Approximate string matching in the high-throughput sequencing era

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Abstract

Abstract...

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CHAPTER

1 Introduction

The sequencing of the whole human genome has been one of the major scientific achievements of the last decades. Very surprisingly, this milestone has been achieved twice, by two independent groups. The three billion dollars publicly funded *Human Genome Project* (HGP) in February 2001 published the first draft *covering more than 96 % of the euchromatic part of the human genome* [Consortium, 2001]. The privately funded company *Celera Genomics* concurrently published *a 2.91 billion base pair consensus sequence of the euchromatic portion of the human genome* [Venter *et al.*, 2001]. Celera Genomics and various international sequencing consortiums contributed to characterize the entire genomes of other model organisms, such as mice [Chinwalla *et al.*, 2002], fruit flies [Myers *et al.*, 2000], nematode worms [Sulston *et al.*, 1992] and yeasts.

These achievements are not only due to the efforts of molecular biologists but also of computer scientists. Indeed, both groups used sequencing technologies based on the *shotgun* approach. Shotgun sequencing consists of chopping long DNA fragments up into smaller segments and then generating *reads* of these short nucleotide sequences. Then, it is left up to *bioinformatics* to reassemble these reads and produce a holistic representation of the original genome.

These ambitious sequencing projects used *capillary electrophoresis* based on the *Sanger sequencing* method [Sanger *et al.*, 1977]. This sequencing technology is capable of reading DNA with high fidelity but at low speed: it produces reads of an average length of 700 bp at a throughput of about 150 Kbp/h. Moreover, in order to produce an assembly with high fidelity, DNA must be sequenced multiple times to obtain a manyfold *coverage*. At this pace, the sequencing of the human genome took years and many million dollars. Nonetheless, the success of these huge sequencing projects did not mark the end of the sequencing era, but its beginning.

1.1 High-throughput sequencing

Since then, sequencing technology steadily improved and evolved into what is now called *high-throughput sequencing* (HTS), or *next-generation sequencing* (NGS). In 2004, *454 Life Science* commercialized the *Genome Sequencer FLX*, an instrument based on large-scale parallel *pyrosequencing*, capable of sequencing DNA under the form of 400 bp reads at a throughput of 20–30 Mbp/h. High-throughput sequencing was born.

In 2006, Solexa released its *1G Genetic Analyzer*, based on a massively parallel tech-

nique of *reversible terminator-based sequencing*. The instrument produced reads as short as 30 bp, at lower accuracy than Sanger sequencing, but at very high-throughput: it allowed *resequencing* a human genome in three months for about $100,000. Following this success, Solexa was acquired by *Illumina*, which is nowadays the market leader. At the beginning of 2014, Illumina announced the *HiSeq X Ten*, allowing the sequencing of many human whole-genomes at $1,000 each, in less than three days.

Over the last decade, other sequencing instruments hit the market with mixed success, e.g. the *SOLiD* system of *Applied Biosystems*, as well as the *third-generation sequencing Ion Torrent* instruments by *Life Technologies* and the *RS II* by *Pacific Bioscience*. I return to sequencing technologies in chapter 5.1, to give more insights on the kind of data produced and understand the problematics linked with their analysis.

In the following of this section, I continue to provide the context of this work. I first introduce most relevant *applications* of HTS and then explain how HTS *analysis pipelines* proceed. Then, I outline the structure of this work and state my contributions to this field.

1.1.1 Protocols and applications

In the last years, HTS has become an invaluable method of investigation for molecular biologists. Abundant and cost-effective production of sequencing data permits viewing not only genomic DNA but also transcripts and epigenetic features at unpreceded single-base resolution. For instance, applications of HTS include genotyping and discovery of structural variation (from DNA-seq); assessments of gene expression and alternative splicing events, analysis of microRNAs, discovery of novel non-coding RNAs (through RNA-seq); prediction of transcription factor binding-sites, analysis of methylation patterns (using ChIP-seq). Some HTS applications are already oriented towards clinical settings, e.g. in the context of mendelian disorders and cancer diagnostic.

Whole genome and exome-seq

Whole genome sequencing (WGS, DNA-reseq) allows discovery of genetic variations across the whole genome. These may be in the form of single nucleotide variants (SNVs), small insertions or deletions (indels), or large structural variants such as transversions, translocations, and copy number variants (CNVs). *Whole exome sequencing* (WES, exome-seq) is a cost-effective yet powerful alternative to WGS. This protocol consists in the targeted sequencing of the *exome*, i.e. the protein coding subset of the human genome.

RNA-seq

RNA sequencing (RNA-seq) is a protocol to sequence the *transcriptome*, i.e. the set of RNA molecules of an organism, including mRNAs, rRNAs, tRNAs, and other non-coding RNAs. Actual HTS technologies perform deep-sequencing of RNA molecules after they have been reverse-transcribed into cDNA. RNA-seq provides a myriad of information on gene expression, alternative splicing, intron/exon boundaries, untranslated regions (UTRs), and genetic variation with single-base accuracy.

ChIP-seq

Chromatin immunoprecipitation with next-generation sequencing (ChIP-seq) is a protocol that allows the selective sequencing of genomic DNA bound by a specific protein. The process isolates chromatin-protein complexes and sheares them by sonication. Subsequently, immunoprecipitation with a protein-specific antibody pulls down genomic DNA sequences bound by a specific protein. These DNA sequences are finally sequenced by HTS. ChIP-seq is used to study the mechanisms of gene regulation. Through this sequencing protocol it is possible to determine global methylation patterns, identify transcription factor binding sites, histone modifications, chromatin remodelling proteins.

1.1.2 Analysis pipelines

The analysis of HTS data consists of numerous steps, ranging from the initial instrument specific data processing to the final application specific interpretation of the results. It is conventional wisdom to subdivide such data analysis pipelines in three stages of *primary*, *secondary*, and *tertiary* analysis. The primary stage of analysis consists of instrument specific processes for generation, collection, and processing of raw sequencing data. The secondary stage reconstructs the original sequence of the donor genome by applying sequence analysis methods to the raw sequencing data. The tertiary stage characterizes features of the donor genome specific to the sequencing application e.g. genetic variations in exome-seq, then provides interpretations e.g. by aggregating multiple samples and performing data mining.

Primary analysis

Primary analysis consists of instrument specific steps to call base pairs and compute quality metrics. The base caller processes instrumental signals and assigns a base to each peak, i.e. A, C, G, T, or N. The software assigns a quality value to each called base, estimating the probability of a base calling error. On early generation instruments, users could provide their own base calling tool. Now this process happens automatically on special hardware (e.g. FPGAs or GPUs) bundled within the instrument. The result of primary analysis is a standard *FASTQ* file containing DNA read sequences and their associated quality scores in *Phred* format (see section **??**).

Secondary analysis

Secondary analysis aims at reconstructing the original sequence of the donor genome. There are two main *plans* to reassemble the original genome: (A) *de novo* assembly, and (B) *reference-guided* assembly (commonly called *read mapping*). *De novo* assembly is very involved as it essentially requires finding a *shortest common superstring* (SCS) of the reads, which is a NP-complete problem [Maier and Storer, 1977; Gallant *et al.*, 1980; Turner, 1989]. Computational methods in plan A first scaffold the reads by performing *overlap alignments* [Myers, 2005] or equivalently by constructing *de Bruijn graphs* [Pevzner *et al.*, 2001]. The knowledge of a *reference genome*, highly similar to the donor,

simplifies the problem and opens the door to plan B. The reads are simply aligned to the reference, tolerating a few base pair errors. It is worth mentioning that some combinations of plans A and B have been proposed [Li, 2012].

Plan B is always preferred in resequencing projects, as it is more computationally viable than plan A and directly provides a way to assess genetic variation w.r.t. a reference genome. In this manuscript, I follow only plan B and present methods that work within this specific plan. Nonetheless, many of the algorithmic components that I expose in the first part of this manuscript are ubiquitous in bioinformatics, thus applicable, if not already applied, to plan A. According to plan B, the secondary analysis step consists of three tasks: *quality control*, *read mapping*, and *pile up*.

Quality control (Q/C) checks the quality of raw reads. Reads produced by current HTS technologies contain sequencing artefacts, in form of single miscalled bases or stretches of oligonucleotides. In order to circumvent this problem, various techniques have been developed, ranging from the simple *trimming* of low quality read stretches to sophisticated methods of *read error correction* [Weese *et al.*, 2013]. Nonetheless, sometimes Q/C is simply omitted.

Read mapping takes care of aligning the reads to the reference genome. Read mappers adopt state of the art *approximate string matching* methods to efficiently analyze the deluge of data produced by HTS instruments. Approximate matching accounts for two kinds of errors: residual sequencing artefacts not removed by Q/C, and small genetic variations in the donor genome to which reads belong. Thus, the read mapper must take into account errors when mapping reads.

Mapped reads, often stored in de-facto standard BAM files, are *piled up* in order to construct a *consensus sequence* of the donor genome. The height of the pileup denotes the sequencing depth at each locus in the donor genome, thus the average height corresponds to the average sequencing coverage; higher depth implies more confidence in the consensus sequence of the donor genome and thus more accuracy in tertiary analysis.

Tertiary analysis

Tertiary analysis aims at interpreting the deluge of information provided by secondary analysis. This pipeline stage groups a wide range of analyses specific to the sequencing application. In many pipelines, downstream analysis performs data mining over aggregated data coming from multiple samples.

Within DNA resequencing, *genotyping* consists of determining the variations between the donor and the reference genome. The result of *variant calling* is usually a VFC file annotating the variations of the donor genome. Subsequently, *genome-wide association studies* (GWAS) associate genetic variants with phenotypic traits by examining *single-nucleotide polymorphisms* (SNPs), variants relatively common among individuals of the same population.

In RNA-seq, tertiary analysis consists of computing transcripts abundance by measuring *reads per kilobase per million mapped reads* (RPKM) [Mortazavi *et al.*, 2008]. Subsequently, relative gene expression is determined by comparing multiple RNA samples. In ChIP-seq, this stage consists of calling peaks in correspondence of mapped reads, de-

termining which peaks identify feasible transcription factor binding sites, then interesting sites affecting gene regulation.

1.2 Outline

In this work, I present novel methods for the efficient and accurate mapping of high-throughput sequencing reads, based on state of the art approximate string matching algorithms and data structures. Read mapping is an ubiquitous and non-trivial task in all resequencing applications. Efficiency is required to keep the pace of HTS technologies constantly increasing their throughput. Accuracy is required to provide data analysis with single-base resolution.

I decided to subdivide this work in two parts: part I is about approximate string matching, while part II is about read mapping. The initial ingenuity of approximate string matching methods turns out to be beneficial in the design of an accurate method for read mapping.

1.2.1 Approximate string matching

In chapter 2, I introduce basic stringology concepts.

In chapter 3, I expose indexed methods for approximate string matching.

In chapter 4, I expose filtering methods for approximate string matching.

1.2.2 Read mapping

In chapter 5, I return to read mapping. I give a solid background.

In chapter 6, I present my first attempt at engineering a read mapping tool.

In chapter 7, I present Yara, a state of the art read mapping tool.

Part I

APPROXIMATE STRING MATCHING

CHAPTER

2 Preliminaries

In this chapter I introduce fundamental definitions and problems of stringology. The reader familiar with basic stringology can skip this chapter and proceed to chapter **??**.

2.1 Definitions

I start by introducing primitive objects of stringology: alphabets and strings.

Definition 2.1. An *alphabet* is a finite ordered set of symbols (or characters); a *string* (or word) over an alphabet is a finite sequence of symbols from that alphabet. I denote the length of a string s by $|s|$, and by ϵ the empty string s.t. $|\epsilon| = 0$.

Definition 2.2. Given an alphabet Σ, the set $\Sigma^0 = \{\epsilon\}$ contains the empty string, Σ^n contains all strings of length n over Σ, and $\Sigma^* = \cup_{n=0}^{\infty} \Sigma^n$ all strings over Σ.

Definition 2.3. The concatenation operator of two strings is defined as $\cdot : \Sigma^* \times \Sigma^* \to \Sigma^*$. Given two strings $x \in \Sigma^m$ with $x = x_1 x_2 \dots x_m$ and $y \in \Sigma^n$ with $y = y_1 y_2 \dots y_n$, their concatenation $x \cdot y$ (simply denoted xy) is the string $z \in \Sigma^{m+n}$ consisting of the symbols $x_1 x_2 \dots x_m y_1 y_2 \dots y_n$.

Definition 2.4. A string x is a *prefix* of y iff there is some string z s.t. $y = x \cdot z$; analogously, x is a *suffix* of y iff there is some string z s.t. $y = z \cdot x$; moreover, x is a *substring* of y iff there is some string w, z s.t. $y = w \cdot x \cdot z$. I denote by $y_{1\dots i}$ the prefix of y ending at position $i \in \mathbb{N}$, by $y_{i\dots n}$ (or simply $y_{i\dots}$) the suffix of y beginning at position $i \in \mathbb{N}$, and by $y_{i\dots j}$ the substring of y within positions $i \leq j \in \mathbb{N}$.

Definition 2.5. Given an alphabet Σ of size σ, I denote by the function $\rho : \Sigma \to [1 \dots \sigma]$ the *lexicographic rank* of any alphabet symbol, s.t. $\rho(a) < \rho(b) \iff a < b$ for any distinct $a, b \in \Sigma$.

Definition 2.6. The *lexicographical order* $<_{lex}$ between two non-empty strings x, y is defined as $x <_{lex} y \iff x_1 < y_1$, or $x_1 = y_1$ and $x_{2\dots} <_{lex} y_{2\dots}$

Definition 2.7. A *string collection* is an ordered multiset $\mathbb{S} = \{s^1, s^2, \dots, s^c\}$ of non necessarily distinct strings over a common alphabet Σ. I denote by $\|\mathbb{S}\| = \sum_{i=1}^{c} |s^i|$ the total length of the string collection. I extend the notation of prefix, suffix and substring also to multisets, e.g. $\mathbb{S}_{(d,i)\dots(d,j)}$ denotes the substring $s^d_{i\dots j}$.

Definition 2.8. I call *terminator symbol* a symbol $\$ \notin \Sigma$ s.t. $\rho(\$) < \rho(a)$ for any $a \in \Sigma$.

Definition 2.9. Given a string s over Σ, I call *padded string* the concatenation of s with a terminator symbol \$.

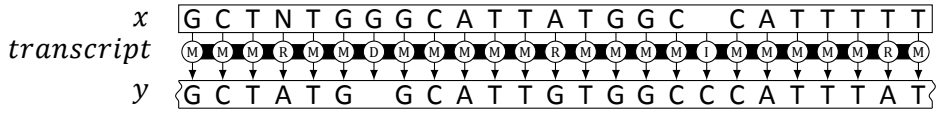
Definition 2.10. Given a string collection $\mathbb{S}$ over Σ, I call *padded string collection* the collection consisting of strings $s^i \in \mathbb{S}$ padded with terminator symbols $\$^i$ s.t. $\rho(\$^i) < \rho(\$^j) \iff i < j$.

2.2 Alignments

The next step is to define the minimal set of edit operations to transform one string into another: substitutions, insertions and deletions. Given two strings x, y of equal length n, the string x can be transformed into the string y by substituting (or replacing) all symbols x_i s.t. $x_i \neq y_i$ into y_i, for $1 \leq i \leq n$. If the given strings have different lengths, insertion and deletion of symbols from x become necessary to transform it into y.

Definition 2.11. An edit transcript for any two given strings x, y is a finite sequence of substitutions, insertions and deletions transforming x into y.

Figure 2.1: *Example of edit transcript transforming the string $x = AAAA$ into $y = CCCC$. The transcript character M indicates a match, R a replacement, I an insertion, and D a deletion.*



An alignment is an alternative yet equivalent way of visualizing a transformation between strings. While an edit transcript provides an explicit sequence of edit operations transforming one string into another, an alignment relates pairs of corresponding symbols between two strings. Because some symbols in one string are not related to any symbol in the other string, i.e. some symbols are inserted or removed, a gap symbol $-$, not being part of the string alphabet Σ, has to be introduced first.

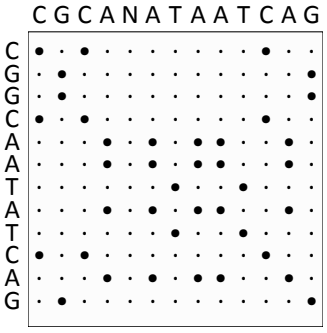
Definition 2.12. An alignment of two strings of length m, n over Σ is a string of length between $\min\{m, n\}$ and $m + n$ over the pair alphabet $(\Sigma \cup \{-\}) \times (\Sigma \cup \{-\})$.

Example 2.1. An alignment of the strings $x = AAAA$ and $y = CCCC$ is given by the string $z = \binom{A}{A}\binom{A}{-}\binom{A}{C}\binom{G}{G}$

A dotplot is a way to visualize any alignment between two strings and highlight their similarities. Given two string x, y of length m, n, a dotplot is a $m \times n$ matrix containing a dot at position (i, j) iff the symbol x_i matches symbol y_j. A dotplot trace is a monotonical

path in the matrix connecting non-decreasing positions of the matrix. A dotplot trace corresponds to an alignment and vice versa. In a trace, match and mismatch columns of the corresponding alignment appear as diagonal stretches, while insertions and deletions are horizontal or vertical stretches. See Figure 2.2.

Figure 2.2: *Example of dotplot of the strings $x = AAAA$ and $y = CCCC$. The highlighted trace corresponds to the alignment of example 2.1.*



2.3 Distance functions

A cost is assigned to any alignment, and to its associated edit transformation, by defining a weight function $\omega : (\Sigma \cup \{-\}) \times (\Sigma \cup \{-\}) \to \mathbb{R}_0^+$, where:

- $\omega(\alpha, \beta)$ for all $(\alpha, \beta) \in \Sigma \times \Sigma$ defines the cost of substituting α with β,
- $\omega(\alpha, -)$ for all $\alpha \in \Sigma$ defines the cost of deleting the symbol α,
- $\omega(-, \beta)$ for all $\beta \in \Sigma$ defines the cost of inserting the symbol β,

and by defining the total cost $C(z)$ of an alignment z between two strings as the sum of the weights of all its alignment symbols:

$$C(z) = \sum_{i=0}^{|z|} \omega(z_i) \tag{2.1}$$

Consequently, the distance function $d : \Sigma^* \times \Sigma^* \to \mathbb{R}_0^+$ is defined to take the minimum cost over all possible alignments of x, y:

$$d(x, y) = \sum_{z \in \mathbb{A}(x,y)} C(z) \tag{2.2}$$

Definition 2.13. The *Hamming distance* between two strings $x, y \in \Sigma^n$ is defined as the function $d_H : \Sigma^n \times \Sigma^n \to \mathbb{N}_0$ counting the number of substitutions necessary to transform x into y. It is obtained by defining $\omega(\alpha, \beta)$ as in the edit distance, and by setting all $\omega(\alpha, -)$ and $\omega(-, \beta)$ to be ∞ in order to disallow indels.

Definition 2.14. The *Levenshtein* or *edit distance* between two strings $x, y \in \Sigma^*$ is defined as the function $d_E : \Sigma^* \times \Sigma^* \to \mathbb{N}_0$ counting the *minimum* number of edit operation necessary to transform x into y. It is obtained by defining for all $(\alpha, \beta) \in \Sigma \times \Sigma$, $\omega(\alpha, \beta) = 1$ iff $\alpha \neq \beta$ and 0 otherwise, and $\omega(\alpha, -)$ and $\omega(-, \beta)$ as 1.

2.4 Optimal alignments

The problem of finding an optimal alignment between two strings is equivalent to the problem of finding their minimum distance [Gusfield, 1997]. A solution to this optimization problem can be efficiently computed via dynamic programming (DP). Below I describe the three essential components of the DP approach: the recurrence relation, the DP table, and the traceback.

Given two strings x, y of length m, n, for all $1 \leq i \leq m$ and $1 \leq j \leq n$ I define with $d(x_{1..i}, y_{1..j})$ the distance between their prefixes $x_{1..i}$ and $y_{1..j}$. The base conditions of the recurrence relation are:

$$d(\epsilon, \epsilon) = 0 \tag{2.3}$$

$$d(x_{1..i}, \epsilon) = \sum_{l=1}^{i} \omega(x_l, -) \text{ for all } 1 \leq i \leq m \tag{2.4}$$

$$d(\epsilon, y_{1..j}) = \sum_{l=1}^{j} \omega(-, y_l) \text{ for all } 1 \leq j \leq n \tag{2.5}$$

and the recursive case is defined as follows:

$$d(x_{1..i}, y_{1..j}) = \min \begin{cases} d(x_{1..i-1}, y_{1..j}) & + \quad \omega(x_i, -) \\ d(x_{1..i}, y_{1..j-1}) & + \quad \omega(-, y_j) \\ d(x_{1..i-1}, y_{1..j-1}) & + \quad \omega(x_i, y_j) \end{cases} \tag{2.6}$$

The above recurrence relation is computed in time $\mathcal{O}(nm)$ using a dynamic programming table D of $(m+1) \times (n+1)$ cells, where cell $D[i, j]$ stores the value of $d(x_{1..i}, y_{1..j})$. The sole distance without any alignment is computed in space $\mathcal{O}(\min\{n, m\})$, as only column $D[: j-1]$ is needed to compute column $D[: j]$ (or row $D[i-1 :]$ to compute $D[i :]$), and the table D can be filled either column-wise or row-wise. An optimal alignment is computed in time $\mathcal{O}(m+n)$ via *traceback* on the table D: the traceback starts in the cell $D[m, n]$ and goes backwards (either left, up-left, or up) to the previous cell by deciding which condition of equation 2.6 yielded the value of $D[m, n]$.

2.5 String matching

I now define *exact string matching*, one of the most fundamental problems in stringology.

Definition 2.15. [Gusfield, 1997] Given a string p of length m, called the *pattern*, and a string t of length n, called the *text*, the exact string matching problem is to find all occurrences of pattern p into text t.

Figure 2.3: *DP table representing the computation of the edit distance* $d_E(x_{1..5}, y_{1..4})$.

	ϵ	C	G	C	A	N	A	T	A	A	T	C	A	G
ϵ	0	1	2	3	4	5	6	7	8	9	10	11	12	13
C	0	1	2	3	4	5	6	7	8	9				
G	0	1	2	3	4	5	6	7	8	9				
G	0	1	2	3	4	5	6	7	8	9				
C	0	1	2	3	4	5	6	7	8	9				
A	0	1	2	3	4	5	6	7	8	9				
A	0	1	2	3	4	5	6	7	8	•				
T														
A														
T														
C														
A														
G														

This problem has been extensively studied from the theoretical standpoint and is well solved in practice [Faro and Lecroq, 2013]. Nonetheless, the definition of distance functions between strings lends to the generalization of exact string matching to a more challenging problem: *approximate string matching*.

Definition 2.16. [Galil and Giancarlo, 1988] Given a text t, a pattern p, and a *distance threshold* $k \in \mathbb{N}$, the approximate string matching problem is to find all occurrences of p into t within distance k.

The approximate string matching problem under the Hamming distance is commonly referred as the *k-mismatches* problem and under the edit distance as the *k-differences* problem. For k-mismatches and k-differences, it must hold $k > 0$ as the case $k = 0$ corresponds to exact string matching, and $k < m$ as a pattern occurs at any position in the text if all its m characters are substituted.

Definition 2.17. Under the edit or Hamming distance, the *error rate* is defined as $\epsilon = \frac{k}{m}$, with $0 < \epsilon < 1$ given the above conditions.

String matching problems are subdivided in two categories, *online* and *offline*, depending on which string, the pattern or the text, is given first. Algorithms for online string matching work by preprocessing the pattern and scanning the text from left to right (or right to left). Algorithms for offline string matching are instead allowed to preprocess the text, hence they build an index of the text beforehand to speed up subsequent searches. In practice, if the text is long, static and searched frequently, provided the necessary amount of memory for text indexing, offline methods outperform online methods in terms of runtime.

It goes without saying that offline string matching algorithms are tightly bound to text indexing data structures. Almost all of these algorithms require a *full-text index*, i.e. a data structure representing all substrings of the text. Very often, such *full-text index* is the *suffix tree* [Weiner, 1973], a fundamental data structure in stringology. Among its virtues [Apostolico, 1985], the suffix tree natively provides exact string matching in optimal time and also approximate string matching via backtracking [Ukkonen, 1993]. Often the suffix tree finds its use within hybrid *filtering methods* rather than on its own.

Filtering methods first discard uninteresting portions of the text and subsequently use a conventional method to verify only narrow areas. These methods work either online or offline. Online filtering methods try to jump over the text while scanning it, while offline filtering methods use an index to place anchors in the text. Any filtering method then requires an online verification method. Filtering methods outperform *native* online and indexed methods for a vast range of inputs, e.g. when the error rate is low, and are thus very appealing from a practical standpoint. Nonetheless, filtering methods are just opportunistic combinations of native online and indexed methods.

In this manuscript, I often consider *multiple* string matching problems, i.e. variants in which many patterns are given at once, instead of *single* problems where they are given one by one in an online fashion. Obviously, any method for the single case can solve the multiple case and vice versa. However, it is clear that multiple methods have an advantage over single methods. For instance, multiple online methods are allowed to preprocess all patterns and then scan the text only once, while single online methods have to scan the text every time a pattern is provided. Thus, provided multiple patterns at once, multiple string matching methods are more appealing than single methods.

In the following of this section, I give a quick overview of the fundamental algorithms and data structures adopted in string matching methods. This overview serves as an introduction to the indexed and filtering methods presented in the next chapters. For an extensive treatment of this subject, the reader is referred to complete surveys on online [Navarro, 2001] and indexed [Navarro *et al.*, 2001] approximate string matching methods.

2.5.1 Online methods

The dynamic programming algorithm **??** to compute the distance of two strings can be easily turned into a string matching algorithm. Since an occurrence of the pattern can start and end anywhere in the text, k-differences consists of computing the edit distance between the pattern and any substring of the text. The problem can be thus solved by computing the edit distance between the text and the pattern without penalizing leading and trailing deletions in the text.

Consider equation 2.6 and pose $x = p$ and $y = t$. Since an occurrence of the pattern can start anywhere in the text, the initialization of the top row $D[0 :]$ of the DP matrix is changed to:

$$d(\epsilon, y_{1..j}) = 0 \text{ for all } 1 \leq j \leq n \tag{2.7}$$

and since an occurrence of the pattern can end anywhere in the text, all cells $D[m, j]$ for all $1 \leq j \leq n$ in the bottom row of D have to be checked for the condition $D[m, j] \leq k$.

2.5.2 Indexed methods

Here I introduce *suffix tries*, idealized data structures to index full-texts. Moreover, I define a set of generic operations to traverse suffix tries in a top-down fashion. In chapter 3, I will expose various data structures replacing suffix tries in practice. The generic

Figure 2.4: *DP table representing the match of $p = ...$ in $t = ...$*

	ϵ	C	G	C	A	N	A	T	A	A	T	C	A	G	A	A	A
ϵ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	1	1	2	3	4	5	6	7	8	9							
G	2	1	2	3	4	5	6	7	8	9							
G	3	1	2	3	4	5	6	7	8	9							
C	4	1	2	3	4	5	6	7	8	9							
A	5	1	2	3	4	5	6	7	8	9							
A	6	1	2	3	4	5	6	7	8	•							

traversal operations here introduced lead to the formulation of generic algorithms solving string matching problems on any of these data structures.

Trie

Consider a padded string collection $\mathbb{S}$ (definition 2.10) consisting of c strings. Note that padding is necessary to ensure that no string $s^i \in \mathbb{S}$ is a prefix of another string $s^j \in \mathbb{S}$.

Definition 2.18. The trie $\mathcal{S}$ of $\mathbb{S}$ is a lexicographically ordered tree data structure having one node designated as the root and c leaves, denoted as $l_1 \ldots l_c$, where leaf l_i points to string s^i. The entering edge of any node of $\mathcal{S}$ is labeled with a symbol in Σ, while the entering edge of any leaf of $\mathcal{S}$ is labeled with a terminator symbol. Any path from the root to a leaf l_i spells the string s^i, including its terminator symbol $\$^i$.

Suffix trie

The suffix trie is the trie of all suffixes of a string.

Definition 2.19. Given a padded string s (definition 2.9) of length n, the suffix trie $\mathcal{S}$ of s has n leaves where leaf l_i points to suffix $s_{i..n}$.

The suffix trie generalizes to index string collections.

Definition 2.20. Given a padded string collection $\mathbb{S}$ (definition 2.10), any leaf of the *generalized suffix trie* is labeled with a pair (i, j) where i points to the string $s^i \in \mathbb{S}$ and $1 \leq j \leq n_i$ points to one of the n_i suffixes of s^i. Thus each path from the root to a leaf (i, j) spells the suffix $\mathbb{S}_{(i,j)...}$.

Note that the suffix trie so defined contains $\mathcal{O}(n^2)$ nodes, yet I only consider the suffix trie as an idealized data structure to expose generic algorithms. The optimal data structure to represent in linear space all suffixes of a given string is the *suffix tree* [Morrison, 1968]. However, the suffix tree comes with the restriction that internal nodes must have more than one child and with the property that edges can labeled by strings of arbitrary length (see Figure 2.5). This latter property slightly complicates the exposition of string matching algorithms but it does not affect their runtime complexity nor their result. For this reason, in the following of this manuscript I always consider w.l.o.g. suffix tries instead of suffix trees.

Figure 2.5: *Suffix trie and suffix tree for the string ANANAS$.*

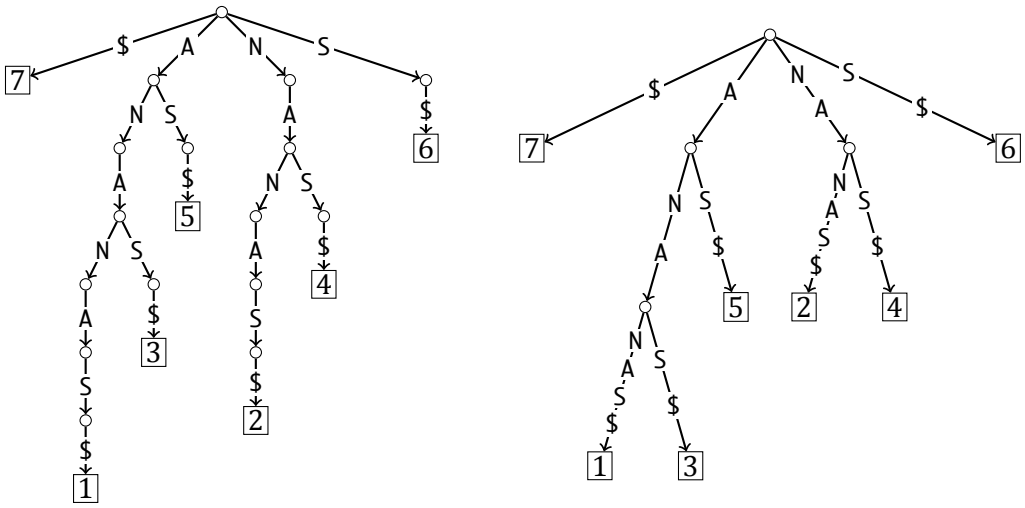
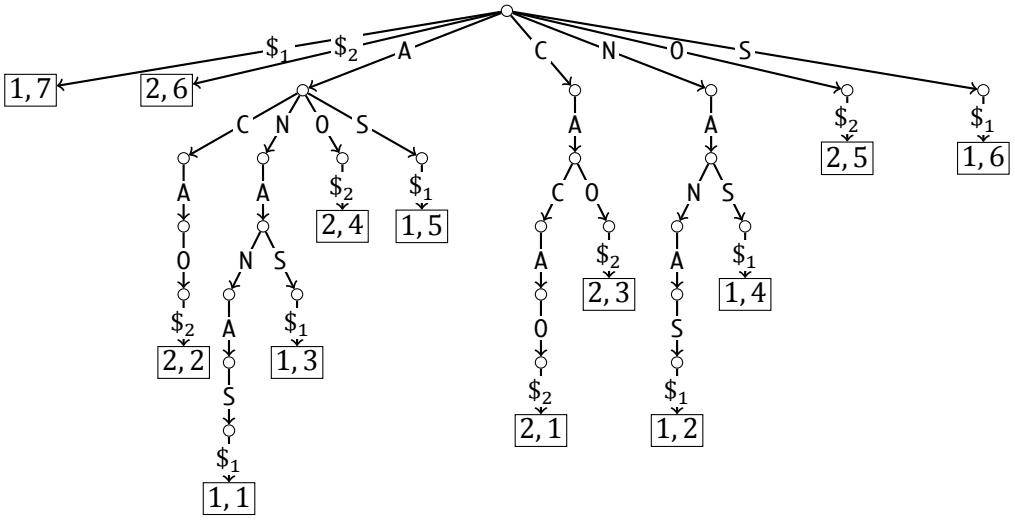


Figure 2.6: *Generalized suffix trie for the string collection* $\mathbb{S} = \{$ ANANAS$\$_1$, CACAO$\$_2$ $\}$.



Top-down traversal

I now give a set of generic operations to traverse tries in a top-down fashion. Given a trie $\mathcal{T}$, I define the following operations inspecting any pointed node x of $\mathcal{T}$:

- ISROOT(x) returns true iff the pointed node is the root;
- ISLEAF(x) returns true iff all outgoing edges are labeled by terminator symbols;
- LABEL(x) returns the symbol labeling the edge entering x;
- OCCURRENCES(x) returns the list of positions pointed by leaves below x;

and the following operations moving from pointed node x, and returning true on success and false otherwise:

Algorithm 2.1 GODOWN(x)

Input x : pointer to a suffix trie node
Output boolean indicating success

```
1: if ISLEAF(x) then
2:     return false
3: if GODOWN(x, min_lex Σ) then
4:     return true
5: else
6:     return GORIGHT(x)
```

Algorithm 2.2 GORIGHT(x)

Input x : pointer to a suffix trie node
Output boolean indicating success

```
1: if not ISROOT(x) then
2:     while c ← next_lex Σ, LABEL(x) do
3:         GOUP(x)
4:         if GODOWN(x, c) then
5:             return true
6: return false
```

- GODOWN(x) moves to the lexicographically smallest child of x;
- GODOWN(x, c) moves to the child of x whose entering edge is labeled by c;
- GORIGHT(x) moves to the lexicographically next child of x;
- GOUP(x) moves to the parent node of x.

Time complexities of the above operations depend on the data structure implementing the trie. Usually LABEL is $\mathcal{O}(1)$, both variants of GODOWN and GORIGHT can be $\mathcal{O}(1)$ or logarithmic in n, OCCURRENCES can be linear in the number of occurrences, GOUP is $\mathcal{O}(1)$ but with an additional $\mathcal{O}(n)$ space complexity to stack all parent nodes. Note that is always possible to implement GODOWN and GORIGHT by relying on GODOWN a symbol and GOUP, but their complexity becomes $\mathcal{O}(\sigma)$. In chapter 3, I consider various data structures to implement suffix tries, I show how to implement these operations and give their complexities.

2.5.3 Filtering methods

Filtering methods work in two stages: the *filtration stage* discards portions of the text unlikely or unable to contain an occurrence of the pattern, subsequently the *verification stage* checks the remaining portions. The filtration stage proceeds online by scanning the text or alternatively offline using an index of the text. The verification stage uses a conventional method, e.g. the online dynamic programming method or some variation of it. The crux of filtering methods is thus to accurately and efficiently classify text portions as containing or not an occurrence of the pattern.

Table 2.1: *Classification of text locations by filtering methods.*

Occurrence	Filtered in	Filtered out
Yes	True positive (TP)	False negative (FN)
No	False positive (FP)	True negative (TN)

Specificity and sensitivity

Any filtering method is thus a binary classification method. Any text location is *true* if it coincides with the beginning of an occurrence of the pattern and *false* if it does not. The outcome of the classification method is *positive* for text locations filtered in and *negative* for locations filtered out. Therefore, as shown in table 2.1, any text location represents either a *true positive* (TP), a *false positive* (FP), a *true negative* (TN), or a *false negative* (FN).

Specificity and *sensitivity* measure the accuracy of filtering methods. The specificity of a filter is defined as:

$$\frac{|TN(t)|}{|TN(t)| + |FP(t)|} \tag{2.8}$$

and the sensitivity as:

$$\frac{|TP(t)|}{|TP(t)| + |FN(t)|} \tag{2.9}$$

An important case is its sensitivity is 1.

Definition 2.21. A filter is *lossless* or *full-sensitive* if its sensitivity is 1, i.e. it produces no false negatives, otherwise it is *lossy*.

Most practical applications, e.g. read mapping, do not require strictly lossless filtration. Nonetheless, a predictable or controlled lossy filter helps to interpret the results and insure their quality. For this reason, I focus on criteria yielding filters which are lossless or lossy in a predictable fashion.

Efficiency

The total runtime of a filtering method is given by the sum of the runtimes of its filtration and verification stages. Filtration specificity determines how much time goes in the verification stage. Clearly, the number of false positives must be low to keep verification time small. Nonetheless, the filtration stage must also run in a reasonable amount of time. Hence, efficient filtering methods balance their runtime between filtration and verification. In any way, no filtering method can be efficient when the number of true positive locations approaches the text length.

Filtering methods for string matching work under the assumption that patterns occur in the text with a *low average probability*. For k-differences, the occurrence probability is a function of the error rate ϵ, in addition to the alphabet size σ, and can be computed or estimated under the assumption of the text being generated by a specific random source. Under the uniform Bernoulli model, where each symbol of Σ occurs with probability $\frac{1}{\sigma}$, Navarro and Baeza-Yates estimate that $\epsilon < 1 - \frac{1}{\sigma}$ is a conservative bound on the error rate which ensures few occurrences and for which filtering algorithms are effective. For higher error rates, non-filtering methods, either online or offline, work better.

Seeds versus q-grams

Filtering methods apply combinatorial criteria to determine which portions of the text might contain some occurrence of the pattern. These criteria are in general valid for both online and offline variants of the problem. In practice, one specific criterion might be more convenient for one variant of the problem rather than the other. The combinatorial criterion underlying a filter is of paramount importance as it provides guarantees on filtration sensitivity.

In chapter 4, I consider two classes of combinatorial filtering methods: those based on *seeds* and those based on *q-grams*. Filters in the former class partition the pattern into *non-overlapping* factors called seeds. Application of the pigeonhole principle yields full-sensitive partitioning strategies. Instead, filters in the latter class consider all *overlapping* substrings of the pattern having length q, the so-called q-grams. Simple lemmata give lower bounds on the number of q-grams that must be present in a narrow window of the text, as necessary condition for an approximate occurrence of the pattern.

CHAPTER

3 Indexed methods

Suffix trees are elegant data structures but they are rarely used in practice. Although suffix trees provides optimal construction and query time, their high space consumption prohibits practical applicability to large string collections. A practical study on suffix trees [Kurtz, 1999] reports that efficient implementations achieve sizes between 12 n and 20 n bytes per character. For instance, two years before completing the sequencing of the human genome, Kurtz conjectured the resources required for computing the suffix tree for the complete human genome (consisting of about $3 \cdot 10^9$ bp) in 45.31 GB of memory and nine hours of CPU time, and concluded that *"it seems feasible to compute the suffix tree for the entire human genome on some computers"*.

One might be tempted to think that such memory requirements are not anymore a limiting factor as, at the time of writing, standard personal computers come with 32 GB of main memory. Indeed, over the last decades, the semiconductors industry followed the exponential trends dictated by Moores' law and yielded not only exponentially faster microprocessors but also larger memories. Unfortunately, memory latency improvements have been more modest, leading to the so called memory wall effect [Wilkes, 1995]: data access times are taking an increasingly fraction of total computation times. Thus, if in 1973 Knuth wrote that *"space optimization is closely related to time optimization in a disk memory"*, forty years later one can simply say that space optimization is always related to time optimization.

Over the last years, a significant effort has been devoted to the engineering of more space-efficient data structures to replace the suffix tree in practical applications. In particular, much research has been done into designing succinct (or even compressed) data structures providing efficient query times using space proportional to that of the uncompressed (or compressed) input. Thanks to this research, I am able to index the human genome in as little as 3.5 GB of memory and at the same time improve query time over classic indices.

In this chapter, I introduce some classic full-text indices (suffix arrays and q-gram indices) and subsequently succinct full-text indices (uncompressed FM-index variants). Afterwards, I give generic string matching algorithms working on any of these data structures and at the same time provide experimental evaluations. My implementation of all these algorithms and data structures is publicly available in source form within the C++ library SeqAn [Döring *et al.*, 2008].

3.1 Classic full-text indices

3.1.1 Suffix array

The key idea of the suffix array [Manber and Myers, 1990] is that most information explicitly encoded in a suffix trie is superfluous for string matching. The explicit representation of suffix trie's internal nodes and outgoing edges can be therefore omitted. Leaves pointing to the sorted suffixes are sufficient to perform exact string matching or even trie traversals. Indeed, any path from the root to an internal node can computed on the fly via binary search over the leaves. In this way, an additional logarithmic time complexity has to be paid to reduce space by a linear factor.

I define the suffix array and later show how to emulate suffix trie traversal.

Definition 3.1. The suffix array of a string s of length n is defined as an array A containing a permutation of the interval $[1, n]$, such that $s_{A[i]\ldots n} <_{lex} s_{A[i+1]\ldots n}$ for all $1 \leq i < n$.

Figure 3.1: *Suffix array for the string* ANANAS$.

i	$A[i]$	$s_{A[i]\ldots n}$
1	7	$
2	1	ANANAS$
3	3	ANAS$
4	5	AS$
5	2	NANAS$
6	4	NAS$
7	6	S$

I define the generalized suffix array to index string collections, analogously to the generalized suffix trie introduced in section 2.5.2.

Definition 3.2. The generalized suffix array of a padded string collection $\mathbb{S}$ (definition 2.10), consisting of c strings of total length n, is defined as an array A of length n containing a permutation of all pairs (i, j) where i points to a string $s^i \in \mathbb{S}$ and $1 \leq j \leq n_i$ points to one of the n_i suffixes of s^i. Pairs are ordered such that $\mathbb{S}_{A[i]\ldots} <_{lex} \mathbb{S}_{A[i+1]\ldots}$ for all $1 \leq i < n$.

The suffix array is constructed in $\mathcal{O}(n)$ time, for instance using the [Kärkkäinen and Sanders, 2003] algorithm, or using non-optimal but practically faster algorithms, e.g. [Schürmann and Stoye, 2007]. The space consumption of the suffix array is $n \log n$ bits. When $n < 2^{32}$, a 32 bit integer is sufficient to encode any value in the range $[1, n]$. Consequently, the space consumption of suffix arrays for texts shorter than 4 GB is $4n$ bytes.

Weese gives a generalization of Kärkkäinen and Sanders algorithm to construct the generalized suffix array in $\mathcal{O}(n)$ time. The space consumption of the generalized suffix array is $n \log cn^*$ bits, where $n^* = \max n_i$. For instance, the human genome GRCh38 is a

Figure 3.2: *Generalized suffix array for the string collection* $\mathbb{S} = \{$ ANANAS$\$_1$, CACAO$\$_2$ $\}$.

i	$A[i]$	$\mathbb{S}_{A[i]\ldots}$
1	(1,7)	$\$_1$
2	(2,6)	$\$_2$
3	(2,2)	ACAO$\$_2$
4	(1,1)	ANANAS$\$_1$
5	(1,3)	ANAS$\$_1$
6	(2,4)	AO$\$_2$
7	(1,5)	AS$\$_1$
8	(2,1)	CACAO$\$_2$
9	(2,3)	CAO$\$_2$
10	(1,2)	NANAS$\$_1$
11	(1,4)	NAS$\$_1$
12	(2,5)	O$\$_2$
13	(1,6)	S$\$_1$

collection of 24 sequences, among whose the largest one consists of 248 Mbp. Hence, to represent the generalized suffix array of GRCh38 I use pairs of 1+4 bytes. The suffix array of GRCh38 fits in 15 GB of memory and is constructed in about one hour on a modern computer [Weese, 2013].

Top-down traversal

I now concentrate on implementing suffix trie functionalities. Any suffix trie node is univocally identified by an interval of the suffix array A. Thus, while traversing the trie, I maintain the interval $[l, r]$ associated to the pointed node. In addition, I also remember the depth d of the pointed node. Recall from section 2.5.2 that any leaf node is defined by an interval containing only terminator symbols. The edge label entering any internal node at depth d is defined by the d-th symbol in any suffix $\mathbb{S}_{A[i]}$ with $i \in [l, r]$. The occurrences below any node correspond by definition to the interval $[l, r]$ of A. Summing up, I represent the pointed node x by the integers $\{l, r, d\}$ and define the following operations on it:

- ISLEAF(x) returns true iff $A[x.r] + x.d = n_{A[x.r]}$;
- LABEL(x) returns $\mathbb{S}_{A[x.l]+x.d}$;
- OCCURRENCES(x) returns $A[x.l \ldots x.r]$.

Binary search is the key to implement function GODOWN a symbol. Functions L (algorithm 3.1) and R (algorithm 3.2) compute in $\mathcal{O}(\log n)$ binary search steps the position in A of the left and right interval corresponding to the child node following the edge labeled by a given symbol c. Note that line 6 of algorithms 3.1–3.2 may involve a comparison

Algorithm 3.1 L(x, c)

Input x : pointer to a suffix array node
c : character to query
Output integer denoting the left interval

1: $l_1 \leftarrow x.l$
2: $l_2 \leftarrow x.r$
3: **while** $l_1 < l_2$ **do**
4: $\quad i \leftarrow \lfloor \frac{l_1+l_2}{2} \rfloor$
5: $\quad$ **if** $\mathbb{S}_{A[i]+x.d} <_{lex} c$ **then**
6: $\quad\quad l_1 \leftarrow i + 1$
7: $\quad$ **else**
8: $\quad\quad l_2 \leftarrow i$
9: **return** l_1

Algorithm 3.2 R(x, c)

Input x : pointer to a suffix array node
c : character to query
Output integer denoting the right interval

1: $r_1 \leftarrow x.l$
2: $r_2 \leftarrow x.r$
3: **while** $r_1 < r_2$ **do**
4: $\quad i \leftarrow \lfloor \frac{r_1+r_2}{2} \rfloor$
5: $\quad$ **if** $\mathbb{S}_{A[i]+x.d} \leq_{lex} c$ **then**
6: $\quad\quad r_1 \leftarrow i + 1$
7: $\quad$ **else**
8: $\quad\quad r_2 \leftarrow i$
9: **return** r_1

Algorithm 3.3 GoRoot(x)

Input x : pointer to a suffix array node
1: $x \leftarrow \{1, n, 0\}$

Algorithm 3.4 GoDown(x, c)

Input x : pointer to a suffix array node
c : character to query
Output boolean indicating success

1: **if** IsLeaf(x) **then**
2: $\quad$ **return false**
3: $x.d \leftarrow x.d + 1$
4: $x.l \leftarrow$ L(x, c)
5: $x.r \leftarrow$ R(x, c)
6: **return** $x.l < x.r$

beyond the end of strings in $\mathbb{S}$, however I defined t_i as the empty word ϵ if $i > |t|$ and $\epsilon <_{lex} c$ for all $c \in \Sigma$.

Algorithms algorithm 3.5 and 3.6) show how to implement respectively GoDown and GoRight, to have time complexity independent of the alphabet size σ. Indeed, the time complexity of GoDown and GoRight is $\mathcal{O}(\log n)$, as they rely on a single call of R. In this way, the time complexity of exact string matching algorithm 3.15 is $\mathcal{O}(m \log n)$.

Note that the trie can be iterated down spelling a full pattern within a single call of L and R: in line 6 of algorithms 3.1–3.2, instead of comparing a single character, it suffices to compare the full pattern to the current suffix. However, the worst case runtime of algorithm 3.15 remains $\mathcal{O}(m \log n)$, as each step of the binary search now requires a full lexicographical comparison between the pattern and any suffix of the text, which is performed in $\mathcal{O}(m)$ time in the worst case. As shown in [Manber and Myers, 1990], the worst case runtime can be decreased to $\mathcal{O}(m + \log n)$ at the expense of additional $n \log n$ bits, by storing the precomputed longest common prefixes (LCP) between any two consecutive suffixes $\mathbb{S}_{A[i]...}$, $\mathbb{S}_{A[i+1]...}$ for all $1 \leq i < n$. Alternatively, the *average case* runtime

Algorithm 3.5 GODOWN(x)

Input x : pointer to a suffix array node
Output boolean indicating success

1: **if** ISLEAF(x) **then**
2: **return false**
3: $x.d \leftarrow x.d + 1$
4: $x.l \leftarrow \mathrm{R}(x, \epsilon)$
5: $c_l \leftarrow \mathbb{S}_{A[x.l]+x.d}$
6: $c_r \leftarrow \mathbb{S}_{A[x.r]+x.d}$
7: **if** $c_l \neq c_r$ **then**
8: $x.r \leftarrow \mathrm{R}(x, c_l)$
9: **return** $x.l < x.r$

Algorithm 3.6 GORIGHT(x)

Input x : pointer to a suffix array node
Output boolean indicating success

1: **if** ISROOT(x) **then**
2: **return false**
3: $c_l \leftarrow \mathbb{S}_{A[x.l]+x.d}$
4: $c_r \leftarrow \mathbb{S}_{A[x.r]+x.d}$
5: **if** $c_l \neq c_r$ **then**
6: $x.l \leftarrow x.r$
7: $x.r \leftarrow \mathrm{R}(x, c_l)$
8: **return** $x.l < x.r$

is reduced to $\mathcal{O}(m + \log n)$, without storing any additional information, by using the MLR heuristic [Manber and Myers, 1990]. In practice, the MLR heuristic outperforms the SA + LCP algorithm, due to the higher cost of fetching additional data from the LCP table.

3.1.2 q-Gram index

The logarithmic factor introduced by the suffix array can be removed by restricting the traversal of the idealized suffix trie to a fixed depth q. The idea is to supplement the suffix array A with a so-called q-gram directory: an additional array D of length $\Sigma^q + 1$, storing the suffix array ranges computed by algorithm **??** for any possible word of length q.

With the aim of addressing q-grams in the directory D, I impose a canonical code on q-grams through a bijective function $h : \Sigma^q \to [1 \dots \sigma^q]$ defined as in [Knuth, 1973]:

$$h(p) = 1 + \sum_{i=1}^{q} \rho_0(p_i) \cdot \sigma^{q-i} \tag{3.1}$$

where $p \in \Sigma^q$ is any q-gram and ρ_0 is the zero-based lexicographic rank defined on Σ (recall the lexicographic rank function ρ from definition 2.5 and pose $\rho_0(x) = \rho(x) - 1$). This allows us to store in and retrieve from $D[h(p)]$, for each q-gram $p \in \Sigma^q$, the left suffix array interval returned by algorithm 3.1, i.e. $D[h(p)] = \mathrm{L}(1, n, p)$. Note that the right interval returned by algorithm 3.2 is equivalent to the left interval of the lexicographical successor q-gram and therefore available in $D[h(p) + 1]$.

The downside of the q-gram index is that in practice it is only applicable to small alphabet and pattern sizes. For instance, parameters $|\Sigma| = 4$ and $q = 14$ require a q-gram directory consisting of 268 M entries that, using a 32 bits encoding, consume 1 GB of memory.

Figure 3.3: *q-Gram index for the string ANANAS over the alphabet* $\Sigma = \{A, N, S\}$.

p	h	$D[h]$	i	$A[i]$	$s_{A[i]\ldots n}$
AA	1	2	1	7	$
AN	2	2	2	1	ANANAS$
AS	3	4	3	3	ANAS$
NA	4	5	4	5	AS$
NN	5	6	5	2	NANAS$
NS	6	6	6	4	NAS$
SA	7	6	7	6	S$
SN	8	6			
SS	9	6			
	10	6			

Algorithm 3.7 L(x, c)

Input x : pointer to a q-gram node
c : character to query
Output integer denoting the left interval

1: $x.l_h \leftarrow x.l_h + \rho_0(c) \cdot \sigma^{x.d}$
2: **return** $D[x.l_h]$

Algorithm 3.8 R(x, c)

Input x : pointer to a q-gram node
c : character to query
Output integer denoting the right interval

1: $x.r_h \leftarrow x.r_h - \rho_0(c) \cdot \sigma^{x.d}$
2: **return** $D[x.r_h]$

Top-down traversal

I now extend suffix array traversal operations to use the q-gram directory D. Again, I maintain the current range $[l, r]$ and the current depth d. In addition, while traversing the trie, I maintain the interval $[l_h, r_h]$ in D and, in order to answer LABEL(x), the label e of the edge entering the current node. Summing up, I represent the pointed node x by the elements $\{l, r, d, l_h, r_h, e\}$. I define the basic node operations as follows:

- ISLEAF(x) returns true iff $x.d = q$;
- LABEL(x) returns $x.e$;
- OCCURRENCES(x) returns $A[x.l \ldots x.r]$.

I define functions L and R to use the directory D instead of A and obtain GODOWN in $\mathcal{O}(1)$. Note how the canonical code assigned by h preserves the lexicographical ordering for all words not longer than q, i.e. $v <_{lex} w$ iff $h(v) < h(w)$ for all $v, w \in \Sigma^{\leq q}$.

Exact string matching algorithm 3.15 runs in time $\mathcal{O}(q)$, nonetheless it can be improved to perform $\mathcal{O}(1)$ lookups in D. It suffices to compute the canonical code of the pattern in one step, as shown in algorithm 3.11.

Algorithm 3.9 GoRoot(x)

Input x : pointer to a q-gram node

1: $x \leftarrow \{1, n, 0, 1, \sigma^q, \epsilon\}$

Algorithm 3.10 GoDown(x, c)

Input x : pointer to a q-gram node
c : character to query

Output boolean indicating success

1: **if** isLeaf(x) **then**
2: **return false**
3: $x.d \leftarrow x.d + 1$
4: $x.e \leftarrow c$
5: $x.l \leftarrow \mathrm{L}(x, x.e)$
6: $x.r \leftarrow \mathrm{R}(x, x.e)$
7: **return** $x.l < x.r$

Algorithm 3.11 ExactSearch(t, p)

Input t : pointer to the root node of the q-gram index of the text
p : string to query

Output list of all occurrences of the pattern in the text

1: $l \leftarrow D[h(p)]$
2: $r \leftarrow D[h(p) + 1]$
3: **report** $A[l \ldots r]$

If the patterns are shorter or equal to the fixed length q, the suffix array is accessed only to locate the occurrences, as the directory D alone is sufficient to count the occurrences. In this case, the total ordering of the text suffixes in the suffix array can be relaxed to prefixes of length q. This gives us a twofold advantage, as one can: (i) construct the suffix array more efficiently using bucket sorting and (ii) maintain leaves in each bucket sorted by their relative text positions. The latter property allows to compress the suffix array bucket-wise e.g. using Elias δ encoding [Elias, 1975] or to devise cache-oblivious strategies to process the occurrences [Hach *et al.*, 2010].

If the patterns are longer than q, the q-gram index is still usable. An hybrid algorithm can use the directory D to conduct the search up to depth q and later continue with binary searches on the suffix array. This hybrid index cuts the most expensive binary searches and increases memory locality. Furthermore, this hybrid index becomes useful whenever the suffix array is too big to fit in main memory and has to reside in external memory.

3.2 Succinct full-text indices

The Burrows-Wheeler transform (BWT) [Burrows and Wheeler, 1994] is a transformation defining a permutation of an input string. The transformed string exposes two important properties: reversibility and compressibility. The former property allows us to

reconstruct the original string from its BWT, the latter property makes the transformed string more amenable to compression. Thanks to these two properties, the BWT has been recognized as a fundamental method for text compression and practically used in the bzip2 [Seward, 1996] tool.

More recently, Ferragina and Manzini proposed the BWT as a tool for full-text indexing. They showed in [Ferragina and Manzini, 2000] that the BWT alone allows to perform exact string matching and engineered in [Ferragina and Manzini, 2001] a compressed full-text index called FM-index. Over the last years, the FM-index has been widely employed under different re-implementations by many popular Bioinformatics tools e.g. Bowtie [Langmead *et al.*, 2009] and BWA [Li and Durbin, 2009], and is now considered a fundamental method for the indexing of genomic sequences.

In the next subsections I give the fundamental ideas behind the BWT and the FM-index. Subsequently, I discuss my succinct FM-index implementations covering strings and string collections.

3.2.1 Burrows-Wheeler transform

Let s be a padded string (definition 2.9) of length n over an alphabet Σ. In the following, I consider the string s to be cyclic and its subscript s_i to be *modular*, e.g. $s_0 = s_n$ and $s_{n+i} = s_i$ for any $i \in \mathbb{N}$. Consider the square matrix consisting of all cyclic shifts of the string s (the i-th cyclic shift has the form $s_{i\dots n}s_{1\dots i-1}$) sorted in lexicographical order (see figure 3.4). For convenience, I denote by f the first column $s_{A[i]}$, and by l the last column $s_{A[i]-1}$. Note how the cyclic shifts matrix is related to the suffix array A of s: the i-th cyclic shift is $s_{A[i]\dots n}s_{1\dots A[i]-1}$.

Definition 3.3. The BWT of s is the string obtained concatenating the symbols in the last column of the cyclic shifts matrix of s, i.e. it is the string $l = s_{A[i]-1}$.

Figure 3.4: *Burrows-Wheeler transform for the string* ANANAS$*.*

i	$A[i]$	$s_{A[i]}$		$s_{A[i]-1}$
1	7	$	ANANA	S
2	1	A	NANAS	$
3	3	A	NAS$A	N
4	5	A	S$ANA	N
5	2	N	ANAS$	A
6	4	N	AS$AN	A
7	6	S	$ANAN	A

The BWT easily generalizes to string collections. Indeed, definition 3.3 still holds for a padded string collection $\mathbb{S}$ (definition 2.10) and its cyclic shifts matrix sorted in lexicographical order.

The cyclic shifts matrix is conceptual and does not have to be to constructed explicitly in order to derive the BWT of a text. The BWT can be obtained in linear time by scanning the suffix array A and assigning to the i-th BWT symbol the text character $s_{A[i]-1}$. As constructing the suffix array is not desirable, due to its space consumption of $n \log n$ bits, various direct BWT construction algorithms working within $o(n)$ bits plus constant space have been recently proposed in [Bauer *et al.*, 2013; Crochemore *et al.*, 2013].

Inversion

I now describe how to invert the BWT to reconstruct the original text. Inverting the BWT means being able to know where any BWT character occurs in the original text. To this extent, I introduce two permutations $LF : [1,n] \rightarrow [1,n]$ and $\Psi : [1,n] \rightarrow [1,n]$, with $LF = \Psi^{-1}$, where the value of $LF(i)$ gives the position j in f where character l_i occurs and the value $\Psi(j)$ gives back the position i in l where f_j occurs. Figure 3.5 illustrates.

Figure 3.5: *Functions LF and Ψ for the string* ANANAS$. *Note how $LF(\Psi(i)) = \Psi(LF(i)) = i$ for any i. Also note how the i-th occurrence of any character c in l is the i-th occurrence of c in f.*

i	$\Psi(i)$	$LF(i)$	$s_{A[i]}$		$s_{A[i]-1}$
1	2	7	$	ANANA	S
2	5	1	A	NANAS	$
3	6	(5)	A	NAS$A	(N)
4	7	6	A	S$ANA	N
5	(3)	2	(N)	ANAS$	A
6	4	3	N	AS$AN	A
7	1	4	S	$ANAN	A

The character s_i is recovered by $f_{\Psi^{i-1}(j)}$, where the iterated Ψ is defined as

$$\begin{aligned} \Psi^0(j) &= j \\ \Psi^{i+1}(j) &= \Psi(\Psi^i(j)) \end{aligned} \tag{3.2}$$

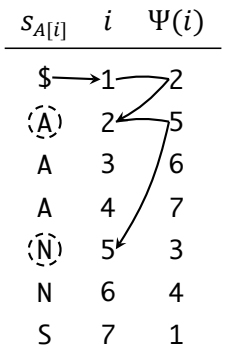
Conversely, $\bar{s}_i$ is recovered as $s_{LF^{i-1}(j)}$, where the iterated LF is defined as

$$\begin{aligned} LF^0(j) &= j \\ LF^{i+1}(j) &= LF(LF^i(j)) \end{aligned} \tag{3.3}$$

The full string s is recovered by starting in f at the position of $ and following the cycle defined by the permutation Ψ. Conversely, the reverse string $\bar{s}$ is recovered by starting in l at the position of $ and following the cycle defined by the permutation LF.

Inverting the generalized BWT works in the same way. Indeed, permutations Ψ and LF are composed of c cycles, where each cycle corresponds to a distinct string in the collection. The character s^i is recovered by starting at the position of $\$^i$ and following the cycle of Ψ (or LF) associated to s^i.

Figure 3.6: *Recovering the string* ANANAS$ *from the permutation* Ψ*. Here I depict only the first two steps of the inversion recovering* AN*.*



Permutation LF

The permutation LF is conceptual: it does not have to be represented explicitly but it can be deduced from the BWT l with the help of some additional character counts. This is possible due to two simple observations on the cyclic shifts matrix [Burrows and Wheeler, 1994]:

- for all $i \in [1, n]$, the character l_i precedes the character f_i in the original string s;
- for all characters $c \in \Sigma$ the i-th occurrence of c in f corresponds to the i-th occurrence of c in l.

These observation are obvious since $f = s_{A[i]}$ and $l = s_{A[i]-1}$ (see figure 3.4). Given the above observations, I define the permutation LF as [Burrows and Wheeler, 1994; Ferragina and Manzini, 2000]:

$$LF(i) = C(l_i) + Occ(l_i, i) \tag{3.4}$$

where I denote with $C : \Sigma \to [1, n]$ the total number of occurrences in s of all characters alphabetically smaller than c, and with $Occ : \Sigma \times [1, n] \to [1, n]$ the number of occurrences of character c in the prefix $l_{1 \ldots i}$.

The key problem of representing the permutation LF is how to represent function Occ, as function C can be easily tabulated by a small array of size $\sigma \log n$ bits. In the next subsection I address the problem of representing function Occ efficiently. Subsequently, in subsection 3.2.3 I show how to build a full-text index out of function LF.

3.2.2 Rank dictionaries

The question "how many times a given character c occurs in the prefix $l_{1 \ldots i}$?", has to be answered efficiently, ideally in constant time and linear space. The general problem on arbitrary strings has been tackled by several studies on the succinct representation of data structures [Jacobson, 1989]. This specific question takes the name of *rank query* and a data structure answering rank queries is called *rank dictionary*.

Definition 3.4. Given a string s over an alphabet Σ and a character $c \in \Sigma$, $\text{rank}_c(s, i)$ returns the number of occurrences of c in the prefix $s_{1...i}$.

The key idea of rank dictionaries is to maintain a succinct (or even compressed) representation of the input string and attach a dictionary to it. By doing so, Jacobson showed how it is possible to answer rank queries in constant time (on the RAM model) using $n + o(n)$ bits for an input binary string of n bits [Jacobson, 1989]. First I consider the binary case $\Sigma_B = \{0, 1\}$ and later I extend it to arbitrary alphabets. In addition, I discuss implementation details that are crucial to obtain practical efficiency.

Binary alphabet

I start by describing a simple rank dictionary answering rank queries in constant time but consuming $2n$ bits and later I extend it to consume only $n + o(n)$ bits. Given the binary string $s \in \Sigma_B$, I partition it in blocks of size b. In the following I assume w.l.o.g. the string length n to be a multiple of b, conversely values in all subsequent formulas must be rounded accordingly.

I attach to the binary string s an array R of length $\frac{n}{b}$, where the i-th entry gives a summary of the number of occurrences of the bit 1 in $s_{1...ib}$, i.e. $R[\frac{i}{b}] = \text{rank}_1(s, \frac{i}{b})$. Note that $\text{rank}_0(s, i) = i - \text{rank}_1(s, i)$ so I consider only $\text{rank}_1(s, i)$. Therefore, the rank query can be rewritten as:

$$\text{rank}_1(s, i) = R[\frac{i}{b}] + \text{rank}_1(s_{\frac{i}{b}...\frac{i}{b}+b}, i \mod b) \tag{3.5}$$

and answered in time $\mathcal{O}(b)$ by (i) fetching the rank summary from R in constant time, and (ii) counting the number of occurrences of the bit 1 within a block of length b. By posing $b = \log n$, step ii is $\mathcal{O}(1)$, by means of the four-Russians tabulation technique [**?**]. Moreover, the array R stores $\frac{n}{\log n}$ positions and each position in s requires $\log n$ bits, so R consumes n bits. Thus, this rank dictionary consumes $2n$ bits.

To squeeze this rank dictionary to consume only $n + o(n)$ bits of space, I add another array R^2 summarizing the ranks on b^2 bits boundaries and let the initial array R store only local positions within the corresponding blocks defined by R^2. I rewrite $\text{rank}_1(s, i)$ accordingly:

$$\text{rank}_1(s, i) = R^2[\frac{i}{b^2}] + R[\frac{i}{b}] + \text{rank}_1(s_{\frac{i}{b}...\frac{i}{b}+b}, i \mod b) \tag{3.6}$$

Each entry of R now has to represent only b^2 possible values and thus consumes only $2 \log b$ bits. Summing up, this two-levels rank dictionary consumes n bits for the input string, $\mathcal{O}(\frac{n \log n}{b^2})$ bits for R^2 and $\mathcal{O}(\frac{n \log b}{b})$ bits for R. By posing $b = \log n$ I have $\mathcal{O}(\frac{n}{\log n})$ bits for R^2 and $\mathcal{O}(\frac{n \log \log n}{\log n})$ bits for R. Hence, the two-levels rank dictionary consumes $n + o(n)$ bits.

I implemented generic multi-levels rank dictionaries where the block size b is a template parameter adjustable at compile time. Whenever the input string has length inferior to 4 GB, I employ one-level rank dictionaries with $b = 32$ bits or two-levels rank

Figure 3.7: *Example of rank dictionaries for the string s = 010101100100. On the one-level rank dictionary, $b = 4$ and $rank_1(s, 6) = R[2] + rank_1(s_{5\ldots8}, 2) = 3$. On the two-levels rank dictionary, $b = 2$ and $rank_1(s, 6) = R^2[2] + R[3] + rank_1(s_{6\ldots6}, 1) = 3$.*

i	s_i	$R[\frac{i}{b}]$
1	0	0
2	1	
3	0	
4	1	
5	0	2
6	1	
7	1	
8	0	
9	0	4
10	1	
11	0	
12	0	

i	s_i	$R[\frac{i}{b}]$	$R^2[\frac{i}{b^2}]$
1	0	0	0
2	1		
3	0	1	
4	1		
5	0	0	2
6	1		
7	1	1	
8	0		
9	0	0	4
10	1		
11	0	1	
12	0		

dictionaries with $b = 16$ bits and $b^2 = 32$ bits; otherwise, I employ two-levels rank dictionaries with $b = 32$ bits and $b^2 = 64$ bits, or three-levels rank dictionaries with $b = 16$ bits, $b^2 = 32$ bits and $b^3 = 64$ bits. In order to reduce the number of cache misses, I interleaved the succinct representation of the input string with the lowest level summaries array R. Moreover, I compute step ii in $\mathcal{O}(1)$ using the SSE 4.2 popcnt instruction [Intel, 2011].

Small alphabets

The extension to small alphabets e.g. Σ_{DNA} is easy. Here I show how to extend the one-level rank dictionary. Given an input string s over Σ_{DNA} of size n bits (and thus of length $\frac{n}{\log \sigma}$ symbols), I partition it in blocks of b symbols (which do not correspond to b bits as in the Σ_B case). I supplement each block of s with an occurrences summary for all symbols in Σ, thus I use a matrix R_σ of size $\frac{n}{b} \times \sigma$ entries. I rewrite $\text{rank}_c(s, i)$ as:

$$\text{rank}_c(s, i) = R_\sigma[\frac{i}{b}][\rho(c)] + \text{rank}_c(s_{\frac{i}{b}\cdots\frac{i}{b}+b}, i \mod b) \tag{3.7}$$

where i now is the i-th symbol in s, not the i-th bit as in the Σ_B case.

In order to answer rank queries in constant time, I have to count the number of occurrences of the character c inside a block of length b. I pose $b = \frac{\log n}{\log \sigma}$ symbols, thus $b = \log n$ bits as in the Σ_B case. The matrix R_σ has $\frac{n}{\log n}$ entries, each one consuming $\sigma \log n$ bits. Thus R_σ consumes $n\sigma$ bits, and the whole rank dictionary $n + n\sigma$ bits.

Figure 3.8: *Example of rank dictionaries for the string* $s = \texttt{CCCGCA}$ *under the binary encoding* $\{A, C, G, T\} = \{00, 01, 10, 11\}$ *of the alphabet* Σ_{DNA}.

i	$s_{\frac{i}{2}}$	s_i	$R_\sigma[\frac{i}{D}]$	σ
1	C	0	0	A
2		1	0	C
3	C	0	0	G
4		1	0	T
5	C	0	0	A
6		1	2	C
7	G	1	0	G
8		0	0	T
9	C	0	0	A
10		1	3	C
11	A	0	1	G
12		0	0	T

3.2.3 FM-index

I now turn to the problem of implementing a full-text index relying on the permutation LF. This is possible because of the relationship between the cyclic shifts matrix and the suffix array A. First I show how to emulate a top-down traversal of the suffix trie, which is sufficient to count the number of occurrences of any substring in the original text. Later I focus on how to represent the leaves, which are necessary to locate occurrences in the original text.

Top-down traversal

I represent the pointed node x by the elements $\{l, r, e\}$, where $[l, r]$ represents the current suffix array interval and e is the label of the edge entering the current node.

- ISLEAF(x) returns true iff $x.l_r = \$$;
- LABEL(x) returns $x.e$.

Given a padded string collection $\mathbb{S}$, its BWT plus its associated permutation LF let us recover any substring of $\bar{\mathbb{S}}$. Nonetheless, I want to recover substrings of $\mathbb{S}$ in forward direction, as the suffix trie $\mathcal{S}$ spells all forward substrings of $\mathbb{S}$. Therefore, given a string $\mathbb{S}$ I consider the BWT of $\bar{\mathbb{S}}$, such that LF let us recover any substring of $\mathbb{S}$. Now I can use the permutation LF to decode the intervals computed during a suffix trie traversal.

From the root node, I easily obtain the interval of its child node labeled by c as $[C(c), C(c+1)]$. Now suppose an arbitrary node v of known interval $[b_v, e_v]$ s.t. the path from the root to v spells the substring s_v; I want to reach the node w of unknown interval $[b_w, e_w]$ s.t.

Algorithm 3.12 GOROOT(x)

Input x : pointer to a FM-index node

1: $x \leftarrow \{1, n, \epsilon\}$

Algorithm 3.13 GODOWN(x, c)

Input x : pointer to a FM-index node
c : char to query

Output boolean indicating success

1: **if** ISLEAF(x) **then**
2: **return false**
3: $x.l \leftarrow \text{LF}(x.l, c)$
4: $x.r \leftarrow \text{LF}(x.r, c)$
5: $x.e \leftarrow c$
6: **return** $x.l < x.r$

the path from the root to w spells $c \cdot s_v$ for some $c \in \Sigma$. Thus, I know all prefixes of $\bar{\mathbb{S}}$ ending with s_v (hence all suffixes of $\mathbb{S}$ starting with s_v) and I am looking for all the prefixes of $\bar{\mathbb{S}}$ ending with $c \cdot s_v$ (hence all suffixes of $\mathbb{S}$ starting with $s_v \cdot c$). All these characters c are in $l_{b_v \ldots e_v}$, since l_i is the character $\mathbb{S}_{A[i]-1}$ preceding the suffix pointed by $A[i]$. Moreover, I know that these characters c are (i) contiguous and (ii) in relative order in f [Ferragina and Manzini, 2000]. If b and e are the first and last position in l within $[b_v, e_v]$ such that $l_b = c$ and $l_e = c$, then $b_w = LF(b)$ and $e_w = LF(e)$. I can rewrite $LF(b)$ as:

$$\begin{aligned} LF(b) &= C(l_b) + Occ(l_b, b) \\ &= C(c) + Occ(c, b) \\ &= C(c) + Occ(c, b_v - 1) + 1 \end{aligned} \tag{3.8}$$

Analogously, I can rewrite $LF(e)$ as $C(c) + Occ(c, e_v)$. Therefore, GODOWN a symbol computes two values of permutation LF and runs in time $\mathcal{O}(1)$. Conversely, GODOWN and GORIGHT run in time $\mathcal{O}(\sigma)$ (see algorithms **??**).

Sampled suffix array

The suffix array A is required to locate occurrences, yet I do not want to maintain the whole array A. As proposed by Ferragina and Manzini, I maintain a *sampled* suffix array A^ϵ containing positions sampled at regular intervals in the input string. In order to determine if and where I sampled any $A[i]$ in A^ϵ, I maintain a binary rank dictionary S of length n: if $S[i] = 1$, then I sampled $A[i]$ in $A^\epsilon[rank_1(S, i)]$. I obtain any $A[i]$ by finding the smallest $j \geq 0$ such that $LF^j(i)$ is in A^ϵ, and then $A[i] = A[LF^j(i)] + j$.

If I sample one text position out of $\log^{1+\epsilon} n$, for some $\epsilon > 0$, then A^ϵ consumes $\mathcal{O}(\frac{n}{\log^\epsilon n})$ space and OCCURRENCES(x) returns all occurrences in $\mathcal{O}(o \cdot \log^{1+\epsilon} n)$ time [Ferragina and Manzini, 2000]. In practice, I usually sample text positions at rates between 2^{-3} and 2^{-5}. The rank dictionary S consumes always $n + o(n)$ extra space.

3.3 Algorithms

In this section, I give generic string matching algorithms, working on any of the data structures presented so far. I first consider a simple algorithm performing top-down traversals bounded by depth. Then, I present algorithms for exact string matching, k-mismatches and k-differences. I finally give, for the first time to the best of my knowledge, algorithms solving multiple variants of exact string matching and k-mismatches.

At the same time, I perform an experimental evaluation of each of these algorithms on various suffix trie implementations. As data structures, I consider the suffix array (SA), the q-gram index for $q = 12$ (q-Gram), the interleaved FM-index with two-levels rank dictionaries (FM-2), the wavelet tree FM-index with two-levels rank dictionaries (FM-WT). As text, I consider the C. elegans reference genome (WormBase WS195), i.e. a collection of 6 DNA strings of about 100 MB total length. As patterns, I use sequences extrapolated from an Illumina sequencing run (SRR065390). The evaluation reports *average* runtimes per pattern, both in single and multiple string matching variants.

3.3.1 Top-down traversal bounded by depth

Before turning to string matching algorithms, I present a simple traversal algorithm. Algorithm 3.14 performs a top-down traversal of a suffix trie in depth-first order. The traversal is bounded, i.e. it stops after visiting any node at depth d. This algorithm helps to comprehend subsequent algorithms backtracking suffix tries. The experimental evaluation provides a first glimpse on what are the practical performances of various suffix trie implementations.

Algorithm 3.14 DFS(x, d)

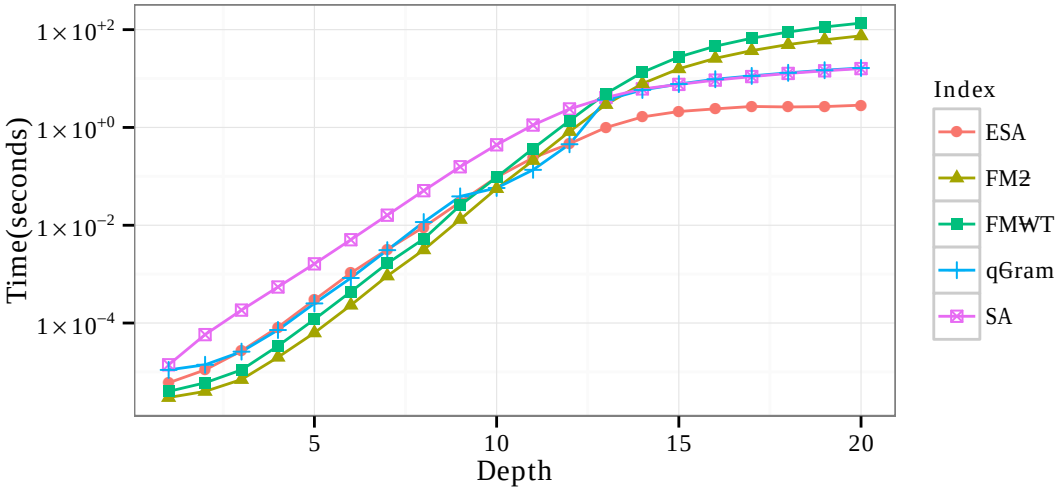
Input x : pointer to the root node of the suffix trie
d : integer bounding the traversal depth

```
1: if d > 0 then
2:     if goDown(x) then
3:         repeat
4:             Dfs(x, d − 1)
5:         until goRight(x)
```

3.3.2 Exact string matching

I now give a simple algorithm performing exact string matching on a generic suffix trie. I assume the text t to be indexed by its suffix trie $\mathcal{T}$. Algorithm 3.15 searches the pattern p by starting in the root node of $\mathcal{T}$ and following the path spelling the pattern. If the search ends up in a node x, each leaf l_i below x points to a distinct suffix $t_{i..n}$ such that $t_{i..i+m}$ equals p. If goDown is implemented in constant time and occurrences in linear time,

Figure 3.9: *Runtime of bounded top-down traversal of various suffix trie implementations.*



all occurrences of p into t are found in optimal time $\mathcal{O}(m + o)$, where m is the length of p and o its number of occurrences in t.

Algorithm 3.15 ExactSearch(t, p)

Input t : pointer to a suffix trie node
p : pointer to a pattern
Output list of all occurrences of the pattern in the text

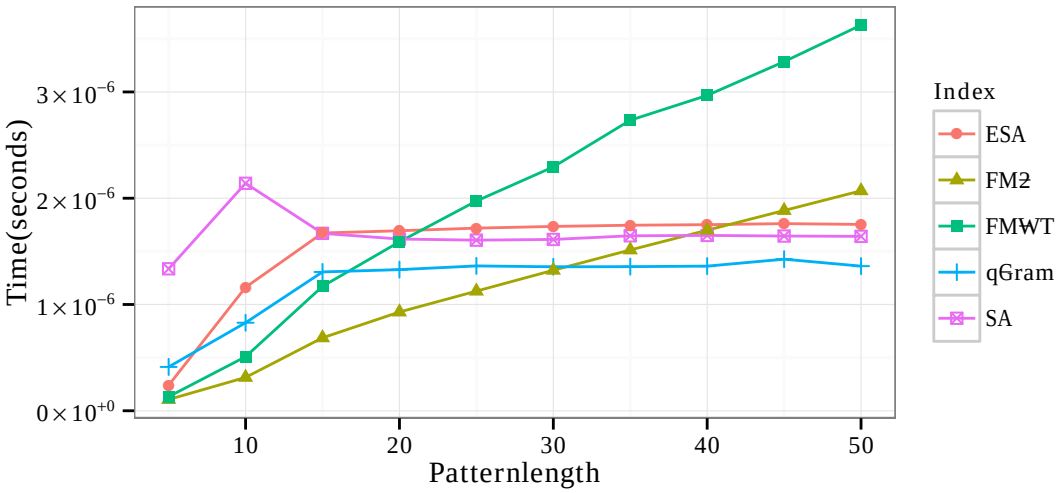
```
1: if atEnd(p) then
2:     report occurrences(t)
3: else if goDown(t, value(p)) then
4:     goNext(p)
5:     ExactSearch(t, p)
```

3.3.3 Backtracking k-mismatches

I now give an algorithm that solves k-mismatches by backtracking a generic suffix trie. The idea of backtracking a suffix tree has been first proposed in [Ukkonen, 1993]. Variations of this method, in conjunction with some FM-index implementation, recently became in vogue for bioinformatics applications [Langmead *et al.*, 2009; Li and Durbin, 2009].

Algorithm 3.16 performs a top-down traversal on the suffix trie $\mathcal{T}$, spelling incrementally all distinct substrings of t. While traversing each branch of the trie, this algorithm incrementally computes the distance between the query and the spelled string. If the

Figure 3.10: *Runtime of exact string matching on various suffix trie implementations.*



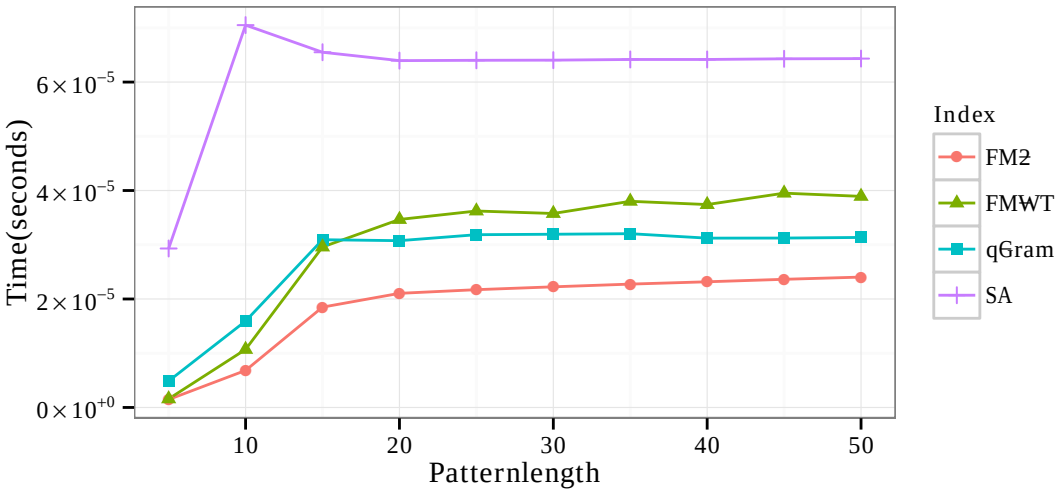
computed distance exceeds k, the traversal backtracks and proceeds on the next branch. Conversely, if the pattern p is completely spelled and the traversal ends up in a node x, each leaf $l_i \in \mathbb{L}(x)$ points to a distinct suffix $t_{i..n}$ such that $d_H(t_{i..i+m}, p) \leq k$.

Algorithm 3.16 KMISMATCHES(t, p, e)

Input t : pointer to the root node of the suffix trie of the text
p : pointer to the root node of the trie of the patterns
e : integer bounding the number of mismatches
Output list of all occurrences of the pattern in the text

```
1:  if e = k then
2:      ExactSearch(t, p)
3:  else if e < k then
4:      if atEnd(p) then
5:          report occurrences(t)
6:      else if goDown(t) then
7:          repeat
8:              d ← ω(label(t), value(p))
9:              goNext(p)
10:             KMismatches(t, p, e + d)
11:             goPrevious(p)
12:         until goRight(t)
```

Figure 3.11: *Runtime of k-mismatches on various suffix trie implementations.*



3.3.4 Backtracking k-differences

I present two alternative algorithms for k-differences. Algorithm 3.17 explicitly enumerates errors while traversing the suffix trie. Conversely, algorithm 3.18 computes the edit distance between the pattern and any branch of the suffix trie. This latter algorithm necessitates of a method capable of checking incrementally whether the edit distance at any node is within the imposed threshold k.

Algorithm 3.17 KDIFFERENCES(t, p, e)

Input t : pointer to the root node of the suffix trie of the text
p : pointer to the root node of the trie of the patterns
e : integer bounding the number of errors
Output list of all occurrences of the pattern in the text

```
1: if e = k then
2:     EXACTSEARCH(t, p)
3: else
4:     GONEXT(p)
5:     KDIFFERENCES(t, p, e + 1)
6:     GOPREVIOUS(p)
7:     if GODOWN(t) then
8:         repeat
9:             KDIFFERENCES(t, p, e + 1)
10:            d ← ω(LABEL(t), VALUE(p))
11:            GONEXT(p)
12:            KDIFFERENCES(t, p, e + d)
13:            GOPREVIOUS(p)
14:        until GORIGHT(t)
```

Algorithm 3.18 KDIFFERENCES(t, p, D)

Input t : pointer to the root node of the suffix trie of the text
p : pointer to the root node of the trie of the patterns
D : vector of integers representing a DP column
Output list of all occurrences of the pattern in the text

```
1: if D[m] ≤ k then
2:     report OCCURRENCES(t)
3: else if minD ≤ k then
4:     if GODOWN(t) then
5:         repeat
6:             D' ← DP(D, LABEL(t), p)
7:             GONEXT(p)
8:             KDIFFERENCES(t, p, D')
9:             GOPREVIOUS(p)
10:        until GORIGHT(t)
```

3.3.5 Multiple exact string matching

Before turning to multiple k-mismatches, I describe a simpler multiple exact string matching algorithm. Algorithm 3.19 necessitates of the trie of the patterns, in addition to the

suffix trie of the text. This algorithm searches simultaneously in the suffix trie all patterns represented by the trie. The traversal of this algorithm corresponds to the intersection of the labeled branches of the two tries.

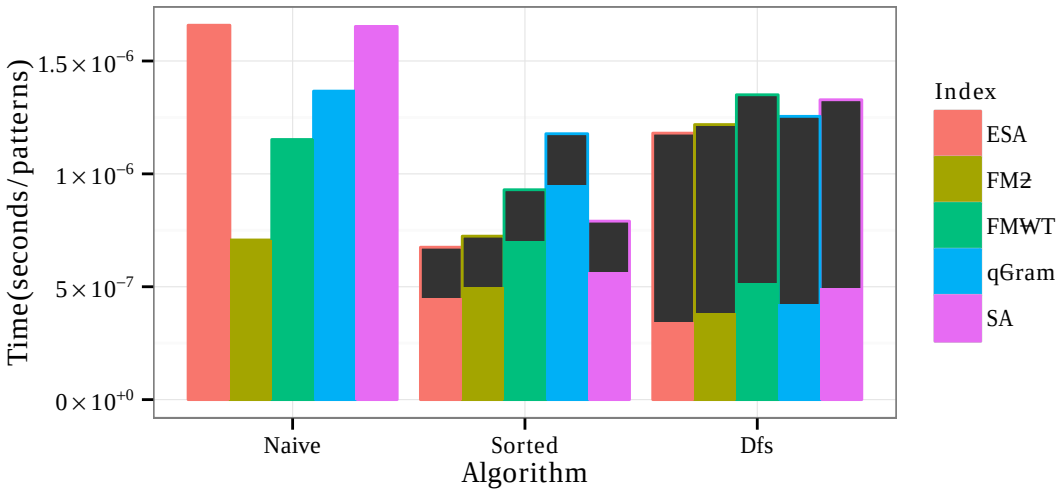
Algorithm 3.19 MULTIPLEEXACTSEARCH(t, p)

Input t : pointer to the root node of the suffix trie of the text
p : pointer to the root node of the trie of the patterns
Output list of all occurrences of any pattern in the text

```
1: if ISLEAF(p) then
2:     report OCCURRENCES(t) × OCCURRENCES(p)
3: else
4:     GODOWN(p)
5:     repeat
6:         if GODOWN(t, LABEL(p)) then
7:             MULTIPLEEXACTSEARCH(t, p)
8:             GOUP(t)
9:     until GORIGHT(p)
```

In the evaluation, I compare algorithm 3.19 (Dfs) with algorithm 3.15 processing patterns in random order (Naive) and in lexicographic order (Sorted). A simple lexicographical sort of the patterns speeds up exact string matching by 2 times. Algorithm 3.19 suffers from the preprocessing time to construct the trie of the patterns.

Figure 3.12: *Runtime of multiple exact string matching on various suffix trie implementations.*



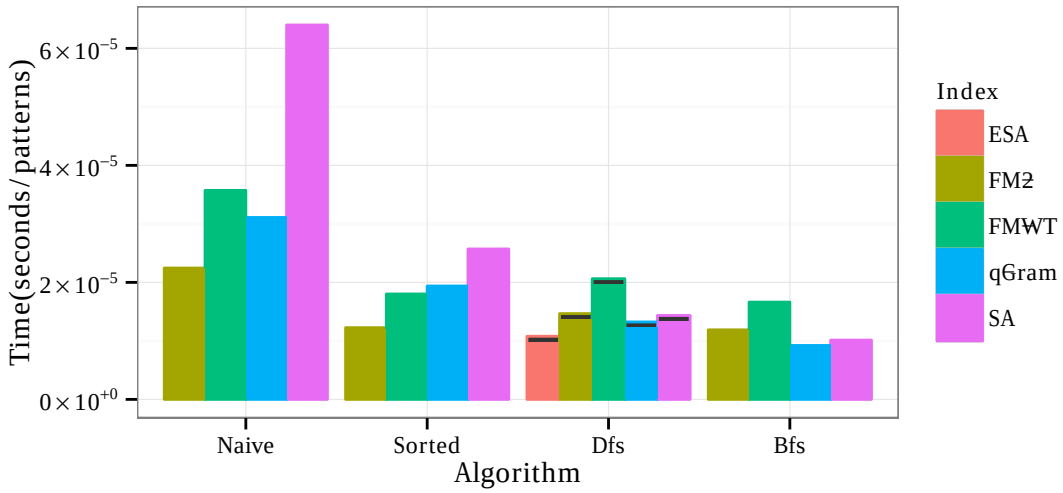
3.3.6 Multiple k-mismatches

Algorithm 3.20 MULTIPLEKMISMATCHES(t, p, e)

Input t : pointer to the root node of the suffix trie of the text
p : pointer to the root node of the trie of the patterns
e : integer bounding the number of mismatches
Output list of all occurrences of any pattern in the text

```
1:  if e = k then
2:      MULTIPLEEXACTSEARCH(t, p)
3:  else if e < k then
4:      if ISLEAF(p) then
5:          report OCCURRENCES(t) × OCCURRENCES(p)
6:      else if GODOWN(t) then
7:          repeat
8:              GODOWN(p)
9:              repeat
10:                 d ← ω(LABEL(t), LABEL(p))
11:                 MULTIPLEKMISMATCHES(t, p, e + d)
12:             until GORIGHT(p)
13:             GOUP(p)
14:         until GORIGHT(t)
```

Figure 3.13: *Runtime of multiple k-mismatches on various suffix trie implementations.*



CHAPTER

4 Filtering methods

In this chapter, I present various filtering methods for approximate string matching. I consider two classes of filtering methods: those based on *seeds* and those based on *q-grams*. Filters of the former class partition the pattern into *non-overlapping* factors called seeds, while filters of the latter class consider all *overlapping* substrings of the pattern having length q, the so-called q-grams. Both classes include various combinatorial filtering methods of increasing specificity and complexity, always providing filtration schemes with guarantees on filtration sensitivity.

I consider the following seed filtering methods: *exact seeds* [Baeza-Yates and Perleberg, 1992], *approximate seeds* [Myers, 1994; Navarro and Baeza-Yates, 2000], *suffix filters* [Kärkkäinen and Na, 2007]. Exact seeds partition the pattern in $k+1$ non-overlapping seeds, to be searched exactly. Approximate seeds increase specificity by factorizing the pattern in less than $k+1$ non-overlapping seeds, to be searched within a smaller distance threshold. Suffix filters further generalize exact and approximate seeds and yield stronger index based filtration.

I consider the following q-gram filtering methods: *contiguous q-grams* [Jokinen and Ukkonen, 1991], *gapped q-grams* [Burkhardt and Kärkkäinen, 2001], *multiple gapped q-grams* [Kucherov *et al.*, 2005]. Contiguous q-grams rely on a counting argument to filter out text regions containing less than a given threshold of q-gram occurrences. Gapped q-grams introduce *don't care positions* to lower the correlation between occurrences of consecutive q-grams. Multiple gapped q-grams conjunct multiple patterns of don't care positions to further increase specificity.

It will become clear through this chapter that seed filters are more practical, flexible, straightforward to design and implement than q-gram filters. All seed filters and contiguous q-grams provide full-sensitive filtration schemes for the k-differences problem, while (multiple) gapped q-grams only for k-mismatches. The design of highly specific yet full-sensitive filtration schemes for q-gram filters is combinatorially hard, while it is quite straightforward for seed filters. Also implementation-wise, q-gram filters are more involved than seeds filter. In fact, seed filters lend themselves well to both online and offline variants of the problem, while q-gram filters are better suited for the online variant. Finally, the experimental evaluation shows that seed filters outperform q-gram filters for most practical inputs. For these reasons, I design the applications of chapters 6 and 7 around seed filtering methods.

4.1 Exact seeds

Filtration with exact seeds is one of the naïvest filtering methods for approximate string matching. I first explain the underlying combinatorial principle, then I discuss implementation details and lastly give some insights on the efficiency of this method.

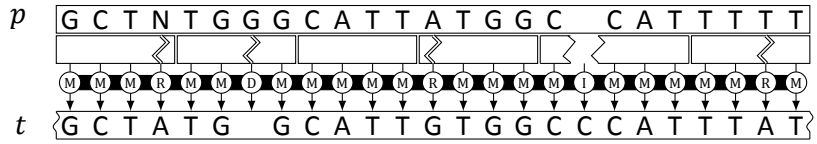
4.1.1 Principle

I consider the case of two arbitrary strings x, y within edit distance k. The generalization to k-differences is straightforward.

Lemma 4.1. *[Baeza-Yates and Perleberg, 1992] Let x, y be two strings s.t. $d_E(x, y) = k$. If y is partitioned w.l.o.g. into $k + 1$ non-overlapping seeds, then at least one seed occurs as a factor of x.*

It is immediate to see that any edit distance error can cover at most one seed. Therefore, at least one seed of y will not be covered by any seed and hence occur as a factor of x. Figure 4.1 shows an example.

Figure 4.1: *Filtration with exact seeds.*



This filtering method reduces the approximate search into multiple smaller exact searches. It solves k-differences by partitioning the pattern into $k + 1$ seeds, searching all seeds into the text, and verifying all their occurrences in the text. As lemma 4.1 is valid for *any substring* of the text within distance k from the pattern, this method finds all approximate occurrences of the pattern in the text.

4.1.2 Efficiency

How many verifications are triggered by filtration with exact seeds? It is straightforward to derive the expected number of verifications under the assumption of the text being generated according to the uniform Bernoulli model. The emission probability of any symbol in Σ is $p = \frac{1}{\sigma}$ and under i.i.d. assumptions the emission (and occurrence) probability of any word of length q is simply

$$\Pr(H > 0) = \frac{1}{\sigma^q} \tag{4.1}$$

thus the expected number of occurrences of a seed of length q in a text of length n is

$$E[H] = \sum_{i=1}^{n-q+1} \Pr(H > 0) = \frac{n - q + 1}{\sigma^q} \leq \frac{n}{\sigma^q}. \tag{4.2}$$

Lemma 4.1 requires to partition the pattern into $k+1$ seeds but leaves the freedom to choose their length. This leads to the problem of finding an optimal pattern partitioning to minimize the expected number of verifications. I fix[1] the length of all seeds to be

$$q = \left\lfloor \frac{m}{k+1} \right\rfloor \tag{4.3}$$

to minimize the expected number of occurrences of any seed. Under these conditions, the expected number of verifications produced by filtration with exact seeds is

$$E[V] = E[H] \cdot (k+1) < \frac{n(k+1)}{\sigma^q}. \tag{4.4}$$

Nonetheless, inputs of practical interest like genomes and natural texts do not fit well the uniform Bernoulli model. On those texts, uniform seed length often leads to suboptimal filtration.

4.2 Approximate seeds

The simple analysis of section 4.1.2 shows that filtration specificity is strongly correlated to the seed length. Therefore, the crux of designing a stronger filter lies into increasing the seed length while maintaining the full-sensitivity constrains. Myers, subsequently followed by Navarro and Baeza-Yates, proposed *approximate seeds* as a practical and effective generalization of exact seeds, yielding stronger filters for k-differences. The key idea of approximate seeds is to reduce the approximate search into smaller approximate searches, as opposed to exact seeds that reduce the approximate search into smaller exact searches.

4.2.1 Principle

Again, I start by considering two arbitrary strings x, y within edit distance k. The result then holds for any substring of the text within distance k from the pattern.

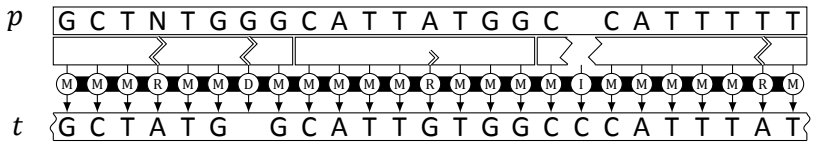
Lemma 4.2. *[Myers, 1994; Navarro and Baeza-Yates, 2000] Let x, y be two strings s.t. $d_E(x, y) = k$. If y is partitioned w.l.o.g. into s non-overlapping seeds s.t. $1 \leq s \leq k+1$, then at least one seed occurs as a factor of x within distance $\lfloor k/s \rfloor$.*

To prove full-sensitivity it suffices to see that, if none of the seeds occurs within its assigned distance, the total distance must be greater than $s \cdot \lfloor k/s \rfloor = k$. Figure 4.2 illustrates.

Lemma 4.2 assigns the same distance threshold to all seeds, yet this is not obligatory. I give here a more general definition of approximate seeds.

[1] For simplicity I ignore that some seed could have length $\left\lceil \frac{m}{k+1} \right\rceil$.

Figure 4.2: *Filtration with approximate seeds.*



Lemma 4.3. *Let x, y be two strings s.t. $d_E(x, y) = k$. Partition y into s non-overlapping seeds $y^1, y^2, \ldots, y^s$. Assign an arbitrary distance threshold k_i to each seed y^i, satisfying the following constraint:*

$$s + \sum_{i=1}^{s} k_i > k. \tag{4.5}$$

Then at least one seed occurs as a factor of x within distance k_i.

4.2.2 Parameterization

Approximate seeds provide filtration schemes of increasing specificity. The fastest but weakest scheme is given by $s = k+1$, while the most specific filtration scheme is obtained for $s = 1$ i.e. perfect filtration without any verification step. Alternatively, filtration specificity is controlled by acting on the minimum seed length q. Fixing q yields $s = \lfloor m/q \rfloor$, or vice versa, fixing the number of seeds s gives $q = \lfloor m/s \rfloor$. As expected, filtration specificity increases with seed length.

How to choose a good filtration scheme in practice? Myers, Navarro and Baeza-Yates carried out involved analysis to estimate the optimal parameterization. Navarro and Baeza-Yates find out that a number of seeds of $\Theta(\frac{m}{\log_\sigma n})$ yields an overall time complexity sublinear for an error rate $\epsilon < 1 - \frac{e}{\sqrt{\sigma}}$. Myers reports an analogous sublinear time when $q = \Theta(\log_\sigma n)$ is the seed length. Yet, these results do not necessarily translate into optimal filtration schemes in practice. The parameterization depends on the full-text index, the verification algorithm, the statistical properties of the text. Missing the optimal number of seeds by one often results in a runtime penalty of an order of magnitude.

Having established the number of seeds, or their length, thresholds have to be assigned. Lemma 4.3 allows to assign arbitrary distance thresholds. In practice, it is convenient to distribute distance thresholds evenly, as seeds with the highest threshold dominate the overall filtration time. The most strict threshold assignment is to give distance $\lfloor k/s \rfloor$ to $(k \bmod s) + 1$ seeds and distance $\lfloor k/s \rfloor - 1$ to the remaining seeds [Siragusa *et al.*, 2013].

4.3 Contiguous q-grams

q-Gram filters rely on counting arguments to filter out text regions containing less than a given threshold of q-gram occurrences. The first q-gram counting filter has been proposed in [Jokinen and Ukkonen, 1991]. More general filters have been proposed and im-

plemented in *QUASAR* [Burkhardt *et al.*, 1999], *SWIFT* [Rasmussen *et al.*, 2006], *STELLAR* [Kehr *et al.*, 2011].

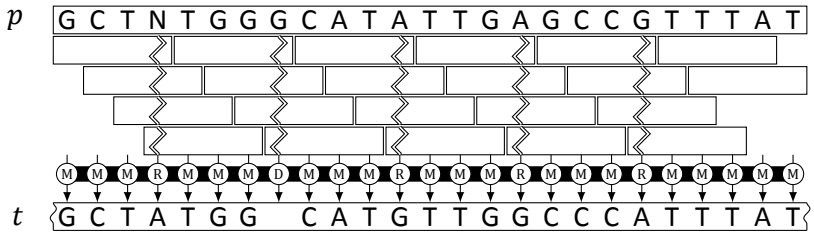
4.3.1 Principle

The counting argument of contiguous q-gram filters is based on the so-called *q-gram similarity measure* $\tau_q : \Sigma^* \times \Sigma^* \to \mathbb{N}_0$, defined as the number of substrings of length q common to two given strings. The following lemma relates q-gram similarity to edit distance. It gives a lower bound on the q-gram similarity $\tau_q(x, y)$ of any two strings x, y within edit distance k. As for seed filters, the result then easily translates to k-differences.

Lemma 4.4 (The q-gram lemma)**.** *[Jokinen and Ukkonen, 1991] Let x, y be two strings s.t. $d_E(x, y) = k$, and assume w.l.o.g. $|x| \leq |y|$ and $|x| = m$. Then x and y have q-gram similarity $\tau_q(m, k) \geq m - q + 1 - kq$.*

The first part of the threshold function τ counts the number of q-grams of x (i.e. $m - q + 1$), while the second part counts how many q-grams can be covered by k errors (kq, i.e. at most q per error). The threshold function τ depends only on parameters q, m, k and not on the specific q-grams. Figure 4.3 illustrates.

Figure 4.3: *Filtration with contiguous q-grams.*

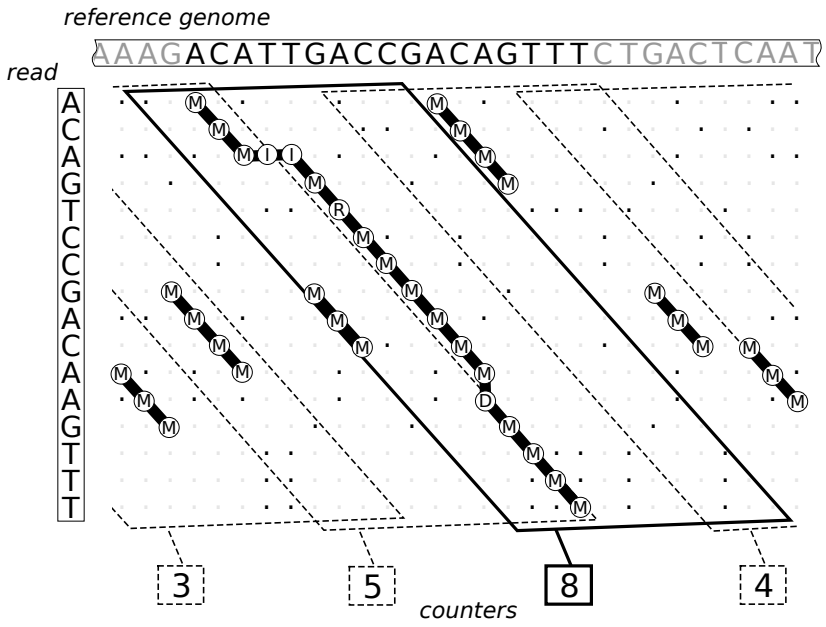


4.3.2 Bucketing

This filtering method requires *bucketing* the text in windows to enforce the counting argument of lemma 4.4. Buckets are obtained by subdividing the implicit DP matrix in parallelograms and projecting them on the text. Figure 4.4 illustrates this concept: any approximate occurrence of the pattern in the text spans at most k diagonals and is thus enclosed inside a parallelogram of width $k + 1$ [Rasmussen *et al.*, 2006]. Hence the projection of any text bucket has length $2k + 1$ and any occurrence has length between $m - k$ and $m + k$. The implementations described in [Rasmussen *et al.*, 2006; Kehr *et al.*, 2011; Weese *et al.*, 2009] use more efficient bucketing strategies with larger, overlapping parallelograms.

This method lends itself to work in a multiple online fashion rather than offline. The filtration stage scans the text and counts how many q-grams of the pattern fall into each bucket. The verification stage then verifies only parallelograms exceeding threshold $\tau_q(m, k)$.

Figure 4.4: *Parallelogram buckets. Picture from [Weese* et al.*, 2009].*



As long as the filter scans the text, such implementation remembers only buckets covering the patterns' lengths. To speed up the filtration phase, an index of the text could be used to count the q-gram. However, this implementation would require more memory, both to keep the text index in memory and to bucket the whole text.

4.3.3 Parameterization

Which is the biggest q-gram length yielding lossless filtration given m and k? In order to satisfy lemma 4.4, the q-gram threshold must be greater than zero, i.e. it must hold $\tau_q(m,k) \geq 1$. Thus, by substituting τ, it follows that the q-gram length must be $q \leq \left\lfloor \frac{m}{k+1} \right\rfloor$, analogously to equation 4.3 of seed filters.

4.4 Gapped q-grams

The idea of *gapped q-grams* is to lower the correlation between consecutive q-grams. The occurrence of any contiguous q-gram is strongly correlated to the occurrences of its preceding and following q-grams. One single edit distance error affects a cluster of q consecutive q-grams, as evidenced by the q-gram lemma 4.4. Gapped q-grams skip characters at fixed positions by defining patterns of *don't care positions*. Such don't care positions are immune to mismatches but not to insertions and deletions. Hence, this generalization of contiguous q-grams is useful to solve k-mismatches but not k-differences.

Gapped q-grams rely on a generalization of the q-gram similarity measure (section 4.3) to *subsequences*. A subsequence is a non-contiguous sequence of symbols of a given

string. Hence, instead of substrings, filtration with gapped q-grams counts the number of subsequences of length q common to two strings, whose positions are taken from a fixed set Q. The formal definition of gapped q-gram follows.

Definition 4.1. A Q-gram is a finite sequence Q of natural numbers starting with the unit element, i.e. $Q \subset \mathbb{N}$ and $1 \in Q$. The cardinality $|Q|$ is called the *weight* of Q and denoted as $w(Q)$. The maximum element of Q is named *span* and indicated by $s(Q)$.

Figure 4.5: *Filtration with gapped q-grams.*

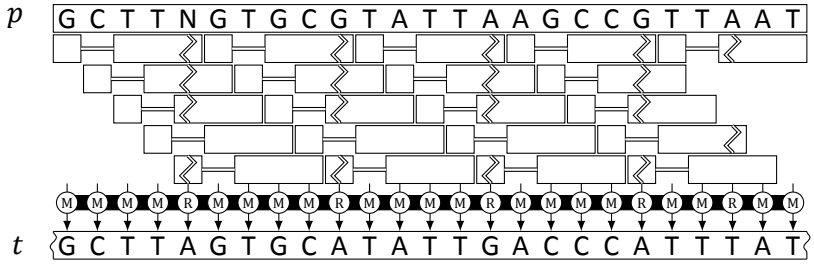


Figure 4.5 shows an example of Q-gram. As in the q-gram lemma, the threshold depends only on Q and parameters m, k. Indeed, the pattern of occurring q-grams does not depend on the text or pattern sequences but only on their transcript, i.e. on the mismatch positions. As mismatches do not affect don't care positions, any gapped Q-gram potentially yields a higher threshold than the contiguous q-gram of the same weight. Unfortunately, the q-gram lemma (**??**) does not give anymore a tight threshold, but only a lower bound.

Gapped q-grams raise hard combinatorial questions. (i) Does a given gapped q-gram yield a full-sensitive filter for k-mismatches? If so, either (ii) which is the maximum q-gram threshold t that guarantees full-sensitivity? Or alternatively, (iii) which is the maximum error k for which full-sensitivity is guaranteed? If the answer to question **??** is negative and the filter is lossy, (iv) how many false negatives the filter discards? Considering filtration efficiency, (v) how many false positives the filter produces?

Question ii has been first considered in [Burkhardt and Kärkkäinen, 2001; Kucherov *et al.*, 2005], the more general questions i has been introduced in [Nicolas and Rivals, 2005], while I consider here for the first time questions iii-v. With the aim of elucidating these questions, I first introduce simple characteristic functions to formally define transcripts detected by gapped q-grams. Afterwards, I recapitulate known results for questions i-v and present new exact and approximate solutions.

4.4.1 Characteristic functions

Consider an arbitrary transcript σ as a m-dimensional vector over $\mathbb{B}$, where $|\sigma|_0$ indicates the Hamming distance of the transcript. Let $\mathbb{B}_k^m \subset \mathbb{B}^m$ be the set containing all transcripts σ such that $|\sigma|_0 = k$.

Definition 4.2. A Q-gram *occurs* at position i in a similarity σ iff $\forall j \in Q\ \sigma_{i+j} = 1$. Fixed a Q-gram threshold t, the Q-gram detects σ iff it occurs at least t times in σ.

Boolean functions

Let $T_Q^m : \mathbb{B}^m \to \mathbb{B}$ denote a *boolean function* such that $T_Q^m(\sigma)$ is true iff the Q-gram occurs at least one time in a similarity σ of length m. In general, (Q, t) detects σ iff σ satisfies at least t clauses of T_Q^m. I define such boolean function as the disjunction

$$T_Q^m(\sigma) = \bigvee_{i=1}^{m-s(Q)+1} \bigwedge_{j \in Q} \sigma_{i+j} \tag{4.6}$$

where each *clause* of T_Q^m represents a single possible occurrence of Q in σ. I define an analogous boolean function for a Q-gram family F as the disjunction

$$T_F^m(\sigma) = \bigvee_{Q_i \in F} T_{Q_i}^m(\sigma) \tag{4.7}$$

By definition, T_Q^m and T_F^m are *monotone nondecreasing* boolean functions in *disjunctive normal form* (*DNF*). Since all monotone boolean functions in DNF are minimal, T_Q^m and T_F^m are *minimal*.

Pseudo-boolean functions

Let the function $t_Q^m : \mathbb{B}^m \to \mathbb{N}_0$ be the boolean function T_Q^m acting on $\mathbb{N}_0$. I define such *pseudo-boolean function* as

$$t_Q^m(\sigma) = \sum_{i=1}^{m-s(Q)+1} \prod_{j \in Q} \sigma_{i+j} \tag{4.8}$$

Here $t_Q^m(\sigma)$ counts how many times a Q-gram occurs in a similarity σ of length m. It is useful to define the complementary function $\bar{t}_Q^m$, counting how many times a Q-gram does not occur in a similarity σ, as

$$\bar{t}_Q^m(\sigma) = m - s(Q) + 1 - t_Q^m(\sigma) \tag{4.9}$$

Analogously, I define a pseudo-boolean function for a Q-gram family F

$$t_F^m(\sigma) = \sum_{Q_i \in F} t_{Q_i}^m(\sigma) \tag{4.10}$$

along with its complementary function

$$\bar{t}_F^m(\sigma) = \sum_{Q_i \in F} (m - s(Q_i) + 1) - t_F^m(\sigma) \tag{4.11}$$

The above functions expose important properties which let me devise approximate solutions. *Nondecreasing monotonicity* of functions t_Q^m and t_F^m follow from nondecreasing monotonicity of their boolean counterparts T_Q^m and T_F^m. Consequently $\bar{t}_Q^m$ and $\bar{t}_F^m$ are *monotone nonincreasing*. From definition **??**, function t_Q^m is *supermodular*, thus it follows that $\bar{t}_Q^m$ is *submodular*. Since super and submodular functions are closed under nonnegative linear combination, functions t_F^m and $\bar{t}_F^m$ are respectively super and submodular.

4.4.2 Full-sensitivity

NON DETECTION [Nicolas and Rivals, 2005]. Does a given Q-gram yield a full-sensitive filter for k-mismatches?

Problem definition

Instance A Q-gram, two integers m, k with $0 < k < m$.
Question Does it exist a similarity $\sigma \in \mathbb{B}_k^m$ such that $T_Q^m(\sigma)$ is false?

Hardness results

NON DETECTION is *strongly* NP-complete [Nicolas and Rivals, 2005]. Nicolas and Rivals introduce an intermediate problem, called SOAPY SET COVER. They reduce EXACT COVER BY 3-SETS to SOAPY SET COVER and SOAPY SET COVER to NON DETECTION. Strong NP-completeness implies that no *FPTAS* nor any *pseudo-polynomial* algorithm for it exist, under the assumption that $P \neq NP$.

4.4.3 Optimal threshold

Which is the highest Q-gram threshold t that guarantees full-sensitivity? This problem has been introduced in [Burkhardt and Kärkkäinen, 2001].

Problem definition

Instance A Q-gram, two integers m, k such that $0 < k < m$.
Solution The largest integer t^* such that NON DETECTION for $(Q, t^*), m, k$ answers *no*.

Recalling Q-gram pseudo-boolean functions 4.8, I can define the optimal threshold problem as the minimization of a supermodular function subject to linear constraints

$$\begin{aligned} \min \quad & t_Q^m(\sigma) \\ w.r.t. \quad & \\ & \sigma \in \mathbb{B}_k^m \end{aligned} \tag{4.12}$$

Exact DP solution

Optimal threshold is fixed-parameter tractable (FPT) in the span of the q-gram shape. Burkhardt and Kärkkäinen give a DP algorithm computing the optimal threshold in time

$O(m \cdot k \cdot 2^{s(Q)})$ [Burkhardt and Kärkkäinen, 2001]. Kucherov *et al.* give an extension for Q-gram families [Kucherov *et al.*, 2005].

Exact ILP solution

I reduce this problem to *maximum coverage* [Vazirani, 2001] and solve it with the following ILP

$$\begin{aligned} \max \quad & |c|_1 \\ w.r.t. \quad & \\ & \sigma \in \mathbb{B}_k^m \\ & c \in \mathbb{B}^{m-s(Q)+1} \\ & \sigma_i \geq c_j \end{aligned} \tag{4.13}$$

where variable c_j indicates the truthfulness of the j-th clause in T_Q^m. The optimal threshold $t^* = |c^*|_1$ is then obtained from the ILP solution c^*.

APX solution

I reduce the complementary optimal threshold problem to the maximization of a submodular function subject to linear constraints

$$\begin{aligned} \max \quad & \bar{t}_Q^m(\sigma) \\ w.r.t. \quad & \\ & \sigma \in \bar{\mathbb{B}}_k^m \end{aligned} \tag{4.14}$$

where the complementary optimal threshold is $\bar{t}^* = m - s(Q) + 1 - t^*$.

I compute an approximate solution via deepest descent. My greedy algorithm for complementary Optimal Threshold has an APX-ratio of $1 + 1/e$ [Vazirani, 2001]. The same *absolute error* applies to Optimal Threshold.

4.4.4 Maximum error

Which is the maximum error k^* for which full-sensitivity is guaranteed?

Problem definition

Instance A Q-gram, an integer $m > 0$.

Solution The largest integer k^* such that Non Detection for Q, m, k^* answers *no*.

Recalling pseudo-boolean functions 4.8, I define this problem as the minimization of a linear function subject to submodular constraints

$$\begin{aligned} \min \quad & |\sigma|_1 \\ w.r.t. \quad & \\ & \sigma \in \mathbb{B}^m \\ & \bar{t}_Q^m(\sigma) \leq 0 \end{aligned} \tag{4.15}$$

ILP solution

I reduce the problem to Minimum Set Cover [Vazirani, 2001], solve it with the following ILP

$$\begin{aligned} &\min && |\sigma|_1 \\ &w.r.t. && \\ & && \sigma \in \mathbb{B}^m \\ & && b \in \mathbb{B}^{m-s(Q)+1} \\ & && A\sigma \geq b \end{aligned} \tag{4.16}$$

where the value A_{ij} of the coefficient matrix A is defined as

$$A_{ij} = \begin{cases} 1 & \text{if } i-j+1 \in Q \\ 0 & \text{if } i-j+1 \notin Q \end{cases} \tag{4.17}$$

and find the maximum error for which full-sensitivity is guaranteed as $k^* = |\bar{\sigma}^*|_1$ given the solution σ^* to the ILP.

Contiguous q-grams provide an interesting special case of this ILP. If A has the *consecutive ones property*, it is *totally unimodular*. The *polytope* defined by a totally unimodular coefficient matrix is *integral*. Hence the optimal solution of the relaxed LP is also the optimal solution of the original ILP.

APX solution

Again, I compute an approximate solution via deepest descent. APX-ratio of $H_{w(Q)}$ [Vazirani, 2001].

4.4.5 Specificity

How many false positives the filter produces?

Problem definition

Instance A Q-gram, two integers m, k such that $0 < k < m$.

Solution The number of false positives produced by the Q-gram.

False positives are true points of the boolean function 4.6 which have weight inferior to $m-k$ and satisfy more than t clauses of $T^m_{Q^t}$. Hence, I define the function FP^m_k counting the number of false positives of filter (Q,t) in instance (m,k) as

$$\mathrm{FP}^m_k(Q,t) = \sum_{\sigma \in \mathbb{B}^m_k} T^m_{Q,t}(\sigma) \tag{4.18}$$

FPRAS solution

I reduce counting false positive transcripts to counting the number of true assignments of a boolean function in DNF. Karp *et al.* introduce a *fully polynomial-time randomized*

approximation scheme (FPRAS) to count the number of true assignments of a DNF [Karp *et al.*, 1989]. This method is importance sampling [Vazirani, 2001].

Part II

READ MAPPING

CHAPTER

5 Background

5.1 High-throughput sequencing data

5.1.1 Read sequences

Illumina

Illumina / Solexa.

Ion Torrent

Life Technologies / Ion Torrent.

Other technologies

Roche / 454 Life Sciences.
SOLiD

5.1.2 Phred base quality scores

Phred base quality scores have been introduced in [Ewing *et al.*, 1998; Ewing and Green, 1998] to assess the quality of sequencing single bases in capillary reads. Instead of directly discarding low-quality regions present in capillary reads, the tool Phred calls each base and annotates it with a quality score encoding the probability that it has been wrongly called. As this method has been widely accepted, base callers annotate reads issue of all sequencing technologies with Phred base quality scores.

To formally define Phred base quality scores, let us fix the alphabet $\Sigma = \{ \text{A, C, G, T} \}$, and consider a known donor genome g over Σ and a read r sequenced at location l from the template $g_{l \dots l+|r|-1}$. The base calling error ϵ_i, at position i in the read r, is defined as the probability ϵ_i of miscalling a base r_i instead of calling its corresponding base g_{l+i-1} in the donor genome. Therefore, the Phred base quality Q_i at position i is:

$$Q_i = -10 \log_{10} \epsilon_i. \tag{5.1}$$

Given the above, the probability $p(r_i | g_{l+i-1})$ of calling the base r_i in the read r, given

the donor genome base g_{l+i-1}, is:

$$p(r_i|g_{l+i-1}) = \begin{cases} 1-\epsilon_i & \text{if } g_{l+i-1} = r_i \\ \frac{\epsilon_i}{|\Sigma|-1} & \text{if } g_{l+i-1} \in \Sigma \setminus \{r_i\} \end{cases} \tag{5.2}$$

and assuming i.i.d. base calling errors, it follows that the probability $p(r|g,l)$ of observing the read r, given the donor genome template $g_{l\ldots l+|r|-1}$, is:

$$p(r|g,l) = \prod_{i=1}^{|r|} p(r_i|g_{l+i-1}) \tag{5.3}$$

5.2 Data analysis paradigms

The goal of secondary analysis is to reconstruct the original sequence of the donor genome. The *reference-guided* assembly plan assumes a prior knowledge of a reference genome similar to the donor. Reads are thus mapped (i.e. aligned) to the reference genome w.r.t. a given scoring scheme and threshold. The scoring scheme should account for eventual genomic variation, as well as for any sequencing artefacts. An alignment of optimal score for a read implies its *original location* on the reference genome. Conversely, no alignment within the score threshold implies too many sequencing errors, too much genetic variation, or sample contamination. A problem arises in presence of co-optimal or close sub-optimal alignments: the read cannot be mapped confidently.

The problem of confidently mapping high-throughput sequencing reads comes from the non-random nature of genomic sequences. Genomes evolved through multiple types of duplication events, including whole-genome duplications [Wolfe and Shields, 1997; Dehal and Boore, 2005] or large-scale segmental duplications in chromosomes [Bailey *et al.*, 2001; Samonte and Eichler, 2002], transposition of repetitive elements as short tandem repeats (microsatellites) [Wang *et al.*, 1994; Wooster *et al.*, 1994] and interspersed nuclear elements (LINE, SINE) [Smit, 1996], proliferation of repetitive structural elements such as telomeres and centromeres [Meyne *et al.*, 1990]. As a result of these events, for instance, about 50 % of the human genome is composed of repeats.

Repeats present in general technical challenges for all *de novo* assembly and sequence alignment programs [Treangen and Salzberg, 2011]. Due to repetitive elements, a non-ignorable fraction of high-throughput sequencing reads cannot be mapped confidently. In general, the shorter the reads, the higher the challenges due to repeats. I quantify this phenomenon more precisely in section 5.3. Here I focus on analysis strategies to deal with *multi-reads*, i.e. reads that cannot be mapped confidently as they align equally well to multiple locations.

It is not evident how to treat *multi-reads*. According to Treangen and Salzberg, common strategies to deal with multi-reads are (i) to discard them all, (ii) to randomly pick one best mapping location, (iii) to consider all or up to k best mapping locations within a given distance threshold. A *de facto* standard strategy emerged over the last years, combining strategies i and ii. The read mapper randomly picks one best mapping location and complements it with its *mapping quality*, i.e. the probability of the mapping location

being correct (see section **??**). Subsequently, downstream analysis tools apply a mapping quality score cutoff to discard reads not mapping confidently to any location. The other popular strategy adopted by analysis tools is to consider all mapping locations within an edit distance threshold. In this case, it is not clear whether downstream analysis tools consider equally all mapping locations regardless of their distance.

In the light of these facts, I define two broad paradigms for the secondary and tertiary analysis of HTS data: *best-mapping* and *all-mapping*. The best-mapping paradigm considers a single mapping location per read along with its confidence, while the all-mapping paradigm considers a comprehensive set of mapping locations per read. It goes without saying that read mapper and downstream analysis tools must agree on a common paradigm. Thus these paradigms are valid not only for read mappers but also for any downstream analysis tool, e.g. variant callers. Read mapping and variant calling are indeed tightly coupled steps within reference-based HTS pipelines.

5.2.1 Best-mapping

As said, best-mapping methods rely on one single mapping location per read. In order to maximize recall, best-mappers often adopt complex scoring schemes taking into account gaps and base quality values, and at the same time implement sophisticate heuristics to speed up the search. Best-mappers should always complement any mapping location with its mapping quality. Subsequently, in order to maximize precision, variant calling tools decide whether to consider or discard reads not mapping confidently to any location. The GATK [DePristo *et al.*, 2011] and Samtools [Li *et al.*, 2009a] are popular best-mapping tools to call small variants. In section **??**, I show how these methods are limited to the analysis of high mappability regions, as they systematically discard reads belonging to low mappability regions.

Mapping quality score

Mapping quality has been introduced in [Li *et al.*, 2008]. The study considers short reads of length ranging from 30 bp to 40 bp, produced by early Illumina/Solexa and ABI/SOLiD sequencing technologies, whose sequencing error rates were quite high. Given the short lengths and high error rates, a significant fraction of such reads can be aligned to multiple mapping locations, even considering only co-optimal Hamming distance locations.

The key point is that the Hamming distance is not an adequate scoring scheme to guess the correct mapping location of many reads. Li *et al.* claim that: *it is possible to act conservatively by discarding reads that map ambiguously at some level, but this leaves no information in the repetitive regions and it also discards data, reducing coverage in an uneven fashion, which may complicate the calculation of coverage.* However, they do not show in their study what is the effect of relying on mapping quality rather than on mapping uniqueness.

Since base callers output base call probabilities in Phred-scale along with the reads, Li *et al.* propose a novel probabilistic scoring scheme called mapping quality, giving the probability that a given read has been aligned correctly at a given mapping location in

the reference genome.

The posterior probability $p(l|g,r)$, that location l in the reference genome g is the correct mapping location of read r, is derived by applying Bayes' theorem. Assuming uniform coverage, each location $l \in [1, |g| - |r| + 1]$ has equal probability of being the origin of a read in the donor genome, thus the prior probability $p(l)$ is simply:

$$p(l) = \frac{1}{|g| - |r| + 1} \tag{5.4}$$

Therefore, recalling $p(r|g,l)$ from equation 5.3, the posterior probability $p(l|g,r)$ equals the probability of the read r originating at location l normalized over all possible locations in the reference genome:

$$p(l|g,r) = \frac{p(r|g,l)}{\sum_{i=1}^{|g|-|r|+1} p(r|g,i)} \tag{5.5}$$

which in Phred-scale becomes:

$$Q(l|g,r) = -10 \log_{10}[1 - p(l|g,r)] \tag{5.6}$$

Computing the exact mapping quality as in equation 5.6 requires aligning each read to all positions in the reference genome. On one hand, this computation would not be practical, indeed the vast majority of a reference genome is discarded when mapping reads by means of filtering and fully-indexed methods. On the other hand, the contribution of discarded locations to the sum in equation 5.5 can be neglected. Therefore, equation 5.5 is approximated using only relevant mapping locations found by the read mapper.

Mapping quality has been initially used in [Li *et al.*, 2008] and [Li and Durbin, 2009] to maximize variant calling confidence by discarding reads whose best mapping location is below a given mapping quality threshold. This measure has been widely accepted: nowadays it is computed by most popular read mappers and used by almost all variant calling tools e.g. the Genome Analysis ToolKit (GATK) [DePristo *et al.*, 2011].

Nonetheless, some important objections can be moved against mapping quality. First, the mapping quality score is derived under the unlikely assumption of the reference genome being equal to the donor genome. In other words, mapping quality considers only errors due to base miscalls and disregards genetic variation; thus the risk is to prefer mapping locations supported by known low base qualities rather than by true but unknown SNVs. Second, mapping quality is nonetheless strongly correlated to mapping uniqueness, as discussed in section 5.3; it is easy to see that the mapping probability in equation 5.5 is diluted in presence of a large number of co-optimal mapping locations. Third, mapping quality tends to become less relevant as base calls improve, due to advances of sequencing technologies, and thus degenerates in a shallow measure of uniqueness.

5.2.2 All-mapping

All-mapping analysis methods consider a comprehensive set of locations per read. Almost all read mappers in this category adopt edit distance, the simplest scoring scheme,

and report all mapping locations within an error threshold, absolute or relative w.r.t. to the length of the reads. Variant calling algorithms based on all-mapping have the potential to detect a wider spectrum of genomic variation events than in best-mapping. For instance, variant callers based on the all-mapping paradigm detect CNVs [Alkan *et al.*, 2009], and SNVs in homologous regions [Simola and Kim, 2011]. A practical challenge of all-mapping is represented by reporting and handling huge sets of mapping locations.

5.3 Limits of high-throughput sequencing

Due to repetitive elements, a non-ignorable fraction of high-throughput sequencing reads cannot be mapped confidently. Which regions of a model organism's genome cannot be resequenced confidently by a high-throughput sequencing technology? And how accurate is downstream analysis on these low confidence regions? Two recent studies [Derrien *et al.*, 2012; Lee and Schatz, 2012] answer these questions. Below, I report their key ideas and most relevant findings.

5.3.1 Genome mappability

In [Derrien *et al.*, 2012], *genome mappability* is defined for a given q-gram length, a distance measure i.e. the Hamming or edit distance, and a distance threshold k. Given a genomic sequence g, the (q,k)-frequency $F_k^q(l)$ of the q-gram $g_{l\ldots l+q-1}$ at location l in g denotes the number of occurrences of the q-gram in g and its reverse complement $\bar{g}$. The (q,k)-mappability $M_k^q(l)$ is the inverse (q,k)-frequency, i.e. $M_k^q(l) = F_k^q(l)^{-1}$ with $M_k^q : \mathbb{N} \rightarrow]0,1]$. Note that $M_k^q(l)$ can be seen as the prior probability that any read of length q originating at location l will be mapped correctly. The values of (q,k)-frequency and mappability obviously vary with the distance threshold k. Nonetheless, under any distance measure, it hold that the q-gram at location l is unique up to distance k iff $M_k^q(l) = 1$ and repeated otherwise.

Unique mappability determines which fraction of a genome can be analyzed according to strategy i (i.e. discarding non-unique reads, see section 5.2). Derrien *et al.* quantify the *unique mappability* of whole human, mouse, fly, and worm genomes. Mimicking typical Illumina read mapping setups, they consider q-grams of length 36, 50 and 75 bp, and Hamming distance 2. They find out that about 30 % of the whole human genome is not unique w.r.t. $(36,2)$-mappability. At $(75,2)$-mappability, 17 % of the human genome is not yet unique. This last result is quite optimistic, as typical mapping setups call for 3–4 edit distance errors in order to map a significant fraction of the reads. Table shows some results extrapolated from [Derrien *et al.*, 2012].

To estimate resequencing accuracy at a single location, Derrien *et al.* consider the mappability of all possible q-grams spanning it. They define *pileup mappability* P_k^q at position i as the average mappability of all q-grams spanning position i, i.e.:

$$P_k^q(i) = 1/q \sum_{j=i}^{i+1} M_k^q(j) \tag{5.7}$$

Table 5.1: *Mappability of model genomes. Data extrapolated from [Derrien* et al.*, 2012].*

	H.sapiens (hg19)	M.musculus (mm9)	D.mel (dm3)
Repeats content [%]	45.25	42.33	26.50
Uniqueome (36 bp, 2 msm) [%]	69.99	72.07	68.09
Uniqueome (50 bp, 2 msm) [%]	76.59	77.06	69.44
Uniqueome (75 bp, 2 msm) [%]	83.09	81.65	71.00

Derrien *et al.* find out in their own resequencing studies that *low pileup-mappability regions are more prone to show a high value of heterozygosity than those with high mappability* [Derrien *et al.*, 2012]. Variant callers ideally call a locus heterozygous whenever its consensus alignment column, consisting of piled up reads, contains two distinct bases. This situation tends to arise whenever the consensus alignment contains reads originating from similar yet distinct regions.

5.3.2 Genome mappability score

Genome mappability score (GMS) [Lee and Schatz, 2012], analogously to pileup mappability, estimates single-locus resequencing accuracy for a specific sequencing technology. Instead of considering the inverse q-gram frequency, Lee and Schatz use mapping quality (see subsection 5.2.1) to estimate the probability that a read originating at a given position can be mapped correctly. Subsequently, they derive average mapping probability of any read spanning a location l of a reference genome g as[1]:

$$p(l|g) = \sum_{r \in \mathcal{R}(l)} \frac{p(l|g,r)}{|\mathcal{R}(l)|} \tag{5.8}$$

which in Phread-scale becomes:

$$Q(l|g) = \sum_{r \in \mathcal{R}(l)} \frac{1 - 10^{-\frac{Q(l|g,r)}{10}}}{|\mathcal{R}(l)|} \tag{5.9}$$

Thus, fixed a genomic sequence g, they define the genome mappability score $\mathrm{GMS}(l)$ in percentual value:

$$\mathrm{GMS}(l) = 100\, Q(l|g) \tag{5.10}$$

Lee and Schatz proceed as follow to compute GMS. They first simulate reads from all genomic locations, having length and error profiles similar to those issue by actual sequencing technologies. Subsequently, they compute mapping quality scores by mapping

[1] Equation 3 in [Lee and Schatz, 2012] is not precise, please consider equation 5.8 instead.

all simulated reads with BWA (see section **??**). Then, as just explained, they compute GMS at any location by averaging the quality scores. Finally, they define *low GMS* regions as those locations for which GMS(l) ≤ 10, and *high GMS* otherwise. Table **??** shows performance of various sequencing technologies on the whole human genome (data extrapolated from [Lee and Schatz, 2012]).

Table 5.2: *Human genome mappability score of various sequencing technologies. Data extrapolated from [Lee and Schatz, 2012].*

Sequencing technology	Read length [bp]	Error rate [%] (msm, ins, del)	Low GMS [%]	High GMS [%]
Illumina-like	100	(0.10, 0.00, 0.00)	10.51	89.49
Ion Torrent-like	200	(0.04, 0.01, 0.95)	9.35	90.65
Roche/454-like	800	(0.18, 0.54, 0.36)	8.91	91.09
PacBio-like	2000	(1.40, 11.47, 3.43)	100.0	0.00
PacBio EC-like	2000	(0.33, 0.33, 0.33)	8.61	91.39

Lee and Schatz simulate an Illumina-like resequencing study. They measure variant calling accuracy by GMS for the popular combination of best-mapping tools BWA and SAMtools [Li *et al.*, 2009a]. They find out that at 30 × sequencing coverage accuracy tends to 100 % in high GMS regions, while it levels off to 25 % in low GMS regions. Their analysis *shows that most SNP detection errors are false negatives, and most of the missing variations are in regions with low GMS scores* [Lee and Schatz, 2012]. These are the limits of *de facto* standard tools for the analysis of high-throughput sequencing data.

5.4 Popular read mappers

Following the boom of NGS technologies, recent bioinformatics research has produced dozens of tools to perform read mapping. Two surveys [Li and Homer, 2010; Fonseca *et al.*, 2012] try to help bioinformaticians to extricate themselves from the jungle of read mapping tools. The survey by Li and Homer first classifies read mapping algorithms by data structure: those based on hash tables and those based on suffix/prefix trees. However, the adopted data structure is often an implementation detail, indeed most algorithms covered in the survey fit into both classes. The survey primarily considers the application of SNP calling; in the considered setup, tools enumerating a comprehensive set of locations always lag behind those designed to report only one location per read. The survey by Fonseca *et al.* catalogs read mappers by the features exposed to the user. It considers supported input–output formats, rate of errors and variation, number and type (i.e. local or semi-global read alignments) of mapping locations reported. After this exhaustive catalog, the survey concludes that the choice of a read mapper *involves application-specific requirements such as how well it works in conjunction with downstream analysis tools (i.e. variant callers)*.

Read mapping and variant calling are indeed tightly coupled steps within reference-based HTS analysis pipelines. Secondary and tertiary analysis methods are based on one of the two following paradigms: best-mapping and all-mapping. In the light of the above consideration, the most important feature of a read mapper is the number of mapping locations reported, followed by their type, while the other features are mostly of technical relevance. Most read mappers are specifically designed to fit one paradigm, while others are versatile enough to work well in both cases.

The rest of this section presents most popular read mapping tools. Among them, BWA [Li and Durbin, 2009, 2010], Bowtie [Langmead *et al.*, 2009; Langmead and Salzberg, 2012] and Soap [Li *et al.*, 2009b] are prominent tools designed for best-mapping, while mr(s)Fast [Alkan *et al.*, 2009; Hach *et al.*, 2010], RazerS [Weese *et al.*, 2009, 2012], SHRiMP [Rumble *et al.*, 2009; David *et al.*, 2011] are designed for all-mapping. Grosso modo, most prominent best-mappers recursively enumerate substrings on a suffix/prefix tree of the reference genome via backtracking algorithms. Backtracking alone is impractical as its time complexity grows exponentially with the number of errors considered, hence best-mappers apply heuristics to reduce and prioritize enumeration. Conversely, all-mappers are based on filtering algorithms for approximate string matching. They quickly determine, often with the help of an index, locations of the reference genome candidate to contain approximate occurrences, then verify them with conventional methods. Their efficiency is bound to filtration specificity and thus deteriorates with increasing error rates and genome lengths. Finally, the most recent tools GEM [Marco-Sola *et al.*, 2012], Masai [Siragusa *et al.*, 2013], and Yara, fit both best and all-mapping paradigms. They speed up best-mapping by stratifying mapping locations by edit distance and prioritizing filtration accordingly. In addition to that, they also speed up all-mapping by means of more specific filters based on backtracking.

5.4.1 Bowtie

Bowtie [Langmead *et al.*, 2009] is a mapper designed to have a small memory footprint and quickly report a few good mapping locations for early generation Illumina/Solexa and ABI/SOLiD short reads of length up to 50 bp. It achieves the former goal by indexing the reference genome with an FM-index and the latter goal by performing a greedy depth-first traversal on it.

The greedy depth-first traversal visits first the subtree yielding the least number of mismatches and stops after having found a candidate (not guaranteed to be optimal when $k > 1$). In addition, Bowtie speeds up backtracking by applying case pruning, a simple application of the pigeonhole principle. However this technique is mostly suited for $k = 1$ and requires the index of the forward and reverse text.

Bowtie can be configured to search by strata, however the search time increases significantly while the traversal still misses a large fraction of the search space due to seeding heuristics. Main practical drawbacks of the tool are too many cryptic options.

Bowtie 2 [Langmead and Salzberg, 2012] has been designed to quickly report a couple of mapping locations for recent Illumina/Solexa, Ion Torrent and Roche/454 reads, usually having lengths in the range from 100 bp to 400 bp.

This tool uses an heuristic seed-and-extend approach, collecting seeds of fixed length, partially overlapping, and searching them exactly in the reference genome using an FM-index. Candidate locations to verify are chosen randomly, to avoid uncompressing large CSA intervals and executing many DP instances. Each mapping location is verified using a striped vectorial dynamic programming algorithm, implemented using SIMD instructions, previously introduced by [Farrar, 2007] and extended to compute end-to-end alignments.

Bowtie 2 can be configured to report end-to-end or local alignments, scored using a tunable affine scoring scheme. For this reason, it is believed to be good at reporting alignments containing indels. However, its completely heuristic filtration method, independent of the scoring scheme, makes it hard to believe what it promises.

5.4.2 BWA

BWA [Li and Durbin, 2009] is designed to map Illumina/Solexa reads up to 100 bp and report a few best end-to-end alignments. The program performs a greedy breadth-first search on an FM-index of the reference genome. Nodes to be visited are ranked by edit distance score: the best node is popped from a priority queue and visited, its children are then inserted again in the queue. The traversal considers indels using a more involved 9-fold recursion. Backtracking is sped up by adopting a more stringent pruning strategy that nonetheless takes some preprocessing time and requires the index of the reverse reference genome.

BWA performs paired-end alignments by trying to anchor both paired-end reads and verifying the corresponding mate, within an estimated insert size, using the classic DP-based Smith-Waterman algorithm. Consequently, the program in paired-end mode aligns reads at a slower rate than in single-end mode. The program is not fully multi-threaded, therefore BWA scales poorly on modern multi-core machines.

BWA-SW [Li and Durbin, 2010] is designed to map Roche/454 reads, which have an average length of 400 bp. It is an heuristic version of BWT-SW, designed to report a few good local alignments.

This version of BWA adopts a double indexing strategy: it indexes all substrings of one read in a DAWG. It performs Smith-Waterman of all read substrings directly on the FM-index, by backtracking as soon as no viable alignment can be obtained. As in BWA-backtrack, the traversal proceeds in a greedy fashion. In addition, BWA-SW implements some seeding heuristics to limit backtracking and jump in the reference genome to verify candidate locations whenever this becomes favorable.

This version of BWA does not support paired-end reads, presumably because it was meant for Roche/454 reads.

5.4.3 Soap

Soap 2 [Li *et al.*, 2009b] is very similar to Bowtie: it has been designed to produce a very quick but shallow mapping of Illumina/Solexa reads up to 75 bp with no more than 2 mismatches and no indels. However, its underlying algorithm is based on the so-called

bi-directional (or 2-way) BWT. The tool support paired-end mapping but at a slower alignment rate. Practical drawbacks are the lack of native output in the de-facto standard SAM format and is closed source. Soap 3 [Liu *et al.*, 2012] is algorithmically similar to Soap 2 but targets only NVIDIA CUDA accelerators.

5.4.4 SHRiMP

SHRiMP 2 TODO.

5.4.5 RazerS

RazerS [Weese *et al.*, 2009] has been designed to report all mapping locations within a fixed hamming or edit distance error rate. It is based on a full-sensitive q-gram filtration method (SWIFT semi-global) combined with the Myers edit distance verification algorithm. On demand, the SWIFT filter can be configured to become lossy within a fixed loss rate. The lossy filter becomes more stringent and produces a lower number of candidates to verify, thus improving the overall speed of the program. All in all, the SWIFT filter is very slow while not highly specific.

RazerS 3 [Weese *et al.*, 2012] is a faster version featuring shared-memory parallelism, a faster banded-Myers verification algorithm, and a faster filtration scheme based on exact seeds that however turns out to be very weak on mammal genomes. Because of this, RazerS 3 is one-two orders of magnitude slower than Bowtie 2 and BWA-backtrack on mammal genomes.

All RazerS versions index the reads and scan the reference genome. One positive aspect of this strategy is that no preprocessing of the reference genome is required. However, other mapping strategies beyond all-mapping, e.g. mapping by strata, cannot be efficiently implemented. Moreover, the program exhibit an high memory footprint as it must remember the mapping locations of all input reads until the whole reference genome has been scanned.

5.4.6 mr(s)Fast

The tools mrFast [Ahmadi *et al.*, 2012] and mrsFast [Hach *et al.*, 2010] are designed to report all mapping locations within a fixed absolute number errors, respectively under the hamming and edit distance, given Illumina/Solexa reads of length ranging from 50 bp to 125 bp. Similarly to RazerS 3, they are based on a full-sensitive filtration method using exact seeds, which turns out to be very weak on mammal genomes.

The peculiarity of their underlying method is a cache-oblivious strategy to mitigate the high cost of verifying clusters of candidate locations. In addition, mrsFast computes the edit distance between one read and one mapping location in the reference genome with an antidiagonal-wise vectorial dynamic programming algorithm, implemented using SIMD instructions.

These tools are as slow as RazerS 3 and appealing for nothing more than all-mapping.

They lack multi-threading support and exhibit various bugs. Furthermore, they only accept reads of fixed length and produce files of impractical size.

5.4.7 GEM

The GEM mapper [Marco-Sola *et al.*, 2012] is a flexible read aligner for Illumina/Solexa, ABI/SOLiD, and Ion Torrent reads. It is full-sensitive and can be configured either as an all-mapper, as a best/unique-mapper, or to search by strata.

GEM uses a combination of state of the art approximate string matching methods, e.g. approximate seeds and suffix filters. The program indexes the reference genome with an FM-index, tries to find an optimal filtration scheme per read, and verifies candidate locations using Myers algorithm. Paired-reads are either mapped independently and then combined, or left/right are mapped and their mates verified using an online strategy.

Unfortunately the tool lacks direct SAM output, it is not open source, and provides many obscure parameters.

	sequencer			paradigm			alignment			index		
	Illumina	Ion	454	best	strata	all	type	optimal	method	type	reference	reads
Bowtie	≤ 75 bp	✗	✗	✓	✓	•	mismatches	✗	backtracking	FM-index	✓	✗
Bowtie 2	≥ 75 bp	✓	✓	✓	✗	✗	local	✗	exact seeds	FM-index	✓	✗
BWA	✓	✗	✗	✓	✗	•	indels	✗	backtracking	FM-index	✓	✗
BWA-SW	✗	✓	✓	✓	✗	✗	local	✗	backtracking	FM-index	✓	✓
Soap 2	≤ 75 bp	✗	✗	✓	✓	•	mismatches	✗	backtracking	FM-index	✓	✗
RazerS	✓	✗	✗	✗	•	✓	indels	✓	q-grams	q-gram index	✗	✓
RazerS 3	✓	✓	✗	✗	•	✓	indels	✓	exact seeds	q-gram index	✗	✓
SHRiMP 2	✓	✓	✓	✓	✗	✓	local	✗	q-grams	q-gram index	✓	✗
mrsFast	≤ 75 bp	✗	✗	✗	✗	✓	mismatches	✓	exact seeds	q-gram index	✓	✓
mrFast	≤ 125 bp	✗	✗	✗	✗	✓	indels	✓	exact seeds	q-gram index	✓	✓
GEM	✓	✓	✗	✓	✓	✓	indels	✓	apx seeds	FM-index	✓	✗
Masai	✓	✗	✗	•	✗	✓	indels	✓	apx seeds	generic	✓	✓
Yara	✓	✓	✗	✓	✓	✓	indels	✓	apx seeds	FM-index	✓	✗

CHAPTER

6 Masai

In this chapter I present my first attempt to engineer an efficient all-mapper. When I started this project, in October 2011, the fastest all-mappers (mrFast and RazerS 3) were two order of magnitude slower than prominent best-mappers (Bowtie and BWA). On one hand, all-mappers were using filtration based on exact seeds, which is fine for short reference genomes but becomes too weak for mammal genomes; clearly, a stronger filtration method would had been beneficial. On the other hand, best-mappers were based on heuristic backtracking, which was becoming inadequate to map reads of increasing length. After a thorough literature review, I came out with a novel read mapping method combining seed-based filtering with backtracking, published in [Siragusa *et al.*, 2013].

In the engineering section, I expose how Masai's filtration method works, which data structures it uses for indexing, and how it performs seed extension. In particular, the filtration method is based on exact or approximate seeds: by employing approximate seeds instead of exact seeds, the tool obtains a stronger filtration for long reference genomes, which is still non-heuristic and quasi full-sensitive. Masai find approximate seeds by backtracking the index of the reference genome. Moreover, the tool speeds up the backtracking phase by searching all seeds simultaneously, with the help of an additional index and the multiple backtracking algorithm. Lastly, Masai implements a method to perform best-mapping in a more efficient way.

My method is packaged in a C++ tool nicknamed *Masai*, which stands for *m*ultiple backtracking of *a*pproximate seeds on a *s*uffix *a*rray *i*ndex. Masai is part of the SeqAn library, it is distributed under the BSD license and can be downloaded from `http://www.seqan.de/projects/masai`.

In the evaluation section, I extensively compare Masai with popular read mappers, both on simulated and real datasets. Compared to all-mappers mrFast and RazerS 3, Masai is an order of magnitude faster and has comparable sensitivity. In addition, Masai as a best-mapper is 2–4 times faster and more accurate than Bowtie 2 [Langmead and Salzberg, 2012] and BWA [Li and Durbin, 2009]. Finally, I discuss the limitations of Masai that led us to engineer Yara, yet another read aligner.

6.1 Engineering

I start by giving an outline of the read mapping method of Masai. Later, I give a detailed explanation of each mapping step, explaining and motivating relevant engineering

choices that led us to the final implementation.

Masai requires an index capable of simulating a top-down traversal of the suffix trie of the reference genome. The tool gives to users the possibility to choose among various indices (see section 6.1.2). Similarly to all read mappers relying on an index of the reference genome, the tool indexes the reference genome only once, stores it on disk and reuses it for all subsequent read mapping jobs.

At mapping time, Masai requires two parameters to be provided: a maximum number of errors per read and a minimum seed length. Default parameters work well for actual Illumina reads, otherwise the user has to parametrize adequately the tool for optimal performance. Nonetheless, independently of the chosen parameterization, filtration is guaranteed to be quasi full-sensitive (see section 6.1.1).

Masai partitions all reads (and their reverse complements) in non-overlapping seeds and subsequently arranges all seeds in a conceptual *trie*. Using the *multiple backtracking* algorithm of section **??**, the tool backtracks simultaneously all indexed seeds in the suffix trie of the reference genome. The program performs seed extension on all hits reported by the multiple backtracking algorithm; it extends both ends of each seed using a banded version of *Myers bit-vector algorithm* [Myers, 1999] (details in section 6.1.3).

6.1.1 Filtration

My original intent was to improve the speed of the all-mapper RazerS [Weese *et al.*, 2009] while preserving full-sensitivity under the edit distance. RazerS was based on a q-gram filter; I as aware that gapped q-grams could have brought a huge speedup, but I could not see any straightforward generalization of gapped q-grams to the edit distance. At the same time, I experienced that weaker but quicker filtration using exact seeds was more advantageous than filtration using q-grams (indeed, a typical Illumina read mapping setup requires only moderate error rates, in the range of 4–6 %). Thus RazerS 3 [Weese *et al.*, 2012] went back to filtration with exact seeds (similarly to mrFast). Nonetheless, I wanted to improve again filtration specificity, as the runtime of RazerS 3 on mammal genomes became dominated by verifications, and I knew that to improve filtration specificity I had to increase the seed length, as these two things are strongly correlated.

While reviewing past literature in the field of approximate string matching, I rediscovered the works of Myers, Navarro and Baeza-Yates on approximate seeds, providing stronger filtration than exact seeds while preserving full-sensitivity under the edit distance. Their idea is to partition the pattern into $s \leq k + 1$ non-overlapping seeds, which obviously can be longer than exact seeds but have to be searched within distance $\lfloor k/s \rfloor$ (see section **??**).

Following [Navarro and Baeza-Yates, 2000], I decided to find approximate seeds by backtracking the suffix trie of the reference genome (in section 6.1.2 I recall my engineering work to find approximate seeds efficiently). For simplicity, I decided to find approximate seeds only under the hamming distance. For this reason, when resorting to approximate seeds, Masai does not attain strict full-sensitivity under the edit distance. Nonetheless, in section **??** I show that such implementation detail sacrifices less than 1% sensitivity.

Then, I slightly improved the filtration lemma of [Navarro and Baeza-Yates, 2000]: I search $(k \bmod s)+1$ seeds within distance $\lfloor k/s \rfloor$ and the remaining seeds within distance $\lfloor k/s \rfloor - 1$. To prove full-sensitivity it suffices to see that, if none of the seeds occurs within its assigned distance, the total distance must be at least $s \cdot \lfloor k/s \rfloor + (k \bmod s) + 1 = k + 1$. Hence all approximate occurrences will be found.

Finally, I chose to parameterize Masai's filter by the seed length rather than by the number of seeds. Clearly, these two parameterization are dual: if I choose the number of seeds to be s, the minimum seed length l has to be $\lfloor |r|/s \rfloor$; vice versa, if I fix the minimum seed length to l, the number of seeds s has to be $\lfloor |r|/l \rfloor$. Nonetheless I prefer the latter, as the minimum seed length gives us a direct estimate of the expected number of verifications produced by the filter. The resulting filter is flexible, indeed by increasing l filtration becomes more specific at the expense of a higher filtration time.

The optimal seed length l depends on the reference genome as well as on read length and the absolute number of errors. I experimentally evaluated filtration with exact and approximate seeds (see section **??**). When mapping current Illumina reads on short to medium length genomes, exact seeds are still more efficient than approximate seeds. Conversely, on larger genomes (e.g. mammalian genomes) approximate seeds outperform exact seeds by an order of magnitude.

Best-mapping

Masai is a tool designed primarily to perform all-mapping rather than best-mapping. In best-mapping, Masai simply reports the first optimal mapping location encountered per read. Clearly, this policy makes sense if the edit distance is effective at identifying original mapping locations. Section **??** shows that Masai is competitive in best-mapping with tools using more complex scoring schemes. Nonetheless, Masai's best-mapping method is ad-hoc and limited. In best-mapping, Masai does not produce mapping qualities, it does not even support paired-end and mate-pair protocols. The reader is thus referred to the next chapter (section 7.1) for the complete description of an efficient best-mapping method that, in standard scenarios, is an order of magnitude faster than all-mapping.

6.1.2 Indexing

Within the SeqAn library, I initially disposed of two indices capable of simulating a top-down suffix trie traversal: the enhanced suffix array (ESA) [Abouelhoda *et al.*, 2004] and the lazy suffix tree (LST) [Giegerich *et al.*, 1999]. To improve the efficiency of Masai, I implemented a generic top-down traversal for some additional indices, namely the suffix array (SA) [Manber and Myers, 1990], the q-gram index, and various flavours of the full-text minute index (FM-index) [Ferragina and Manzini, 2001]. Below I discuss the performance of these indices within Masai, while I refer the reader to chapter 3 for their extensive explanation.

Indexing the reference genome

I initially chose the ESA over LST because of better construction times. Indeed, I dispose of a linear time construction algorithm for the ESA (an adaptation of the DC7 algorithm [Dementiev *et al.*, 2008] to multiple sequences [Weese, 2013] for the generalized SA, followed by the algorithms proposed in [Kasai *et al.*, 2001; Abouelhoda *et al.*, 2004]), while the LST construction algorithm takes quadratic time (using the radix sort based *wotd*-algorithm [Giegerich *et al.*, 1999]). Apart from that, both ESA and LST implementations require 13 bytes per base pair and exhibit comparable query speed. Thus, for the human reference genome (GRCh38), I had a suffix trie constructed in about 1.5 hours and consuming 39 GB of memory (see figure **??**).

At this point, Masai required high-end hardware to process large reference genomes. Therefore, thinking of a space-time trade-off, I designed a generic suffix trie top-down traversal for the SA (see section **??**); indeed, the SA consumes only 5 bytes per base pair but is theoretically slower than the ESA, as it adds a logarithmic factor to query times. However, with surprise I found out that, within Masai, the SA had equal or better performance than the ESA (see figure **??**). Ultimately, I brought down the memory footprint of the index from 39 GB to 15 GB but preserved query speed.

I tried to further improve query speed by removing the logarithmic factor introduced by the SA. Therefore, to cut the most expensive binary searches, I put a q-gram index on top of the SA and extended my generic suffix trie top-down traversal accordingly (see section **??**). Yet, the q-gram index did not bring significant speedup to the application; indeed, the lookup table turned out to be useful when searching patterns one by one, but not when coupled with the multiple backtracking algorithm as it performs a factorization of the top-down traversal.

Finally, I explored additional space-time trade-offs. I started implementing[1] a generalized FM-index based on a wavelet tree [Grossi *et al.*, 2003]. This initial FM-index consumed about 1.5 bytes per base pair with a SA sampling of 10 %. Thus the memory footprint of the index went down to 4.5 GB, but Masai became significantly slower (less than twice as slow though).

In definitive, I prefer the SA as it provides a good compromise between query speed and memory consumption. Nevertheless, Masai leaves to the user the possibility to choose among the aforementioned data structures.

Indexing the reads

In order to improve index query speed, I designed and implemented an algorithm to search simultaneously many exact or approximate seeds, achieving a speedup of 3–5 times (see section **??**). As the multiple search algorithm requires a trie of the seeds, I also engineered an efficient trie implementation.

It was straightforward to reuse SeqAn's suffix trie implementations to emulate tries. It goes without saying that the easiest way to implement a trie is by means of a partial SA: I index only the first suffix of each seed in the collection and construct the SA-based

[1] Thanks to the master's thesis of Jochen Singer.

trie via quicksort in time $\mathcal{O}(n \log n)$, where n is the number of seeds; then, the top-down traversal based on binary search still works. I adapted the LST in an analogous way: I fill the partial SA as above and then apply the *wotd*-algorithm [Giegerich *et al.*, 1999] to construct the trie in linear time.

Quicksorting the SA turned out to be faster than radix sorting the LST but, within Masai, the more involved LST data structure payed off at query time (see section **??**). Indeed, the LST stores all trie nodes and thus provides node traversal in constant time, while the SA explicitly stores only the leaves and thus internal nodes have to be worked out via binary search. As the memory footprint of the trie is negligible within this application, I chose the LST to perform multiple backtracking of approximate seeds.

When performing multiple backtracking of exact seeds, the LST construction time dominates the overall filtration time (see section **??**). Therefore, I decided to resort to the *q-gram index* to emulate a trie in this case: I build a partial q-gram index efficiently and in linear time by bucket sort, again considering only the first suffix of each seed in the collection. Such index represents a trie truncated at depth q (which I fixed to 12 in Masai). Truncation is only a minor concern: at depth q the search continues via single backtracking algorithm on each active node.

6.1.3 Verification

To verify hits reported by the filtration algorithm, Masai employs a banded version of Myers bit-vector algorithm [Myers, 1999]. Myers' algorithm is an efficient DP alignment algorithm [Needleman and Wunsch, 1970] for edit distance. Instead of computing DP cells one after another, this algorithm encodes the whole DP column in two bit-vectors and computes the adjacent column in a constant number of 12 logical and 3 arithmetical operations. Within SeqAn, I disposed of a bit-parallel version that computes only a diagonal band of the DP matrix, faster and more specific than the original algorithm by Myers. More details can be found in section **??**.

RazerS 3 [Weese *et al.*, 2012] already used Myers' algorithm. However, instead of performing a semi-global alignment to verify a parallelogram surrounding the seed, Masai performs a global alignment on both ends of a seed. Given a seed occurring with e errors, Masai first performs seed extension on the left side within an error threshold of $k - e$ errors. Only if the seed extension on the left side succeeds, the tool performs a seed extension on the right side within the remaining error threshold. Moreover, Masai first computes the longest common prefix on each side of the seed and let the global alignment algorithm start from the first mismatching positions. I observed that this approach is up to two times faster than RazerS 3.

6.2 Evaluation

In order to evaluate Masai, I propose three experiments: (i) the Rabema benchmark and (ii) variant detection on simulated data, and (iii) performance on real data.

It should be noted that in this evaluation I am interested on the capability of the mapper to retrieve the location of a single read without the help of read pairs, which can of course disambiguate mapping locations of the partner.

As references, I use whole genomes of E. coli (NCBI NC_000913.2), C. elegans (WormBase WS195), D. melanogaster (FlyBase release 5.42), and H. sapiens (GRCh37.p2).

I compare Masai with the best-mappers Bowtie 2, BWA and Soap 2 as well as with the all-mappers RazerS 3, Hobbes, mrFAST and SHRiMP 2. I remark that Bowtie 2, BWA, Soap 2 and SHRiMP 2 rely on scoring schemes taking into account base quality values, while Masai, RazerS 3, Hobbes and mrFAST use edit distance. When relevant, I configured some read mappers with the appropriate absolute number of errors (Masai, mrFAST, Hobbes, Soap 2) or error rate (RazerS 3). In section , I give the exact parameterization for the read mappers considered in the evaluation.

6.2.1 Rabema benchmark on simulated data

I first consider the Rabema benchmark [Holtgrewe *et al.*, 2011] (v1.1) for a thorough evaluation and comparison of read mapping sensitivity. The benchmark contains the categories *all*, *all-best*, *any-best*, *precision*, and *recall*. In the categories all, all-best, and any-best a read mapper has to find all, all of the best, or any of the best edit distance locations for each read. The categories precision and recall require a read mapper to find the *original* location of each read, which is a measure independent of the used scoring model, e.g. edit distance or quality based. A read is mapped *correctly* if the mapper reports its original location, and it is mapped *uniquely* if the mapper reports only one location. Rabema defines *recall* to be the fraction of reads which were correctly mapped and *precision* the fraction of uniquely mapped reads that were mapped correctly.

Similarly to [Langmead and Salzberg, 2012], I used the read simulator Mason [Holtgrewe, 2010] with default profile settings to simulate from each whole genome 100 k reads of length 100 bp having sequencing errors distributed like in a typical Illumina run. I performed the benchmark for an error rate of 5 %, which corresponds to edit distance 5 for reads of length 100 bp. Therefore, I built a Rabema gold standard for each dataset by running RazerS 3 in full-sensitive mode up to edit distance 5. I further classified mapping locations in each category by their edit distance.

For a more fair and thorough comparison, I also consider BWA and Bowtie 2 as all-mappers (Soap 2 cannot be configured accordingly). To this extent, I parametrized these tools to be highly sensitive and output all found mapping locations. Since BWA and Bowtie 2 were not designed to be used as all-mappers, they spent much more time than proper all-mappers, i.e. up to 3 hours in a run compared to several minutes. However, the aim of this experiment is to investigate read mapping sensitivity, therefore I do not report running times. Results for H. sapiens are shown in table 6.1.

Best-mappers

Masai shows the best recall values, not loosing more than 3.3 % recall on edit distance 5. Conversely, recall values of BWA and Bowtie 2 drop significantly with increasing edit

Table 6.1: *Rabema benchmark results on* $100\,k \times 100\,bp$ *Illumina-like reads. Rabema scores are given in percent (average fraction of edit distance locations reported per read). Large numbers show total scores in each Rabema category and small numbers show the category scores separately for reads with* $\binom{0\ 1\ 2}{3\ 4\ 5}$ *errors.*

	method	all		all-best		any-best		precision		recall	
best-mappers	Masai	93.26	99.18 98.73 97.93 95.60 85.77 43.60	97.91	97.79 97.88 98.03 97.98 98.20 96.70	99.95	100.00 100.00 100.00 99.98 99.93 98.71	97.79	97.88 97.84 97.79 97.68 97.61 97.93	97.75	97.88 97.84 97.79 97.68 97.56 96.74
	Bowtie 2	92.04	99.18 98.72 96.80 93.44 81.94 40.19	96.16	97.79 97.85 95.80 94.83 93.37 88.86	98.08	100.00 99.96 97.55 96.62 94.93 90.46	96.58	98.01 97.72 95.98 95.19 95.22 94.37	95.94	98.01 97.72 95.55 94.24 92.79 89.52
	BWA	92.18	99.18 98.72 97.81 94.25 80.92 37.65	96.81	97.79 97.87 97.88 96.59 92.63 83.47	98.81	100.00 99.95 99.81 98.55 94.28 85.37	97.50	97.93 97.70 97.37 97.11 97.17 97.57	96.41	97.93 97.69 97.25 95.77 91.98 84.61
	Soap 2	65.93	99.18 95.55 91.34 8.67 0.70 0.00	69.89	97.79 94.74 91.37 8.98 0.79 0.00	71.37	100.00 96.78 93.18 9.21 0.81 0.00	97.69	98.05 97.74 97.73 94.87 84.13 91.67	69.91	98.05 94.62 91.20 11.85 1.41 0.36
all-mappers	Masai	99.90	100.00 100.00 100.00 100.00 99.94 98.58	99.96	100.00 100.00 100.00 100.00 99.93 98.71	99.96	100.00 100.00 100.00 100.00 99.93 98.71	100.00	100.00 100.00 100.00 100.00 100.00 100.00	99.96	100.00 100.00 100.00 100.00 99.93 98.78
	Bowtie 2	95.69	99.98 99.91 99.45 97.99 90.69 55.14	98.85	99.74 99.79 98.61 98.21 97.55 93.84	99.16	100.00 99.98 99.01 98.63 97.94 94.17	99.84	100.00 99.95 99.87 99.64 99.67 99.29	98.54	99.74 99.58 98.27 97.64 96.87 94.40
	BWA	95.89	99.96 99.88 99.49 97.13 87.79 64.11	97.98	98.81 99.01 99.02 97.83 93.95 85.20	98.82	100.00 99.95 99.82 98.56 94.34 85.37	98.12	93.21 97.63 98.36 98.49 98.68 99.56	97.80	99.03 98.96 98.75 97.35 93.43 86.36
	RazerS 3	100.00	100.00 100.00 100.00 100.00 100.00 100.00	100.00	100.00 100.00 100.00 100.00 100.00 100.00	100.00	100.00 100.00 100.00 100.00 100.00 100.00	100.00	100.00 100.00 100.00 100.00 100.00 100.00	100.00	100.00 100.00 100.00 100.00 100.00 100.00
	Hobbes	96.56	99.41 99.00 98.76 97.80 93.20 73.05	97.08	97.23 96.59 97.01 97.38 98.16 97.42	98.01	97.92 97.51 97.96 98.43 99.12 98.46	99.97	99.96 99.97 99.97 99.98 99.95 99.96	96.41	95.49 95.84 96.54 97.03 97.98 97.79
	mrFAST	99.97	100.00 100.00 100.00 100.00 99.99 99.53	99.97	100.00 100.00 100.00 100.00 100.00 99.10	99.97	100.00 100.00 100.00 100.00 100.00 99.13	100.00	100.00 100.00 100.00 100.00 100.00 100.00	99.97	100.00 100.00 100.00 99.99 100.00 99.18
	SHRiMP 2	96.53	99.87 99.82 99.53 98.37 92.58 64.63	99.50	99.34 99.50 99.60 99.64 99.65 98.32	99.85	99.87 99.90 99.91 99.89 99.84 98.57	99.95	100.00 100.00 100.00 99.93 99.89 99.23	99.25	99.35 99.30 99.24 99.30 99.09 98.48

distance and loose up to 15.4 % and 11.5 % on edit distance 5. As expected, Soap 2 turns out to be inadequate for mapping reads of length 100 bp at this error rates.

Precision values have less variance than recall values. Masai shows the best precision values with 97.8 %, followed by Soap 2 with 97.7 %, and BWA with 97.5 %. Interestingly, Bowtie 2 shows the worst precision values, loosing up to 5.6 % on edit distance 5.

All-mappers

As expected, RazerS 3 shows full-sensitivity and mrFAST looses only a minimal percentage of mapping locations. Overall, Masai does not loose more than 0.1 % of all mapping locations. In particular, Masai is full-sensitive for low-error locations and looses only a small percentage of high-error locations, i.e. its loss is limited to 0.1 % and 1.4 % of mapping locations at edit distance 4 and 5.

Conversely, BWA and Bowtie 2 miss 35 % and 45 % of all mapping locations at edit distance 5 and their recall values as all-mappers do not substantially increase. Likewise, SHRiMP 2 is not able to enumerate all mapping locations, although its recall values are good. Again, Hobbes has the worst performance.

I remark that Masai is not full-sensitive whenever approximate seeds are used, e.g. on H. sapiens. Indeed, Masai loses 0.1 % overall sensitivity in respect to RazerS 3. In general, RazerS 3 should be used when full-sensitivity is required, i.e. for read mappers benchmarking. However, these results show that Masai can replace RazerS 3 or mrFAST as an all-mapper in practical setups.

6.2.2 Variant detection on simulated data

The second experiment analyzes the theoretical performance of Masai and other read mappers in genomic variation pipelines. Similarly to [David *et al.*, 2011], this experiment

considers simulated reads containing sequencing errors, SNPs and indels, such that each read has an edit distance of at most 5 to its genomic origin. Reads are grouped according to the number of contained SNPs and indels, where class (s, i) consists of all reads with s SNPs and i indels. The experiment considers a read to be mapped *correctly* if a mapping location is reported within 10 bp of its genomic origin; it considers a read to map *uniquely* if only one location is reported by the mapper. For each class, the experiment defines *recall* to be the fraction of reads which were correctly mapped and *precision* the fraction of uniquely mapped reads that were mapped correctly.

I simulated 5 million Illumina-like reads of length 100 bp from the whole human genome using Mason. I mapped the reads with each tool and measured its sensitivity in each class. Table 6.2 shows the results of each read mapper by class.

Best-mappers

Among best-mappers, Masai shows the highest precision and recall in all classes. In particular, Masai does not loose more than 3.2 % recall in class (4,0), whether Bowtie 2 and BWA loose respectively 17.5 % and 14.9 % and Soap 2 is not able to map any read.

Interestingly, recall values of Bowtie 2, BWA and Soap 2 are negatively correlated with the amount of genomic variation. For instance, in the Rabema benchmark, Bowtie 2 looses respectively 7.2 % and 11.5 % of mapping locations at distance 4 and 5, but in class (4,0) of this experiment it looses 17.5 % recall. A similar trend is observable for BWA and Soap 2. The low performance of Soap 2 is also due to its limitation to at most 2 mismatches and no support for indels.

All-mappers

Looking at all-mappers results, Masai shows 100 % precision and recall in all classes, except for classes (2,0) and (1,1) where it looses only 0.1 % and 0.7 % recall. Masai is therefore roughly comparable to the full-sensitive read mappers RazerS 3 and mrFAST. SHRiMP 2 shows 100 % precision in all classes but looses between 0.3 % and 0.8 % recall in each class. Hobbes has the lowest performance among all-mappers: it appears to have problems with indels, indeed it looses 9.5 % recall in class (0,3).

6.2.3 Performance on real data

The last experiment focuses on comparing read mappers performance on real data. I mapped the first 10 M×100 bp reads from an Illumina lane of E. coli (ERR022075, Genome Analyzer IIx), D. melanogaster (SRR497711, HiSeq 2000), C. elegans (SRR065390, Genome Analyzer II), and H. sapiens (ERR012100, Genome Analyzer II). Whenever possible, I configured the tools to map the reads within edit distance 5.

I measured mapping times on a cluster of nodes with 72 GB RAM and 2 Intel Xeon X5650 processors running Linux 3.2.0. For an accurate running time comparison, I ran the tools using a single thread and used local disks for I/O. I measured running times, peak memory consumptions, mapped reads and Rabema any-best scores.

Table 6.2: *Variant detection results on* $5\,M \times 100\,bp$ *Illumina-like reads. The table shows percentages of found origins (recall) and fraction of unique reads mapped to their origin (precision) classed by reads with* s *SNPs and* i *indels* (s, i).

		(0,0)		(2,0)		(4,0)		(1,1)		(1,2)		(0,3)	
	method	prec.	recl.	prec.	recl.	prec.	recl.	prec.	recl.	prec.	recl.	prec.	recl.
best-mappers	Masai	98.2	98.2	97.6	97.5	96.8	96.8	97.8	97.2	97.9	97.9	97.2	97.2
	Bowtie 2	97.6	97.3	94.6	92.0	92.6	82.5	95.3	93.3	93.5	92.3	96.1	95.4
	BWA	98.2	97.9	97.6	95.3	94.9	85.1	97.4	90.9	97.1	80.3	96.3	66.5
	Soap 2	98.1	82.9	97.4	31.0	0.0	0.0	90.6	6.2	0.0	0.0	0.0	0.0
all-mappers	Masai	100.0	100.0	100.0	99.9	100.0	100.0	100.0	99.3	100.0	100.0	100.0	100.0
	RazerS 3	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Hobbes	99.9	99.9	99.9	99.9	100.0	100.0	100.0	99.8	100.0	93.6	99.6	90.5
	mrFAST	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	SHRiMP 2	100.0	99.4	100.0	99.7	100.0	99.7	100.0	99.5	100.0	99.2	100.0	99.6

I cannot measure precision and recall values as real reads have unknown origins. Therefore, for this evaluation, I adopt the commonly used measure of percentage of *mapped reads*, i.e. the fraction of reads for which the read mapper reports a mapping location. However, as some mappers report mapping locations without constraints on the number of errors, I also include Rabema *any-best* scores. I recall that the Rabema any-best benchmark assigns a point for a read if the mapper reports at least one mapping location with the optimal (minimum) number of errors; final Rabema any-best scores are normalized by the number of reads.

Results for C. elegans and H. sapiens are shown in table 6.3.

Best-mappers

On the C. elegans dataset, Masai is 7.7 times faster than Bowtie 2, 8.2 times faster than BWA and 1.5 times faster than Soap 2. On the H. sapiens dataset, Masai is 2.6 times faster than Bowtie 2, 3.6 times faster than BWA but 2.1 times slower than Soap 2.

On one end, Soap 2 is not able to map a consistent fraction of reads because of its limitation to 2 mismatches. On the other end, Bowtie 2 reports more mapped reads than Masai but, taking any-best scores into account, it reports less mapping locations than Masai. In fact, Bowtie 2 uses a scoring scheme based on quality values and does not impose a maximal error rate threshold. On the C. elegans and H. sapiens datasets, Bowtie 2 misses respectively 22.0 % and 20.7 % of reads mappable at edit distance 5.

All-mappers

On the C. elegans dataset Masai is 2.0 times faster than RazerS 3, 10.9 times faster than Hobbes, 6.3 times faster than mrFAST and 50.1 times faster than SHRiMP 2. Hobbes constantly crashes and maps less reads than all other mappers in this category.

On the H. sapiens dataset Masai is 11.9 times faster than RazerS 3, 14.6 times faster than mrFAST, and 7.6 times faster than Hobbes. I note that the current version of Hobbes

Table 6.3: *Performance on real data using* $10\,M \times 100\,bp$ *Illumina reads.*
Rabema any-best: in large are shown the percentage of reads mapped with the minimal number of errors (up to 5%) and in small the percentage of reads that were mapped with $\left(\begin{smallmatrix} 0 & 1\% & 2\% \\ 3\% & 4\% & 5\% \end{smallmatrix}\right)$ *errors.*
Mapped reads: in large are shown the percentage of mapped reads and in small the cumulative percentage of reads that were mapped with $\left(\begin{smallmatrix} 0 & 1\% & 2\% \\ 3\% & 4\% & 5\% \end{smallmatrix}\right)$ *errors.*
Remarks: SHRiMP 2 is not able to map the H. sapiens dataset within 4 days; Hobbes constantly crashes and is not able to map completely nor the C. elegans nor the H. sapiens dataset.

	dataset	SRR065390 C. elegans				ERR012100 H. sapiens			
	method	time [min:s]	memory [Mb]	Rabema any-best [%]	mapped reads [%]	time [min:s]	memory [Mb]	Rabema any-best [%]	mapped reads [%]
best-mappers	Masai	3:10	2936	100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00	89.49 75.01 83.80 86.38 87.83 88.79 89.49	22:35	19711	99.99 100.00 100.00 100.00 99.94 99.91 99.53	93.76 75.99 87.84 90.67 92.02 92.99 93.76
	Bowtie 2	24:14	135	99.21 100.00 99.30 93.38 88.61 84.03 77.96	92.58 75.01 83.74 86.20 87.61 88.57 89.27	57:41	3180	99.45 100.00 99.75 96.02 92.88 87.86 79.26	96.72 75.99 87.81 90.54 91.85 92.76 93.44
	BWA	25:53	325	99.33 100.00 99.09 95.57 89.70 85.86 82.29	89.33 75.01 83.72 86.25 87.64 88.59 89.32	80:58	4475	99.54 100.00 99.50 98.01 93.39 88.92 84.42	93.53 75.99 87.78 90.59 91.91 92.82 93.53
	Soap 2	4:37	748	95.98 100.00 96.57 92.38 0.33 0.04 0.02	85.95 75.01 83.50 85.94 85.95 85.95 85.95	11:11	5357	95.66 100.00 94.94 86.54 0.32 0.16 0.16	89.73 75.99 87.24 89.73 89.73 89.73 89.73
all-mappers	Masai	10:49	2821	100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00	89.49 75.01 83.80 86.38 87.83 88.79 89.49	307:16	20130	100.00 100.00 100.00 100.00 100.00 99.97 99.53	93.76 75.99 87.84 90.67 92.02 92.99 93.76
	RazerS 3	21:18	11489	100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00	89.49 75.01 83.80 86.38 87.83 88.79 89.49	3653:03	17298	100.00 100.00 100.00 100.00 100.00 100.00 100.00	93.77 75.99 87.84 90.67 92.02 92.99 93.77
	Hobbes	117:46	3885	89.77 91.04 80.63 86.47 88.32 88.47 85.17	80.34 68.29 75.38 77.61 78.89 79.74 80.34	2319:27	71685	59.02 59.24 58.65 57.48 56.92 56.70 56.32	55.35 45.01 51.96 53.59 54.36 54.91 55.35
	mrFAST	67:41	875	99.99 100.00 99.98 99.88 99.87 99.93 99.51	89.49 75.01 83.80 86.38 87.83 88.78 89.49	4462:25	929	99.98 100.00 100.00 100.00 99.99 99.99 97.46	93.75 75.99 87.84 90.67 92.02 92.99 93.75
	SHRiMP 2	541:20	2735	98.51 99.59 96.81 91.76 87.60 81.88 74.77	91.91 74.71 83.22 85.59 86.88 87.69 88.27	–	–	–	–

constantly crashes and maps only half of the reads. SHRiMP 2 is not able to map the H. sapiens dataset within 4 days.

Likewise for Bowtie 2, also SHRiMP 2 does not impose a maximal error rate threshold and reports more mapped reads than Masai. However, its Rabema any-best score is inferior to Masai. This could be due to the use of a different scoring scheme where two mismatches cost less than opening a gap. Anyway, this hypothesis does not explain why SHRiMP 2 does not report some mapping locations at distance 0.

6.2.4 Filtration efficiency

This experiment assesses the contribution of approximate seeds and multiple backtracking on runtime results. To this intent, I performed all-mapping with Masai on each previously considered dataset, this time using either exact or approximate seeds in combination with either single or multiple backtracking. Table 6.4 shows the results. Filtration time consists of the time spent to index the seeds (in case of multiple backtracking) and to perform backtracking. Candidates reports the number of candidate locations reported by the filter for which seed extension is subsequently performed. I report in bold the optimal combination of seeding and backtracking that I used to parameterize Masai.

Since this experiment focuses on filtration, I do not consider the time spent performing seed extensions and I/O, i.e. loading the reference genome and its index, loading the reads, writing the results. Such time is independent of any combination of seeding or backtracking and can be extrapolated by subtracting bold filtration times of table 6.4

from respective Masai all-mappers times of table 6.3 and table **??**.

On E. coli, D. melanogaster and C. elegans approximate seeds reduce the number of candidates respectively by 2.1 times, 9.9 times, and 4.3 times. Nevertheless I still prefer exact seeds as filtration dominates the total runtime. Multiple backtracking on exact seeds compared to single backtracking speeds up filtration by 2.9 times on E. coli, and 3.8 times on D. melanogaster and C. elegans. Without the contribution of multiple backtracking Masai would not be faster than RazerS 3, the second fastest all-mapper.

Approximate seeds become effective on H. sapiens, where they reduce the number of candidates by 10.8 times. On H. sapiens seed extensions largely dominate the total runtime, therefore I prefer approximate seeds. Multiple backtracking on approximate seeds provides a speed-up of 3.2 times over single backtracking. The combination of the two methods makes Masai an order of magnitude faster than any other all-mapper.

Table 6.4: *Masai filtration efficiency results for all-mapping. Filtration time is given as [min:s] and includes seeds indexing time.*

organism	dataset	seeding	backtracking	filtration time	candidates
E. coli	ERR022075	exact	single	3:55	69.17 M
E. coli	ERR022075	**exact**	**multiple**	**1:20**	**69.17 M**
E. coli	ERR022075	approximate	single	38:42	33.08 M
E. coli	ERR022075	approximate	multiple	9:00	33.08 M
D. melanogaster	SRR497711	exact	single	8:15	1020.28 M
D. melanogaster	SRR497711	**exact**	**multiple**	**2:11**	**1020.28 M**
D. melanogaster	SRR497711	approximate	single	100:18	102.78 M
D. melanogaster	SRR497711	approximate	multiple	20:48	102.78 M
C. elegans	SRR065390	exact	single	8:25	1065.70 M
C. elegans	SRR065390	**exact**	**multiple**	**2:11**	**1065.70 M**
C. elegans	SRR065390	approximate	single	102:02	246.65 M
C. elegans	SRR065390	approximate	multiple	21:33	246.65 M
H. sapiens	ERR012100	exact	single	55:54	294943.86 M
H. sapiens	ERR012100	exact	multiple	41:52	294943.86 M
H. sapiens	ERR012100	approximate	single	165:45	27396.01 M
H. sapiens	ERR012100	**approximate**	**multiple**	**52:15**	**27396.01 M**

6.3 Discussion

Masai consists of three important algorithmic methods: (i) approximate seeds, (ii) multiple backtracking and (iii) greedy filtration. Approximate seeds are of paramount importance to obtain very specific yet full-sensitive filtration; their adoption speeds up Masai by one order of magnitude. Multiple backtracking further speeds up the filtration phase by 3–5 times on a (enhanced) suffix array index; this technique makes Masai twice as

fast. Greedy filtration prioritizes analysis of optimal mapping locations; because of this method, Masai in best-mapping is an order of magnitude faster than in all-mapping.

Is the edit distance sufficient to perform best-mapping? Both Rabema benchmark and variant detection results show that Masai has constantly better accuracy than other best-mappers relying on more complex scoring schemes. In particular, the Rabema benchmark results show that Rabema any-best values are tightly bound to recall values. Hence, the edit distance is a pertinent and adequate scoring scheme for best-mapping. Vice versa, best-mappers using scoring schemes based on quality values show a generalized and substantial loss of mapping accuracy. This is likely due to the heuristics on which these tools rely. To sum up, it is better to stick to edit distance and guarantee full-sensitivity rather than to adopt an involved scoring scheme and explore the alignment space heuristically, hence partially.

How many mapping locations do heuristic best-mappers miss? By looking at precision and recall values on simulated data, or at Rabema any-best values on real data, it can be deduced that Bowtie 2, BWA and Soap 2 miss up to 20 % of reads mappable at 5 % error rate. Yet, it is not evident how these results affects variant calling pipelines.

Summing up, Masai as an all-mapper is an order of magnitude faster and thus a valid alternative to tools like RazerS 3 and mrFast. Computational requirements of all-mapping now become close to those of best-mapping: Masai as an all-mapper is only 4 times slower than BWA, despite reporting two orders of magnitude more mapping locations. Masai as a best-mapper is 2–4 times faster and more accurate than Bowtie 2 citepLangmead2012 and BWA [Li and Durbin, 2009]. The achieved speedup is huge when RazerS 3 has to be used as a best-mapper: in this scenario, Masai is roughly 200 times faster!

Despite the good results, Masai is not being widely used. This is mainly because it lacks some commonly requested features, including: parallelization via multi-threading, low memory footprint, direct support of paired-end or mate-pair protocols, computation of mapping qualities, automatic parameterization. Because of initial inexperience and unclear (or wrong) goals, I neglected these requirements while designing the tool. The next chapter introduces *Yara*, *y*et *a*nother *r*ead *a*ligner, a tool fulfilling these requirements.

CHAPTER 7

Yara

Yara (*Y*et *a*nother *r*ead *a*ligner) is an exhaustive, non-heuristic read mapper, capable of quickly reporting all stratified mapping locations within a given error rate. Yara offers parallelization via multi-threading, has a low memory footprint by using the FM-index, directly supports paired-end or mate-pair protocols, computes accurate mapping qualities, does not require ad-hoc parameterization and works on Illumina or Ion Torrent reads.

7.1 Engineering

7.1.1 Ad-hoc filtration

Specific yet rapid filtration is fundamental in the design of an efficient read mapping tool. Read mappers like RazerS 3 [Weese *et al.*, 2012] and mrFast [Ahmadi *et al.*, 2012] are designed around naïve filtration with exact seeds. This filtration method is always very quick, however it is not specific enough on long, repetitive reference genomes like the human genome. Masai [Siragusa *et al.*, 2013] circumvents this problem by enforcing a minimum seed length, whose optimal value must be tuned for a specific reference genome, and eventually resorting to approximate seeds in order to guarantee full-sensitivity. This filtration method speeds up Masai by an order of magnitude but is still rough: it needs external parametrization, lacks flexibility and is suboptimal in practice.

Yara applies an ad-hoc filtration scheme *per read*. Under any fixed filtration scheme, the number of verifications per read is not uniform: within a typical mapping, most reads produce very few verifications and are easily mappable, while a few others are problematic and often not even confidently mappable to one single location. Consequently, any fixed filtration scheme turns out to be too weak for some reads yet too strong for others, thus suboptimal in practice. An ad-hoc filtration scheme per read improves filtration efficiency by optimizing the ratio between filtration speed and specificity. Yara thus automatically chooses an ad-hoc filtration scheme per read, without requiring manual parameterization by the user.

Ad-hoc filtration works as follows. Yara initially applies filtration with exact seeds to all reads. The tool counts the number of verifications to be performed for each read, thus decides if it is worth proceeding with the verification phase or alternatively applying a stronger filtration scheme. This decision depends on fine-tuned internal verification thresholds. Under standard Illumina setups, exact seeds provide efficient filtration for

up to 70–80 % of the reads; on the remaining reads, a filtration scheme using 1– or 2–approximate seeds works better. Thus, Yara starts with the quickest filtration scheme and becomes more specific whenever it pays off to do so.

7.1.2 Stratified filtration

All-mapping methods consider a set of relevant mapping locations per read. Yet, this definition leaves open what relevant means. In all-mapping under the edit distance, the user defines relevant mapping locations by imposing a distance threshold. Despite being sound, this definition does not work well in practice. On the one hand a very low threshold leaves a consistent fraction of the reads unmapped, on the other hand a moderate threshold produces a deluge of mapping locations for some reads. In practice, at 5 %, error rate, Illumina reads map to hundreds of mapping locations on the human genome. It is questionable whether all these locations are relevant for the downstream analysis. Thus, a finer definition of all-mapping relevance is necessary in practice.

Stratification of mapping locations yields an equally sound yet practical definition of all-mapping under the edit distance. The e-stratum

$$S(r, e) = \{(i, j, e) : d_E(g_{i\ldots j}, r) = e\} \tag{7.1}$$

denotes the set of all mapping locations of a read r at edit distance e from the reference genome g. According to the above definition, conventional all-mapping under the edit distance defines the set

$$S(r, 0) \cup S(r, 1) \cup \ldots \cup S(r, k) \tag{7.2}$$

as relevant mapping locations within an *absolute* error threshold k. Stratified all-mapping refines this definition by considering only mapping locations being co-optimal, or sub-optimal up to a certain degree. Formally, if the distance of any optimal mapping location for read r is

$$e^* = \min\{e \in [0, k] : S(r, e) \neq \emptyset\} \tag{7.3}$$

stratified all-mapping considers mapping locations

$$S(r, e^*) \cup \ldots \cup S(r, \min\{e^* + l, k\}) \tag{7.4}$$

within a *relative* error threshold l to be relevant.

Yara significantly improves the runtime of stratified all-mapping over conventional all-mapping. Obviously, the most straightforward way to achieve stratified all-mapping consists into performing conventional all-mapping and subsequently filtering out any irrelevant mapping location. For instance, RazerS 3 implements this method and gets no speedup. Another naïve method consists into applying up to k rounds of conventional all-mapping, with filtration schemes for thresholds going from 0 to $\min\{e^* + l, k\}$. It is easy to see that also this method performs redundant computation: the total work for any read mapping at distance greater or equal to k corresponds to the sum of all k filtration schemes.

The following stratified all-mapping method, adopted by Yara, guarantees not to perform more work than conventional all-mapping. Indeed, the key idea is to simply reduce any filtration scheme full-sensitive within distance k to be full-sensitive within distance $\min\{e^* + l, k\}$. Given any filtration scheme full-sensitive within distance k, with s seeds having thresholds $\mathbb{k} = (k_1, \ldots, k_s)$, any subset consisting of $s^* < s$ seeds with thresholds $\mathbb{k}^* = (k_1^*, \ldots, k_{s^*}^*)$ is full-sensitive within distance $\min\{e^* + l, k\}$ if it satisfies

$$s^* + \sum \mathbb{k}^* > \min\{e^* + l, k\}. \tag{7.5}$$

The proof is analogous to that one given in section **??**.

Example 7.1. Let $k = 5$ be the absolute threshold, and $l = 0$ be the relative threshold, restricting relevant locations to co-optimal ones. A read r maps at distance 1, i.e. $|S(r, 0)| = 0$, $|S(r, 1)| > 0$ thus $e^* = 1$. Given the filtration scheme $\mathbb{k} = (1, 1, 1)$, any subset full-sensitive up to distance $\min\{e^* + l, k\} = 1$ finds all relevant mapping locations, i.e. all subsets of $\mathbb{k}$ are: $(0, 0, -)$, $(0, -, 0)$, $(-, 0, 0)$, $(1, -, -)$, $(-, 1, -)$, $(-, -, 1)$ are full-sensitive. Thus, verification of all candidates, produced by *any* two exact seeds or one 1-approximate seed, yields all mapping locations in the 1-stratum of r.

In addition, Yara implements a simple greedy strategy to minimize the number of verifications to find all relevant stratified mapping locations. As candidate locations can be verified in any order, Yara chooses the ordering of seeds producing the minimum number of verifications. The tool first finds all seeds and ranks them by number of candidate locations produced. Then it processes all candidate locations, from the least to the most frequent seed, until it explores l strata from the first non-empty one, or until it attains the absolute distance threshold k.

Yara performs best-mapping by means of stratified filtration. Best-mapping requires one primary mapping location along with its confidence. Under the edit distance, without any further assumptions, any co-optimal location is equally likely to be correct. Thus, Yara performs stratified all-mapping with a relative threshold $l = 0$, picks one random co-optimal location, and subsequently estimates its mapping quality using all found mapping locations (see section 7.1.4). Because of this method, Yara in best-mapping is an order of magnitude faster than in conventional all-mapping.

7.1.3 Paired-end and mate-pair protocols

Paired-end and mate-pair protocols are the sequencing protocols of choice of Illumina instruments. Reads are sequenced in pairs from both ends of the same insert. Properly paired reads are expected to map within the insert size adopted in the sequencing protocol. The lack of any proper pair of mapping locations signals a potential structural variation, e.g. a long indel or an inversion. Thus, the added information of an expected insert size allows a read mapper to map read pairs to their original locations more confidently than in the single-end protocol. Nonetheless, a read mapper should report equally important unpaired mapping locations.

In the paired-end or mate-pair workflows, Yara maps paired reads independently, exactly as in the single-end workflow, and reports all relevant mapping locations per read. However, in addition to the single-end workflow, Yara implements a finer strategy to choose primary mapping locations. For any reads pair, among all pairs of co-optimal mapping locations, the tool selects the one with minimal deviation from the expected insert size. Since Yara outputs all relevant mapping locations, the choice of primary locations can be always corrected a posteriori.

7.1.4 Mapping qualities

Yara computes mapping qualities using the number of mapping locations stratified by error rate.

7.1.5 Indexing

Yara uses an efficient FM-index specialization for the DNA alphabet, based on interleaved rank dictionaries (see section **??**). This interleaved FM-index exhibit a fourfold speedup over the first FM-index implementation bundled with Masai. Surprisingly, the interleaved FM-index is also faster than any other index, both in exact and approximate search (see figure **??**). Moreover, this index consumes only 1.23 bytes per base pair with a SA sampled at 10 %, thus its memory footprint is 3.7 GB for the human genome. Under these terms, the there is no indexing space-time trade-off: the FM-index always provides the most convenient suffix trie implementation.

Yara does not use multiple search algorithms of section **??** to search seeds on the FM-index. These algorithms work according to a *cache-friendly* memory access pattern, which holds for forward search but not for backward search. Using forward search, navigation in a suffix trie becomes less expensive as it proceeds towards bottom nodes. Indeed, navigation towards a child node involves the computation of a subinterval of the current suffix array interval; such computation accesses memory locations within the current interval, that have good chances to be in the cache. Conversely, using backward search, navigation becomes more expensive as it proceeds deeper in the trie; navigation downwards involves the computation of intervals outside of the current one, unlikely to be in the cache as they are accessed less often than top intervals. As multiple backtracking factorizes the navigation of top nodes, it pays off with forward search rather than with backward search. Hence, on the FM-index, it is always faster to search exact queries in a naïve way and approximate queries simply sorted in lexicographical order (see figure **??**).

7.2 Evaluation

The evaluation consists of three experiments: (i) accuracy on simulated data, (ii) Rabema benchmark on simulated and real data, and (iii) throughput on real data. In each experiment, I compare Yara in best-mapping with GEM, Bowtie 2 and BWA, while in all-mapping with GEM, RazerS 3, and Hobbes 2.

7.2.1 Experimental setup

Read mappers parametrization

In appendix B.2, I give the exact parametrization of each read mapper considered in the evaluation. Whenever possible, I configured the tools with the appropriate error rate (Yara, GEM, RazerS 3) or absolute number of errors (Hobbes 2). When processing paired-end reads, I provided the tools with appropriate insert size information.

Infrastructure

All tools run on a desktop computer running Linux 3.10.11, equipped with one Intel Core i7-4770K CPU @ 3.50 GHz, 32 GB RAM and a 2 TB HDD @ 7200 RPM. For maximum throughput, all tools run using eight threads. For accurate running time comparisons, I disabled Intel Turbo Boost; therefore, real throughputs might be slightly lower than the measured ones.

Datasets

The reference in all experiments is the human whole genome (GRCh38).

The simulated data consists of 1 M Illumina-like 2×100 bp paired-end reads, simulated from the reference genome using Mason [Holtgrewe, 2010]. The mean insert size is `INS = 175` and the deviation `ERR = 225`.

The real data is a publicly released sequencing run (SRA/ENA id: ERR161544) by the Beijing Genome Institute; the genomic DNA used in this study came from an anonymous male Han Chinese individual who has no known genetic diseases. This dataset consists of 2×100 bp whole genome sequencing reads, produced by an Illumina HiSeq 2000 instrument. BWA reports mean insert size `INS = 178` and deviation `ERR = 200`.

7.2.2 Accuracy on simulated data

I introduce an *accuracy benchmark* to measure read mappers accuracy of finding the *original* location of simulated reads. This benchmark considers for each read only the *first primary mapping location* encountered while scanning the SAM file [Li *et al.*, 2009a] produced by each tool; this policy mimics the behavior of de-facto standard *best-mapping analysis pipelines*, e.g. the GATK [DePristo *et al.*, 2011]. This accuracy benchmark counts a simulated read as *correctly mapped* if the found mapping location corresponds to its original location, it computes the *recall* of each tool as the fraction of correctly mapped reads and the *precision* as the fraction of mapped reads that are correct; for a thorough evaluation, it also classes all simulated reads by the *error rate* of their original locations, then computes recall and precision within each error rate class.

I repeated this experiment twice: first providing the simulated reads as unpaired, then as paired-end with additional insert size information. Results are shown in table 7.1.

Table 7.1: *Accuracy results on the human whole genome. The left panel shows the results of mapping 1 M Illumina-like 2 × 100 bp reads as unpaired; the right panel shows the results of mapping the same reads as paired-end, providing additional insert size information. Big numbers show total scores, while small numbers show marginal scores for the reads at $\binom{0\ 1\ 2}{3\ 4\ 5}$ % error rate.*

		hiseq_hg19_like_se H. sapiens SE								hiseq_hg19_like_pe H. sapiens PE							
	tool	recall				precision				recall				precision			
best	Yara	97.67	97.70	97.62	97.57	97.67	97.70	97.62	97.57	98.50	98.55	98.42	98.28	98.50	98.55	98.42	98.28
			97.32	97.76	97.03		97.32	97.82	97.19		97.90	98.51	97.61		97.90	98.56	97.77
	Gem	97.65	97.69	97.56	97.56	97.65	97.69	97.56	97.56	98.50	98.54	98.48	98.34	98.50	98.54	98.48	98.34
			96.54	96.86	97.20		96.56	96.91	97.20		97.49	97.71	98.43		97.49	97.71	98.43
	Bowtie 2	97.56	97.70	97.61	95.60	97.59	97.70	97.61	96.01	98.46	98.50	98.47	98.08	98.47	98.50	98.47	98.12
			94.27	94.68	95.80		95.13	95.44	96.35		97.58	96.59	97.53		97.74	96.96	98.17
	BWA	97.53	97.69	97.58	97.28	97.64	97.69	97.58	97.35	98.39	98.54	98.47	98.19	98.50	98.54	98.47	98.26
			90.86	76.53	68.01		96.30	95.80	97.40		91.56	77.06	68.34		97.05	96.47	97.87
all	Yara	97.67	97.70	97.61	97.61	97.67	97.70	97.61	97.61	98.50	98.55	98.42	98.27	98.50	98.55	98.42	98.27
			97.18	97.50	96.95		97.18	97.55	97.11		97.90	98.56	97.61		97.90	98.62	97.77
	Gem	97.65	97.70	97.57	97.58	97.65	97.70	97.57	97.58	98.50	98.53	98.45	98.35	98.50	98.53	98.45	98.35
			96.59	96.86	97.20		96.59	96.91	97.20		97.41	97.66	98.43		97.41	97.66	98.43
	Hobbes 2	98.34	98.38	98.29	98.20	90.00	89.63	90.68	91.74	89.22	89.10	89.46	89.99	89.92	89.60	90.47	91.53
			97.56	97.76	97.77		91.83	94.01	95.18		89.41	87.33	84.09		91.92	93.72	96.41
	RazerS 3	91.00	90.52	91.90	93.14	91.00	90.52	91.90	93.14	94.13	93.95	94.48	94.95	94.17	93.98	94.51	94.99
			94.01	96.11	96.87		94.01	96.11	96.87		95.40	96.38	92.75		95.53	96.79	97.74

7.2.3 Rabema benchmark on simulated and real data

The *Rabema benchmark* [Holtgrewe *et al.*, 2011] (v1.1) measures read mappers sensitivity of finding *relevant* mapping locations of simulated or real reads. This experiment considers the Rabema benchmark category *all* for all-mappers and *all-best* for best-mappers. In the category all, Rabema counts as relevant, for each read, all mapping locations within a maximal error rate; in the category all-best it considers just co-optimal mapping locations. Rabema computes the *sensitivity* of each tool as the fraction of relevant mapping locations found per read. Analogously to the accuracy benchmark, Rabema classes mapping locations by their *error rate*, then computes sensitivity within each error rate class. The benchmark reports percentual scores normalized by the number of reads.

I applied the Rabema benchmark both on simulated and real data, within an error rate of 5 %. Therefore, I built a Rabema gold standard for each dataset by running RazerS 3 in full-sensitive mode up to 5 % error rate. I provided unpaired reads to each tool as the Rabema benchmark by definition does not consider paired-end reads. Results are shown in table 7.2.

7.2.4 Throughput on real data

This experiment complements the sensitivity evaluation on real data provided by the Rabema benchmark. The goal of this experiment is to determine if read mappers are able to sustain sequencing throughput of the instrument or constitute a potential bottle-

Table 7.2: *Rabema benchmark results on the human whole genome. The left panel shows the results of mapping* 1 *M Illumina-like* 2 × 100 *bp simulated reads; the right panel shows the results of mapping* 1 *M Illumina* 2×100 *bp real reads. Big numbers show total Rabema scores, while small numbers show marginal scores for the mapping locations at* $\left(\begin{smallmatrix} 0 & 1 & 2 \\ 3 & 4 & 5 \end{smallmatrix}\right)$ *% error rate.*

		hiseq_hg19_like H. sapiens				ERR161544 H. sapiens			
	tool	all	all-best	any-best		all	all-best	any-best	
best	Yara	92.09 100.00 97.99 85.94 / 40.28 10.10 2.56	100.00 100.00 100.00 100.00 / 100.00 99.94 99.71	100.00 100.00 100.00 100.00 / 100.00 99.94 99.83		90.49 100.00 94.64 75.66 / 50.19 30.86 14.27	99.99 100.00 100.00 100.00 / 99.96 99.88 99.40	99.99 100.00 100.00 100.00 / 99.96 99.90 99.53	
	Gem	93.71 100.00 98.73 90.88 / 61.29 31.48 15.01	99.99 100.00 99.99 99.95 / 99.84 99.23 97.97	100.00 100.00 100.00 99.98 / 99.95 99.71 98.39		93.25 100.00 96.64 84.54 / 72.12 55.35 31.75	99.94 100.00 99.98 99.91 / 99.71 99.48 94.16	99.95 100.00 99.99 99.97 / 99.84 99.77 95.12	
	Bowtie 2	90.98 98.86 96.87 83.98 / 38.88 9.79 2.47	97.60 97.67 97.81 95.73 / 94.89 95.59 95.64	99.88 100.00 99.99 97.74 / 96.83 97.14 97.72		88.40 98.59 92.21 70.69 / 44.59 25.30 9.41	95.82 97.17 95.00 87.74 / 81.88 76.13 64.68	99.57 100.00 99.94 97.32 / 94.98 90.74 81.12	
	BWA	90.93 98.86 96.87 84.84 / 37.15 7.77 1.73	97.59 97.67 97.82 97.70 / 91.33 76.10 67.27	99.88 100.00 99.99 99.88 / 93.38 77.51 68.61		88.40 98.59 92.22 71.29 / 44.08 24.74 9.45	95.90 97.17 94.99 89.67 / 82.49 75.82 65.10	99.68 100.00 99.93 99.56 / 96.06 90.95 82.74	
all	Yara	99.82 100.00 100.00 100.00 / 99.99 99.56 96.27	100.00 100.00 100.00 100.00 / 100.00 99.94 99.71	100.00 100.00 100.00 100.00 / 100.00 99.94 99.83		99.83 100.00 100.00 100.00 / 99.98 99.72 97.17	99.99 100.00 100.00 100.00 / 99.96 99.88 99.43	99.99 100.00 100.00 100.00 / 99.97 99.89 99.54	
	Gem	95.27 100.00 99.04 94.93 / 70.97 48.00 34.47	99.75 100.00 99.06 99.61 / 99.64 99.20 97.88	100.00 100.00 100.00 99.99 / 99.98 99.71 98.39		95.18 100.00 98.13 92.41 / 80.50 67.39 47.99	99.65 100.00 98.32 98.97 / 99.03 99.02 93.72	99.95 100.00 99.98 99.97 / 99.82 99.76 95.10	
	Hobbes 2	99.91 100.00 100.00 100.00 / 100.00 99.89 98.04	100.00 100.00 100.00 100.00 / 99.99 100.00 99.91	100.00 100.00 100.00 100.00 / 100.00 100.00 100.00		–	–	–	
	RazerS 3	100.00 100.00 100.00 100.00 / 100.00 100.00 100.00	100.00 100.00 100.00 100.00 / 100.00 100.00 100.00	100.00 100.00 100.00 100.00 / 100.00 100.00 100.00		100.00 100.00 100.00 100.00 / 100.00 100.00 100.00	100.00 100.00 100.00 100.00 / 100.00 100.00 100.00	100.00 100.00 100.00 100.00 / 100.00 100.00 100.00	

neck in the data analysis pipeline. The Illumina HiSeq 2500 in a six days run produces[1] up to 800 Gbp as 2 × 100 bp paired-end reads. The experiment measures read mapping throughput in *giga base pairs per hour* (Gbp/h); under this measure the maximum throughput of the Illumina HiSeq 2500 is 5.56 Gbp/h.

For an accurate throughput estimation, best-mappers processed 10 M Illumina 2 × 100 bp reads, while for all-mappers it was sufficient to process 1 M reads. For a fair comparison, best-mappers produced a SAM file as expected by de-facto standard best-mapping pipelines, while all-mappers output a file in native format (SAM for Yara and Hobbes 2, custom for Gem and RazerS 3).

[1] According to the specifications at `http://res.illumina.com/documents/products/datasheets/datasheet_hiseq2500.pdf` for high output run mode with dual flow cell.

Table 7.3: *Read mapping throughput on the human whole genome. All tools run using 8 threads on a desktop computer equipped with an Intel Core i7-4770K CPU. The left panel shows the results of mapping* 2×100 *bp Illumina HiSeq 2000 reads as single-end; the right panel shows the results of mapping the same reads as paired-end. The maximum throughput of an Illumina HiSeq 2500 is* 5.56 *Gbp/h.*

		ERR161544 100 bp		ERR161544 2x100 bp	
	tool	throughput [Gbp/h]	memory [Mb]	throughput [Gbp/h]	memory [Mb]
best	Yara	12.59	5072	11.39	5093
	Gem	8.19	4438	13.35	4430
	Bowtie 2	6.60	3326	6.69	3370
	BWA	4.36	4579	3.77	4759
all	Yara	1.27	5549	1.34	6210
	Gem	0.84	5356	1.64	4733
	Hobbes 2	–	–	–	–
	RazerS 3	0.10	19065	0.17	9139

APPENDIX

A Dictionary search and join

Dictionary search is a restriction of string matching. Given a set of database strings $\mathbb{D}$ and a query string q, the approximate dictionary search problem is to find all strings in $\mathbb{D}$ within distance k from q. Note that usually the query string q has length similar to strings in $\mathbb{D}$, as $||d| - |q|| \leq k$ is a necessary condition for $d_E(d, q) \leq k$.

A.1 Online methods

The problem can be solved by checking whether $d_E(d, q) \leq k$ for all $d \in \mathbb{D}$. Answering the question whether the distance $d_E(d, q) \leq k$ is an easier problem than computing the edit distance $d_E(d, q)$: a band of size $k + 1$ is sufficient.

Lemma A.1. *The k-differences global alignment problem can be solved by computing only a diagonal band of the DP matrix of width $k+1$, where the leftmost band diagonal is $\lfloor \frac{m-n+k}{2} \rfloor$ cells left of the main diagonal (see Figure* **??***).*

Proof. Indirect. Assume that a cell outside the band is part of a global alignment with at most k errors. If the cell is left of the band, the traceback that starts in the top left corner would go down at least $c = \lfloor \frac{m-n+k}{2} \rfloor + 1$ cells. Then it needs to go right at least $n - m + c$ cells to end in the bottom right corner. Hence it contains at least $n - m + 2c > n - m + 2\frac{m-n+k}{2} = k$ errors. The assumption that the cell is right of the band can be falsified analogously. □

Figure A.1: *DP table representing the match of $p = \ldots$ in $t = \ldots$.*

	ϵ	C	G	C	A	N	A	T	A	A	T	C	A	G
ϵ	0	1	2	3	4	5	6	7						
C	0	1	2	3	4	5	6	7	8					
G	0	1	2	3	4	5	6	7	8	9				
G	0	1	2	3	4	5	6	7	8	9	10			
C		0	1	2	3	4	5	6	7	8	9	10		
A			0	1	2	3	4	5	6	7	8	9	10	
A				0	1	2	3	4	5	6	7	8	9	10
T														
A														
T														
C														
A														
G														

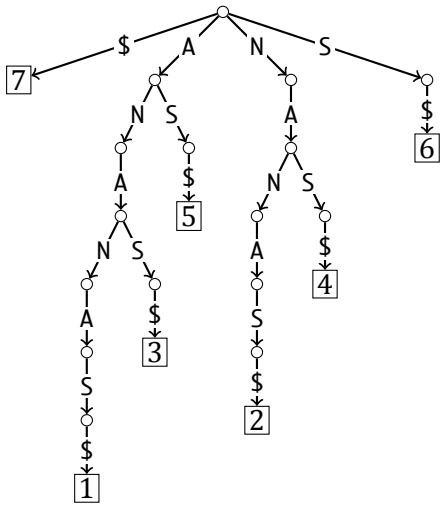
A.2 Indexed methods

Using a radix tree $\mathcal{D}$ we can find all strings in $\mathbb{D}$ equal to a query string q, in optimal time $\mathcal{O}(|q|)$ and independently of $||\mathbb{D}||$.

Algorithm A.1 Exact dictionary search on a radix trie.

```
1: procedure ExactSearch(x, p)
2:     if p = ϵ then
3:         report 𝔼(x)
4:     else if ∃ c ∈ ℂ(x) : label(c) = p_1 then
5:         ExactSearch(c, p_{2..|p|})
```

Figure A.2: *Exact dictionary search on a suffix trie.*



A.3 Filtering methods

Filtering methods of section 2.5.3 can be directly applied to solve the dictionary search problem. Database strings satisfying the filtering condition can be verified with algorithm **??**.

Appendix

B Read mappers parameterization

B.1 Masai evaluation

In the following, I give the exact parameterization of each read mapper considered in the evaluation of section **??**.

Masai Version 0.5 was used. In order to use Masai as an all-mapper, I passed the argument `–all`, otherwise the argument `–any-best` is used by default. I set the maximal edit distance using the parameter `-e`. I configured the seed length with the parameter `–seed-length`; on E. coli, D. melanogaster and C. elegans I chose a seed length of 16, while on H. sapiens I chose a seed length of 33. I selected the SAM output format with `-os` and enabled CIGAR output with `-oc`.

Bowtie 2 Version 2.0.0-beta6 was used. I used the parameter `–end-to-end` to enforce semi-global read alignments. For the Rabema experiment I used the parameter `-k 100`.

BWA Version 0.6.1-r104 was used. For the Rabema experiment I passed the parameter `-N` to `aln` and `-n 100` to `samse`.

Soap 2 Version 2.1 was used.

RazerS 3 Version 3.1 was used. I mapped with indels using the pigeonhole filter (default) and set the error rate through the parameter `-i`, e.g. `-i 95` to map within an error rate of 5 %. I selected the native or SAM output format with `-of 0` or `-of 4`.

Hobbes Version 1.3 was used. I built the index using the recommended q-gram length 11. Since I focus on edit distance, I used the 16 bit bit-vector version. I enabled indels with `–indels` and set maximal edit distance using the parameter `-v`. For resource measurement I used the output without CIGAR, for analyzing the results I enabled CIGAR output using `–cigar`.

mrFAST Version 2.1.0.6 was used. I set maximal edit distance using the parameter `-e`.

SHRiMP 2 Version 2.2.2 was used.

B.2 Yara evaluation

In the following, I give the exact parameterization of each read mapper considered in the evaluation of section 7.2. Below, `MIN` and `MAX` are placeholders for minimal and maximal insert size, while `INS` is the mean insert size and `ERR` its allowed deviation, i.e. `INS = (MIN + MAX) / 2`, `ERR = (MAX - MIN) / 2`.

Yara Version 1.0 was used. To perform all-mapping, I passed the argument `–all`; by default, the tool runs as a best-mapper. I set the error rate using the parameter `-e`. In paired-end mode, the parameters used were `–library-length INS –library-error ERR`. The number of threads was set with the parameter `-t`.

GEM Version 1.376 was used. I set the error rate using the parameters `-m` and `-e`, then I disabled adaptive mapping using the parameter `–quality-format ignore`. In best-mapping, to analyze only the best stratum, I passed the argument `-s 0`; in all-mapping, to analyze all strata, I passed `-d all -D all -s all –max-big-indel-length 0`. In single-end mode, I passed the parameter `–expect-single-end-reads`; in paired-end mode, I passed `–paired-end-alignment`, along with `–min-insert-size MIN –max-insert-size MAX`, and `–map-both-ends` to select the workflow mapping both reads independently. The number of threads was selected using the parameter `-t`.

Bowtie 2 Version 2.2.1 was used. I used the parameter `–end-to-end` to enforce semi-global read alignments. In paired-end mode, I used the parameters `–minins MIN –maxins MAX`. The number of threads was selected using the parameter `-p`.

BWA Version 0.7.7-r441 was used. I used the parameter `-t` to select the number of threads in the `aln` step; the `sampe` and `samse` steps were performed using one thread since BWA does not offer any parallelization here.

Hobbes 2 Version 2.1 was used. I built the index using the recommended q-gram length 11. I enabled edit distance with `–indels` and set the distance threshold using the parameter `-v`. In paired-end mode, I used the parameters `–pe –min MIN –max MAX`. Multi-threading was enabled using `-p`.

RazerS 3 Version 3.2 was used. I set the error rate through the parameter `-i`, e.g. `-i 95` to map within an error rate of 5 %. I passed the option `-rr 100` to set the recognition rate to 100 % and `-m 1000000` to output all mapping locations per read. In paired-end mode, the parameters used were `–library-length INS –library-error ERR`. The number of threads was set with the `-tc` parameter.

Appendix C

Declaration

I declare that this thesis is my own work and has not been submitted in any form for another degree or diploma at any university or other institute of tertiary education. Information derived from the published and unpublished work of others has been acknowledged in the text and a list of references is given.

Enrico Siragusa
August 13, 2014

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