Closeness to the Diagonal for Longest Common Subsequences

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Abstract

We investigate the nature of the alignment with gaps corresponding to a Longest Common Subsequence (LCS) of two random sequences. We show that such an alignment, which we call optimal, typically matches pieces of similar length. This is of importance in order to understand the structure of optimal alignments. We also establish a method for showing that a certain class of properties typically holds in most parts of the optimal alignment. The assumption being that the property considered has high probability to hold for strings of similar short length. The present result is part of our general effort to obtain the order of the variance of the LCS of random strings.

1 Introduction

Let $x$ and $y$ be two finite strings. A common subsequence of $x$ and $y$ is a subsequence which is a subsequence of $x$ as well as of $y$. A Longest Common Subsequence (LCS) of $x$ and $y$ is a common subsequence of $x$ and $y$ of maximal length.

Throughout, let $X$ and $Y$ be two random strings $X = X_1 \ldots X_n$ and $Y = Y_1 \ldots Y_n$, and let $LC_n$ denote the length of the LCS of $X$ and $Y$.

As well known, common subsequences can be represented as alignments with gaps; and this is illustrated next with some examples:

First take the binary strings $x = 0010$ and $y = 0110$. A common subsequence is 01. We represent this common subsequence as an alignment with gaps. We allow only for alignments which align the same letters or letters with gaps. We represent a common subsequence by aligning the letters of the subsequences from each word. The letters which do not appear in the common subsequence get aligned

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with a gap; several alignments can represent the same common subsequence. In this first example, an alignment corresponding to the common subsequence 01 is given by

\[
\begin{array}{c|c|c|c|c|c}
 & 0 & 0 & 1 & 0 & 0 \\
 x & 0 & 0 & 1 & 0 & 0 \\
y & 0 & 1 & 1 & 0 & 0
\end{array}
\] (1.1)

However, the LCS is not 01, but 010. We call an alignment corresponding to the LCS an **optimal alignment**. Hence, (1.1) is not an optimal alignment, but an optimal alignment is given by:

\[
\begin{array}{c|c|c|c|c|c}
 & 0 & 0 & 1 & 0 & 0 \\
 x & 0 & 0 & 1 & 0 & 0 \\
y & 0 & 1 & 1 & 0 & 0
\end{array}
\]

Here the LCS is \(LCS(x, y) = 010\), and its length is 3 a fact that we denote by 

\[|LCS(x, y)| = 3.\]

Let us consider another example: let \(x = \text{christian}\) and \(y = \text{krystyan}\). In this situation, the LCS of \(x\) and \(y\) is \(LCS(x, y) = \text{rstan}\) and the alignment with gaps representing the LCS is:

\[
\begin{array}{c|c|c|c|c|c|c|c|c|c|c|c}
 & c & k & h & r & i & s & t & i & a & a \\
 x & h & r & y & s & t & y & s & t & y & h & a
\end{array}
\]

(1.2)

Again, all the letters which are part of the LCS get aligned with each other, while the other letters get aligned with gaps. Often, we say that, in a given alignment, a part of \(x\) gets aligned with a part of \(y\), and here is what is meant: In the above example, \(x_5x_6x_7x_8x_9 = \text{stan}\) is aligned with \(y_5y_6y_7y_8 = \text{styan}\) and the alignment with gaps representing the LCS is:

For further clarification see that in the alignment (1.2), the interval [1, 4] is aligned with [1, 2]. In other words, we say that in an alignment a piece of \(x\) gets aligned with a piece of \(y\), if and only if the letters from the piece of \(x\) which get aligned to letters get only aligned with letters from the piece of \(y\) and vice versa.

Longest Common Subsequences (LCS) and Optimal Alignments (OA) are important tools used in Computational Biology and Computational Linguistics for string matching, e.g., see [10], [3]. It is known and due to Chvátal and Sankoff [4] that the expected length of the LCS divided by \(n\) converges to a constant \(\gamma\). But even for the simplest distributions, the exact value of \(\gamma\) is not known.

In several special cases (e.g., [5], [6], [7]), the long open problem of finding the order of the variance of the LCS and the OA has been solved. Such is the case, for example, with binary sequences with 0 and 1 having very different probabilities from each other. In all these cases, it turned out that the variance of the LCS is of linear order in the length of the sequences. This is the order conjectured by Waterman [9], for which Steele [8] has an upper bound of such order, whilst Alexander [1] determined the speed of convergence. The most important cases, like for example i.i.d. sequences with equiprobable letters remain, however, open as far as this order is concerned.
In \cite{6} and \cite{7}, for determining the linear order of the variance of the LCS, we used ad-hoc (somewhat intricate) combinatorial arguments, despite the fact that the situation there is less involved than for the general case. In this paper, we show a general method to prove certain properties of the optimal alignment, given that typically the property holds for alignments of short strings.

We investigate here the nature of the optimal alignments of random strings, i.e., of the alignments corresponding to LCSs. For this, and throughout, we take two independent random strings \(X = X_1 \ldots X_n\) and \(Y = Y_1 \ldots Y_n\) and further assume that \(X\) and \(Y\) are both iid sequences drawn from a finite ordered alphabet. We denote by \(LC_n\) the length of the LCS of \(X\) and \(Y\).

To do so, we are going to partition \(X\) into pieces of length \(k\), fixed, as \(n\) goes to infinity, and prove that typically, in any optimal alignment, most of these pieces get aligned with pieces of \(Y\) of similar length. More precisely, we assume throughout that

\[ n = m \cdot k. \]

Assume that the integers

\[ r_0 = 0 < r_1 < r_2 < r_3 < \ldots < r_{m-1} < r_m = n, \]

are such that

\[ LC_n = \sum_{i=1}^{m} |LCS(X_{k(i-1)+1}X_{k(i-1)+2} \ldots X_{ki}; Y_{r_{i-1}+1}Y_{r_{i-1}+2} \ldots Y_{ri})|. \] (1.4)

The above condition just indicates that there exists an optimal alignment which maps \([k(i-1) + 1, ki]\) onto \([r_{i-1} + 1, ri]\) for all \(i = 1, 2, \ldots, m\).

The first goal of the present paper is to show that for \(k\) fixed, and \(n\) large enough, any generic optimal alignment is such that the vast majority of the intervals \([r_{i-1} + 1, ri]\) are close in length to \(k\). Another goal is to show that if a certain property \(P\) holds with high probability for any optimal alignment of strings of (short) length order \(k\), then typically any optimal alignment has a large proportion of parts of order \(k\) having the property \(P\). This is proven in Section 4.

Let us get back to the first goal of this paper. That is, we will show that with high probability if the integers \(r_0, r_1, \ldots, r_m\) satisfy (1.3) and (1.4) then most of the lengths \(r_i - r_{i-1}\) are close to \(k\).

Of course, we need to quantify what is meant by ”close to \(k\)”. To do so, we first need a definition. For \(p > 0\), let

\[ \gamma^*(p) := \lim_{n \to \infty} \frac{\mathbb{E}[|LCS(X_1X_2 \ldots X_n; Y_1Y_2 \ldots Y_m)|]}{n(1 + p)/2}. \] (1.5)

This function \(\gamma^*\) is just a new parametrization of the usual function
\[
\gamma(q) = \lim_{n \to \infty} \frac{\mathbb{E}[|LCS(X_1X_2\ldots X_{n-nq};Y_1Y_2\ldots Y_{n+qn})|]}{n},
\]

\(q \in [-1, 1]\), i.e.,

\[
\gamma^*(p) = \gamma\left(\frac{p-1}{p+1}\right). \tag{1.6}
\]

A subadditivity argument as in Chvátal and Sankoff [4] shows that the above limits do exist. When \(X\) and \(Y\) are identically distributed, then the function \(\gamma\) is symmetric about the origin, while a further subadditivity argument shows that it is concave and so it reaches its maximum at \(q = 0\). In general, it is not clear, whether or not it is strictly concave at \(q = 0\). From simulations it seems almost certain that the function \(\gamma\) is strictly concave at \(p = 1\). This however might be very difficult to prove. (The LCS problem is a Last Passage Percolation problem with correlated weights. In general, proving for First/Last passage percolation that the shape of the wet zone is strictly concave seems difficult and in many cases has not been done yet.) Note that \(q(p) = (p-1)/(p+1) = 1 - (2/(p+1))\) is strictly increasing in \(p\) and is equal to 0 for \(p = 1\). So, if \(\gamma(\cdot)\) is strictly concave at \(q = 0\), then it reaches a strict maximum at that point. In that case, \(\gamma^*(\cdot)\) would reach a strict maximum at \(p = 1\). Without the strict concavity of \(\gamma(\cdot)\), \(p = 1\) would not be the unique point of maximal value.

Usually however, there are specific methods for showing that \(\gamma^*(p)\) is strictly smaller than \(\gamma^*(1)\) as soon as \(p\) is further away, than a given small quantity, from 1. Here, \(\gamma^*\) is non-decreasing on \([0, 1]\) and then non-increasing on \([1, \infty)\). The value of \(\gamma^*\) at 1 is simply denoted by \(\gamma^* := \gamma(0) = \gamma^*(1)\).

So assume that we know that \(p_1\) and \(p_2\) are such that

\[
\gamma^*(p_1) < \gamma^*(1), \quad \gamma^*(p_2) < \gamma^*(1) \tag{1.7}
\]

while

\[
0 < p_1 < 1 < p_2. \tag{1.8}
\]

The main result of this paper is that if \(n\) is large enough (we take \(k\) fixed and let \(n\) go to infinity), then for all optimal alignment typically we have that most of the intervals \(r_{i-1} + 1, r_i\) (for \(i = 1, 2, \ldots, m\)) have their length between \(kp_1\) and \(kp_2\). By most, we mean that by taking \(k\) fixed, and \(n\) large enough, that proportion gets typically as close to 100% as we want.

Let \(\epsilon > 0\), \(p_1, 0\) and \(p_2 > 0\) be constants. Let \(A_{\epsilon,p_1,p_2}^n\) be the event that a proportion of no less then \(1 - \epsilon\) of the intervals \([r_{i-1} + 1, r_i]\), \(i = 1, 2, \ldots, m\) have their length between \(kp_1\) and \(kp_2\) for any optimal alignment of \(X_1\ldots X_n\) and \(Y_1\ldots Y_n\). More precisely, let \(A_{\epsilon,p_1,p_2}^n\) be defined as the event that for all integer vectors \((r_0, r_1, \ldots, r_m)\) satisfying (1.3) and (1.4), we have that

\[
\text{card}(\{i \in 1, 2, \ldots, m : kp_1 \leq r_i - r_{i-1} \leq kp_2\}) \geq (1 - \epsilon)m. \tag{1.9}
\]
Theorem 1.1 \ Let \( \epsilon > 0 \) \ Let \( p_1 < 1 < p_2 \) be such that \( \gamma^*(p_1) < \gamma^*(1), \gamma^*(p_2) < \gamma^*(1) \). Let \( k \geq 1 \) and let \( \delta \in (0, \min(\gamma^*(1) - \gamma^*(p_1), \gamma^*(1) - \gamma^*(p_2))) \). Then,
\[
P \left( A_{\epsilon, p_1, p_2} \right) \geq 1 - \exp\left(-n \left(-\ln(ek)/k + \delta^2 \epsilon^2 / 16\right)\right),
\]
for all \( n = n(k, \epsilon, \delta) \) large enough.

Before proving the above theorem, let us mention that the results presented here are yet another step in our attempt at finding the order of the variance of \( LC_n \) (see \[5\], \[7\], \[6\] and the references therein), and they will prove useful towards our ultimate goal (\[2\]).

2 Proof of the main theorem

In this section we prove our main Theorem 1.1. To do so, we will need to define a few things: So far we have looked at the intervals on which an optimal alignment would map the intervals \([k(i-1) + 1, ki]\); and we are now going to take the opposite stand: we will give non-random integers \( r_0 = 0 < r_1 < r_2 < \ldots < r_m = n \) and request that the alignment aligns \([k(i-1) + 1, ki]\) onto \([r_{i-1} + 1, r_i]\) for every \( i = 1, 2, \ldots, m \). In general, such an alignment is not optimal and the best score an alignment can reach under the above constraint is given by:
\[
L_n(\vec{r}) := L_n(r_0, r_1, \ldots, r_m) := \sum_{i=1}^{m} |LCS(X_{k(i-1)+1}X_{k(i-1)+2} \ldots X_{ki}; Y_{r_{i-1}+1}Y_{r_{i-1}+2} \ldots Y_{r_i})|.
\]

where \( \vec{r} = (r_0, r_1, \ldots, r_m) \). Hence, the quantity \( L_n(\vec{r}) = L_n(r_1, \ldots, r_m) \) represents the maximum number of aligned identical letter pairs under the constraint that the string \( X_{(i-1)k+1}X_{(i-1)k+2} \ldots X_{ki} \) gets aligned with \( Y_{r_{i-1}+1}Y_{r_{i-1}+2} \ldots Y_{r_i} \) for all \( i = 1, 2, \ldots, m \). Note that for non-random \( \vec{r} = (r_0, r_1, \ldots, r_m) \), the partial scores
\[
|LCS(X_{(i-1)k+1}X_{(i-1)k+2} \ldots X_{ki}; Y_{r_{i-1}+1}Y_{r_{i-1}+2} \ldots Y_{r_i})|,
\]
are independent of each other, and concentration inequalities will prove handy when dealing with \( L_n(\vec{r}) = L_n(r_0, r_1, \ldots, r_m) \). Let
\[
\mathcal{R}_{\epsilon, p_1, p_2},
\]
denote the (non-random) set of all integer vectors \( \vec{r} = (r_0, r_1, \ldots, r_m) \) satisfying the conditions (1.3), and (1.9). Let
\[
\mathcal{R}_{\epsilon, p_1, p_2}^c,
\]
denote the (non-random) set of all integer vectors \( \vec{r} = (r_0, r_1, \ldots, r_m) \) satisfying the condition (1.3), but not (1.9).
Hence we get the following upper bound for the number of elements in the set \( R_{\epsilon,p_1,p_2}^{c} \):

\[
\text{card } ( R_{\epsilon,p_1,p_2}^{c} ) \leq \left( \frac{n}{m} \right) \leq \left( \frac{en}{m} \right)^m = (ek)^m, \tag{2.1}
\]

by a well known and simple bound on binomial coefficients.

Now, let \( \delta := \min(\gamma^* - \gamma^*(p_1), \gamma^* - \gamma^*(p_2)) \). By definition \( LC_n \) is always larger or equal to \( L_n(\vec{r}) \). For \( \vec{r} \) to “define an optimal alignment” we need to have:

\[
L_n(\vec{r}) \geq LC_n. \tag{2.2}
\]

Hence for the event \( \mathcal{A}_{\epsilon,p_1,p_2}^{nc} \) not to hold, there needs to be at least an element \( \vec{r} \) in \( R_{\epsilon,p_1,p_2}^{c} \) for which (2.2) is satisfied. This means that

\[
\mathcal{A}_{\epsilon,p_1,p_2}^{nc} = \bigcup_{\vec{r} \in R_{\epsilon,p_1,p_2}^{c}} \{ L_n(\vec{r}) - LC_n \geq 0 \},
\]

and thus

\[
\mathbb{P}(\mathcal{A}_{\epsilon,p_1,p_2}^{nc}) \leq \sum_{\vec{r} \in R_{\epsilon,p_1,p_2}^{c}} \mathbb{P}(L_n(\vec{r}) - LC_n \geq 0). \tag{2.3}
\]

When \( \vec{r} \in R_{\epsilon,p_1,p_2}^{c} \), the expectation of \( L_n(\vec{r}) - LC_n \) is, for \( n \) large enough, bounded above as follows:

\[
\mathbb{E}[L_n(\vec{r}) - LC_n] \leq -0.5\delta \epsilon mk.
\]

(The proof of this fact is given in Lemma 2.1.) With the last inequality above, we find that

\[
\mathbb{P}(L_n(\vec{r}) - LC_n \geq 0) \leq \mathbb{P}(L_n(\vec{r}) - LC_n - \mathbb{E}[L_n(\vec{r}) - LC_n] \geq 0.5\delta \epsilon m) \tag{2.4}
\]

Note that the quantity \( L_n(\vec{r}) - LC_n \) changes by less than 2 units, when we change any of the i.i.d. entries \( X_1, X_2, \ldots, X_n; Y_1, Y_2, \ldots, Y_n \). Hence, we can apply Hoeffding’s martingale inequality to the right side of (2.4), to obtain

\[
\mathbb{P}(L_n(\vec{r}) - LC_n \geq 0) \leq \mathbb{P}(L_n(\vec{r}) - LC_n - \mathbb{E}[L_n(\vec{r}) - LC_n] \geq 0.5\delta \epsilon n) \leq \exp(-n\delta^2 \epsilon^2 / 16).
\]

(Recall that Hoeffding’s inequality ensures that if \( f \) is a map in \( l \) entries, so that changing any one single entry affect the value by less than \( a \), then

\[
\mathbb{P}(f(W_1, W_2, \ldots, W_l) - \mathbb{E}[f(W_1, W_2, \ldots, W_l)] \geq \Delta l) \leq \exp(-2l\Delta^2 / a^2),
\]

provided the variables \( W_1, W_2, \ldots \) are independent.) Combining the last inequality above with (2.3), one obtains

\[
\mathbb{P}(\mathcal{A}_{\epsilon,p_1,p_2}^{nc}) \leq |R_{\epsilon,p_1,p_2}^{c}| \exp(-n\delta^2 \epsilon^2 / 16). \tag{2.5}
\]

But, by the equation (2.1), the set \( R_{\epsilon,p_1,p_2}^{c} \) contains less than \((ek)^m\) elements so that out of (2.5), we get

\[
\mathbb{P}(\mathcal{A}_{\epsilon,p_1,p_2}^{nc}) \leq (ek)^m \exp(-n\delta^2 \epsilon^2 / 16) = \exp(-n (-\ln(ek)/k + \delta^2 \epsilon^2 / 16)). \tag{2.6}
\]

This will finish the proof of Theorem 1.1 provided we prove:
Lemma 2.1 Let \( \delta > 0 \) be such that \( \delta < \min(\gamma^*(1) - \gamma^*(p_1), \gamma^*(1) - \gamma^*(p_2)) \). Assume that \( \vec{r} = \langle r_0, \ldots, r_m \rangle \in \mathcal{R}_{\epsilon, p_1, p_2}^c \). Then for \( n \) large enough, we have

\[
\mathbb{E}[L_n(\vec{r}) - LC_n] \leq -0.5 \delta \epsilon n
\]

(2.7)

\textbf{Proof.} Assume that we compute the LCS of the string \( X_{(i-1)k+1}X_{(i-1)k+2} \cdots X_{ik} \) and of the string \( Y_{r_{i-1}+1}Y_{r_{i-1}+2} \cdots Y_{r_i} \). Let \( \delta^* := \min(\gamma^*(1) - \gamma^*(p_1), \gamma^*(1) - \gamma^*(p_2)) \). If \( r_i - r_{i-1} \) is not between \( p_1k \) and \( p_2k \), then the rescaled expected value is below \( \gamma^* \) by at least \( \delta^* \). (Rescaled by the average of the lengths of the two strings). Hence,

\[
\gamma^* - \frac{\mathbb{E}[|LCS(X_{(i-1)k+1}X_{(i-1)k+2} \cdots X_{ik}, Y_{r_{i-1}+1}Y_{r_{i-1}+2} \cdots Y_{r_i})|]}{0.5(k + r_i - r_{i-1} - 1)} \geq \delta^*
\]

if the length \( r_i - r_{i-1} \) is not in \([kp_1, kp_2]\). One of the strings has length \( k \). Hence, not rescaled we are below \( \gamma^* \) by at least \( \delta^* k/2 \). By definition, any alignment belonging to \( \mathcal{R}_{\epsilon, p_1, p_2}^c \) has a proportion of at least \( \epsilon \) of the intervals \( X_{(i-1)k+1}X_{(i-1)k+2} \cdots X_{ik} \) which get matched on strings of length not in \([p_1k, p_2k]\). This corresponds to a total number of \( \epsilon m \). For each of these intervals we are below the expected value, which would correspond to \( \gamma^* \) times the average length, by at least \( \delta^* k/2 \). Hence, the expected value for any alignment of \( \mathcal{R}_{\epsilon, p_1, p_2}^c \) is below \( \gamma^* n \) by at least \( (\delta^* k/2)(\epsilon m) = n \delta^* \epsilon /2 \). This means that

\[
\gamma^* n - \mathbb{E}L_n(\vec{r}) \geq n \delta^* \epsilon /2, \tag{2.8}
\]

as soon as \( \vec{r} = \langle r_0, r_1, \ldots, r_m \rangle \) is in \( \mathcal{R}_{\epsilon, p_1, p_2}^c \). Now \( \mathbb{E}[LC_n]/n \to \gamma^* \) as \( n \) goes to infinity. Note, that by definition, \( \delta^* - \delta > 0 \), and so for all \( n \) large enough, we will have

\[
\left| \gamma^* - \frac{\mathbb{E}[L_n]}{n} \right| \leq (\delta^* - \delta) \epsilon /2. \tag{2.9}
\]

Combining (2.8) and (2.9) yields that for all \( n \) large enough, we have

\[
\mathbb{E}[L_n] - L_n(\vec{r}) \geq 0.5 \delta \epsilon n
\]

as soon as \( \vec{r} \in \mathcal{R}_{\epsilon, p_1, p_2}^c \). The proof is now completed. \qed

3 Closeness to the diagonal

Let us start by explaining how we can represent alignments in two dimensions by considering an example. Take the two related words: the English \( X = \text{mother} \) and the German \( Y = \text{mutter} \). The longest common subsequence is \( \text{mutter} \) and hence \( LC_6 = 4 \). As mentioned, we represent any common subsequence as an alignment with gaps. The letters appearing in the common subsequence are aligned one on top of the other. The letters which are not aligned with the same letter in the other text get aligned with a gap. In the present case the common subsequence \( \text{mutter} \) corresponds to the following alignment:

\[
\begin{array}{cccccccc}
  m & o & t & h & e & r & m \\
  m & u & t & t & e & r \\
\end{array}
\]

(3.1)
An alignment corresponding to a LCS is called an optimal alignment. The optimal alignment is, in general, not unique. For example, to the same common subsequence mter corresponds also the following optimal alignment:

\[
\begin{array}{cc|ccc|cc}
m & o & t & h & e & r \\
m & u & t & t & e & r \\
\end{array}
\] (3.2)

In the following, we represent alignments in 2 dimensions. For this we view alignments as subsets of \( \mathbb{R}^2 \), in the following manner: If the \( i \)-th letter of \( X \) gets aligned with the \( j \)-th letter of \( Y \), then the set representing the alignment is to contain \((i, j)\). For example, the alignment (3.1) can be represented as follows: \((1, 1), (3, 3), (5, 5), (6, 6)\) with the corresponding plot

\[
\begin{array}{cccc}
r & x & x & x \\
e & x & x & x \\
t & t & x & x \\
t & u & u & u \\
m & x & x & x \\
\end{array}
\] (3.3)

Here, the symbol \( x \) indicates pairs of aligned letters. We say that these points represent the optimal alignment.

The main result of the previous section implies that the optimal alignment must remain close to the diagonal. This is the content of the next theorem. But first we need a definition. Let

\[
D^n_{\epsilon, p_1, p_2}
\]

be the event that all points representing any optimal alignment of \( X_1X_2\ldots X_n \) with \( Y_1Y_2\ldots Y_n \) are above the line \( y = p_1 x - p_1 n \epsilon - p_1 k \) and below the line \( y = (1/p_1)x + (1/p_1)n \epsilon + (1/p_1)k \).

**Theorem 3.1** Let \( p_1 < 1 < p_2 \) be such that \( \gamma^*(p_1) < \gamma^*(1) \) and \( \gamma^*(p_2) < \gamma^*(1) \). Let \( k \geq 1 \), let \( \delta \in (0, \min\{\gamma^*(p_1), \gamma^*(p_2)\}) \) be a constant which does not depend on \( n \). Then, for any \( \epsilon > 0 \) fixed, we have for \( n \) large enough,

\[
\mathbb{P}(D^n_{\epsilon, p_1, p_2}) \leq 2 \exp(-n (-\ln(ek)/k + \delta^2 \epsilon^2/16)).
\]

**Proof.** Let \( D^n_\alpha \) be the event that any optimal alignment of \( X_1X_2\ldots X_n \) with \( Y_1Y_2\ldots Y_n \) is above the line \( y(x) = p_1 x - p_1 n \epsilon - p_1 k \); and let \( D^n_\beta \) be the event that any optimal alignment of \( X_1X_2\ldots X_n \) with \( Y_1Y_2\ldots Y_n \) is below the line \( y = (1/p_1)x + (1/p_1)n \epsilon + (1/p_1)k \). Note that

\[
D^n_\alpha \cap D^n_\beta \subset D^n_{\epsilon, p_1, p_2}
\]

and thus

\[
\mathbb{P}(D^n_{\epsilon, p_1, p_2}) \leq \mathbb{P}(D^n_\alpha) + \mathbb{P}(D^n_\beta).
\]
By symmetry we have that $\mathbb{P}(D_a^{nc}) = \mathbb{P}(D_b^{nc})$. The last inequality above then yields

$$\mathbb{P}(D_{a, \epsilon, p_1, p_2}^{nc}) \leq 2\mathbb{P}(D_a^{nc}).$$

(3.4)

Next, we are going to prove that

$$A_{a, \epsilon, p_1, p_2}^n \subset D_a^n.$$  

(3.5)

Let $x \leq \epsilon n$ be a multiple of $k$. Let thus $a$ be a natural number such that $ak = x$. Let us first consider the case where $x \leq \epsilon n$. In this situation, we have that $p_1 x - p_1 \epsilon n$ is negative. But any alignment (and optimal alignment) we consider maps any $x \in [0, n]$ onto $[0, n]$. Hence for every $x \epsilon n$ the condition is always verified, that is any optimal alignment aligns $x$ onto a point which is no less than $p_1 x - p_1 \epsilon n$.

Let us next consider the case where $x \geq \epsilon n$. When the event $A_{a, \epsilon, p_1, p_2}^n$ holds, then any optimal alignment aligns all but a proportion $\epsilon$ of the interval $[(i - 1)k + 1, ik], i \in \{1, \ldots, m\}$ onto intervals of length longer or equal to $p_1 k$. The maximum number of intervals which could be matched on intervals of length less than $p_1 k$ is thus $\epsilon m$. In the interval $[0, x]$ there are $a$ intervals from the partition $[(i - 1)k + 1, ik], i \in \{1, \ldots, m\}$. Hence, at least $a - \epsilon m$ of these intervals are matched onto intervals of length no less than $p_1 k$. This implies that, when the event $A_{a, \epsilon, p_1, p_2}^n$ holds, we find that the point $x$ gets matched by the optimal alignment on a value no less than

$$(a - \epsilon m)kp_1.$$  

Noting that $ak = x$ and that $mk = n$ the above bound becomes

$$p_1 x - p_1 \epsilon n.$$  

If $x$ is not a multiple of $k$, let $x_1$ denote the largest multiple of $k$ which is less than $x$. By definition, we have that

$$x - x_1 < k.$$  

(3.6)

The two-dimensional alignment curve cannot go down, hence, we have that $x$ gets aligned to a point which cannot be below to where $x_1$ gets aligned. Now, for $x_1$, since it is a multiple of $k$, we have that it gets aligned on a point which is larger or equal to

$$p_1 x_1 - p_1 \epsilon n.$$  

Using (3.6), we find

$$p_1 x_1 - p_1 \epsilon n \geq p_1 x - p_1 \epsilon n - p_1 k.$$  

We have just proven that when the event $A_{a, \epsilon, p_1, p_2}^n$ holds, the point $x$ gets aligned above or on the point $p_1 x - p_1 \epsilon n - p_1 k$. This finishes proving that the event $A_{a, \epsilon, p_1, p_2}^n$ is a subevent of $D_a^n$.

Since $A_{a, \epsilon, p_1, p_2}^n \subset D_a^n$, we get

$$\mathbb{P}(D_a^{nc}) \leq \mathbb{P}(A_{a, \epsilon, p_1, p_2}^{nc}).$$

But by Theorem 1.1 the last probability above is upper bounded by:

$$\exp(-n \left(-\ln(ek)/k + \delta^2 \epsilon^2 / 16\right)).$$
so that \( P(D^n_{\text{nc}}) \leq \exp(-n (-\ln(ek)/k + \delta^2 \epsilon^2/16)) \). Hence, (3.4) becomes:

\[
P(D^n_{\epsilon, p_1, p_2}) \leq 2 \exp(-n (-\ln(ek)/k + \delta^2 \epsilon^2/16)).
\]

Theorem 3.1 allows to reduce the time to compute the LCS for two random sequences. First note that by rescaling the two-dimensional representation of optimal alignments by \( n \), it implies that, with high probability, up to a distance of order \( \epsilon > 0 \) any optimal alignment is above the line \( x \to p_1 x \) and below \( x \to p_2 x \). Moreover, in the theorem we can take \( \epsilon > 0 \) as small as we want, (leaving it fixed though when \( n \) goes to infinity).

Simulations seem to indicate that the mean curve \( \gamma^* \) is strictly concave at \( p = 1 \). If this is indeed true then we can take \( p_1 \) as close to one as we want and it will satisfy the conditions of the theorem. That is, we could then take \( \epsilon \) as close to \( 0 \) as we want and \( p_1 \) as close as close as we want to \( 1 \). Hence, the rescaled two-dimensional representation of the optimal alignments gets uniformly as close to the diagonal as we want when \( n \) goes to infinity.

Figure 1, below, is the graph of a simulation with two i.i.d binary sequences of length \( n = 1000 \). All the optimal alignments are contained between the two lines in the graph below. We see that all the optimal alignments stay extremely close to the diagonal:
4 Proving a property of the optimal alignment

Let $\mathcal{P}$ be a map which assigns to every pair of strings $(x, y)$ a 1 if the pair $(x, y)$ has a certain property and 0 otherwise. Hence, if $\mathcal{A}$ is the alphabet we consider, then

$$\mathcal{P} : (\cup_k \mathcal{A}^k) \times (\cup_k \mathcal{A})^k \rightarrow \{0, 1\}.$$ 

If $\mathcal{P}(x, y) = 1$ we will say that the string pair $(x, y)$ has the property $\mathcal{P}$.

Let $\epsilon > 0$ be any fixed number strictly larger than 0 and let $\vec{r} = (r_0, r_1, \ldots, r_m)$ be an integer vector satisfying condition (1.3). Let $B^m_n(\vec{r}, \epsilon)$ denote the event that there is a proportion of at least $1 - \epsilon$ of the string pairs

$$(X_{(i-1)k+1} \ldots X_{ik}; Y_{r_{i-1}+1} \ldots Y_{r_i})$$

satisfying the property $\mathcal{P}$. In other words, the event

$$B^m_n(\vec{r}, \epsilon)$$

holds if and only if

$$\sum_{i=1}^{m} \mathbb{P}(X_{(i-1)k+1} \ldots X_{ik}; Y_{r_{i-1}+1} \ldots Y_{r_i}) \geq (1 - \epsilon)m.$$
Let $B^n_P(\epsilon)$ denote the event that for every optimal alignment the proportion of aligned string pairs (4.1) satisfying the property $\mathcal{P}$, is more than $1 - \epsilon$. Hence, the event $B^n_P(\epsilon)$ holds if and only if for every vector $\vec{r} = (r_0, r_1, \ldots, r_m)$ satisfying (4.3) and such that $LC_n = L_n(\vec{r})$, the event $B^n_P(\vec{r}, \epsilon)$ holds.

Most of the time, the properties we want for string pairs only holds with high probability if the two strings have their lengths not too far from each other. Let $q$ be a (small) constant so that $q \in [0, 1]$. Assume that as soon as $r_i - r_{i-1} \in [kp_1, kp_2]$, the probability that string pairs (4.1) has the required property is above $1 - q$. Hence, assume that for every $r_i \in [kp_1, kp_2]$ we have:

$$\mathbb{P}(\mathcal{P}(X_1 \ldots X_k, Y_1Y_2 \ldots Y_{r_1}) = 1) \geq 1 - q.$$ 

We are going to investigate next how small $q = q(k)$ needs to be, in order to insure that a large proportion of the aligned string pairs (4.4) have the property $\mathcal{P}$ (for every optimal alignment). Recall that $A^\alpha_{\epsilon,p_1,p_2}$ denotes the event that every optimal alignment aligns a proportion larger/equal to $1 - \epsilon$ of the substrings $X(i-1)_{k+1} \ldots X_{ik}$ to substrings of $Y$ with length in $[p_1k, p_2k]$. Also, recall that $\mathcal{R}_{\epsilon,p_1,p_2}$ denotes the set of integer vectors $\vec{r} = (r_0, r_1, \ldots, r_m)$, satisfying (4.3) and such that there is more than $(1 - \epsilon)m$ of the differences $r_i - r_{i-1}$ in $[kp_1, kp_2]$.

We will need a small modification of the event $B^n_P(\vec{r}, \epsilon)$. For this let $\tilde{B}_P^P(\vec{r}, \epsilon)$ denote the event that among the aligned string pieces (4.1), there are no more than $m\epsilon$ which do not satisfy the property $\mathcal{P}$ and have their length $r_i - r_{i-1}$ in $[kp_1, kp_2]$. We find that

$$A^n(\epsilon_1, p_1, p_2) \cap \left( \cap_{\vec{r} \in \mathcal{R}_{\epsilon_1, p_1, l_2}} \tilde{B}^n_P(\vec{r}, \epsilon_2) \right) \subset B^n_P(\epsilon_1 + \epsilon_2),$$

so that

$$\mathbb{P}(B^n_P(nc(\epsilon_1 + \epsilon_2)) \leq \mathbb{P}(A^n_{nc}(\epsilon_1, p_1, p_2)) + \sum_{\vec{r} \in \mathcal{R}_{\epsilon_1, p_1, l_2}} \mathbb{P}(\tilde{B}^n_P(\vec{r}, \epsilon_2)) \quad (4.2)$$

We find the bound

$$\mathbb{P}(\tilde{B}^n_P(\vec{r}, \epsilon_2)) \leq \left( \frac{m}{\epsilon_2 m} \right)^{2m} q^{2m} \exp(H_\epsilon(\epsilon_2)m).$$

Noting that $\binom{m}{\epsilon_2 m}$ is bounded above by $\exp(H_\epsilon(\epsilon_2)m)$, where $H_\epsilon$ is the base $\epsilon$ entropy function, given by $H_\epsilon(x) = \epsilon x \ln x - (1 - \epsilon) \ln(1 - \epsilon), 0 < x < 1$, we find the bound

$$\mathbb{P}(\tilde{B}^n_P(\vec{r}, \epsilon_2)) \leq q^{2m} \exp(H_\epsilon(\epsilon_2)m). \quad (4.3)$$

We can now apply inequality (4.3) to inequality (4.2). For this note that in the set $\mathcal{R}_{\epsilon,p_1,p_2}$ there are less than $(3k)^m$ elements as we proved in Section 2. Thus we obtain

$$\mathbb{P}(B^n_P(nc(\epsilon_2)) \leq \mathbb{P}(A^n_{nc}(\epsilon_1, p_1, p_2)) + (3k)^m q^{2m} \exp(H_\epsilon(\epsilon_2)m) \quad (4.4)$$

Taking $q(k)$ equal to $1/((6k)^{1/\epsilon_2})$, yields

$$\mathbb{P}(B^n_P(nc(\epsilon_1 + \epsilon_2)) \leq \mathbb{P}(A^n_{nc}(\epsilon_2, p_1, p_2)) + \exp((H_\epsilon(\epsilon_2) - \ln(2))m) \quad (4.5)$$
Note that $H_\epsilon(\epsilon) < \ln 2$ as soon as $\epsilon < 0.5$. So, if we assume that $\epsilon < 0.5$, then expression $\exp\left((H_\epsilon(\epsilon) - \ln(2))m\right)$ is a (negatively) exponentially small quantity in $m$. We already, learned how to bound the probability of the event $A^{nc}(\epsilon_1, p_1, p_2)$ in the previous sections. Hence, the inequality (4.5), allows to show that a high percentage of the aligned string pairs (4.1), have property $\mathcal{P}$ in any optimal alignment. For this we just need to show that for pairs (4.1) with similar length, the probability $q(k)$ is less or equal to

$$\frac{1}{(12k)^{1/\epsilon}},$$

where

$$q(k) := \max_{r_1 \in [kp_1, kp_2]} \mathbb{P}(\text{the pair } (X_1 \ldots X_k; Y_1 \ldots Y_{r_1}) \text{ has not property } \mathcal{P}).$$

This is the content of the next theorem, which is obtained by putting $\epsilon_1 = \epsilon_2 = \epsilon/2$:

**Theorem 4.1** Assume that $p_1$ and $p_2$ are such that $p_1 < 1 < p_2$. Let $\delta > 0$ be strictly less than $\min(\gamma^* - \gamma(p_1), \gamma^* - \gamma(p_2))$. Let $\epsilon > 0$. Assume that there is a natural number $k \geq 1$ such that

$$\mathbb{P}(\text{the pair } (X_1 \ldots X_k, Y_1 \ldots Y_l) \text{ does not satisfy property } \mathcal{P}) \leq \frac{1}{(6k)^{2/\epsilon}}$$

for any $l \in [kp_1, kp_2]$. Then, for any optimal alignment $\vec{r}$ (i.e., such that $LC_n = L(\vec{r})$), the proportion of string pairs $((X_{(i-1)k+1} \ldots X_{ik}; Y_{r_{i-1}+1} \ldots Y_{r_i})$ which have property $\mathcal{P}$ is above $1 - \epsilon$ with probability bounded below as given in the next inequality:

$$\mathbb{P}(B_p^a(\epsilon) \geq 1 - \mathbb{P}(A^{nc}(0.5\epsilon, p_1, p_2) - \exp((H_\epsilon(0.5\epsilon) - \ln 2)m))$$

and hence by Theorem [1.1]:

$$\mathbb{P}(B_p^a(\epsilon) \geq 1 - \exp(-n(-\ln(ek)/k + \delta^2\epsilon^2/64)) - \exp(n(H_\epsilon(0.5\epsilon) - \ln 2)/k),$$

for all $n$ large enough. Hence, the probability that there are not at least a proportion of $1 - \epsilon$ string pairs (4.1) having property $\mathcal{P}$ in every optimal alignment is exponentially small as $n$ goes to infinity (while holding $k$ and $\epsilon$ fixed) as soon as there exists $k \geq 1$, such that:

$$k > \frac{64\ln(ek)}{\epsilon^2\delta^2}$$

and

$$\max_{l \in [p_1 k, p_2 k]} \mathbb{P}(\text{the pair } (X_1 \ldots X_k, Y_1 \ldots Y_l) \text{ does not have property } \mathcal{P}) \leq \frac{1}{(6k)^{2/\epsilon}}.$$

The above theorem is very useful for showing that when a certain property holds for aligned string pairs with similar lengths of order $k$, then the property holds typically in most parts of the optimal alignment. From our experience, for most properties we are interested in, when $p_1$ and $p_2$ are close to 1 but fixed, then the probability that

$$(X_1 \ldots X_k, Y_1 Y_2 \ldots Y_l)$$
does not have a certain property is about the same for all \( l \in [kp_1, kp_2] \). In other words, how the alignment of \( X_1 \ldots X_k \) with \( Y_1 \ldots Y_l \), behaves does not depend very much on \( l \) as soon as \( l \) is close to \( k \) and \( k \) fixed. (We are not necessarily able to prove this formally in many situation though). Looking at (4.7) we see that we need a bound for the probability on the left side of (4.7) which is smaller than any negative polynomial order in \( k \). (At least if we want to be able to take \( \epsilon \) as close as we want to 0. If we just want \( \epsilon > 0 \) small but fixed, then a negative polynomial bound with a huge exponent will do). So, if the probability is for example of order \( k^{-\ln k} \) or \( e^{-k^\alpha} \) for a constant \( \alpha > 0 \), we get condition (4.7) satisfied by taking \( k \) large enough. Similarly, condition (4.6) always gets satisfied for \( k \) large enough.

On the other hand, we could envision using Montecarlo simulation in order to find a likely bound for the probability on the left side of (4.7). Things then become much more difficult. Assume that you want \( \epsilon \) to be 0.2 and take \( \delta = 0.1 \). Then, by condition (4.6) you find that \( k \) must be larger than:

\[
k \geq \ln(64) + \ln(25) + \ln(100))64 \cdot 25 \cdot 100 \approx 1260000.
\]

The probability not to have property \( P \) for strings of length approximately \( k \) must be less (see (4.7)) than \( (6k)^{-10} \), so that with our previous bound on \( k \), we would get less than \( 10^{-66} \).

The above number is way too small for Montecarlo simulations! Indeed, to show that a probability is as small as \( 10^{-66} \), one would need to run an order of \( 10^{66} \) simulations.

### 4.1 Further improvements

There are several ways to improve on our bounds. First, we took as upper bound for \( R_{\epsilon,p_1,p_2} \) the value \( \binom{n}{m} \). One can find a better upper bound as follows: first note that if \( \vec{r} = (r_0, r_1, \ldots, r_m) \in R_{\epsilon,p_1,p_2} \), then at least \((1 - \epsilon)m\) of the lengths \( r_{i+1} - r_i \) are in the interval \([p_1k, p_2k]\). to determine these lengths we have at most

\[
\binom{(p_2 - p_1)k}{m} \quad (4.8)
\]

choices. Then, there can be as many as \( \epsilon m \) of the lengths \( r_{i+1} - r_i \), which are not in \([p_1k, p_2k]\). Choosing those lengths is like choosing at most \( \epsilon m \) points from a set of at most \( n \) elements. Hence, we get as upper bound \( \binom{n}{\epsilon m} \) which, in turn, can be bounded by

\[
\binom{n}{\epsilon m} \leq \left( \frac{ek}{\epsilon} \right)^{\epsilon m} \quad (4.9)
\]

Finally, we have to decide which among the \( m \) lengths \( r_i - r_{i-1} \) have there length in \([kp_1, kp_2]\) and which have not. That choice is bounded as follows:

\[
\binom{m}{\epsilon m} \leq \exp(H_\epsilon(\epsilon)m). \quad (4.10)
\]

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Combining the bounds (4.8), (4.9) and (4.10), yields

\[ |R_{\epsilon,p_1,p_2}| \leq \left( (p_2 - p_1)k \left( \frac{ek}{\epsilon} \right)^{\epsilon} \exp(H_\epsilon(\epsilon)) \right)^m \]  

(4.11)

With this improvement in the bound for the cardinality of \( R_{\epsilon,p_1,p_2} \), the inequality (4.4) becomes:

\[ \mathbb{P}(B_{nc}^P(\epsilon_1 + \epsilon_2)) \leq \mathbb{P}(A_{nc}^P(\epsilon_1, p_1, p_2)) + \left( (p_2 - p_1)k \left( \frac{ek}{\epsilon_1} \right)^{\epsilon_1} \exp(H_\epsilon(\epsilon_1)) \right)^m q^{\epsilon_2 m} \exp(H_\epsilon(\epsilon_2)m). \]  

(4.12)

The last inequality above combined with Theorem 1.1 yields that

\[ \mathbb{P}(B_{nc}^P(\epsilon_1 + \epsilon_2)) \]

is less than

\[ \exp \left( -n(-\ln(ek)/k + \delta^2\epsilon_1^2/16) \right) + \left( (p_2 - p_1)k \left( \frac{ek}{\epsilon_1} \right)^{\epsilon_1} \exp(H_\epsilon(\epsilon_1))q^{\epsilon_2} \exp(H_\epsilon(\epsilon_2)) \right)^m. \]  

(4.13)

The last expression above is exponentially small in \( n \) (we assume that we hold \( k \) fixed), if the following two conditions are satisfied:

(i) \[ k > \frac{16 \ln(ek)}{\epsilon_1^2\delta^2}. \]  

(4.14)

(ii) Assuming that \( q(k) \) denotes the maximum for \( l \) ranging over \([kp_1, kp_2]\) of the probability that the property \( P \) does not holds for \((x_1 \ldots X_k; Y_1 \ldots Y_l)\), the second condition is

\[ q(k) < \frac{1}{\left( (p_2 - p_1)k \left( \frac{ek}{\epsilon_1} \right)^{\epsilon_1} \exp(H_\epsilon(\epsilon_1) + H_\epsilon(\epsilon_2)) \right)^{1/\epsilon_2}}. \]  

(4.15)

Combining the last two conditions above yields:

\[ q(k) < \left( \frac{\epsilon_1^2\delta^2}{(p_2 - p_1)16 \ln(ek) \left( \frac{ek}{\epsilon_1} \right)^{\epsilon_1} \exp(H_\epsilon(\epsilon_1) + H_\epsilon(\epsilon_2))} \right)^{1/\epsilon_2}. \]  

(4.16)

The typical situation is that \( \epsilon_1 + \epsilon_2 \) should be of a given order. So, we will try to find \( \epsilon_1 \) and \( \epsilon_2 \) under the constraint \( \epsilon = \epsilon_1 + \epsilon_2 \), so that the right bound in (4.16) is least small. For this note first that the power \( 1/\epsilon_2 \) has much more effect on making the bound small than the expression \( \epsilon_1^2 \) on top of the fraction bar.

Note that \( \exp(H_\epsilon(\epsilon_1) + H_\epsilon(\epsilon_2)) \) is just going to be a value between 1 and 2, and so will not have a lot of influence. Also, \((3k)/\epsilon_1\) is somewhat negligible compared to \(3k\). So
we are first going to disregard the quantities \(((3k)/\epsilon_1)^1_1\) and \(\exp(H_\epsilon(\epsilon_1)) + H_\epsilon(\epsilon_2))\). for this let \(g(k, \epsilon_1, \epsilon_2)\) be equal to

\[
g(k, \epsilon_1, \epsilon_2) = \left( \frac{\epsilon_1^2 \delta^2}{(p_2 - p_1)16 \ln(3k)} \right)^{1/\epsilon_2}
\]

Note that \(g(k, \epsilon_1, \epsilon_2)\) is larger than the bound on the right side of (4.16). This means that if \(g(k, \epsilon_1, \epsilon_2)\) is too small for allowing some Monte Carlo simulation, then the bound (4.16) is also too small!

Note also, that when we hold all the parameters \((p_1, p_2, \delta)\) fixed, the function \(g(k, \epsilon_1, \epsilon_2)\) is decreasing in \(\epsilon_2\) as well as in \(\epsilon_1\). However, as already mentioned, \(\epsilon_2\) “has more effect” in decreasing \(g(k, \epsilon_1, \epsilon_2)\) than \(\epsilon_1\). Hence, given \(\epsilon\) and given all that all the parameters are fixed (including \(k\)), when we want to maximize \(g(k, \epsilon_1, \epsilon_2)\) under the constrain \(\epsilon_1 + \epsilon_2 = \epsilon\), \(\epsilon_1, \epsilon_2 > 0\) we get something where \(\epsilon_2\) will be quite a bit larger than \(\epsilon_1\).

Could Monte Carlo simulations be realistic with \(\epsilon = 0.1\) and the bounds which we have? The answer is no. For this note that \(\delta/(p_2 - p_1)\) gets at first better when we increase \(|p_2 - p_1|\), since \(\gamma^*\) has 0 derivative at \(p = 1\). when the interval \([kp_1, kp_2]\) becomes too big however, than the property might no longer hold with high probability for all couple \((X_1, \ldots, X_k, Y_1, \ldots, Y_l)\) with \(l \in [kp_1, kp_2]\). So, we will take \([p_1, p_2]\) so large as possible around 1, so that property still holds with high probability for all the string pairs mentioned before. With such a choice we get that \(\delta/(p_2 - p_1)\) can be treated as a constant. Somewhat optimistically say that the constant is less than 1/3. Now if \(\epsilon = 0.1\), then \(\epsilon_1, \epsilon_2 \leq 0.1\). In that case,

\[
g(k, \epsilon_1, \epsilon_2) \leq g(k, 0.1, 0.1) \leq \left( \frac{0.01\delta}{3 \times 16 \ln(ek)} \right)^{10}.
\]

Returning to inequality (4.14) and taking \(\delta = 0.2\), we find that \(k\) must be larger than \(10^{10}\), so that \(\ln(ek)\) is more than 21. With this in mind, we find that \(g(k, \epsilon_1, \epsilon_2)\) in the present case where \(\epsilon_1 + \epsilon_2 = 0.1\) is less than \(10^{40}\), so no hope for Monte Carlo simulation here!

Motecarlo with \(\epsilon_1 = 0.1\) and \(\epsilon_2 = 0.2\): Take also \(\delta = 0.2\) and \(\delta/(p_2 - p_1) = 1/2\). With these values, using (4.14) we find that \(k\) must be somewhat larger than \(10^2 \cdot 10 \cdot 8 \ln(24000) \approx 10^5\). Then, also \(q(k)\) by (4.15) should be less than

\[
(10^2 \cdot 10 \cdot 11 \cdot 8)^{-5} \approx 10^{-25}.
\]

This is still an order that is difficult for Monte Carlo simulation, but we get closer to something which could be realistic. Now if we had \(\epsilon_2 = 0.3\) instead, then we would get a bound \(10^{-15}\) which still does not look too good for Monte Carlo simulation!
When only dealing with the inequality (4.15), things look somewhat better. Take $k = 1000$ and $(p_1 - p_1)k = 100$, then the order for the left bound for $q(k)$ is about $10^{-5}$ which is feasible with Montecarlo! So, if we could find another method than the one described here to make sure that most of the pieces of strings $X_{(i-1)k+1} X_{(i-1)k+2} \ldots X_{ik}$ are aligned with pieces of similar length we would be in business!

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