignment exists, s should be classified as *unalignable*.

Defining a bounded adaptation of the problem is obviously done in order to reduce the computational complexity, but it also present a powerful notion of control to the model: We can choose the degree of similarity required for elements to be considered equal. This simplifies the concept of equality into a classification problem where the border between the two classes can be easily manipulated through the threshold variable.

3.3 “Fuzzy context-based search”

We now present the algorithm we propose as a solution to the bounded optimal alignment score problem. The algorithm consists of two distinct subproblems which are solved in consecutive steps:

1. Create a new graph G' for an input triplet $\{G, s, T\}$
2. Search G' for an optimal alignment

Both the motivation behind each step and the conceptual approach for solving the subproblem will be explained in its corresponding subsection. In addition to the three involved components set as input parameters, the algorithm has a preset scoring schema.

In presenting the algorithm we introduce a new variable λ . λ represents the *error margin* allowed in an alignment and is computed by taking the difference between the highest possible alignment score for s and the scoring threshold T . The highest possible score for any string can be found by aligning the string against itself with regular string alignment operations, using the already defined scoring schema. Introducing λ gives us the opportunity to do strict pruning throughout the entire alignment process: Any alignment which contains a single element, be it a gap or a sequence of mappings, which is penalized more than *lambda* compared to the corresponding element in an optimal alignment can never have a total alignment score higher than T (Appendix A).

3.3.1 Creating a new graph

The motivation behind building an entirely new graph is the realization that whenever reads are mapped against a reference genome the read is typically vastly shorter than the reference. We can therefore do a *horizontal pruning* where we determine which sections along the horizontal axis of the graphs are interesting for the alignment. The same argument can be made for extremely complex graphs, where only a small number of the branches are relevant, in an operation we have called a *vertical pruning*. The result should be a new graph G' with a vertex set V' and an edge set E' .

We first let V' be a subset of the original vertex set V . In order to guarantee optimality we put a restriction on V' :

1. Every $v_x \in V$ should be in V' if there exists an optimal alignment A with a higher score than T which contains the index x

Through the definition of the alignments we know they are ordered and that the indexed elements refer to the vertices which map to a specific position in the string. We can use this knowledge to more specifically define V' as an ordered set of sets V'_x where every indexed set is related to the corresponding position in the alignment:

1. Every $v_x \in V$ should be in V'_y if there exists an optimal alignment A with a higher score than T where $a_y = x$

This is a restriction which is strictly enforced throughout the algorithm, to continue ensuring the optimal solution is still a possibility. We formulate a second restriction, to reduce the number of vertices which are not interesting for final alignments:

2. Every vertex $v_x \in V$ which is not referenced by a_i in any optimal alignment should not be in V'_i

If we manage to create V' from these two restrictions we can guarantee a vertex set where every element of every optimal alignment is still present and all excesses vertices has been dropped. However, finding these vertices requires knowledge of every alignment A of every string s for every threshold T , a number of possibilities which quickly become infeasible. In order to make the operation more tractable we identify the second restriction as only being related to the computational complexity, which means it does not have to be strictly enforced. We can thus relax it:

2. Every vertex $v_x \in V$ should be in V'_i for every $0 \leq i < |s|$.

This is a complete relaxation and puts every vertex $v \in V$ in every subset of V' . The resulting parenting vertex set V' is a set far greater than V and this is obviously suboptimal. So, we propose a compromise:

2. Every subset V'_x should be as small as possible

Finding the elements of V' can then be formulated as finding the optimal compromise to the second restriction without violating the first.

We let a vertex v be a *candidate vertex* for index i if it is a part of the *candidate set* V'_i . In order to find candidate vertices we apply *fuzzyness* to the context-based mapping schema proposed by Paten et al.[19]. We say a vertex is a candidate vertex for an index if it has a context which is similar enough to the context of the corresponding position in s . The vagueness of “similar enough” is controlled through the fuzzyness, which again is controlled through the error margin parameter λ . The contexts of the vertex represents the paths passing through it, and because we know that if a context is penalized more than λ compared to the maximal possible score we know that the context can never be a part of a longer incomplete path with a total score higher than T . Thus, more formally, for every index $0 \leq i < |s|$ we put v_x in V'_i if and only if the context set $c(v_x)$ of v_x contains a context which can be aligned against $c(s_i)$ with a score higher than T_c . T_c is a *context threshold score* and is computed by taking the max possible score for a context in s and subtract λ .

After deciding which vertices make up G' we need to decide how we combine them, through the edge set E' . Because the subsets of candidate vertices follow a natural ordering there is already defined a direction in the

graph. Every vertex of every candidate set V'_i should have an incoming edge from every vertex in the preceding candidate set V'_{i-1} to account for this direction. Because we allow gaps in our alignments we have to extend the number of steps a vertex looks back for possible paths: Every vertex in every candidate set V'_i should have an incoming edge from *every* preceding candidate set V'_j , where $0 \leq j < i$. These edges represent the relationships between the elements of the string. We do also want to represent the relationships between the vertices in the graph they originate from. This is done through introducing *weighted edges*:

Definition 17 (Graph genome weighted edge (Weighted edge))

A triplet $e' = \{i_s, i_e, w\}$ where the two first elements are indexes for vertices in V' and the latter is an integer value

We let the weight w denote the distance $d(P)$ of the shortest path P where $P_0 = i_s$ and $P_{-1} = i_e$. These weights can be found through a regular graph search in G , if no distance is found we let it be inf. At this point we have a complete graph G' .

Corollary 3

For every edge $e = \{i_s, i_e\} \in E$ where $v_{i_s} \in V'_x, v_{i_e} \in V'_y$ and $x > y$ there exists a weighted edge $e' = \{i_s, i_e, 0\} \in E'$

The resulting graph is still very complex . Every vertex is connected to every preceding vertice, and in order to find the weights of these edges we need to do graph searches for every possible pair of vertices. However, we still know we are not interested in incomplete paths which have a lower score than T and we thus can limit the edges to only the ones that are passable without being penalized more than λ . This sets a bound both on how far back in the candidate sets a vertex looks for neighbours and, more importantly, puts a strict upper bound on the complexity of the individual graph searches done in G .

3.3.2 Searching the newly formed graph

We have built G' in a specific way to guarantee the optimal alignments still exist, which means the next step is finding them. Searching for an alignment means combining vertices, representing bases, into a path representing a string. This linear sequence can be aligned against the input sequence with regular string alignment tools and the scores are therefore easily verifiable.

In order to continue securing optimal results the algorithm does the search using dynamic programming. The search algorithm is conceptually very similar to PO-MSA[12], except the roles are switched around: Instead of searching through the reference graph with an input string we are searching through the indices of the string with the candidate nodes from the reference graph as our input. When we dynamically compute scores we are still doing the same thing as a regular PO-MSA, letting a candidate

vertice v_x in a candidate set V'_i be an intersection at position x, i in a two-dimensional space where the dimensions represent the string and the path. We set the scores to be the highest possible score for aligning the substring of s ending in i against a path ending in v_x . In this way we can find the highest possible score for the entire alignment in the highest scoring node in the last candidate set.

The base case of the dynamic programming are the candidate vertices in the first candidate set, $v_x \in V'_0$. We initialize these scores to $\text{mappingScore}(b(v_x), s_0)$, which is equivalent to aligning them against the substring containing exactly the first character of the string. During the following bottom-up procedure we will be faced with another set of base cases: Vertices which have no incoming edges. If the vertices are reachable by gapping over the preceding indexes of the string without the gap penalty exceeding λ we initialize them to their mapping score combined with the gap penalty. In all other cases we set the score to $-2 * \lambda$, which yields any path starting with the vertex score lower than T and thus not be considered candidates for the optimal alignment.

The recurrence relation of the dynamic programming algorithm is concerned with setting the score for any vertex/index pair which is not a base case. The score for these candidate vertices $v_x \in V'_i$ are set by looking at all incoming edges, find the one yielding the highest score and add $\text{mappingScore}(b(v_x), s_y)$. The score for an edge is found by taking the score in the vertice $v_y \in V'_j$, represented by the start-index i_s in the edge, and adding the gap penalties corresponding to traversing the edge. There are two gap penalties related to the edge: one penalty for the distance represented by the weight w and one penalty for jumping from index i to index j . However, in all edges traversed in the final alignment will only be penalized for one of them.

When the scores have been computed for every candidate vertice we can start looking for the highest score, which represents the alignment score for one of the optimal alignments. We will find this score in as a score for one of the vertices in the candidate set corresponding to the last index of the string. At this point we just have to backtrack the procedure which lead to the score to find the actual alignment, which is guaranteed to be one of the optimal alignments.

Chapter 4

Implementation

In this section we will present the implementation of the algorithm “Fuzzy context-based search” which is found in the *GraphGenome* tool (Appendix C). The algorithm will be coupled by a concrete example which is found in figures 4.2-4.4 and table 4.1. Throughout this chapter, and in the example, the scoring schema is assumed to be the *negated edit distance* schema. This scoring schema is chosen due to its intuitive nature: A final score of $-x$ means there is something wrong in exactly x places. The scoring schema is also practical for doing complexity analysis: A gap which is penalized by y means traversing exactly y vertices or indexes.

Definition 18 (Negated edit distance scoring schema)

A scoring schema where the substitution matrix is a variant of an identity matrix where matches are scored 0 and mismatches are scored -1. Both the gap opening and gap extension penalty is -1

The chapter is divided into two sections. The first explains the implementation of the algorithm corresponding to the previous chapter. The second is a brief overview of how the tool merges sequences into the graph after they have been aligned. This section is included to better provide an intuition as to how the graphs are built and what readers can expect when seeing the results and using the tool themselves.

4.1 Aligning sequences

The alignment process consists of the two steps described in the previous chapter which each has their corresponding subsection. In addition to this the tool needs to do a precomputation of the original graph in order to build a searchable index. This is not counted as a step in the alignment process as the precomputation is determined by only the graph and the index is thus reusable.

4.1.1 Building the index

There are two data structures needed for aligning a string against the graph: a suffix tree for left contexts and a suffix tree for right contexts.

Before either of the two are built the algorithm needs to decide a length for the contexts. Currently in the tool there are two ways of setting the context length: A user given parameter or an approximation based on the probability of sharing contexts (Appendix D). The length of the contexts does not impact the quality of the alignments found by the algorithm (Appendix A) but will have an impact on the runtime (Appendix B).

When a context length $|c|$ is set, the algorithm can start building the index. Two sets of strings, a left context set and a right context set, is generated for every vertex in the graph G . The generation of the two sets happen by the same procedure by swapping around the starting point and the direction of the iteration. When creating left contexts the algorithm starts in the start-node of G and traverses following the direction of the edges, for right contexts the opposite is done. Apart from this the two are equal. To generate the context set $c(n_x)$ for a given node n_x the algorithm looks at every string $c \in c(n_y)$ for every incoming neighbouring node n_y . Every c is modified into a new context string c' by trimming away the last character and prefixing the context with the character $b(n_y)$. All the generated strings c' is added to $c(n_x)$. As sets per definition does not allow duplicates the impact of a branching occurring in the graph will fade away after exactly $|c|$ steps as the difference is trimmed away (see Fig. 4.2), and thus avoid explosive exponentiality in the context set sizes. Unlike Paten et al. [19] there are no requirements for contexts to be uniquely mappable to exactly one vertex. Because the last step of the algorithm does a search for an incomplete path through all the candidate vertices this presents no difficulties when finding the alignment. Furthermore, dropping this precondition assures every node has two valid contexts and are thus present in both suffix trees.

The iteration starts in the node defined as the starting point which has

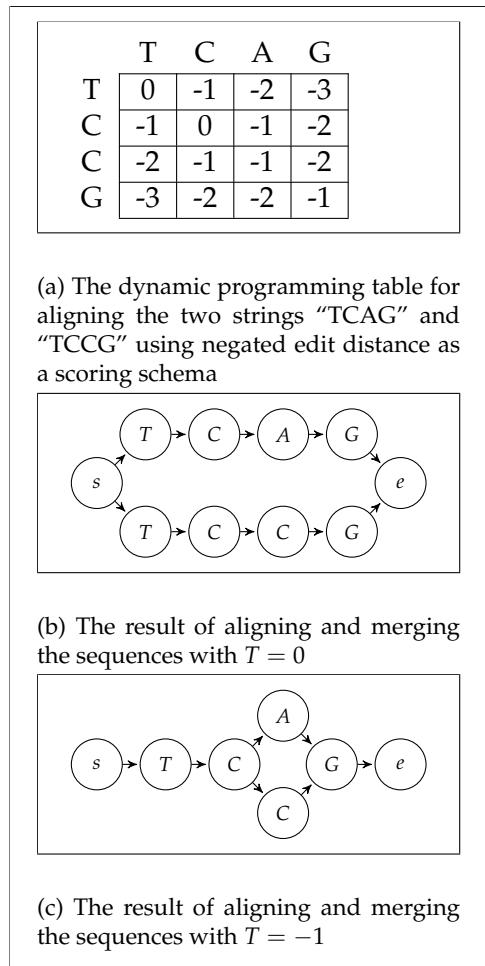


Figure 4.1: Different scoring thresholds T yields different reference graphs

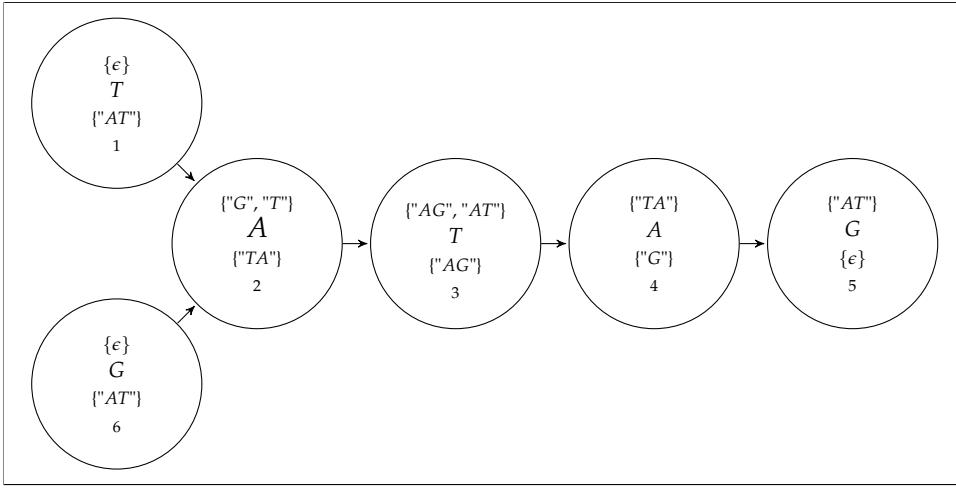


Figure 4.2: A small reference graph with left contexts (top) and right contexts (bottom) of length 2 shown

the empty string ϵ as its only context. Whenever a node has finished producing its contexts it enqueues everyone of its outgoing neighbours in a regular FIFO queue. If a vertex has more actual incoming neighbours than incoming neighbours which are finished generating contexts, the node puts itself back in the queue. Thus happens to ensure that when a vertex is finished generating context, both the vertex itself and all preceding vertices are finished, and the remaining nodes can safely fetch contexts from its neighbours knowing they are finished. The algorithm halts when the queue is empty. Every node has to be visited exactly once to generate its context, looking up its approximately b neighbours, and as the procedure runs twice to generate both sets the total runtime for the operation is $O(2|G|b)$.

After generating the two context sets for every node, the elements of each one is inserted into their corresponding suffix tree. Every suffix is stored as a key with the index of its originating node as a value (fig. 4.3). In theory every node can have $4^{|c|}$ contexts in each set, in practice a more fair approximation is $b^{|c|}$ where b is the observed branching factor for the graph. **Should contain something about probable values of B. Find an article on it.** The current implementation uses a naive suffix tree implementation where insertion is $O(|c|)$, giving a total time complexity of $O(b^{|c|}|c|)$ per node per context set and $O(2|G|b^{|c|}|c|)$ for the entire graph. Building the entire index can thus be done in $O(2|G|b + 2|G|b^{|c|}|c|)$.

4.1.2 Generating the modified graph

The produced graph G' is a function of both the original graph G , the input sequence s and the threshold T . For every character $s_x \in s$ a left-context string and a right-context string is generated by looking at the $|c| + maxPossibleGapGivenFuzziness(\lambda)$ surrounding characters. The two

context strings are used as a basis for a fuzzy search in it's corresponding suffix tree. The search is a recursive function based on PO-MSA. The root node is supplied with a one-dimensional scoring array corresponding to the context string c , which is initialized with all zeroes. Then, for every child, a new scoring array is computed by regular edit distance rules: For each index i take the maximal score for either a gap in the graph, a gap in the string or matching the character c_i with the character contained in the child node (Reference actual code in supplementary?), (more explanation needed?). This newly created array is supplemented to the same recursive function in the child. When a leaf node is reached the last index of the supplied scoring array corresponds to mapping the entire string c against the entire context achieved by concatenating the characters contained in the path through the tree traversed by the recursion. If the score is higher than the context threshold T_c for the given context string, every index contained in the node is stored as a pair on the form $\{index, score\}$ in the candidate set. If an index is stored several times, only the pair containing the highest score is saved.

In order to also be able to look up contexts which are shorter than the contexts stored in the tree, the suffix tree search implementation has built in a concept which we called **something smart**. This concepts allow all vertices at a depth greater than the length of the string which is looked up to pass on their highest possible score, and avoids deterioration of context scores due to different length and are typically used for the shorter contexts at the beginning and end of reads.

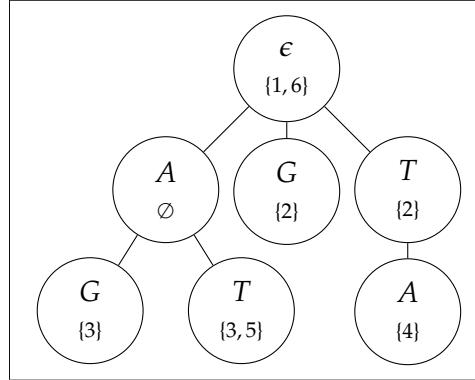


Figure 4.3: The left suffix tree corresponding to the graph in 4.2

In theory every leaf node has to be visited in order to check the score for every represented context in the tree. In practice the tree can be pruned by cutting off the search whenever the *maximal potential score* falls below the threshold T_c for the provided context. The maximal potential score for a node is found by adding together the currently highest score in the scoring array with the maximal matching score for the remainder of the string. This reduces the number of nodes to be searched from $O(4^c)$ to (something alot smaller. Needs calculations).

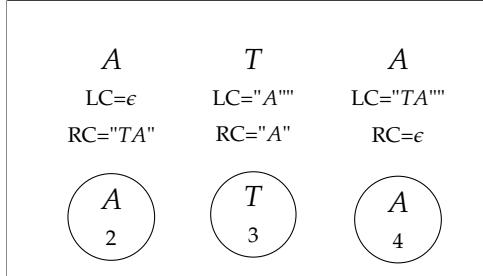
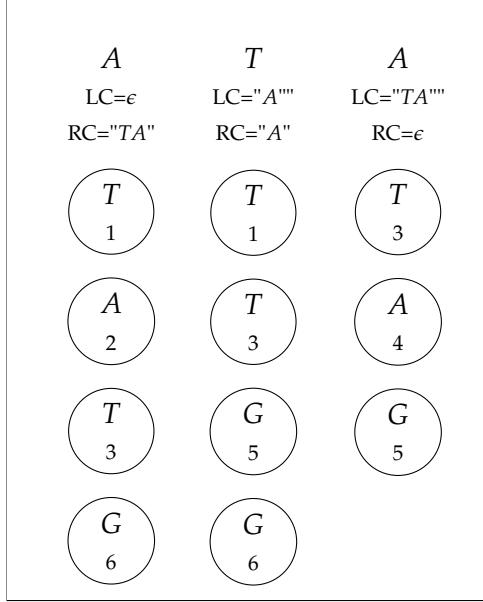
(a) $T = 0$ (b) $T = 1$

Figure 4.4: The resulting candidate sets for mapping the string "ATA" against the reference genome from fig. 4.2 with varying T values

After the fuzzy search is concluded there are two sets of candidates for every index, one containing the nodes matching the left context and an equivalent for nodes matching the right context. These two sets are intersected to produce a final candidate set for the index i , where the score is created by adding together the scores from the two original sets. When the intersection happens the final set can again be pruned by removing all vertices which has a combined score that is lower than the combined threshold T for both contexts. When the vertices are found the edges need to be generated in order to finish the graph. Intuitively there should be an edge wherever there is a gap which is traversable without having the gap penalty exceeding λ . In practice this is a step which is done during the next step of the algorithm.

The newly formed graph G' can be defined formally:

$$G'(G, s, T) = \{V', E'\}$$

where V' is an ordered set of sets of length $|s|$ where each set V'_i is a set of nodes such that

$$V'_i = \{v_x | v_x \in G \wedge \exists [c \in c(v_x)] (\text{alignmentScore}(c, c(s_i)) \geq T)\}$$

and E' is a list of weighted edges such that

$$\begin{aligned} E' = \{e' = \{i_s, i_e, w\} | & v_{i_s} \in V'_x \wedge v_{i_e} \in V'_y \wedge \text{gapPenalty}(y - x) \leq \lambda \wedge \\ & w = \text{distance}(v_{i_s}, v_{i_e}) \wedge \text{gapPenalty}(w) \leq \lambda\} \end{aligned}$$

where $\text{alignmentScore}(x, y)$ and $\text{gapPenalty}(x, y)$ are scoring functions provided by the scoring schema and $\text{distance}(x, y)$ is the distance of the shortest path from node x to node y in the graph. (**Mixing up nodes and indexes in the definitions**)

4.1.3 Searching G' with a modified PO-MSA search

SOMETHING ABOUT SCORES

Table 4.1: The 4 arrays used by the searching algorithm when using the candidate sets from Fig 4.4 and $T = -1$

contained in the preceding entry, $scores[i'][j']$, a gap penalty, and a mapping score for the current index $mappingScore(n_{indexes[i][j]}, s_i)$. The gap penalty is found by combining a gap penalty for a gap of length $i - i'$ and for a gap of length $distance(n_{indexes[i'][j']}, n_{indexes[i][j]})$. The final score stored in $scores[i][j]$ is the maximal achievable score θ produced by one of these pairs. $backpointers[i][j]$ is set to the index-pair (i', j') responsible for producing this score. The recursive formulas for the three arrays are defined by:

$$\begin{aligned}
 \text{indexes}[i][j] &= x \quad \text{for } n_x \in V'_i \\
 \text{scores}[i][j] &= \max_{i', j'} \theta((i, j), (i', j')) \quad \text{for } 0 \leq i' \leq i, 0 \leq j' < \text{length}(\text{scores}[i']) \\
 \text{backPointers}[i][j] &= \underset{i', j'}{\operatorname{argmax}} \theta((i, j), (i', j')) \quad -|+-
 \end{aligned}$$

where θ is a scoring function defined as:

$$\theta((x_1, y_1), (x_2, y_2)) = scores[x_2][y_2] + gapPenalty(x_1 - x_2) + gapPenalty(distance(n_{indexes[x_1][y_2]}, n_{indexes[y_1][x_2]})) + mappingScore(b(n_{indexes[y_1][x_2]}), s_{y_1}))$$

SOMETHING ABOUT FINDING THE HIGHEST SCORE AND BACK-POINTERS. COMPLEXITY ANALYSIS

2

Finding all optimal alignments

4.1.4 Handling invalid threshold values

4.2 Merging aligned sequences

Chapter 5

Experiments

The following chapter describes the details of the experiments conducted to produce the results in the succeeding chapter. The experiments are divided along a natural border, decided by the size of the input data, into two classes. Each class has its own section describing the motivation behind the experiments and the details specific to that class. Elements which are common to both classes are described once in the section preceding the class-specific sections.

5.1 Common elements

5.1.1 Scoring schema

5.1.2 Hardware/runtime environment

5.2 Proof of concept

Whenever a graph is built from a set of sequences one can get an intuition concerning what the final result should look like. These experiments are attempts to formalize the notion of intuition into stable, testable results. Due to readability and shortcomings of printed media only a small set of the experiments are presented here. A more exhaustive set of tests can be found as unit tests in the tool (Appendix C).

5.2.1 Test data

Because the motivation behind these tests are to determine the behaviour of the algorithm, the input data consists of small, handcrafted sequences which for each experiment contains exactly one easily identifiable trait. These traits are crafted in a way which reflects the nature of variation in genetic sequences. Because the negated edit distance scoring schema is a flat scoring schema which penalizes all errors the same it is prone to display order of operations characteristics of the underlying algorithm. Because the order of operations of the implementation is well known to the authors this is taken into account when creating the data.

5.2.2 Validation

There are two main concepts which the validation of this experiment class wish to capture: The intuition and the formalization. The intuition is captured through visualizable results. Every experiment will provide a visualization of both the inputs and the outputs. When the inputs are visualized, one of the sequences will be chosen as a basis for the graph. The output visualizations will be directly produced by the tool using the -print parameter, followed by porting the resulting dot-file to the tikz syntax used in this thesis^{5.1}. The formalization is carried out through a set of statements from first order logic concerning the state of either the resulting graph or the alignment, which are verifyable in the visual outputs. The mentioned unit tests are created to represent these statements through Java syntax.

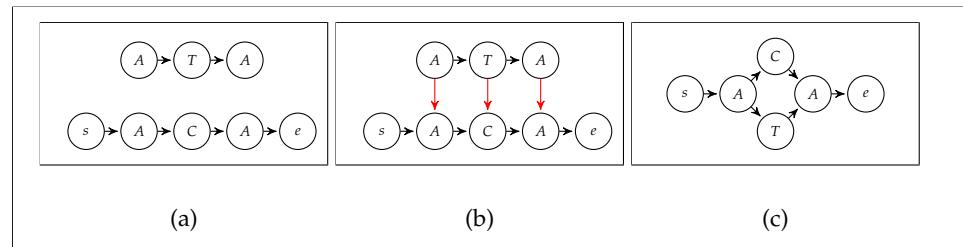


Figure 5.1: The syntax of the visual outputs. Two input sequences “ACA” and “ATA” are given, and the first is chosen as a basis for the reference graph (a). Then the second sequence is mapped against the graph (b) and merged (c)

5.3 Efficiency

In order to determine the usefulness of a new approach it should be compared to other already available approaches. The goal of these experiments is to run the implementation in the tool against similar applications to determine the grade of correctness and the computational feasibility of the approach. Because of its guarantee for optimality PO-MSA (Section 2.2.3) is chosen as a baseline, through an own implementation in Java. The results are compared with the vg implementation[vg] and the tool corresponding to the article “Canonical, Stable, General Mapping using Context Schemes”[sequence_graphs].

5.3.1 Test data

Because the experiments are meant to reflect usage in an everyday situation the tests are run on real genetic data fetched from the vg github repo[vg], and from the test-set provided for the previously mentioned tool made by Noval et al. The sequences correspond to alleles of the MHC region^{2.1.4} and chromosome 6 in the human genome. All the data used can be found in the github of the “Fuzzy context-based search” tool (Appendix C).

In order to do an alignment there needs to exist reads as well as the reference graph itself. A read for a graph G is generated by the following procedure:

1. Choose a read length l , an SNP-probability p_s a deletion probability p_d and an insertion probability p_i
2. Choose a random vertex $v_x \in G$ where every path to the end vertex t_G has a length $\geq l$
3. For r steps:
 - (a) Append $b(v_x)$ to the read r
 - (b) Set the new v_x as a random neighbour of the old v_x
4. Add noise to r according to p_s , p_i and p_d .

Because this thesis is concerned with the mathematical properties of the model the noise in the reads does not necessarily depict the true nature of either genetic variation (Section 2.1.2) or read errors (Section 2.1.5). **why is this ok.** In order to provide reproducibility the randomness in the reads are generated from a seed.

5.3.2 Validation

When an alignment is produced for a read it is classified either as optimal or not optimal. Intuitively this can be determined by whether the generated read aligns back to the path it was generated from. However, when noise is introduced an interesting phenomenon can occur: The modified read

can be more similar to another path than its origin. This can also occur whenever there exists actual equal paths in the graph, typically in the case of repeats. In order to stick with mathematical properties, optimality holds no relation to the origin of a read but is purely defined as the path which produces the highest possible alignment score. As PO-MSA is an exhaustive search we define optimally aligned as alignments which produce the same alignment score as the highest score found by PO-MSA. Consequently, as only the scores are compared, even when the approaches produce different alignments than PO-MSA these can be classified as optimal. This falls within the problem definition (Definition 16).

Chapter 6

Results

6.1 Proof of concept

6.1.1 Equal sequences

6.1.2 SNPs

6.1.3 Indels

6.1.4 Structural variations

6.2 Efficiency

6.2.1 Building the index

6.2.2 Alignment

Runtime as a function of $|G|$

Runtime as a function of $|s|$

Runtime as a function of λ

Chapter 7

Discussion

Chapter 8

Conclusion

Chapter 9

Further work

9.1 Improvements to the algorithm

9.2 Heuristical approaches

Appendices

Appendix A

Proving optimality

Appendix B

Complexity analysis

Appendix C

The GraphGenome tool

Appendix D

The birthday problem

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