A NEW SIMILARITY FUNCTION FOR MUSIC RHYTHM COMPARISON

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ABSTRACT
This extended abstract is for MIREX 2008 Query by Tapping task. The submission presents a rhythm similarity function to compare MIDI extract with user tapping. Algorithm can also use for QBT Content-Base Music Retrieval system.

Keywords: MIREX, QBT, CBMR.

1 IMPLEMENTATION OVERVIEW
QBT task uses recorded tapping rhythm in WAV audio format as query files. Retrieve the top 10 candidates MIDIs from QBT test collection. There are two execution files in this submission both are implemented by Matlab 7:

1.1 indexMidi.exe
Extract the time interval between every consecutive Note On event for each MIDI in collection and save as intermediate form. Note On with velocity=0(rest note) or time interval smaller than 100 ms will be discard. For example the rhythm intermediate form for the first 12 Note On events in “Happy birthday” would be:
450,150,600,600,600,1200,450,150,600,600,600

1.2 running_wav.exe
Extract the wav query files onset time by “aubioonset.exe”. Setting the threshold value for the onset peak picking=0.7. Then compare the similarity between extract onset peak and rhythm intermediate form. Finally report result in answer file for each task run order by their similarity.

2 SIMILARITY FUNCTION
Most MIR system compares rhythm by symbolic form using warping distance[1] or editing distance[2] to compute the similarity. This extended abstract propose a new way to measure the rhythm similarity by “Rhythm Quotient Standard Deviation”. RQSD compares rhythm directly by numerical form instead of symbolic form. Normalization from numerical to symbolic will cause losing some detail for distance comparison. For example we have a query sequence Q and index document sequence D, RQSD processes by the following step:

A. Cut Q and D into grams by 4-gram method, and every gram with 4 rhythm elements. Then calculate each corresponding gram similarity between Q and D.

B. Suppose a 4-gramm in Q is called QG and the corresponding 4-gramm in D is called DG. Divide each rhythm element in QG and DG to obtain four rhythm quotient values

\[
q1=\frac{QG(1)}{DG(1)}
\]
\[
q2=\frac{QG(2)}{DG(2)}
\]
\[
q3=\frac{QG(3)}{DG(3)}
\]
\[
q4=\frac{QG(4)}{DG(4)}
\]

C. Calculate the standard deviation of these 4 rhythm quotient values. The smaller the standard deviation is, the more similar QG and DG are.

\[
\sigma = \text{StdDev} (q1, q2, q3, q4)
\]

D. The standard deviation value allows changing in wider range for bigger rhythm quotient values. In other words, for the same similarity degree, bigger q1, q2, q3, q4 will get a bigger standard deviation value. So it is necessary to create a factor \(\bar{\sigma}\) to reduce this kind of effect

\[
\bar{\sigma} = \frac{q1+q2+q3+q4}{4}
\]

E. Gram similarity can be calculated:

\[
\text{Gram Similarity} = (1 - (\sigma / \bar{\sigma})) \times 100\%
\]

F. Finally calculate the global similarity of Q and D. Sums the gram similarity of all grams and divides the summation by the number of gram pairs compared.

\[
\text{Similarity} = \frac{\sum \text{GramSimilarity}}{\text{compared gram count}}
\]

REFERENCES