Deep rank-based transposition-invariant distances on musical sequences

Gaëtan Hadjeres\textsuperscript{1, 2} and Frank Nielsen\textsuperscript{3, 4}

\textsuperscript{1}LIP6, Université Pierre et Marie Curie
\textsuperscript{2}Sony CSL, Paris
\textsuperscript{3}École Polytechnique, Palaiseau, France
\textsuperscript{4}Sony CSL, Tokyo

Abstract

Distances on symbolic musical sequences are needed for a variety of applications, from music retrieval to automatic music generation. These musical sequences belong to a given corpus (or style) and it is obvious that a good distance on musical sequences should take this information into account; being able to define a distance ex nihilo which could be applicable to all music styles seems implausible. A distance could also be invariant under some transformations, such as transpositions, so that it can be used as a distance between musical motives rather than musical sequences. However, to our knowledge, none of the approaches to devise musical distances seem to address these issues. This paper introduces a method to build transposition-invariant distances on symbolic musical sequences which are learned from data. It is a hybrid distance which combines learned feature representations of musical sequences with a handcrafted rank distance. This distance depends less on the musical encoding of the data than previous methods and gives perceptually good results. We demonstrate its efficiency on the dataset of chorale melodies by J.S. Bach.

1 Introduction

Determining whether two musical sequences are similar or not is a key ingredient in music composition. Indeed, the repeated occurrences of a given pattern (transformed or not) is easily perceived by an attentive listener. Among possible transformations of a pattern, we can cite

- transposition
- mode change
- augmentation / diminution
- ornamentation / simplification.

These patterns in music gives the listener expectations of what could follow. This latter is then gratified to have guessed right or can be surprised by a pleasing or unexpected change. The musical pieces may then appear more coherent and organized. It is then up to the composer to play with this series of fulfilled/unfilled expectations. From a compositional point of view, this allows a composer to create long pieces of music while retaining the listener’s attention.

Many musical pieces are intrinsically-based on the different repetitions of a given pattern. Fugues or sonatas are examples of such pieces where the overall structure results from how the occurrences and transformations of a given pattern unfold through time. But this is also true on a local scale in many musical genres since patterns give coherence between musical phrases. This is particularly observable in pop and jazz songs (see Fig. \ref{fig:example} for instance for an example of a pattern and its transformation).
Due to the omnipresence of patterns in music, good distances on musical sequences are essential and can be used for a wide variety of tasks:

- plagiarism detection \cite{5}
- music retrieval \cite{1}
- automatic musical analysis \cite{10, 12}
- automatic music generation \cite{27}.

The traditional distance used for sequence comparison is the edit-distance (also known as the Levenshtein distance \cite{21}). On sequences of symbols, it basically consists in assigning a cost to different basic edit operations such as the insertion, the deletion or the substitution of a single symbol. The distance between two sequences is then the cost of the minimal sequences of basic edit operations allowing to change the first sequence into the second one. This minimal cost is easily calculated using a dynamic programming algorithm.

Most of the existing distances on musical sequences are based on generalizations of the aforementioned distance by taking into account the specificity of the set of musical sequences (the edit distance was primarily designed for text).

For instance, \cite{24} propose to extend the set of basic edit operations by two other operations that are more specific to musical sequences: fragmentation and consolidation.

The main issue with this approach is that the edit-distance strongly depends on the choice of the encoding of the musical content. Indeed, contrary to textual data, musical content (such as monophonic melodies) can be encoded in many ways and there are a priori no representation which is better than another.

The importance of the choice of the data representation is pinpointed in \cite{4}. In this paper, the authors argue that the MIDI pitch representation is insufficient for applications in tonal music as it disregards the hierarchical importance of diatonic scale tones over the 12-tone discrete pitch space. To address this issue, they propose a new representation, called the General Pitch Interval Representation. It is a representation that takes into account the diatonic intervals in scale steps and other more abstract representations such as contour strings (the contour string of a melody is a representation where only the following events are considered: repeat, ascending or descending step, ascending or descending leap).

The interest in such a representation is that it introduces perceptually salient information directly into the sequence encoding.

This idea is further explored in \cite{14} where they propose to encode a melody using its Implication/Realization structure. It is a concept drawn from the theory of perception and cognition of melodies from \cite{26} which is based on
the Gestalt theory. It consists in assigning different basic structures depending on the contour of a sequence and can be considered as a generalization of the contour string encoding.

Using contour strings encoding implies that a melody is only considered up to a transposition since only intervals with respect to the previous note is considered \cite{20}. The same idea can also be used by considering ratios of rhythmic patterns instead of their absolute values. We refer the reader to \cite{16} where the authors study the advantages and drawbacks of many monophonic sequence representations on the edit-distance algorithms.

Geometric interpretations of the distance between two musical sequences have also been proposed \cite{23, 30}. Their advantage is to be applicable on polyphonic sequences contrary to the methods based on the edit-distance. \cite{19} compares the two approaches on a variety of music retrieval tasks.

However, defining how close two sequences are is in fact an ill-defined problem. This notion is very subjective and it seems implausible to find a universal rule applying to every musical style and sequences: sequences can be “close” with respect to a given music style and “far” in another music style. Furthermore, attempts to ground it on a psychological basis using an appropriate representation still suffer from the arbitrariness of the underlying distance.

In this work, we introduce a corpus-dependent distance between two musical sequences. Our distance relies on a permutation-based distance \cite{21} applied on high-level features obtained via a sequence-to-sequence autoencoder. This approach is general and we believe more independent of the choice of the representation than all previous methods, and can be applied to both monophonic and polyphonic music.

We then extend our method in order to obtain a way to generate transposition-invariant distances, which means that a sequence and its transposition should be close. Contrary to other methods, this distance is made transposition-invariant without changing the sequence encoding.

In the following, we focus on monophonic sequences with a given representation, but these ideas can easily be generalized to other representations of musical material, from monophonic to polyphonic ones.

Our contributions are the following:

- introduction of a framework to build distances on sequences,
- extension of this approach in order to construct invariant distances with respect to a given set of transformations,
- introduction of corpus-dependent musical distances in music.

We believe that linking the distance between musical sequences to the specific genre of these musical sequences is a way to address issues related to the choice of a perceptually-appropriate distance and is more likely to yield better results.

The outline of this paper is the following: In Sect. \ref{related_works} we expose related works about transformation-invariant features and transformation-invariant distances; Section \ref{methodology} introduce our method to construct a data-dependent distance on sequences and Sect. \ref{implementation} improves this method in order to obtain a distance which is invariant with respect to a set of transformations; Finally, in Sect. \ref{results} we present experimental results about the introduced distances and highlight their efficiency on the dataset of the chorale melodies from the J.S. Bach chorale harmonizations.

## 2 Related works

Finding transformation-invariant distances is a problem which was primarily addressed on image datasets. Indeed, learning distances from a corpus of images is crucial in many applications (classification, clustering, or retrieval tasks) and it is often desirable that this distance be independent under some natural transformations on images such as rotations and translations.

Taking into account the “natural” set of transformations which acts on a dataset is of a great interest since we can use this information to obtain more robust and more informative feature representations.

The feature representations need not necessarily be invariant with respect to a set of transformations, but sometimes only equivariant \cite{7}. Equivariance here means that the feature representation of a transformed image can be obtained by applying a known transformation directly to the feature representation of the original image.

Convolutional Neural Networks (CNNs) \cite{18, 28} for instance take into account the importance of translations on image datasets by using the same transposed filter. A generalization of the regular CNN filters has been proposed \cite{31}.
Figure 2: (a) a 2-beat sequence and (b) its transposition a major third lower.

It aims at obtaining a CNN which is equivariant to both translations and rotations. It is in fact possible to devise more general approaches which are able to deal with any symmetry group acting on images as shown in [11, 8, 3]. In [3], the proposed model is suitable for a theoretical analysis about the stability of the learned invariant representations.

However, equivariant feature representations are not particularly suitable for building invariant feature representations. Indeed, in order to obtain an invariant representation, one would have to average all feature representations of all possible image transformations under the chosen group, which is either intractable or computationally demanding.

An approach in the context of shape matching which shares the same motivations as ours can be found in [22]. Contrary to images, two shapes are considered to be identical if we can obtain one by applying a group transformation on the other one. These group transformations can be as above the group of displacements (translations and rotations), but can also be, in the context of shapes, the affine group (translations, rotations and rescalings). A distance between shapes is then constructed by introducing a distance on the integral invariants of a shape. These handcrafted quantities are invariant with respect to the group of transformations acting on shape contours and thus assert that the constructed distance is well-defined on shapes. The main difference with the approaches in image is that the feature representations (here the integral invariants) is not learned from data but constructed by hand.

In comparison, our method is able to learn transformation-invariant feature representations from data resulting in a transformation-invariant distance.

3 Corpus-based distance

3.1 Rank-based distance

Our method to construct distances on sequences relies on the rank-based (or permutation-based) distances described in [2]. The idea is to define a distance based solely on the ranking of the high-level activations of a Deep Neural Network (DNN) [13]. Indeed, activations of neurons from high-level hidden layers can be used as features for describing the input. Each of this feature can encode a particular concept about the input and how these concepts are ranked with respect to one another is sufficient to determine if two inputs are similar.

More precisely, let $x$ be a $N$-dimensional feature vector. We define $\Pi(x)$ to be the vector of ranks of $x$. This vector is a permutation of the $N$-tuple $[N]$ such that

$$\forall i, j \in [N], \quad i < j \implies x_{\Pi(x)_i} \geq x_{\Pi(x)_j}.$$  \hspace{1cm} (1)

With this notation, $\Pi(x)_1$ is the index $i$ such that $x_i$ is the greatest coordinate of $x$.

Given two feature vectors $x$ and $y$, we can define their distance to be the distance between their permutations $\Pi(x)$ and $\Pi(y)$ using popular distances between permutations. In the following, we will consider two popular rank correlation measures: Spearman’s rho distance and Kendall’s tau distance.

In its simplest formulation, Spearman’s rho distance $\rho$ between feature vectors $x$ and $y$ is defined to be the $\ell_2$ norm between their vectors of ranks. This gives us:

$$\rho(x, y) = \sqrt{\sum_{i=1}^{N} (\Pi(x)_i - \Pi(y)_i)^2}.  \hspace{1cm} (2)$$

The Kendall tau distance is a measure of similarity between two rank variables. It is based on the number of pairwise inversions needed to change one ordering into the other. Given two vectors of ranks $\Pi(x), \Pi(y)$ of size
In the following, we consider that we have an i.i.d. dataset \( D \) of \( K \) sequences of length \( L \)

\[
D := \left\{ s^{(k)} = (s_1^{(k)}, \ldots, s_L^{(k)}), \ s_i \in [A] \right\}_{k \in [K]},
\]

where sequences are composed of tokens in \([A]\) with \( A \) the size of the alphabet. The objective is to obtain a mapping from the space of sequences \( A^L \) to a feature representation in \( \mathbb{R}^N \).

In order to build a high-level representation of musical sequences in an unsupervised manner, we consider using a sequence-to-sequence model [29, 6] (Fig. 3a) as an autoencoder [13]. An autoencoder is a Neural Network (NN) parametrized by \( \theta \) which is composed of two parts: an encoding NN \( \text{enc}_\theta \) which usually maps the high-dimensional observation space to a feature representation (or code) of smaller dimensionality and a decoding NN \( \text{dec}_\theta \) whose aim is to predict the original sequence given its code.

The decoder returns a probability distribution \( \pi = (\pi_1, \ldots, \pi_L) \) over the sequences in \( A^L \) where each \( \pi_i = (\pi_{i,1}, \ldots, \pi_{i,A}) \) is a categorical distribution over \([A]\) (\( \pi_{i,a} \geq 0 \) and \( \sum_{a=1}^{A} \pi_{i,a} = 1 \) for all \( i \)).

The parameters \( \theta \) of the RNN are chosen to minimize the following loss:

\[
\mathcal{L}(\theta; D) := \sum_{k=1}^{K} \sum_{i=1}^{N} H \left[ s_i^k; \text{dec}_\theta(\text{enc}_\theta(s^k))_i \right]
\]

where

\[
H \left[ s_i^k; \text{dec}_\theta(\text{enc}_\theta(s^k))_i \right] := -\sum_{a=1}^{A} \delta_a(s_i^k) \log \left[ \text{dec}_\theta(\text{enc}_\theta(s^k))_{i,a} \right],
\]

Figure 3: Seq2seq autoencoder and its generalization. Boxes represent RNN cells. Only the output of the last RNN cell is used. The feature representation is displayed as an oval.

\( N \), we say that a pair of integers \( i < j \) is concordant if \( \Pi(x)_i < \Pi(x)_j \) and \( \Pi(y)_i < \Pi(y)_j \) and discordant if \( \Pi(x)_i < \Pi(x)_j \) and \( \Pi(y)_i > \Pi(y)_j \) (and these definitions also hold when we reverse all inequalities). Since there are \( N(N-1)/2 \) such pairs, we can define a similarity on feature vectors \( x \) and \( y \) by

\[
\tau(x, y) = \frac{\# \{ \text{concordant pairs} \} - \# \{ \text{discordant pairs} \}}{N(N-1)/2},
\]

where \( \# \{ \text{concordant pairs} \} \) indicates the number of concordant pairs when considering the rank vectors of \( x \) and \( y \). This similarity measure is in \([-1, 1]\) and equals 1 when the ranks are equal.

It is worth noting that computing Kendall’s tau distance is more computationally-demanding than computing Spearman’s rho distance due to the quadratic number of terms.

### 3.2 Sequence-to-Sequence autoencoder

In the following, we consider that we have a i.i.d. dataset \( D \) of \( K \) sequences of length \( L \)

\[
D := \left\{ s^{(k)} = (s_1^{(k)}, \ldots, s_L^{(k)}), \ s_i \in [A] \right\}_{k \in [K]},
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In our case, these neural networks are implemented using Recurrent Neural Network (RNN) [13]. The feature representation \( \text{enc}_\theta(s) \) for a sequence \( s \) is obtained by considering only the output of the RNN on the last time step.

The decoder returns a probability distribution \( \pi = (\pi_1, \ldots, \pi_L) \) over the sequences in \( A^L \) where each \( \pi_i = (\pi_{i,1}, \ldots, \pi_{i,A}) \) is a categorical distribution over \([A]\) (\( \pi_{i,a} \geq 0 \) and \( \sum_{a=1}^{A} \pi_{i,a} = 1 \) for all \( i \)).

The parameters \( \theta \) of the RNN are chosen to minimize the following loss:

\[
\mathcal{L}(\theta; D) := \sum_{k=1}^{K} \sum_{i=1}^{N} H \left[ s_i^k; \text{dec}_\theta(\text{enc}_\theta(s^k))_i \right]
\]

where

\[
H \left[ s_i^k; \text{dec}_\theta(\text{enc}_\theta(s^k))_i \right] := -\sum_{a=1}^{A} \delta_a(s_i^k) \log \left[ \text{dec}_\theta(\text{enc}_\theta(s^k))_{i,a} \right],
\]
denotes the categorical cross-entropy with \( \delta_a \) such that \( \delta_a(x) = 1 \) iff. \( x = a \) and 0 otherwise.

Details about our implementation are discussed in Sect. 5.1.

3.3 ReLU non-linearity and truncated Spearman rho distance

In exposing the rationale behind the permutation-based distance in Sect. 3.1, we put forward the idea that each feature of a sequence encodes a particular high-level concept. An ordering of these concepts would then act like a fingerprint for this sequence. However, in the model described above, the “most-relevant concepts” (the coordinates \( x_i \) which have supposedly the greatest impact on the sequence decoding) are the coordinates with the greatest absolute value. Coordinates near zero are unlikely to be particularly relevant but have a great influence on the ordering \( \Pi(x) \) of Eq. (1) and on the distance Eq. (2).

A way to deal with this consists in adding a Rectifier Linear Unit (ReLU) activation on top of the encoder RNN. The resulting feature vector will then contain only non-negative elements with a substantial number of null elements. In doing so, we impose that the “most-relevant concepts” are within the first values of the permutation \( \Pi(x) \). It is then possible to modify the Spearman rho distance by only considering the \( l \) most important coordinates, which results in the truncated Spearman rho distance of order \( l < N \):

\[
\rho_l(x, y) = \sqrt{\frac{\sum_{i=1}^{l} (\Pi(x)_i - \Pi(y)_i)^2}{\sum_{i=1}^{N} (\Pi(x)_i - \Pi(y)_i)^2}}.
\]

(7)

We finally define the corpus-dependent distance \( D_D \) between two sequences \( s \) and \( s' \) truncated up to \( l \) by

\[
D_D(s, s'; l) = \rho_l(\text{enc}_\theta(s), \text{enc}_\theta(s')),
\]

(8)

where \( \text{enc}_\theta \) is the encoder RNN (with a ReLU non-linearity on its top-most layer) of a trained sequence-to-sequence autoencoder.

4 Transformation-invariant distances

We now suppose that we have a set of transformations \( T \) that act on sequences. We suppose that this action defines an equivalence relation on \( \mathcal{D} \). This means that if there exists \( t \in T \) such that \( s = t.s' \) for sequences \( s, s' \in \mathcal{D} \), then there exists \( t' \in T \) such that \( s' = t'.s \). In such a case, we note \( s \sim s' \) and their equivalence class is notated \( T.s \).

A typical example on musical sequences would be the set of transpositions (see Fig. 6). The sequence dataset is then split between the different equivalence classes \( T.s \). Our objective is to devise a distance between sequences that would be invariant relatively to this set of transformations, i.e. the distance only depends on the equivalence classes and not on the sequences themselves.

A simple way to achieve this goal is to directly obtain transformation-invariant feature representations. For this, we need to modify the preceding architecture so that the feature representation (represented as a circle in Fig. 3a) is the same for a sequence and all its transformations. We introduce the sequence-to-sequence architecture depicted in Fig. 3b. It is a model which takes as an input a sequence \( s \in \mathcal{D} \) and a transformation \( t \in T \) and learns to predict the transformed sequence \( t.s \). In this model, the encoder \( \text{enc}_\theta(s) \) is only a function of \( s \) while the decoder \( \text{dec}_\theta(x, t) \) takes as an input a feature representation \( x \) together with the transformation \( t \) applied to \( s \).

This architecture is trained using the following loss function:

\[
L(\theta; D, T) := \sum_{t \in T_k} \sum_{k=1}^{N} \sum_{i=1}^{K} H \left[ (t.s^k)_i; \text{dec}_\theta(\text{enc}_\theta(s^k), t)_i \right],
\]

(9)

where the first sum over \( t \in T_k \) denotes the set of transformations \( t \in T \) such that \( t.s^k \in \mathcal{D} \).

Note that, in the case of musical transpositions, we can specify how we want to transpose our input sequence \( s \) by two means:
\begin{itemize}
  \item \textit{relatively to} $s$, by specifying the interval by which we transpose $s$ (relative representation),
  \item \textit{independently of} $s$, by specifying, for instance, the name of the starting note of $t.s$ (absolute representation).
\end{itemize}

Since we want a feature representation which depends only on equivalence classes $T.s$ and not on its representatives $s' \in T.s$, we must use an absolute representation when specifying the transformations $t \in T$. Indeed, using a relative representation would otherwise force the feature representation to contain absolute information. Plugging this representation in a rank-based distance would lead to a distance which is not transformation-invariant.

Even when doing so, the distances we obtain are not fully-invariant: the feature representation can still contain absolute information about sequence $s$. We propose to overcome this issue by forcing the model to compute averaged feature representations. Ideally, using the mean representation

$$
\overline{\text{enc}}_{\theta}(T.s) := \frac{1}{|T.s|} \sum_{s' \in T.s} \text{enc}_{\theta}(s') \tag{10}
$$

for an equivalence class $T.s$ gives a transformation-invariant representation, but it is computationally-expensive. A simple approximation is to compute this mean representation using only two sequences belonging to the same equivalent class. For two sequences $s, s' \in T.s$, we consider the averaged representation

$$
\overline{\text{enc}}_{\theta}(s, s') := \frac{1}{2} (\text{enc}_{\theta}(s) + \text{enc}_{\theta}(s')) \tag{11}
$$

this representation is then passed to the decoder together with the absolute transformation representation. This architecture is represented in Fig. 4.

We finally add a $\ell_1$-penalty on the difference between the two feature representations to encourage the model to make these two representations equal. The loss function we obtain in this case is then given by

$$
\mathcal{L}_{\text{invariant}}(\theta; D, T, \lambda) := \sum_{t, t' \in T_k} \sum_{k=1}^{K} \sum_{i=1}^{N} \left[ H \left( \left( t', s^k \right)_i ; \text{dec}_{\theta} \left( \overline{\text{enc}}_{\theta}(s^k, t.s^k) , t'_i \right) \right) \right] + \lambda \ell_1 \left[ \text{enc}_{\theta}(s^k) - \text{enc}_{\theta}(t.s^k) \right], \tag{12}
$$

where $\lambda$ is a hyper-parameter controlling the trade-off between accuracy and enforcing the invariance property.

We thus define a transformation-invariant $D_{D,T}$ distance relative to a corpus $D$ and a set of transformations $T$ as in Eq. (8), except that the encoder network $\text{enc}_{\theta}$ is the encoder network of the modified architecture schematically displayed in Fig. 4 and trained with loss $\mathcal{L}_{\text{invariant}}(\theta; D, T, \lambda)$ given by Eq. (12).

This transposition-invariant distance has the advantage that the notion of invariance is directly encoded into the learned model. Indeed, a simpler way to produce a transposition-invariant distance would be to apply the corpus-based distance of Eq. (8) to a corpus where all sequences would start with the same note, say C4. The distance
between any two sequences would thus be the distance between their transposed version starting in C4. However, these transpositions cannot be implemented effectively: the first note has to be found in order to know how to transpose (we can have rests or hold symbols, see Sect. 5.1). This operation takes some time and it cannot be easily parallelizable on a GPU. The proposed transposition-invariant distance thus transfer these costly operations from the evaluation phase to the data-preprocessing phase.

5 Experimental results

We report experiments on the chorale melodies from the chorale harmonizations by J.S. Bach. This dataset is obtained by extracting all soprano parts from the J.S. Bach chorales dataset included in the music21 Python package.

5.1 Implementation details

We choose to encode our data using the melodico-rhythmic encoding proposed in [15]. More specifically, time is quantized with sixteenth notes and we use the full name of the notes instead of the traditional MIDI pitch representation. We introduce two additional tokens in order to handle rhythm and pitch in a unified fashion: a hold symbol HOLD indicating that a note is being played but not attacked, and a rest symbol REST. In this setting, a musical sequence is only an ordered sequence of tokens drawn from the set of all possible notes \{C3, C#3, Db3, D3, D#3, \ldots\} together with the HOLD and REST tokens.

The set of transformations \( T \) we choose is the set of all transpositions. But for a given sequence \( s \), we only define as its equivalence class the set of its transpositions which fits within the original voice range. In doing so, we do not need the set of transformations to be a group, but require only that it defines an equivalence relation.

The RNN we use is a 2-layer stacked LSTM [17] with 512 hidden units each. The ReLU non-linearity is used and the truncation order \( l \) of Eq. (7) is set to 256.

5.2 Nearest neighbor search

We empirically demonstrate the efficiency of these distances by displaying examples of nearest neighbor requests. Fig. 5a shows examples of melodies which are “close” according to the corpus-dependent distance \( D_D \). All the results that we display are obtained using Spearman’s rho distance, but we obtain similar results by replacing it with Kendall’s tau similarity measure.

The nearest neighbors query of Fig. 5a reveals interesting behaviors of the corpus-dependent distance \( D_D \). The overall shape of the target melody (ascending then descending) is present in every neighboring sequence under various aspects. There are interesting rhythmic variations and also key changes. But, what is the most striking here, is that some other characteristic elements of the target sequence are also taken into account. For instance, the importance of the ascending leap on the fourth beat is present in many sequences. Another such example is the note repetition at beats 2 and 3 which also occurs in some neighboring sequences. We believe that the last sequence in the example displayed in Fig. 5a is a good illustration of how characteristic elements are captured with our distance. Even if there are only two notes in common with the target sequence, we still have an impression of proximity between both. This may be due to the following facts

- the most important notes of the target sequence (the highest and the lowest) are replicated,
- the key and the rhythm are identical,
- there is an ascending fourth in both (on beat 2 for the neighboring sequence instead of on beat 4 for the target sequence),
- there is a note repetition on beats 2 and 3,
- they both conclude by a descending conjunct movement.
Figure 5: A target melody and its nearest neighbors according to different distances on sequences. Duplicates have been removed.
This has to be compared with the nearest neighbors returned using the edit distance on the same target sequence. This is displayed in Fig. 5b. This presents some unwanted behaviors. For instance, sequences identical to the target sequence but with a sixteenth note offset are considered to be almost identical. However, from a musical point of view, the importance of the difference between notes on and notes off the beat is crucial. In the other cases, the edit only manages to find sequences containing common notes (and played at the exact same time) with the target sequence. Since the HOLD symbol is seen as note like any other one, we can see that replacing a half note by a quarter note has a cost of only one, independently of the chosen note. The importance here is not on the melodic contours nor on an intuitive perception of similarity.

The behavior of the edit distance seems more erratic and less predictable. It is also “less smooth” than our proposed distances (see Fig. 6) since the edit distance can only take a finite (and smaller) number of values. The important difference is that the number of possible values returned by the edit distance depends on the sequences size, while it depends on the feature vector size in the case of corpus-dependent distances.

5.3 Invariance by transposition

In this section, we check to which extent the distance $D_{D,T}$ is invariant under the set of transformations $T$. In Fig. 6 we plot the distance $D_{D,T}(s, s')$ when $s$ and $s'$ are in the same equivalence class under $T$ and when they are not.

Two things are two be noted in this example. Firstly, the obvious difference between the two densities and the sharp peak when the sequences are in the same equivalence class show that our distance indeed captures the invariance by transposition on musical sequences. Secondly, the behavior of the density of the distance between two randomly-chosen sequences is interesting: it is multimodal and widespread. This distance can take numerous different values and can then have more discriminative power. We have experimentally seen in Sect. 5.2 that the corpus-dependent distance is able to capture high-level musical concepts. It is the same for its transposition-invariant counterpart.

To show this, we do not replicate the results about the nearest neighbor search of Fig. 5a since it only returns exact transpositions of the target sequence. Instead, we only make a nearest neighbor search on a small subset of the J.S. Bach chorales using $D_{D,T}$. The result is displayed in Fig. 7.

The same analysis as the one conducted for Fig. 5a can be made, except that it is now irrespective of the transposi-
tion of the neighboring sequences. We conclude that this transposition-invariant distance allows to detect characteristic patterns and musical motives independently of the key they are in.

6 Conclusion

We proposed a novel framework to build distances learned from musical corpora. Because they take into account the style to which musical sequences belong, these learned distances are not subject to the usual problems encountered using the edit-distance generalizations: they are less dependent on the input encoding while being more satisfactory from a perceptive point of view. Indeed, using neural-network-learned features instead of handcrafted features allows to define a natural notion of proximity between sequences which is rooted on an objective and non-biased a priori basis. The choice of the rank-based distance applied on the feature representations does not seem to influence much the final distance behavior. This framework can be modified so that the distances we obtain are invariant with respect to a given a set of transformations. This is made possible by the fruitful combination between a quasi-invariant feature representation learned from a regularized sequence-to-sequence architecture and a rank-based distance. Since the feature representations are not necessarily equal for sequences within the same equivalence class, the usage of a rank-based distance over these representations helps to make the distance over sequences invariant.

Future work will aim at improving the proposed method by taking into account multiple hidden layers in the rank-based distance. On a more practical side, we will also aim at using this distance on music generation tasks in order to design algorithms capable of generating highly-structured melodies.

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