



Extracting music genes for era classification



Yang Liu, Xiongfei Li, Rigen Te, Chi Pan, Xuebai Zang*

Symbol Computation and Knowledge Engineer of Ministry of Education, Jilin University, Changchun, China

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ABSTRACT

With the growth of computational culture, the concept of cultural syntactic unit has been investigated quite intensively in recent years. The existing approaches of extracting music feature always consider putting notes together according to certain rules. However, sometimes, it might be better take the integrity of melody into account. In this paper, we introduce a syntactic unit named music gene and propose a music feature extraction method for era classification. Music genes are extracted from XML files and estimated utilizing their intervals to investigate their representation of music feature. We evaluate the performance of music gene and the previous proposed motif to illustrate the effectiveness of music gene in classification. Support vector machines are applied to classify XML files into their respective classes by learning from training data. We obtain the classification accuracy for a collection of 764 music genes, demonstrating that significant classification can be achieved using higher level music feature.

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1. Introduction

The challenge of processing music automatically with computer has involved much research in musical domains. Processing music is a very complex work that involves many disciplines. Music feature extraction is just one of these aspects.

The concept of music feature has been investigated quite intensively in recent years. Music feature, chord for example, is an aspect of a piece of music. Researchers extract music features from a music score for further discussion on music computable. Nowadays, cultural heritage like music has become computable with the accelerated advancement of AI. Michel et al. constructed a corpus of digitized texts and investigated cultural trends quantitatively. Their analysis of 'culturomics' extends the boundaries of rigorous quantitative inquiry to a wide way of new phenomena spanning the social sciences and the humanities (Michel et al., 2011). Culturomics focused on words in English language as words are considered to be complete grammar units. Studies show that words can provide insights about fields as diverse as lexicography, the evolution of grammar and collective memory.

From Michel's research we see that the frequency of words can be more informative than the letters'. Similarly, music should also have syntactic units that can be the minimum meaningful units in the whole score. We call such unit music gene instead. In this study we focus on music features from the perspective of music gene. A

related theory named 'computer expressive performance' (Kirke & Miranda, 2013) has developed in a variety of directions. The major concern is to express music with a hierarchical representation. Kirke divides the music score into five levels from the perspective of Linguistics: note, motif, phrases, section and piece. Current studies are basically on the motif level. For example, Nieto and Farbood (2012) argues that 6 notes already have the ability to describe a melody and Jiménez, Molina-Solana, Berzal, and Fajardo (2011) believes that the length of a motif is 10 notes at most. In general, researchers consider that 6–9 notes compose a motif. However, motif ignores the concepts of tempo and measure in a score; it simply puts the sequential notes together to compose a motif. This perspective overpasses the integrity of music measures, which may lead to an important problem of missing information in music feature analysis. The proposed music gene in this paper takes integrity into consideration, it is considered to be a syntactic unit that can map music features to a certain emotion under specific historical and social conditions. We briefly understand it as a function from music notes to more abstract values. Music gene provides a syntactic aspect for music feature and makes up for the imperfection of Kirke's levels.

Various approaches have been proposed, utilizing music features such as rhythm, gamut and melody (Lu & Tseng, 2009; Shan, Kuo, Chiang, & Lee, 2009). According to researchers in musicology (Hashida, Nagata, & Katayose, 2006; Katayose, Fukuoka, Takami, & Inokuchi, 1990), a melody can express emotions, and pitch interval is one of the basic essentials of melody. Approaches to intervals are generally applied to distinctive pattern recognition in music, while they do not consider the integrity of melody. Moreover, more studies extract pitch from the audio sound format, which is not

* Corresponding author. Tel.: +86 13596081669.

E-mail address: zangxbjlu@gmail.com (X. Zang).

convenient and accurate as the pitch is obtained from a mixed sound wave.

There are two main formats utilized in music feature extraction: audio sound and MusicXML. Audio sound such as WAVE and MIDI has no exact information of every note, so researchers need to extract notes from channels first. The other format MusicXML is a new kind of format provided by Recordare LLC in 2004. To date, it has gained the status of a *de facto* standard and is accepted by most academic and commercial applications (Szwoch, 2008). In this paper we propose a method for extracting music genes according to Sheet-MusicXML, which is an improvement of MusicXML. We prefer MusicXML as it is based on the mature XML technology and is clear structured for the semi-structured format. Above all, MusicXML has its respective score for each track while audio sound is only a sound wave, that is to say, information in MusicXML is more completed than audio sound during the analysis of extracting music gene.

Furthermore, classification is essentially a recognition problem in culture heritage. In the past few years, numerous studies have been devoted to music classification. For example, Conklin (2010) studied distinctive patterns in music for geographical classification. Anagnostopoulou, Giraud, and Poulakis (2013) utilized melodic contour in the analysis for children songs' classification. We see that the above studies are all associated to music computable. In our work, we aim at discovering syntactic units for music computable and utilizing them to assist humanities scholars in culture heritage protecting engineering. This thesis discusses the topic of music era classification, mainly including era classification. A classifier for processing music automatically with computer is generated in this research, which can be an assist while judging music's era.

In this paper, we propose a method for extracting music gene to achieve two goals: to explain the importance of music genes in classification, and to investigate the classification accuracy under various conditions. Compared to other music features that have been proposed, our music gene takes the integrity of melody into consideration, making up for their imperfection. As is comprised of one or more continuous measures, music gene has the character that the length of extracted genes is not fixed. According to the study of music theory, classical music expresses emotions in a longer melody than the modern one. Consequently, the corresponding genes with different lengths show more strengths in classification of classical and modern. On the other hand, music gene helps us find the implied superiority in the classification for era. We also discuss some existing researches on music feature extraction, which can be used in the classification. Experimental results show that the accuracy achieved by our method can reflect eras attribute in a way. Furthermore, we find some rules in extracting music gene along with the various conditions.

The remainder of this paper is organized as follows. Section 2 reviews some relevant research work in the field. Section 3 describes the methodology used to conduct the analysis. Section 4 shows experimental results for verifying the proposed model. Finally, a discussion with results is presented in Section 5.

2. Related work

There have been many studies on music feature extraction in areas of Computer Science, Music and Psychology. Concerning the hierarchal representation of music, analysis always starts from the bottom level-note. Then a greater and higher-level representation composed by notes is formed for music feature extraction.

Man-Kwan and Fang-Fei (2003) investigated the mining and classification of music style by melody from a collection of MIDI music. To obtain the main melody, they merged all channels

together and removed all notes which sounded simultaneously except for the highest note. The authors paid attention on chords in music and ignored effects of other parts. To extract music features from the raw data for music retrieval, Chang and Jiau (2003) used the idea of interval between two adjacent notes for representing music. They proposed a method to find repeating figures. Their repeating figure is a sequence of adjacent notes that appears more than once in a music object. However, this perspective disrupted the concept of measures in music theory, which may not guarantee the integrity of melody. The study by Conklin (2010) argued that repeating or recurrent patterns may be syntactic units in a piece of music. A distinctive pattern is one that is overrepresented in a corpus compared to an anti-corpus (Conklin & Anagnostopoulou, 2001; Conklin, 2010). The authors searched notes which have similar viewpoints to comprise a distinctive pattern. They viewed notes from different viewpoints such as during and pitch, but the obtained patterns may not be complete melody. In the approach proposed by Anagnostopoulou et al. (2013), the beat information was considered. Three pattern representations related to melodic contour to classify children's songs were utilized. Experiments show that melodic contour can be a appropriate level for the analysis of children songs. Furthermore, since MusicXML has been widely used, several studies have been done. Lu and Tseng (2009) proposed a novel method for Web-based music recommendation using MusicXML. Its usage facilitated the extraction of tags in XML.

As discussed above, we find that very few studies focused on the integrity of music. In this study we use Sheet-MusicXML to fill this research gap. Sheet-MusicXML views the whole music score with a new angle, considering the relationship among music measures. To maintain the integrity, music gene is comprised of one or more continuous measures. It means that we consider measures to be one music gene if there is a legato between or among measures. Besides, in music theory, each semitone performs different effects in melody. For instance, the 12 semitones (octave for alias in music theory) will bring the whole song to a climax, while the 0 semitone (unison for alias) represents the gentle, quiet feelings. With the development of the times, people also changed their way of expressing feelings in music. This can be reflected in the changes of the intervals. Hence, interval is a particularly significant music feature, which has been studied from several fields. To extract music gene quickly and easily, Sheet-MusicXML alters the tree structure of MusicXML. It argues that melody is a combination of rhythm and gamut. So the MusicXML tree can be separated into two parts. Depth of the tree implies the rhythm and its leaf nodes mean the pitches we mentioned before. In addition, Sheet-MusicXML simplifies the calculation of pitch. Chang and Jiau (2003) and Zhu (2006)'s representations of pitch are composed of character and numeric, while in Sheet-MusicXML pitch is transferred into an exact figure using Twelve Tone. This transfer allows us more convenient when computing the pitch interval.

3. Method

In this section, we describe our method in details. For the genes to obtain, we first illustrate how to obtain the gamut genes from a



Fig. 1. An example of music gene.

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