

SOLVING THE (α, δ) -APPROXIMATE MATCHING PROBLEM UNDER TRANSPOSITION INVARIANCE IN MUSICAL SEQUENCES

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ABSTRACT

In this paper we extend the δ -approximate matching problem with α -bounded gaps to cover the case in which transposition invariance is allowed.

The δ -approximate matching problem arises in many questions concerning musical information retrieval and musical analysis. In the case in which no gap is allowed between consecutive pitches of the melody, such problem is effective in discovering musical similarity, covering transposition invariance, if the musical sequences are encoded using interval pitch encoding. However this property is not maintained if we allow the presence of gaps between consecutive pitches of the musical sequence.

Here we introduce two problems relating the (δ, α) -approximate matching under transposition invariance and propose new solutions obtained by adapting efficient algorithms for δ -approximate matching with α -bounded gaps.

Keywords: approximate string matching, experimental algorithms, musical information retrieval.

1 INTRODUCTION

String matching is an extensively studied problem in computer science, mainly due to its direct applications to such diverse areas as text, image and signal processing, speech analysis and recognition, information retrieval, computational biology and chemistry, etc. Formally the string matching problem consists in finding *all* occurrences of a given pattern P in a text T , over some alphabet Σ .

Such problem has been generalized with various notions of approximate matching.

In this paper we focus on a variant of the approximate string matching problem, namely the *δ -approximate string matching problem with α -bounded gaps*, or *(δ, α) -matching problem* for short. Such problem arises in many questions concerning musical information retrieval and

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musical analysis. This is especially true in the context of monophonic music, in which one wants to retrieve a given melody from a complex musical score.

Musical sequences can be schematically viewed as sequences of integer numbers, representing either the notes in the chromatic or diatonic notation (absolute pitch encoding), or the intervals, in number of semitones, between consecutive notes (interval pitch encoding).

The second representation is generally of greater interest for applications in tonal music, since absolute pitch encoding disregards tonal qualities of pitches. Particularly the interval pitch encoding is *transposition invariant*, i.e. any two melodies that differ by an interval transposition are encoded with the same numeric sequence.

Note durations and note accents can also be encoded in numeric form, giving rise to richer alphabets whose symbols can really be regarded as sets of parameters. This is the reason why alphabets used for music representation are generally quite large.

In the δ -approximate matching problem two integer strings of the same length match if the corresponding integers differ by at most a fixed bound δ .

Notice that for $\delta = 0$, the δ -approximate string matching problem reduces to the exact string matching problem. A significant amount of research has been devoted to adapt solutions for exact string matching to δ -approximate matching (see for instance Cambouropoulos et al. (1999), Crochemore et al. (2001), Crochemore et al. (2002b), Cantone et al. (2004)). In this respect, Boyer-Moore-type algorithms are of particular interest, since they are very fast in practice. Note that the δ -approximate matching problem allows transposition invariance if we use interval pitch encoding.

The δ -approximate matching problem with α -bounded gaps has been first addressed by Crochemore et al. (2002a), where an algorithm based on the dynamic programming approach has been proposed. Then faster solutions have been presented in (Cantone et al., 2005a) and in (Cantone et al., 2005b).

At an intuitive level, we say that a melody has a δ -approximate occurrence with α -bounded gaps within a given musical score, if the melody has a δ -approximate matching with a subsequence of the musical score, in which it is allowed to skip up to a fixed number α of symbols (the *gap*) between any two consecutive positions. For example in classical music compositions, and in particular

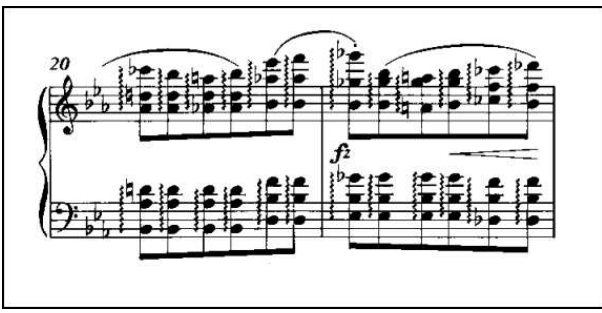


Figure 1: Bars Nr 20 and Nr 21 of the study Opus 10 Nr 11 of Fryderyk Chopin.

in compositions for *Piano Solo*, it is quite common to find musical pieces based on a sweet ground melody, whose notes are interspaced by rapidly executed arpeggios. Figure 1 shows two (partial) bars of the study *Opus 10 Nr. 11 for Piano Solo* by Fryderyk Chopin illustrating such a point. The notes of the melody are the higher notes of each arpeggiated chord.

However the above musical technicality is not by any means the only one for which approximate matching with bounded gaps turns out to be very useful. Examples are given by the use of *musical ornaments, pedal-notes*, etc.

2 MATCHING UNDER TRANSPOSITION INVARIANCE

In the problem of finding musical similarities between given melodies, it is quite natural, among other things, to regard as similar any two melodies when they differ by an interval transposition. However the formal definition of (δ, α) -matching given in previous works does not take into account the requirement of transposition invariance.

Since transposition invariance is a property which depends only on the intervals between the pitches, rather than on the pitches themselves in δ -approximate matching the problem is addressed by simply translating the melodies into interval pitch encoding.

For instance, let us consider the first two melodies, S_1 and S_2 , represented in Figure 2. If we use absolute pitch encoding then an approximation bound of $\delta \geq 7$ is needed to retrieve a match, whereas a value of $\delta = 1$ would suffice if both melodies were encoded in i.p.e. However the use of i.p.e. works well only in the case in which no gap between pitches is allowed. Referring again to Figure 2, although the melody S_3 has a transposed δ -approximate occurrence with α -bounded gaps in melody S_2 , such occurrence is not retrieved by the actual definition of (δ, α) -approximate matching. The main reason of this phenomenon is that when we allow the presence of a gap between two pitches of a melody, we lose the relevant tonal information contained in the pitches of the gap.

Here we give a new formal definition of the δ -approximate matching problem with α -bonded gaps, which take into account transposition invariance and which turns out to be very useful when melodies are represented in the a.p.e.

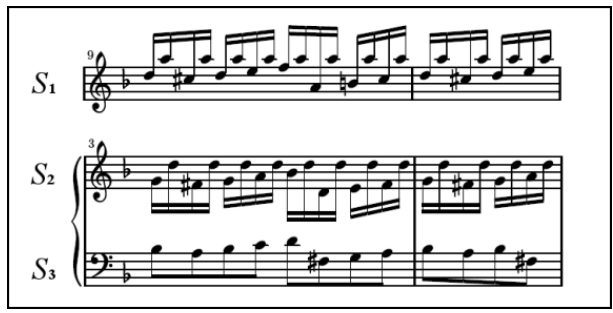


Figure 2: Two excerpts of Toccata and Fuga in D minor of Johann Sebastian Bach.

2.1 The (δ, α) -Approximate Matching Under Transposition Invariance

Let Σ be an alphabet of integer numbers and let δ, α and τ be nonnegative integers. Two symbols a and b of Σ are said to be δ -approximate if $|a - b| \leq \delta$. In this case we say that a and b effect a δ -match and write $a =_\delta b$.

Given a text T of length n and a pattern P of length m , a τ -transposed (δ, α) -occurrence of P in T at position i , is an increasing sequence of indices $(i_0, i_1, \dots, i_{m-1})$ such that

1. $0 \leq i_0$ and $i_{m-1} = i \leq n - 1$,
2. $i_h - i_{h-1} \leq \alpha + 1$, for $0 < h < m$
3. $|P[0] - T[i_0]| = \tau$
4. $P[j] - P[j-1] =_\delta T[i_j] - T[i_{j-1}]$, for $0 < j < m$.

The above definition of δ -approximate occurrence with α -bonded gaps is slightly different from the one given in Cantone et al. (2005a) in that it takes into account the δ -matching of intervals between (immediately consecutive) pitches, rather than δ -matching of the pitches themselves.

Given a text T and a pattern P , we write $P \prec_i^{(\delta, \alpha, \tau)} T$ to mean that P has a τ -transposed (δ, α) -occurrence in T at position i . In such a case we say also that P has a (δ, α, τ) -match within T .

Thus we give the following definition

Definition 1 Given two nonnegative bounds, δ and α , the δ -approximate matching problem with α -bonded gaps under transposition invariance consists in finding all positions i , in the text T , such that exists a nonnegative integer τ for which the pattern P has a τ -transposed (δ, α) -occurrence in T which ends at position i , i.e. $P \prec_i^{(\delta, \alpha, \tau)} T$.

According to this definition of approximate matching with bounded gaps, the melody S_3 of Figure 2 has a (δ, α, τ) -match within the melody S_1 if we set $\delta \geq 1$ and $\alpha \geq 1$, and if both melodies are represented in a.p.e.

Notice that in the case in which $\alpha = 0$ the δ -approximate matching problem with α -bonded gaps under transposition invariance reduces to δ -approximate matching problem with interval pitch encoding.

2.2 The (δ, α) -Matching Under Ranged-Transposition Invariance

The notion of (δ, α) -occurrence given in Definition 1 takes into consideration only the intervals of the “pattern melody” P formed between pitches which are immediately consecutive, i.e. each interval $P[j] - P[j - 1]$, for $j = 1, \dots, m - 1$.

This definition allows to bound the *local* tonal variations between pitches but, generally, leads to large *global* tonal variations along the whole sequence. More formally, a difference δ between any two consecutive pitches, in a sequence P of length m , can lead to an overall difference of $\delta(m - 1)$ between the first and the last symbol of the sequence.

Take Figure 2.2 as example. Here are shown the C major scale (first score) and the A whole tone scale (second score). If we set $\delta = 2$ and $\alpha = 1$ then we retrieve a transposed (δ, α) -occurrence of the whole tone scale as part of the major scale (in fact we retrieve the played arpeggios Dm13 chord) indicated in the first score by the squared notes. Observe, however, that the overall difference between the first and the last symbols of the sequences is 9.

However, to take care of transposition invariance, we do not need to consider necessarily intervals formed between pitches which are immediately consecutive. To bound the global tonal variations of a matched sequence it seems better to fix a particular pitch of the melody and then consider the intervals formed with such pitch.

Choosing the first pitch of a melody leads to a new definition of (δ, α) -occurrence of a pattern P in a text T , which we call τ -ranged-transposed (δ, α) -occurrence of P in T . The new definition differs from the previous in that clause 4. is replaced by:

$$4. \quad P[j] - P[0] =_{\delta} T[i_j] - T[i_0], \text{ for } 0 < j < m.$$

Given a text T and a pattern P , we write $P \triangleleft_i^{(\delta, \alpha, \tau)} T$ to mean that P has a τ -ranged-transposed (δ, α) -occurrence in T at position i . Thus we came with the following definition:

Definition 2 Given two nonnegative bounds, α and δ , the δ -approximate matching problem with α -bounded gaps under ranged-transposition invariance, consists in finding all positions i of the text T such that exists a nonnegative integer τ for which the pattern P has a τ -ranged-transposed (δ, α) -occurrence in T ending at position i , i.e. $P \triangleleft_i^{(\delta, \alpha, \tau)} T$.

Generally the approximate matching under ranged-transposition invariance leads to more “accurate” matching results than the approximate matching under transposition invariance defined previously in Section 2.1.

For instance, in Figure 2.2, to retrieve a ranged-transposed (δ, α) -occurrence, we need a value of $\delta = 9$ for the approximation bound.

Finally, observe that in the case in which $\alpha = 0$ the δ -approximate matching problem with α -bounded gaps under ranged-transposition invariance reduces to δ -approximate matching problem in the case in which we use absolute pitch encoding.

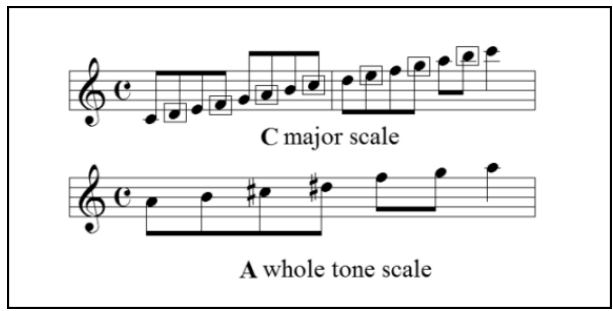


Figure 3: The C major scale and the A whole tone scale. The squared notes in the first score represent an approximate occurrence under transposition invariance of the whole tone scale.

3 TWO SEQUENTIAL-SAMPLING ALGORITHMS

In this section we present two algorithms which solve the δ -approximate matching problem with α -bounded gaps introduced in the previous Section. Such algorithms, named (δ, α, τ) -Sequential-Sampling $((\delta, \alpha, \tau)$ -SS) and $(\delta, \alpha, \hat{\tau})$ -Sequential-Sampling $((\delta, \alpha, \hat{\tau})$ -SS), are modified versions of the (δ, α) -Sequential-Sampling algorithm presented by the authors in Cantone et al. (2005a).

We begin by considering first the (δ, α) -matching problem under transposition invariance, and then we turn our attention to the (δ, α) -matching problem under ranged-transposition invariance.

Given a text T of length n , a pattern P of length m and two integers, $\delta, \alpha \geq 0$, we set, for $i = 0, 1, \dots, n$

$$\mathcal{S}_i = \{(j, k) : 0 \leq j < i, \\ 0 \leq k < m, \text{ and} \\ P_k \triangleleft_i^{(\delta, \alpha, \tau)} T \text{ for some } \tau \geq 0\}.$$

Here P_k denotes the prefix of P of length $k + 1$.

Notice that $\mathcal{S}_0 = \emptyset$. If we put $\mathcal{S} = \mathcal{S}_n$, the problem of finding all positions i in T such that $P_k \triangleleft_i^{(\delta, \alpha, \tau)} T$ for some $\tau \geq 0$, translate to the problem of finding all values i such that $(i, m - 1) \in \mathcal{S}$. To begin with, note that for $i = 0, 1, \dots, n - 1$,

$$\mathcal{S}_{i+1} = \\ \mathcal{S}_i \cup \{(i, k) : k > 0, \\ \exists h \in \{1, \dots, \alpha + 1\} : (i - h, k - 1) \in \mathcal{S}_i, \\ T[i] - T[i - h] =_{\delta} P[k] - P[k - 1]\} \\ \cup \{(i, 0)\}.$$

This recursive relation, coupled with the initial condition $\mathcal{S}_0 = \emptyset$, allows us to compute the set \mathcal{S} in an iterative fashion, by computing in turn the sets $\mathcal{S}_0, \mathcal{S}_1, \dots, \mathcal{S}_n$, starting from the set \mathcal{S}_0 .

Such computation is accomplished by means of the (δ, α, τ) -SS algorithm shown in Figure 4. The time complexity of such algorithm is easily seen to be $O(nm\alpha)$, and the space required is $O(nm)$.

However, since during each iteration of the for-loop at line 4 of the (δ, α, τ) -SS algorithm at most $m(\alpha + 1)$

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 $(\delta, \alpha, \tau)$ -Sequential-Sampling( $T, P, \delta, \alpha$ )
1.  $n = \text{length}(T)$ 
2.  $m = \text{length}(P)$ 
3.  $S = \emptyset$ 
4. for  $i = 0$  to  $n - 1$  do
5.   for  $k = m - 2$  down to  $0$  do
6.     if  $\exists h \in \{1, \dots, \alpha + 1\} : (i - h, k) \in S$  and
7.        $P[k + 1] - P[k] =_{\delta} T[i] - T[i - h]$ 
8.     then  $S = S \cup \{(i, k + 1)\}$ 
9.      $S = S \cup \{(i, 0)\}$ 
10. for  $i = 0$  to  $n - 1$  do
11.   if  $(i, m - 1) \in S$ 
12.   then output( $i$ )

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Figure 4: The algorithm (δ, α, τ) -Sequential-Sampling for the δ -approximate matching problem with α -bounded gaps under transposition invariance.

pairs of S need to be considered, it would be enough to maintain only $m(\alpha + 1)$ pairs of S at each step of the computation. With this modification, the space complexity of the (δ, α, τ) -SS algorithm can be improved to $O(m\alpha)$.

To solve the (δ, α) -matching problem under ranged-transposition invariance, we define, for each pair (i, k) , with $0 \leq i < n$ and $0 \leq k < m$, a set $\Gamma(i, k)$ which collects the starting positions j of a τ -ranged-transposed (δ, α) -occurrence of P_k in T which ends at position i . $\Gamma(i, k)$ is the set of all indexes j such that there is a τ -ranged-transposed (δ, α) -occurrence (i_0, i_1, \dots, i_k) of P_k in T such that $i_0 = j$ and $i_k = i$. Then, the problem of finding all positions i in T such that $P \prec_i^{(\delta, \alpha, \tau)} T$ for some $\tau \geq 0$, translates to the problem of finding all values i such that $\Gamma(i, m - 1) \neq \emptyset$.

We observe that, for $0 \leq i < n$ and $0 < k < m$ we have

$$\Gamma(i, k) = \{j : P[k] - P[0] =_{\delta} T[i] - T[j] \text{ and } j \in \Gamma(\max(0, i - h), k - 1) \text{ for some } h \in \{1, \dots, \alpha + 1\}\}$$

while $\Gamma(i, 0) = \{i\}$, for $0 \leq i < n$.

Thus the computation of the sets $\Gamma(i, k)$ can be done iteratively, as is shown in the $(\delta, \alpha, \hat{\tau})$ -SS algorithm of Figure 5.

4 CONCLUSIONS

We have addressed the problem of approximate matching with bounded gaps allowing transposition invariance, and we have also presented two algorithms that solve it.

The notions of approximate matching which we have devised, turn out to be very useful in discovering musical similarities, covering transposition invariance.

Existing solutions for the approximate matching problem with bounded gaps do not cover well the problem of transposition invariance in either cases in which musical sequences are represented in a.p.e. or in i.p.e. In particular the latter representation of musical sequences could seem to be more appropriate to handle transposition invariance, since transposition invariance is a property which depends only on the intervals between pitches rather than on the pitches themselves.

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 $(\delta, \alpha, \hat{\tau})$ -Sequential-Sampling( $T, P, \delta, \alpha$ )
1.  $n = \text{length}(T)$ 
2.  $m = \text{length}(P)$ 
3. for  $i = 0$  to  $n - 1$  do
4.   for  $k = m - 2$  down to  $0$  do
5.      $\Gamma(i, k + 1) = \emptyset$ 
6.     for  $h = 1$  to  $\alpha + 1$  do
7.       for each  $j \in \Gamma(\max(0, i - h), k)$  do
8.         if  $P[k + 1] - P[0] =_{\delta} T[i] - T[j]$ 
9.         then  $\Gamma(i, k + 1) = \Gamma(i, k + 1) \cup \{j\}$ 
10.     $\Gamma(i, 0) = \{i\}$ 
11. for  $i = 0$  to  $n - 1$  do
12.   if  $\Gamma(i, m - 1) \neq \emptyset$ 
13.   then output( $i$ )

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Figure 5: The $(\delta, \alpha, \hat{\tau})$ -Sequential-Sampling algorithm for the δ -approximate matching problem with α -bounded gaps under ranged-transposition invariance.

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