A survey of mapping algorithms in the long-reads era

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Abstract

It has been ten years since the first publication of a method dedicated entirely to mapping third-generation sequencing long-reads. The unprecedented characteristics of this new type of sequencing data created a shift, and methods moved on from the *seed-and-extend* framework previously used for short reads to a *seed-and-chain* framework due to the abundance of seeds in each read. As a result, the main novelties in proposed long-read mapping algorithms are typically based on alternative seed constructs or chaining formulations. Dozens of tools now exist, whose heuristics have considerably evolved with time. The rapid progress of the field, synchronized with the frequent improvements of data, does not make the literature and implementations easy to keep up with. Therefore, in this survey article, we provide an overview of existing mapping methods for long reads with insights into algorithmic details.

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1 Introduction

With the introduction of PacBio long-read sequencing and later Oxford Nanopore Technologies emerged a need for mapping long and noisy sequencing reads. The data proposed new computational challenges of mapping millions of sequences, initially at expected error rates of 10-20%. From the start, authors noticed that the seed-and-extend paradigm used in short-read mapping was not practical for long-reads. First, seed-and-extend would usually rely on a single match before extending, while long-reads required multiple consistent matches along the read to be confidently mapped. Second, the extending part, which relies on alignment algorithms with quadratic time complexity, had to be avoided given the combined length and the frequent insertions and deletions in such data. Early on, the computational problem was compared to whole-genome alignment, with the additional complexity of high error rates. Such observations lead to the novel *seed-and-chain* paradigm for mapping long-reads (see Figure 1). However, the first long-read alignment algorithms using older seeding techniques

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designed for generic sequence alignment (e.g., BLAST) were not time-competitive in their throughput compared to short-read mappers. Thus, sketching and subsampling techniques imported from comparative genomics started to appear in this domain.

Recently, specific sub-problems in the mapping domain have been identified and investigated, such as partial and gapped alignment of reads for structural variant discovery, aligning reads in repetitive regions or from non-reference alleles to correct loci, and other applications such as spliced-mapping of RNA reads. These specific problems require and motivate novel algorithmic solutions. In this survey article, we give an overview of the techniques that have been proposed over the last decade for mapping long reads to genomes.

2 Definitions and state-of-the-art of tools

2.1 Preliminaries

In this article we restrain ourselves to the problem of mapping a sequence shorter or equal to a genome (a read) to a reference genome. We further assume that the reads come from a genome that is closely related to the reference genome, such as from the same organism or a closely related species.

Let $q = (q_1, \dots q_l)$ be the read sequence of size l and $t = (t_1, \dots t_n)$ the sequence of the reference region of size n. Let $\Sigma = \{A, C, G, T\}$ and $\Sigma_+ = \{A, C, G, T, -\}$ be two alphabets, x and y strings are defined on Σ. Let $f : \Sigma_+^* \to \Sigma^*$ be a transform that maps a string to its subsequence with all "$-$" characters removed. An alignment is a pair of strings $(q', t') \in \Sigma_+^2$ such that:

1. $|q'| = |t'| = S$
2. $f(q') = q$ and $f(t') = t$
3. $(q'[i], t'[i]) \neq (-, -)$, for $0 \leq i < S$

Many alignments exist for a given pair of strings, in theory, the methods described hereafter aim at finding *good* alignments, i.e. alignments that optimize some distance between the pair of strings. The distance is computed using score functions which give rules on the characters pairing.

With *read mapping*, we mean the procedure to find a read's location on the reference genome. Typically, long-read mapping is performed by seeding and chaining the seeds into high-scoring regions on the genome. In this study, a *read alignment* implies both that the read has been mapped to a location, and that a pairwise alignment between the read and the genome at the mapped location has been performed. Algorithms exist to compute optimal semi-global pairwise alignments with respect to a score function. However, their complexity in $\mathcal{O}(n \times l)$, disqualifies them in the context of handling big data such as sequencing data. Therefore, methods of the literature use heuristics to perform read mapping on a reference. They do not guarantee to find the optimal solution.

In our survey, we discuss read mapping to a genome sequence. We will use the terms *query* for a read and *reference* to denote the genome.

2.2 Overview of fundamental ideas

To our knowledge, the first mapper explicitly written for long-reads was `BLASR` [12], although short-reads mappers had been adapted for the long-read usage [37, 41, 47]. While solutions specialized for either Nanopore [5] or PacBio [28] characteristics appeared, most modern mappers work for both technologies with adapted parameters. `BLASR` presented itself as an

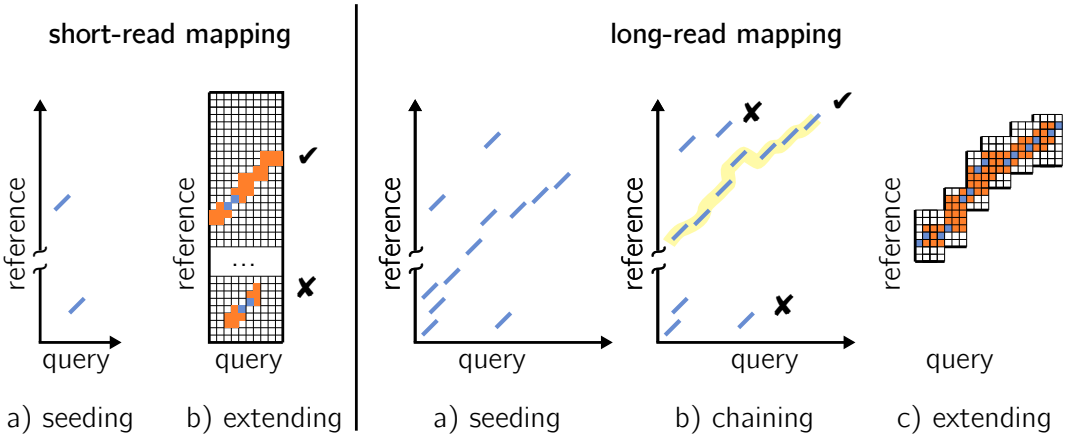


Figure 1 Differences in the main steps between short-read mapping (left) and long-read mapping (right). *Query* denotes the read and *reference* denotes a genome region. Mainly, short-read approaches extend (orange parts) from a single anchor (in blue) on the whole read length while long-read approaches gather multiple anchors, and chain (yellow line) them in for a candidate extending procedure that is done between pairs of anchors.

approach descending from both genome to genome alignment methods (such as `MUMmer` [16]) and short-read mappers. The paper contains seminal ideas used in modern long-read mappers such as the seed-and-chain paradigm.

Seeding Seeding is the first operation in the heuristics used by mapping techniques.

▶ **Definition 1.** *A **seed** is a subsequence extracted from the query or the reference.*

The purpose of seeding is to find relatively small matching segments between the query and the reference that serves as markers for reference regions that potentially are similar to the read. The reason seeding is used is that it is typically computationally efficient to find matching seeds that can narrow down regions of interest compared to, *e.g.*, global alignment of the read to the reference. As we will see in Section 3.1, seeds can be of different nature. Seeding relates to pattern matching, although in sequence bioinformatics, practically all approaches work under the paradigm which indexes the reference and query the index to find matches. The underlying assumption is that once the index is created, it can be used several times to map different query sets. To save space, reference indexes can be in a compressed form. Once matches are found, a second operation aims at finding sets of concordantly ordered seeds between the query and the reference (*chaining*; section 3.3 and to "fill the gaps" between seeds as well as providing the final nucleotide level alignment (*extension*; section 4). Seeding was quickly identified as a critical phase in long-read mapping, which led to novel proposals [49, 42, 71].

Sketching and subsampling An important idea for seeding is *sketching* that was introduced in `MHAP`, a long-read overlap finder implemented in an assembly algorithm [7]. Although long read mappers had already been proven faster than alignment approaches [71], the rationale was to improve the time efficiency of the long-read mapping problem in comparison to the throughput of the second generation sequencing mappers. Sketching consists of compressing the information of a set (here a set of k-mers) into a fixed-length vector (a sketch) of representative elements called fingerprints. By comparing two sketches, one can approximate

a similarity estimation of the two sets quickly and independently of their initial set sizes. Several approaches exist [9, 54, 14]. `MHAP` relied on sketching with a MinHash approach. MinHash [9] is a sketching technique based on locally sensitive hashing, which produces an unbiased estimator for the Jaccard distance between two sets by selecting a subsample for each set and comparing them in a very efficient way. Thus, `MHAP` overcame a space limitation of `BLASR` which would index the whole reference. The type of matches (exact, fixed-size) induced by `MHAP`'s approach also allowed to perform rapid queries. An important limitation of `MHAP` was that the sampling technique gave no guarantee to uniformly cover the query's sequence. This led to the development of subsampling techniques which have been adapted to approximate distances between sequences, starting with `minimap` [42]. Seeding is still an active research area of long-read mapping with several recent developments [35, 70, 22, 60]. Sketching and subsampling are discussed in Section 3.1.2.

Chaining A key intuition is that in short-reads mapping, the extending procedure could start after finding a single shared seed between the query and the reference, called anchors (for details on techniques related to the previous sequencing generation, we refer the reader to a methodological survey of short-read mapping [3]).

▶ **Definition 2.** *An **anchor** is a matching seed between the query and the reference. It is represented by a pair of coordinates on the query and the reference.*

In long-read mapping, the length of the reads and the short seed length used due to the initial high long-read error rates can lead to a large number of seed matches. It is therefore necessary to reduce the search space by selecting subsequences of ordered anchors (chains).

▶ **Definition 3.** *Let $\mathcal{A} = [a_0, a_1, \ldots, a_k]$ be an list of anchors defined by their coordinates on the reference and the query. A **chain** is a subsequence of $\mathcal{A}$ of length $c \leq k$. A colinear chain is a subsequence of $\mathcal{A}$ in which anchors are sorted by such that if $i < j$, a_j is above and to the right of a_i in the $(reference, query)$ plane.*

Drawing inspiration from genome-wide mapping, `BLASR` introduced a chaining step which aims at selecting high-scoring chains from a set of candidate chains. Chaining allows to reduce the final step of a long-read aligner (the base level extension) to alignment of sub-regions between ordered anchors in chains. Chaining in long-reads has been solved using various dynamic programming procedures [71, 61, 43]. In particular, the continuous work effort put in `minimap2` [42, 43, 44] in both seeding and chaining processes made it a baseline for many other tools' development.

While this survey covers the genomic mapping aspects, other important contributions have dealt with adapted procedures in the case of long-read RNA mapping [53, 65, 50, 74], and structural variant identification [68, 48, 24, 73], or other specialized problems [55]. Other related research focused on read-to-read overlap detection [20, 75][2], or alignment-free/pseudo-mapping approaches [33, 13]. Finally, here we describe algorithmic solutions working on the nucleotide sequence, but raw signal mappers for Nanopore long-reads is also an active area of research [29, 76, 38].

[2] and the unpublished `DALIGNER` `https://github.com/thegenemyers/DALIGNER`

3 A survey of algorithmic steps

3.1 Seeding almost always uses sampled, exact, fixed-length matches

Seeding is the procedure that consists in collecting a set $\mathcal{S}$ of seeds from the reference, then finding matches between the query's seeds and $\mathcal{S}$. In order to find matches efficiently, $\mathcal{S}$ is stored using an index data-structure. In the following we detail the different types of seeds that can be encountered and Figure 2 illustrates some of the approaches that have been proposed.

3.1.1 *k*-mers

Substrings of length k, or k-mers, are perhaps the most commonly used seed in bioinformatics. Such seeds can be extracted from the reference and stored for queries with little computational cost. This makes k-mers popular in mapping and alignment applications that require high-performance to scale for millions to billions of reads. A k-mer seed can be indexed by using a hash function to produce an integer value (usually as a 32 or 64-bit integer), which is then added to a hash table. This makes indexing of k-mers computationally cheap, provided that the hash function and hash table implementations are efficient. Methods to efficiently hash k-mers have been proposed [56], which uses the previous k-mers hash value to compute the next one using a rolling hash function.

Both a strength and a weakness with k-mers are that if a k-mer match is found, it is guaranteed to be exact. While it is desirable to produce matches only to identical regions, a downside is that mutations will "destroy" the k-mers in the region. This has been studied theoretically in [6] where the authors derived analytical expressions for the mean and variance of regions without matches for a given mutation rate.

3.1.2 *k*-mer subsampling techniques

As any two consecutive k-mers share most of their sequence and are therefore mostly redundant, we could reduce the memory overhead and query time without losing much of the information if not all adjacent or nearby k-mers were stored. In the following, we present different methods that allow picking a subsample of representative k-mers as seeds. These approaches have proven their efficiency at reducing drastically the number of objects to index while keeping high sensitivity and specificity for matches.

No distance guarantee between seeds: sketching Sketching gives typically no guarantee of distance between two k-mer representatives, which means that a very large gap can appear between two consecutive selected k-mers. An early work [7] bases its long-read mapping strategy on MinHash sketching by using a total ordering on the k-mers' hashes (see (a) in Figure 2), and keeping minimal hashes in the ordering (representing their k-mers). Related to read mapping, it was used to perform genome-length sequences alignment-free mapping [33] and to find read-to-read overlaps in long-read assembly [69]. However, fixed-size sketches do not adapt well to different read lengths since the number of fingerprints remains constant for any distinct k-mer number. Because of this, two similar regions from sequences of different sizes will not automatically have the same representative, which is a desired property for seeding. Therefore this approach was later replaced by other subsampling strategies in following papers.

Distance guaranteed between seeds On the contrary, subsampling techniques have been proposed to guarantee that for a certain amount of consecutive k-mers, at least one will be selected. The first k-mer subsampling technique proposed in the context of long-read mapping was *minimizers* [62]. In our framework, minimizers are sampled k-mers given two parameters m and w. Given the set k-mers starting in a window $[m, m+w-1]$ of w positions on the sequence, a minimizer is the minimal value over this set (and therefore the k-mer associated with this minimal value) (see (b) in Figure 2). Minimizers are produced by extracting a minimizer in each window $w \in [0, |S|-w+1]$ over a sequence S. The techniques used for assigning values to k-mers are discussed in section 3.2.1. Minimizers are agnostic to their relative abundance over a sequence. Different optimizations have been proposed to reduce the density of sampled minimizers in some regions. Weighted minimizers [35] implement a procedure to select k-mers of variable rareness. In order for k-mers from highly repetitive regions not to be as likely as others to be selected, it first counts k-mers, and downweights frequently occurring ones. Then it takes this weight into account for the hashing procedure. Other subsampling techniques include syncmers [18] and minimally overlapping words (MOW) [23]. The first was used in the context of long-read mapping [70] in an alternative implementation of `minimap2` and even more recently in [60][3]. For their construction, syncmers use s-mers of size $k-s+1$ ($s<k$) occurring within k-mers (see (c) in Figure 2, and Supplementary Figure S1 for an illustrated difference with the minimizers). The k-mer is selected if its smallest (in the sense of an ordering, typically on hashes) s-mer meets some criteria. An example criteria is that the s-mer appear at position p within the k-mer ($1 \leq p < k-s+1$). By construction, syncmers tend to produce a more even spacing between sampled seeds while still allowing a distance guarantee.

Context dependency of subsampling techniques Minimizers are generated through a *winnowing* procedure which compares all k-mers of a given window. The choice of representative k-mer in a given window depends on the window's k-mer content. This property has been called *context dependency* [70]. On the contrary, syncmers can be described as context-free since each k-mer's capacity to be selected is independent. Being context-free implies better conservation of the overall sampled region under mutations. Indeed, context-dependent representatives can tend to be broken over several consecutive windows because of the k-mers propagating an error. Finally, other aspects can be considered, such as the related density [70] (informally, the expected number of selected k-mer over the total number of k-mers), or the deviation of minimizer-based strategies from the initial unbiased Jaccard estimator [6].

3.1.3 Fuzzy seeds handling substitutions

Due to read errors and SNPs between the reference and sequenced organism, it is in many scenarios desired that a seed match between the query and the reference even if the seed contains a substitution. Put differently, we would want similar k-mers to hash to identical hash values. A hash function that would produce identical hash values for similar but not necessarily identical inputs is usually referred to as a locality-sensitive hash function. We will refer to seeds produced under such methods as fuzzy or inexact seeds.

Several methods to produce inexact seeds have been described. Perhaps the most common one is spaced-seeds. Within a spaced-seed, some positions are required to match (called

[3] `https://github.com/bluenote-1577/os-minimap2` and `https://github.com/Shamir-Lab/syncmer_mapping`

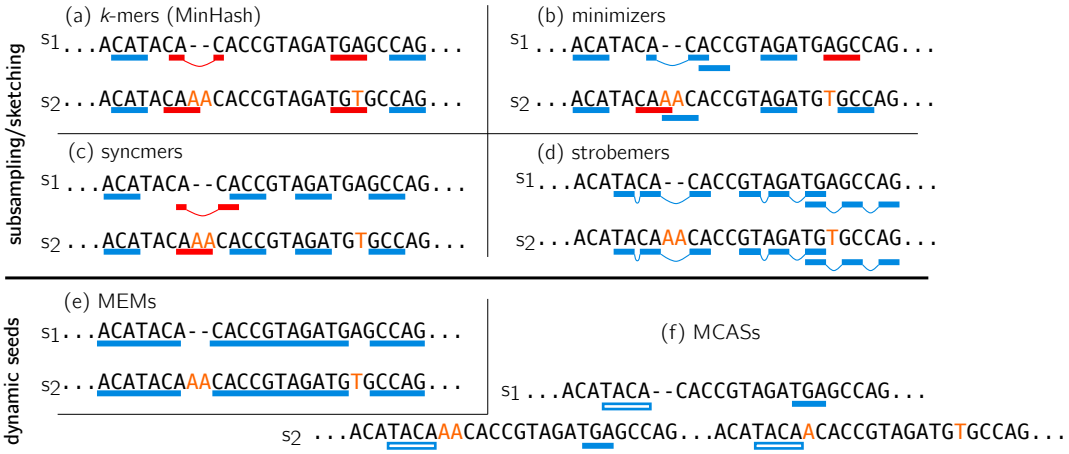


Figure 2 Overview of major seeding techniques used in long-read mapping. The figure presents informally which bases will be selected (underlined) given the technique. For the sake of simplicity, we are not consistent with a hash pattern (for instance lexicographical order) when selecting the seeds in the different panels. A more comprehensive example following a pattern is presented in Supplementary Figure S1.
We use two related sequences s_1 and s_2 which differ from a (A/T) substitution and a AA insertion in s_2 (in orange) to show the possible differences in selected bases (underlined in blue or red) due to mutations/errors. (a) k-mer seeds of length 3 selected with MinHash. k-mers have no distance guarantee and are picked based on having minimal hash value in total ordering of the hashes. (b) Minimizers picked with $k = 3$ a window size of w. Minimizers has a maximum distance guarantee given by w but has no minimal distance guarantee and may therefore subsample densely in some regions. (c) A subset of strobemers consisting of three *strobes* (short k-mers) are illustrated. The first strobe is picked at the seed start position and the remaining strobes are selected in windows downstream from the start strobe. (d) Syncmers selected with $k = 3$, s and the condition for selection are not detailed. Syncmers are context-free and respect a distance guarantee which tends to create pairs of evenly spaced seeds. (e) MEMs computed as exact matches until reaching a position that breaks the exactness. (f) MCAS. s_1 remain the same than in other panels, s_2 now contains two copies of a repeat, each has accumulated different mutations. A blue bordered region gives an example of a substring which is not a MCAS: it is repeated in the two copies. The blue-filled underlined region is a MCAS.

fixed positions) while the remaining positions can be ignored (called wildcards or don't care positions). Within a k-mer, fixed positions can be selected to be wildcards by applying particular masks on the k-mer's bases [32]. A problem with spaced-seeds is to find a fixed-position profile to minimize the overlap of the fixed positions in the seeds [31]. Although the computation of good spaced-seeds has been optimized [32], constructing good spaced-seeds profiles requires extra computational work compared to k-mers and is therefore slower to compute, and in practice, multiple different seeds are used [46] to increase sensitivity, which requires storing multiple hash tables. Another limitation with fuzzy seeds for substitutions is that seeds will, just as for k-mers, not match over indels.

While fuzzy-seeds handling substitutions have been used e.g. in metagenome short-read classification [10] and permutation-based seeds were implemented for short-read mapping [40], few of long-read mapping algorithms implement them. As indels are a frequent source of variability on long-reads, the computations to construct these seeds may not be worth the trade-off in increased sensitivity. An exception to this is a recent seeding mechanism [22], where the authors use a variant of SimHash [14](an alternative locality sensitive hashing to

MinHash) to construct fuzzy seeds over subsampled k-mers using the minimizer technique [62]. The authors showed read alignment can be improved both in terms of speed and accuracy by integrating their seeds into `minimap2` [43].

3.1.4 Fuzzy seeds handling indels

A common source of errors and biological variation is short insertions and deletions. Neither the exact seeds nor the fuzzy seeds discussed so far are designed to match over such variability. Traditionally, matching over indels has typically been solved not by a single query of a fuzzy seed, but instead involved queries of a few short k-mers at a close occurring distance which are then inferred as a matching region. While several queries in a nearby region usually provide gold standard sequence similarity queries [4, 36], it comes at a significant computational cost. Along the same vein [71] proposed to index one so-called spaced k-mer as a seed in each position of the reference and would, query three different seeds for each position in the query (representing a mismatch, a deletion of length one, and a mismatch and a one nucleotide insertion). This design was motivated by overcoming the frequent substitutions and short indels present in third-generation sequencing techniques, but would only handle indels of one nucleotide (we provide details on this scheme in Supplementary Figures S2 and S3). Earlier, there have been works to handle higher error rates with so-called covering template families [26] that can guarantee a match up to any error rate e. Naturally, with higher e, more seeds need to be indexed and queried and it becomes computationally prohibitive to use such seeding.

To remove the overhead of post-processing of nearby seeds [4, 36] or multiple queries [71] per indexed reference seed, one can instead link the k-mers up into a seed before storing it in the index. Such indexing has been favorable in the long-reads era where indels are frequent. One proposed method is to join two nearby minimizers into a seed. Joining nearby minimizers is usually a relatively cheap computation as the minimizers constitute a subset of the positions on the reference. Such a seeding technique has been used for long-read overlap detection for both genome assembly [15] and error correction [66]. While such indexing is relatively fast and matches regions over indels, the joining of nearby minimizers implies that if some minimizer(s) are destroyed due to mutations in a region, all of the seeds in that region will be destroyed. Put another way, nearby seeds share the same information (in the form of a shared minimizer). Therefore, alternative approaches such as strobemers [63] (see (d) in Figure 2) have been described, where the goal has been to reduce the information between closeby seeds by linking k-mers at seemingly random positions within a window. Such pseudorandom linking implies that if one seed is destroyed due to a mutation, a nearby seed may still match. Strobemers have shown effective at finding matches between long-reads and for long-read mapping [63], and have been used in short-read alignment programs [64] but they come at an increased computational cost to joining neighboring minimizers.

Another way to alleviate the issue that mutations will destroy consecutive seeds in the neighboring minimizers technique is to apply the SimHash technique on strobemers instead of k-mers [22]. Such seeds were used for long-read overlap detection [22] and the authors show that for the highest quality long-reads (PacBio HiFi), such seeds can speed up long-read overlap detection by an order of magnitude or more while retaining the same downstream level assembly accuracy.

3.1.5 Dynamic seeds

Previously discussed seeds share the characteristic that they can all be produced and inserted in a hash table, and consequently, only require a single lookup. This is typically fast and, hence, popular to use in long-read alignment algorithms. The downside is that if a seed is different in a region between the reference and the query (e.g., due to an error), there is no way to alternate the seeds in this region at alignment time. There are however other types of constructs, that we here refer to as dynamic seeds, that can be computed on the fly at the mapping step, and then used as seeds downstream in the read alignment algorithm.

Maximal Exact Matches Maximal exact matches (MEMs) [16] are matches between a query and reference sequence that cannot be extended in any direction on the query or reference without destroying the match (see (e) in Figure 2). These are typically produced by first identifying a k-mer match, and then an extension process is applied. MEMs are guaranteed to be an exact match between the query and the reference and are bounded below by length k but do not have an upper threshold for seed size. As there can typically exist many MEMs, a subset of MEMs that has a unique location on both the query and reference is sometimes considered. MEMs or similar approaches have been used in one of the earlier long-read alignment programs (e.g., `BWA-MEM`) [41, 12] and for long-read splice alignment [65], but these seeds are more computationally expensive to compute and are typically slower than single-query seed-based algorithms.

Anchors from minimal confidently alignable substrings (MCASs) If a query was sampled from a repetitive region in the reference, one may likely find several clusters of anchors across the reference. Further dynamic programming operations to decipher the true origin region of the query are typically costly or even unfeasible if too many copies have to be considered. Even in the case a query is located on the reference, it might be attributed to the wrong copy because of the sequencing errors. A recent contribution [34] proposed a solution for handling seeding in repetitive regions. The procedure finds smallest subsequences that *uniquely* match (MCASs) between the query and the reference (see (f) in Figure 2). There can be as many as the query length in theory. In practice, the more the repeats are divergent, the shortest the MCASs since a base pertaining to a single copy is more likely to be met. MCASs are computed using an alignment procedure, which means that *uniquely* matched must be understood as a relative property. For each position on a query, the best and second-best alignment scores are compared, and a substring is considered uniquely matched if the difference between the scores is above a threshold. It is interesting to bound the maximal size of MCASs, both for performance purposes and because they may become less specific as to their size increase. Fixed-size, exact match anchors (minimizers) are then extracted from MCAS regions.

3.2 Implementation of the seeding step

3.2.1 Seeds transformations before indexing

Originally, minimizers use a lexicographical ordering. However, in our four base alphabet, this can tend to select sequences starting with long alphabetically smaller runs such as "AAA...". Random hash functions assigning each k-mer a value between 0 and a maximum integer are preferred [67].

Oxford Nanopore reads are known for accumulating errors in homopolymers, typically adding/removing a base in a stretch of a single nucleotide. Sequences can be homopolymer-

compressed before finding k-mers. Homopolymers longer than a size s are reduced to a single base, then k-mers are computed over the compressed sequence. For instance, for $s = 3$, $k = 4$, an original sequence ATTTTGAAAACC is compressed to ATGACC, and the final k-mers are ATGA, TGAC, GACC. This procedure allows finding more anchors while indexing fewer k-mers/minimizers. Homopolymer compression is ubiquitous in long-read mappers.

In regions of low complexity (e.g. ATATATA, CCCCC) the standard minimizer procedure keeps all minimal k-mers in windows. It is then possible for two k-mers to get the minimal value and to be selected, which tends to over-sample repetitive k-mers. A *robust winnowing* procedure is proposed in [35], which avoids the over-sampling effect by selecting fewer copies of a k-mer, but increases the context dependency phenomenon.

3.2.2 Hash tables prevail for seed indexing

Indexing of fixed size is usually done using hash tables (although FM-indexes for k-mers exist [8]). In the context of subsampling, invertible hash functions have been a key asset for using minimizers as k-mers representatives. In other words, a hash value is associated with one and only one k-mer, and the k-mer sequence can be retrieved from the hash value (using reciprocal operations). This choice allows a very fast k-mer/minimizer correspondence but is costly as it implies that the fingerprints of the hash table are not compressed (which is mitigated by the subsampling). Minimizers are then used to populate a hash table, which associates them to their position(s) in the reference and their strand information (usually hashed seeds are canonical k-mers: the smallest lexicographic sequence between the original k-mer and its reverse complement).

Variable-length seeds are indexed in full-text data structures (suffix arrays, FM-index), which allow to find and count arbitrarily long queries in the reference. They have been used in the first versions of long-read mappers. Variable-length seeds type can be longer to query in the structure, while hashed matches are queried in constant time. Since minimizers represent fixed-length k-mers, hash table solutions mainly prevail.

3.2.3 Seeds selection at the query

In [43], it is proposed to select all minimizers from the reference during the indexing phase (although the latest versions include the weighted k-mers and robust winnowing heuristics), and to soft mask some representative k-mers at the query. The procedure simply avoids k-mers seen too many times according to a fixed cutoff. The authors noticed that in cases where a query is sampled from a repetitive region, such a procedure prevents it to be seeded. Therefore, an update was proposed [44], which detects if low occurrence k-mers are too far away in a query, and in this case, allows sampling minimizers in the repetitive region in between (and keeps some of the lowest possible occurrences among these minimizers). Techniques that use longer fuzzy seeds (e.g., strobemers) [22] reduce the number of masked regions, although it comes at the cost of sensitivity. Another approach [61] computes a new set of minimizers on the targeted reference region in order to obtain finer candidate chains, in particular in repeated or low complexity regions.

3.3 Chaining is dominated by dynamic programming with concave gap score functions

3.3.1 A dynamic programming problem

Once the reference's seeds are indexed, a set of seeds is extracted from the query and looked up in the index to find anchors. Anchors' positions on the query and reference are stored, as well as the forward/reverse information. Instead of directly extending the alignment between anchors, as it is done in short-read mapping, a step of chaining is added and meant to accelerate further extensions. Chaining acts as a filter and a guide for smaller extensions that need to be realized only between selected anchor pairs. Without it, too many extension procedures, most of which would be dead-ends, would have to be started.

In an ideal case, there is a unique way of ordering anchors by ascending Cartesian positions in the $(reference, query)$ space, which passes by all the anchors. In practice, some anchors are spurious, others correspond to repeated regions and yield different possible chains. Moreover, over parameters have to be taken into account. Thus, methods optimize different aspects (also illustrated in Figure 3):

A1) Do not allow anchors which are not ascending either by the anchors' start or end coordinates in both the query and reference (see first case in Figure 3).
A2) Avoid discrepancies in diagonals between anchors (second case in Figure 3).
A3) Do not allow large spaces between consecutive anchors of the chain (see third case in Figure 3).
A4) Favor the longest possible anchor chain (fourth case in Figure 3).
A5) If inexact matches in seeds are possible, find a series of anchors ensuring a minimal Levenshtein distance between the query and the reference.

The problem of finding an optimal chain using non-overlapping anchors has been called the *local chaining problem* [1], although in this application anchors can overlap. The score $f(i+1)$ represents the cost of appending an anchor a_{i+1} to a_i to the chain. This score is often called the *gap score* in the literature, though it includes other constraints, as described above. The chaining problem for long reads seeks to find an optimal colinear chain with a positive gap score.

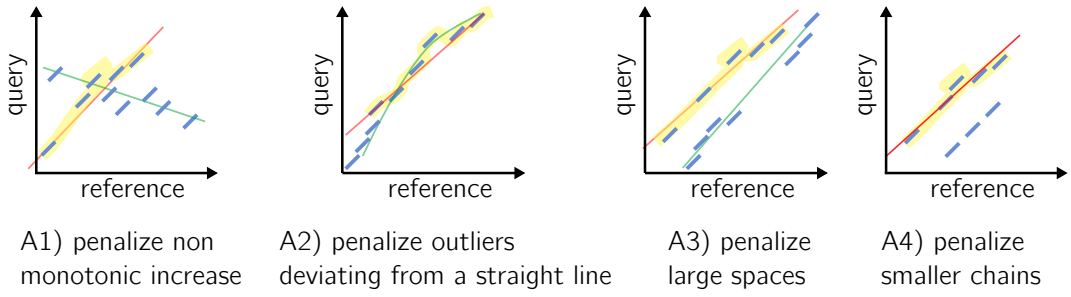


Figure 3 An illustration of the different constraint taken into account in the gap score functions. The reference axis shows a genome region of interest where anchors were found, not the whole reference. A1–A4 correspond to items in the text in section 3.3.1. Anchors are showed in blue. The selected chain with respect to the described constraint is highlighted in yellow and a line approximately passing by its anchors is showed in red. The line passing by the longest chain is showed in green.

Mainly, methods use either a two-step approach: 1-find rough clusters of seeds as putative chains, followed by 2-find the best scored chain among the selected clusters; or work in

a single pass and apply a custom dynamic programming solution to find the best anchor chain. We can start by noting that one of the first mappers dedicated to long-reads solved a global chaining problem to determine a chain of maximum score, by fixing starting and ending points (anchors) such that their interval is roughly the size of the query [12]. Such an approach would easily discard long gaps and spaces in alignments.

3.3.2 Chaining in two steps

Clusters of seeds are found through single-linkage in 2D space The two-step approaches rely on a first clustering step. Although it tends to be replaced by single-step chaining (see Section 3.3.3), in the following we describe the fundamental ideas of the clustering. Methods first find rough clusters of anchors by considering a discrete $(reference, query)$ position space. In this space, an anchor realizing a perfect match is a line of the size of the seed. This line should have a 45-degree angle, which also corresponds to the main diagonal of a $(reference, query)$ alignment matrix. The same idea stands for a set of anchors. However, because of insertions and deletions, each small line materializing an anchor may not be on the exact same diagonal, thus realizing approximate lines in the $(reference, query)$ space. A method from image processing has been proposed to find approximate lines in this space: the *Hough transform* [17], which makes it possible to detect imperfect straight lines in 2D space. Contrary to linear regression which would output the best line explained by the anchor distribution, here an arbitrary number of straight lines can be output and considered (see Supplementary Figure S4 for an illustration). Hough transform or other similar anchor grouping algorithms ([61] proposes to delineate fine-grained clusters in order to increase the chaining specificity in repeated regions) all can be assimilated to single-linkage clustering in 2D space, which finds groups of anchors placed roughly on the same diagonal.

Anchor chaining using longest subsequences of anchors The previous clustering techniques aim at finding lines in groups of anchors that can be approximately colinear. To determine truly colinear chains, a subset of anchors can be ordered by finding a longest increasing subsequence (LIS) of anchors. Let each anchor be mapped to $1 \dots n$ integers. The LIS problem consists in finding a longest increasing subsequence from a permutation P of the set $\{1, 2, \dots c\}$, which can be solved in $\mathcal{O}(c \times log(c))$.

In the case of exact fuzzy seeds, inexact matches are to be dealt with on top of the initial increasing chain problem. Indeed, one wants to obtain the closest base-wise anchor chain. In this case, the problem is converted to LCSk (longest common subsequence in at least k-length substrings). Note that there is a correspondence between LIS and LCS. The LIS of P is the LCS between P and the sequence $(1, 2, \dots c)$. In both cases, neither the longest nor the increasing requirements are sufficient to find correct anchor chains: they lack definitions for other constraints, such as distance between anchors or the possibility to allow large gaps. They are complemented with heuristics or replaced by more recent approaches in Section 3.3.3. In addition, several methods use graphs built over anchors as backbones to the chaining and alignment steps [73, 49, 71] (one approach is described in the Appendix). Because they would fail to take into account distances between anchors, these methods have been replaced by dynamic programming approaches relying on gap score functions.

3.3.3 Chaining in a single step: gap score functions

The main drawback of the approaches previously described in 3.3.2 is that though large spaces between two anchors of a pair must be avoided, some spaces correspond to gaps in

the alignment and can be kept. In order to deal concurrently with these two problems, most recent methods drop the two-step clustering and LIS to directly apply a custom dynamic programming solution. It is globally the same spirit as LIS, but integrates a more fine-grained gap penalty solution. It defines a cost function that grants a maximum penalty for non-monotonic increasing seed chains.

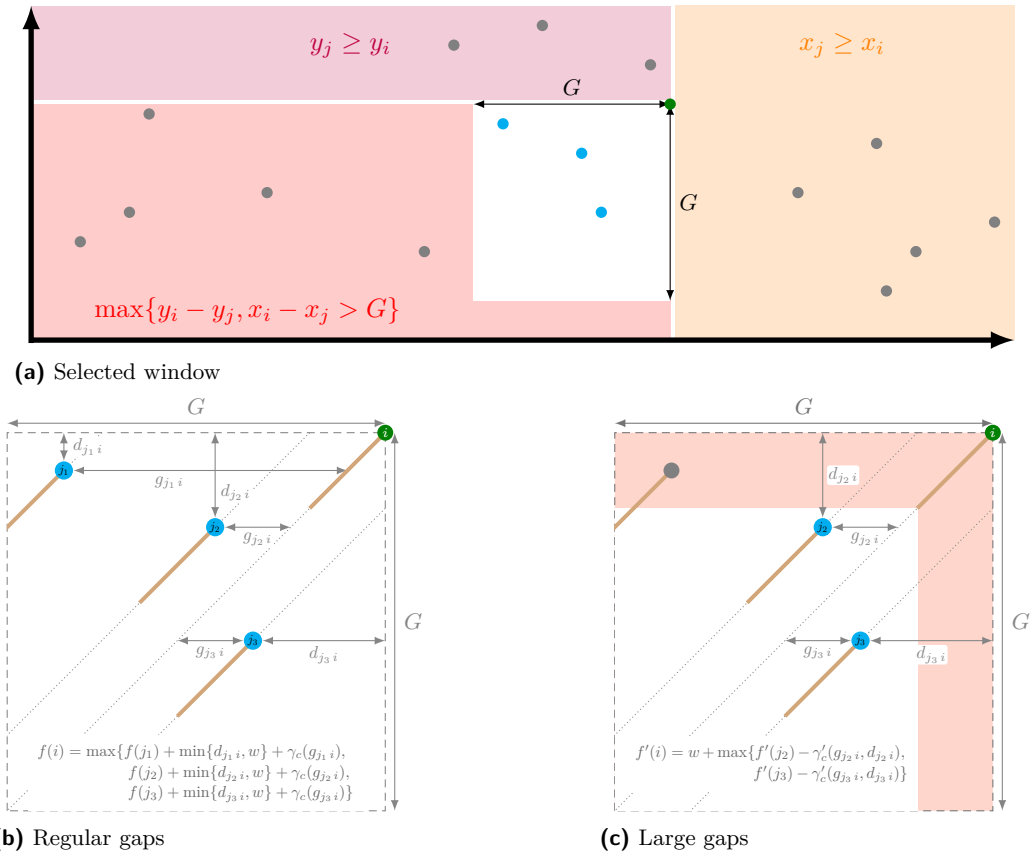
Concave gap functions The cost function is designed to handle the gaps induced by frequent indels in the data. Intuitively, it is likely that indels happen in clusters of n positions rather than at n independent positions in the chain because some regions on the query might be particularly spurious, or because of local repeats on the reference. Therefore, the same cost is not attributed to opening a gap and extending a gap, thus a linear gap function does not fit. The choice of gap functions which are concave (verifying the *Quadrangle Inequality*) improves the time complexity by using the *wider is worse* strategy [25, 21]. In practice, these concave gap functions are affine, a set of affine functions, or a combination of affine and log functions, as proposed in [43]. We chose to present `minimap2`'s [43] gap functions in Figure 4 as they are adopted without modifications in most current papers (with the recent exception of [61]). Chains are built by aggregating close anchors of smaller coordinates to the current anchor by penalizing the shifts compared to the main diagonal. In Figure 4, Panel 4a presents how the set of possible anchors to prolong the chain is selected. Panel 4b illustrates the dynamic function's parameters. The complete description of the functions is available in the Appendix.

Heuristics are applied to rapidly drop a dynamic programming procedure in regions that are unlikely to align and to avoid $O(c^2)$ worst cases. Based on empirical results, these heuristics mostly check if seeds are not separated by too large regions and drop the chaining procedure if the score becomes too low.

Solutions for large gaps Noticing that [43]'s original approach would be failing in large gaps, one contribution [61] proposed techniques to perform dynamic programming with a family of concave functions by relying on a previous work [21] (built on a prior clustering step as described in 3.3.2). Recently, [43] integrated a solution designed for mapping long structural variants in pangenomic graphs [45]. Its recent versions entail a cost function for regular gaps, and a long gap patching procedure. Then it chooses the cheapest solution to move on to the alignment step. The gap patching procedure uses a linear gap cost so that it has a higher long-gap opening cost in comparison to the regular procedure but at a cheaper extending cost. The chaining with a linear function is solved with a range minimum query (RMQ) algorithm using a balanced binary search tree [1, 59]. It allows to solve the linear chaining in $\mathcal{O}(c \times log(c))$. Although this time complexity can be improved in $\mathcal{O}(c)$ by using range maximum queue [11], the implemented algorithm is more costly than the solution for regular gaps, which is preferred if possible. Panel 4c in Figure 4 illustrates the dynamic function for large gaps.

3.3.4 Mapping quality scores have been adapted for ranking chains

The described methods may deliver a set of chains that satisfies the chaining score threshold. To choose among the candidates and decide the final location, chains can then be categorized into primary/secondary chains. Chains with a sufficient score are ranked from highest to lowest score. Primary chains are those with the highest scores which do not overlap with another ranked chain for the most of their length. Secondary chains are others. Mapping quality, which is a measure that had been introduced to assess short-reads mapping, is



(a) Selected window

(b) Regular gaps

(c) Large gaps

Figure 4 Outline of chaining of `minimap2`. Figure a shows for an anchor (in green) the selected region (in white, G is the gap threshold) to find available anchors to continue chaining (in blue). Figures b and c give respectively the dynamic programming functions for regular and large gaps size. Anchors are shown as segments ending with green or blue dots with the same color code as in Figure a. Besides, for the large gap size (Figure c), to improve the complexity, the anchors do not overlap (available anchors are not in the red zone). d_{ji} represents the smallest "distance" between the two anchors (but is not really a distance by definition), w is the minimizer window size, g_{ji} is the gap length, and the γ functions are the concave gap functions.

redefined for long-reads with slight variations according to articles. It reports, for chains, whether the primary is very far in terms of score from the best secondary, and if it is long enough.

4 Extension step and final alignment computation

Extenstion step In order to allow gaps, the methods rely on local alignment between pairs of successive anchors using classical algorithms [27, 57] derived from Needleman and Wunsch [58]. They are based on alignment matrices, which aggregate the base-wise alignment scores from the two prefixes (top left of the matrix) to the two suffixes (bottom right).

To compute the scores and report them in a matrix, affine cost functions allow to allocate different penalties for opening and extending gaps and therefore can favor short or long gaps. More precisely, such algorithms use pairs of affine gap score functions and choose the cheapest cost between the scoring for short gaps (i.e. less costly to open, costly to extend),

and the scoring for long gaps (i.e., more costly to open, cheap to extend). Allowing long gaps has a drastic negative impact on the alignment efficiency because more cells in the alignment matrix have to be considered.

Heuristics for speed-up and quality enhancement Therefore, alignment is commonly accelerated through vectorization, using single instruction multiple data (SIMD) sets of instructions, which increase the computational throughput by passing simultaneously several matrix cells for the processors to evaluate. Second, practical alignment implementation relies on banded alignment, which, simply put, bounds the alignment matrix in a band of size ℓ around the top-left – bottom-right diagonal. Inspired from `BLAST`'s X-drop [4], [43] implements a Z-drop procedure. X-drop quits extending the alignment if the maximum score reached at some point when aligning the prefix drops by more than X. Z-drop adds the possibility not to drop the extension during large gaps.

Due to sequencing errors, some spurious anchors main remain in a chain, which can lead to a suboptimal alignment. At the alignment step, [43] chooses to remove anchors that produce an insertion and a deletion at the same time (>10bp) or that lead to a long gap at the extremity of a chain. Another solutions [12] involves to re-compute a chain with novel anchors computed on a window that comprises the alignment.

5 Future directions

On top of mentioned novel seeding techniques bringing new properties concerning their coverage of the seeded sequence and robustness to errors and mutations (syncmers, strobemers [70, 60, 22]), we can expect to see advances in the chaining and extending parts in the coming months.

Indeed, the usage of *diagonal-transition algorithms* which was initially define for edit distance [72, 39, 30] has been reactivated recently for the gap-affine model with the wavefront alignment algorithm (WFA, including [52, 51, 19]). More precisely, instead of using dynamic programming on the adjacent cells, WFA transposes the optimization problem on the diagonals and the score. In particular, WFA has the potential to make computation faster for similar sequences and large gaps (by setting the score accordingly and adapting the scoring). A current result shows that we can exploit the massive parallel capabilities of modern GPU devices to accelerate this wavefront alignment algorithm [2]. Currently, different implementations exist that have been tested on long reads [52][4], although no dedicated long-read mapper integrates them yet.

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Appendix

Details on subsampling techniques In Supplementary Figure S1, we present an example of the difference in the selected bases between a minimizer approach and a syncmer approach.

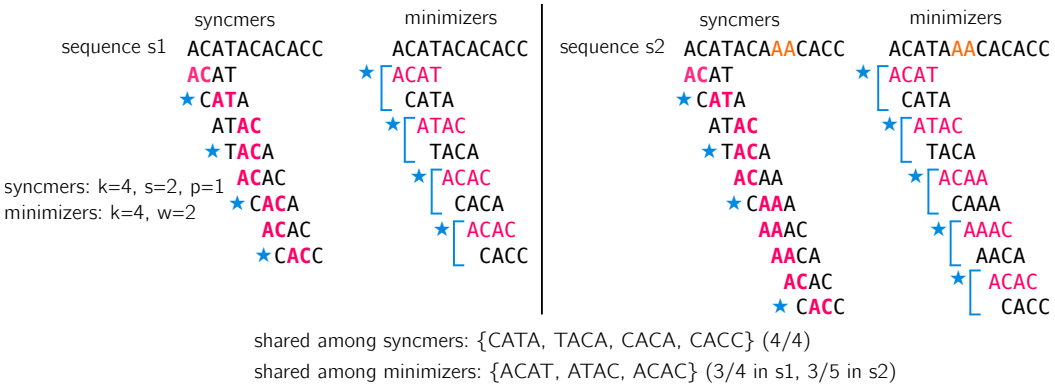

Figure S1 Usage syncmers and minimizers for comparing two similar sequences. Sequences s1 and s2 differ by a AA insertion in orange in S2. We show how selected syncmers and minimizers do not produce the same sets of representative k-mers and therefore yield different fractions of shared k-mers between s1 and s2. The k-mer size is 4, the s-mers in syncmers (smallest showed in pink, we choose the lexicographic order) are of size 2, and in this example we require that the smallest s-mer appears at the first position of the k-mer. Minimizers have windows of size 2, materialized in blue, with the minimizer in pink. The selected k-mers are highlighted using a blue star.

Graphmap's indexing strategy for fuzzy seeds Graphmap builds two hash indexes from two types of shapes , called `6-1-6` and `4-1-4-1-4`. As shown in Supplementary Figure S2, for each position is seeded (no subsampling). A seeded key corresponds to the subsequence at a given position of the reference when applying the shape mask: each *don't care* (*) base is skipped.

Then, for each read in the query, several lookup keys (for mismatch, deletion and insertion) are built from a shape (Supplementary Figure S3). To that extent, the lookup key treats the *don't care* base in three different ways. The mis(match) shape has the same behaviour as the indexed key, i.e., the *don't care* base are skipped. The insertion shape skips two bases: the initial *don't care* base and the base next to it. Finally the deletion shape will simply build the key and keep all the base including the *don't care* base. In total, for a number d of *don't care* base, 3^d different keys are built per shape.

Graphmap's backbone graph for LCSk Because of the possible spurious matches that occur because of the ambiguous bases, `Graphmap`'s fuzzy seeds require more treatments to find proper chains. A first step after seeding finds groups of anchors representing longer shared subsequences between the query and the reference, on which is applied LCSk. Anchors are placed in a vertex-centric positional graph of k-mers, in which k-mers in both sequences appear, and share an arc if they are directly consecutive (or consecutive up to a distance parameter)[5]. Most weighted paths of anchors (i.e. supported by the query and the reference) are found in this graph and output as shared subsequences. After the LCSk pass, a L1 linear

[5] NB: this is different from a de Bruijn graph since nodes with similar contents can be repeated

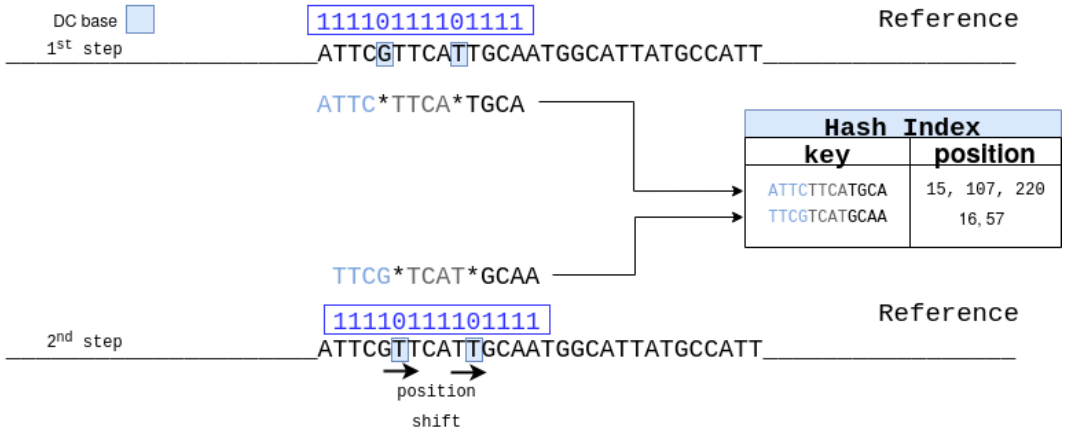

Figure S2 Indexing scheme for fuzzy seeds allowing indels and substitutions in Graphmap. In the figure the shape 4.1.4.1.4 is represented. The zeros represent the don't care positions of the shape. The shape is then applied for each position of the genome. The substring built from the shape is used as key inside a hash index. Each key will correspond to one or more positions on the reference.

regression step is applied to fit a straight line with a 45 degree slope and remove outliers, especially in the beginning and end of the chain (see case 4 in Figure 3 in the main text). Note that other methods use graphs built over anchors as backbones to the chaining and alignment steps without fuzzy seeds [73, 49].

Minimap2's complete formula for regular and large gaps size

- For regular gaps size:

$$f(i) = \max\{ \max_{\substack{i>j\geq 1 \\ x_i - G < x_j \leq x_i \\ y_i - G < y_j < y_i}} f(j) + \min\{d_{j\,i}, w\} - \gamma_r(g_{j\,i}), w\}$$

The property $x_i - G \leq x_j \leq x_i$ and $y_i - G \leq y_j < y_i$ is equivalent to $y_j < y_j$, $x_j \leq x_i$ and $e_{j\,i} < G$.

- For large gaps size:

$$f'(i) = \max_{\substack{i>j\geq 1 \\ x_i - G \leq x_j \leq x_i - w \\ y_i - G \leq y_j \leq y_i - w}} f'(j) + w - \gamma_l(g_{j\,i}, d_{j\,i})$$

where

$d_{j\,i}$	$= \min\{y_i - y_j, x_i - x_j\}$	Smaller "distance" between the two anchors. This is not really a distance by definition : for $(x_i, y_i) = (-n, 0)$, $(x_j, y_j) = (0, 0)$ and $(x_k, y_k) = (0, n)$, we have $d_{i\,j} + d_{j\,k} = 0 < n = d_{i\,j}$.
$e_{j\,i}$	$= \max\{y_i - y_j, x_i - x_j\}$	Discrete Chebyshev distance between the two anchors
$g_{j\,i}$	$= \lvert(y_i - y_j) - (x_i - x_j)\rvert$	Gap length (or Manhattan distance between the diagonals passing by the two anchors)
$\gamma_r(g)$	$= 0.01 \times w \times g + 0.5 \log_2 g$	
$\gamma_l(g, d)$	$= c_1 \times g + c_2 \times d + \log_2 g$	where c_1 and c_2 are parameters

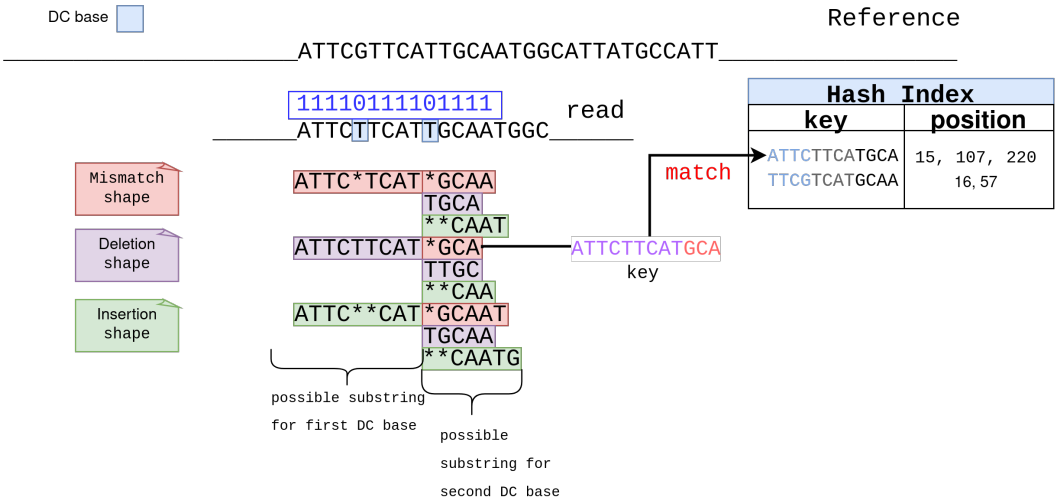

Figure S3 Query in Graphmap, different possible sequences can be matched using a single key. As we can see, there are three types of look-up shapes, and each of them is used to reconstruct a different substring. Each type corresponds to three phenomena that can occur with errors in sequencing, namely substitution, substitution + 1 insertion, and substitution + 1 deletion. Here, two don't care bases are present and nine substrings can be obtained. In this example the substring obtained from the substitution + insertion shape and the mismatch leads to a match with the reference.

Hough transform principle Applying the Hough transform means going from the $S1 = (query, reference)$ space to the Hough S_2 space of coordinates. If a line $(y = ax + b)$ exists in S_1, it is a point of coordinates (a, b) in S_2 (practically, polar coordinates are used for technical reasons). All possible lines intersecting a point in S_1 can be translated in S_2 as a sine wave. Multiple anchors give multiple points in S_2, and the intersection of possible sinusoids intersecting the different points in S_2 correspond to a line roughly intersecting the initial anchors in S_1. The Hough space is rasterized, and by counting and weighing the possible solutions in S_2, lines can be deduced in S_1. Contrary to linear regression which would output the best line explained by the seed distribution in S_1, here an arbitrary number of straight lines can be output and considered (see Supplementary Figure S4 for an overview of the steps).

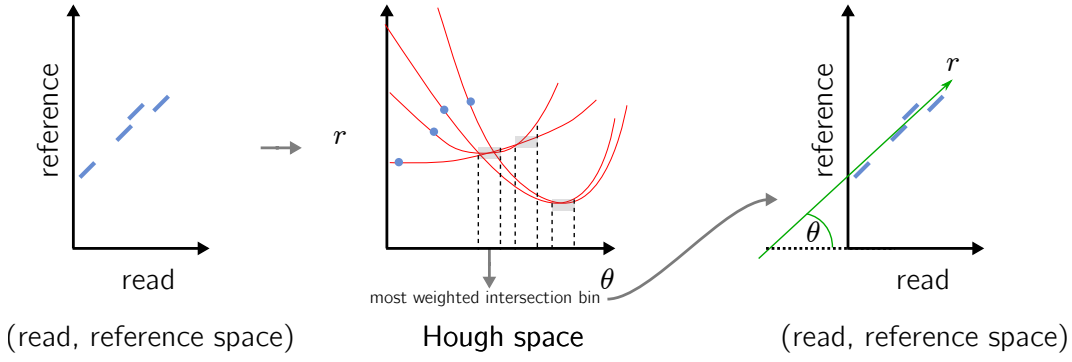

Figure S4 An overview of the Hough transform steps.