Pattern Anal Applic
DOI 10.1007/s10044-016-0582-7

THEORETICAL ADVANCES

A sequential pattern mining approach to design taxonomies for hierarchical music genre recognition

Sylvain Iloga[1,2,3] · Olivier Romain[2] · Maurice Tchuenté[3]

Received: 31 December 2015 / Accepted: 8 September 2016

Abstract In this paper, music genre taxonomies are used to design hierarchical classifiers that perform better than flat classifiers. More precisely, a novel method based on sequential pattern mining techniques is proposed for the extraction of relevant characteristics that enable to propose a vector representation of music genres. From this representation, the agglomerative hierarchical clustering algorithm is used to produce music genre taxonomies. Experiments are realized on the GTZAN dataset for performances evaluation. A second evaluation on GTZAN augmented by Afro genres has been made. The results show that the hierarchical classifiers obtained with the proposed taxonomies reach accuracies of 91.6 % (more than 7 % higher than the performances of the existing hierarchical classifiers).

Keywords Audio processing · Automatic taxonomy generation · Music genre recognition · Hierarchical classification · Sequential pattern mining · Histogram mining

✉ Sylvain Iloga
sylvain.iloga@yahoo.fr

Olivier Romain
olivier.romain@u-cergy.fr

Maurice Tchuenté
maurice.tchuente@gmail.com

[1] Higher Teachers' Training College, Department of Computer Science, University of Maroua, P.O. Box 55, Maroua, Cameroon

[2] Laboratoire ETIS, UMR 8051, Université de Cergy-Pontoise, CNRS, ENSEA, av du ponceau, 95000 Cergy-Pontoise, France

[3] IRD UMI 209 UMMISCO and LIRIMA, University of Yaounde 1, P.O. Box 337, Yaounde, Cameroon

1 Introduction

Nowadays, broadcast radio is a source of multimedia content under-exploited. Digital radio stations broadcast meta-data (traffic, music cover, meteorological data, radio name, etc.), and, by using the RDS norm, FM analogue bands deliver various information. These meta-data enrich not only the diversity of available broadcast content, but also the possibilities of indexing this content, either using the contained meta-data, or via original features extracted from the radio signal themselves. It is necessary to develop new search engines that enable the internet user to navigate efficiently through these multimedia streams produced by radio broadcast. The use of audio indexing techniques in the broadcast media market will also be critical for radio on demand applications. These technologies will provide new services such as criterion-based programming (genre- or artist- specific, publicity filtering, etc.). The two main issues in such applications are the simultaneous demodulation of entire broadcast bands and the music genre classification. While the first issue has been solved [1], the second one remains pending.

The extraction of some information from music samples is currently the subject of many studies. To improve the efficiency of recognition systems, several authors have proposed hierarchical approaches. The main idea is that a classifier applied at an inner node of the taxonomy allows solving a classification problem with a small number of classes. Therefore, these approaches are more efficient than flat multi-class classifiers [2].

Several taxonomies have been designed to perform hierarchical classification in various domains. A detailed review of performance evaluation based on taxonomies can be found in [3]. The 3 following motivations for the use of taxonomies in music genres classification are stated in [4]:

Published online: 27 September 2016

1. Taxonomies improve usability and search success rate.
2. A hierarchy enables to identify the existing links of dependence between the genres.
3. Hierarchical classifiers based on taxonomies implement the divide-and-conquer principle that makes the errors concentrate within the given level of the hierarchy.

In music genre recognition, most of the existing taxonomies are human-generated [2, 4–6]. Other authors [7, 8] proposed techniques to automatically generate taxonomies. However, in some of these publications [4, 6], experiments were not cross-validated, and it is difficult to compare the real performances of the classifiers. Additionally the gain in accuracy provided by the existing methods is generally low. The manually generated taxonomies proposed in [2, 4–6] exhibit accuracy gains not greater than 5.1 %. The same observation is made in [7] where the proposed automatically generated taxonomies provide accuracy gains not greater than 2 %. The highest accuracy gain reached 14.67 % and was obtained by the automatically generated taxonomy proposed in [8].

In this paper, a new approach to extract taxonomies of music genres is proposed. It is mainly based on sequential pattern mining techniques. Given a family G of music genres, these techniques are used to initially identify relevant sets of characteristics for each genre of G. These features enable to propose a vector representation for each genre. The similarities between these vectors are then used as input to the Agglomerative Hierarchical Clustering (AHC) algorithm [9], in order to generate a taxonomy. Finally, the generated taxonomy is tested in a hierarchical classification process.

The rest of this paper is organized as follows: The state of the art is presented in Sect. 2, and a detailed description of the proposed approach is given in Sect. 3. Experimental results are presented in Sect. 4 and the last section is devoted to the conclusion.

2 State of the art

2.1 Hierarchical music genres classification

As noted earlier in Sect. 1, some previous work on hierarchical music genre classification have relied on human-generated taxonomies. A classical way to manually design genre taxonomies consists in gathering the genres according to some general descriptors such as the feeling (soft, noisy, etc.), the geographical origin (Afro, Latino, etc.), the music instruments used (piano, guitar, etc.) and the language (English, French, etc.). Such manually generated taxonomies may not match with the natural groups of genres detected when low-level music descriptors are used [7]. This difference results from the fact that manually generated hierarchies often use *human semantics*, and therefore are mainly suitable for human use, while the automatically generated taxonomies are optimized for computational classifiers [4]. This is why in [10], Pachet analyzed existing taxonomies of music genres and derived some criteria that should lead the design of a taxonomy of music genres.

Fig. 1 Taxonomies proposed in [2, 4–8]. **a** Taxonomy proposed by Brecheisen in [2]. **b** Taxonomy proposed by Tao in [4]. **c** Taxonomy proposed by Silla in [5]. **d** Taxonomy proposed by Burred in [6]. **e** Taxonomy of GTZAN proposed by Hasitha in [7]. **f** Taxonomy proposed by Ulaş in [8]

In [2], Brecheisen relied on the manually generated taxonomy presented in Fig. 1a to design a hierarchical classifier for 11 music genres (500 songs, 30 s each) after extracting the 5 following music descriptors: *Mel Frequency Cepstral Coefficients (MFCCs), spectral flux, spectral rolloff, beat histogram* and *pitch histogram*. He used Support Vector Machines (SVMs) as classifiers and after a 90–10 % cross-validation, his hierarchical classifier performed slightly worse than the flat classifier: This method reached 72.01 % for the flat classifier and 70.03 % for the hierarchical classifier.

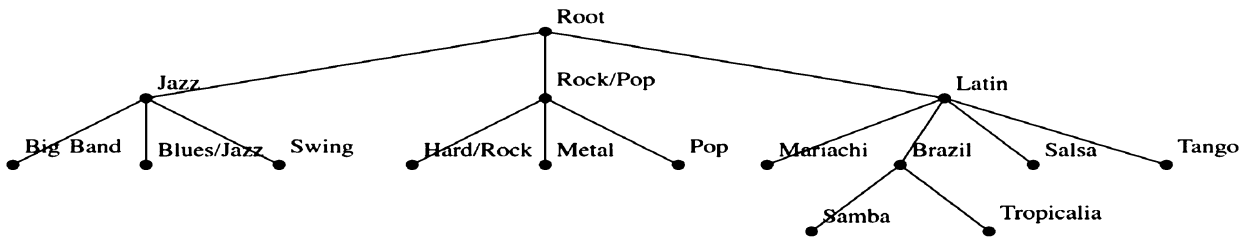
Tao manually generated in [4] the taxonomy presented in Fig. 1b to realize the hierarchical classification of the 10 genres of GTZAN [11]. After extracting 7 music descriptors, he used SVMs with linear kernels implemented in the *LibSVM* library as classifier. No cross-validation was realized. He performed one single training step including 70 % of the data and one test step including 30 % of the data. He obtained accuracies of 72 % for the flat classifier and 72.7 % for the hierarchical classifier. Tao also proposed in [4] an approach to automatically design music genres taxonomies. The taxonomy was then generated by applying a hierarchical clustering algorithm. The main limitation of this method is the fact that the taxonomy depends on the selected classifier. Indeed, two genres naturally different may be represented by vectors close to one another, due to a poor classifier. These automatically generated taxonomies were not used for hierarchical classification in that work.

Figure 1c depicts the manually generated taxonomy proposed by Silla in [5] to perform the hierarchical classification of 15 genres :10 genres coming from the Latin Music Database (3000 songs) and 5 genres coming from the ISMIR2004 database ('world' genre excluded, 1188 songs). He extracted the following music descriptors for each window: Inset-Onset Interval Histogram Coefficient, Rhythm Histogram, Statistical Spectrum Descriptors[1] and the MARSYAS framework.[2] The following classifiers were experimented using the WEKA[3] datamining tool [12] with

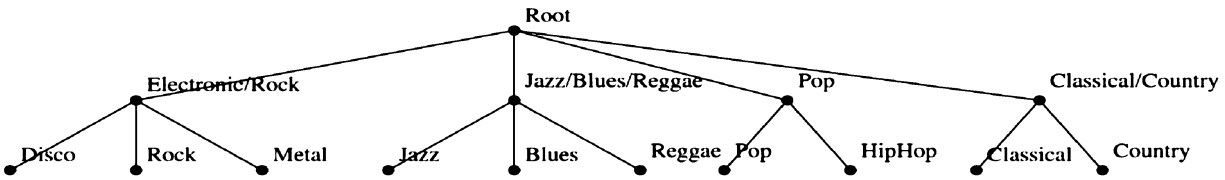
[1] http://www.ifs.tuwien.ac.at/mir/audiofeatureextraction.html.

[2] http://marsyas.sness.net/.

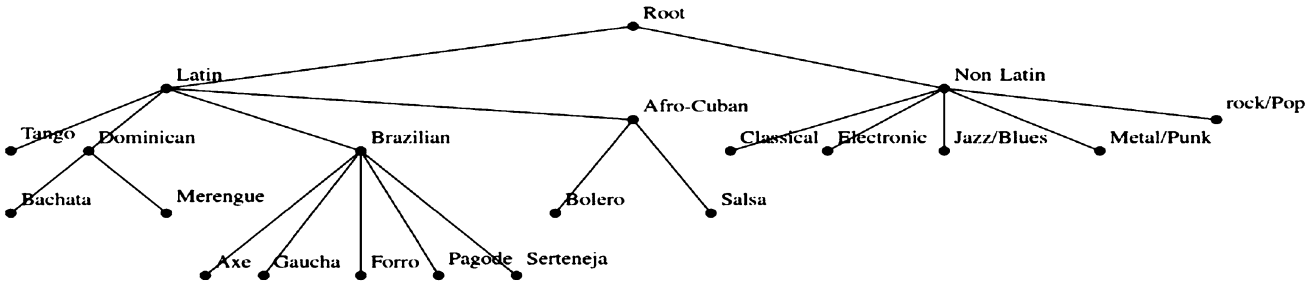
[3] http://www.cs.waikato.ac.nz/ml/weka/.


Root
Jazz
Rock/Pop
Latin
Big Band
Blues/Jazz
Swing
Hard/Rock
Metal
Pop
Mariachi
Brazil
Salsa
Tango
Samba
Tropicalia

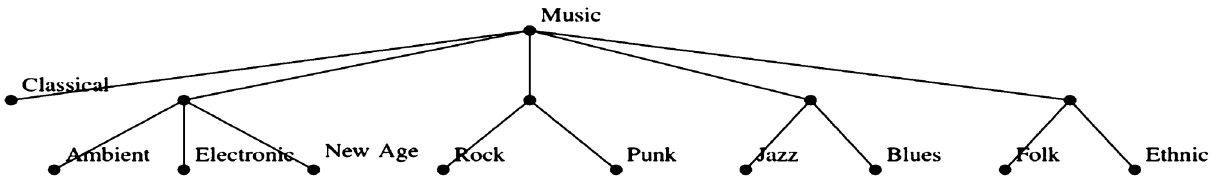
(a)


Root
Electronic/Rock
Jazz/Blues/Reggae
Pop
Classical/Country
Disco
Rock
Metal
Jazz
Blues
Reggae
Pop
HipHop
Classical
Country

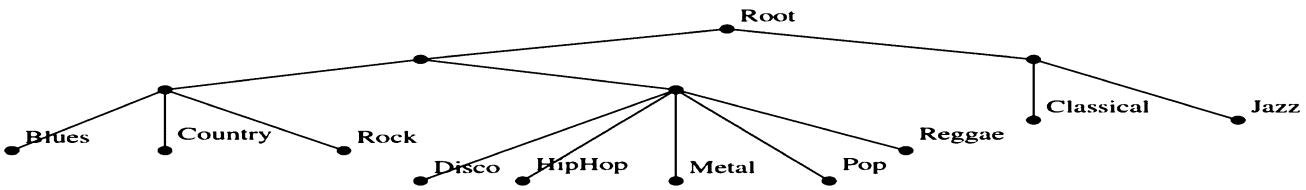
(b)


Root
Latin
Non Latin
Afro-Cuban
rock/Pop
Tango
Dominican
Brazilian
Classical
Electronic
Jazz/Blues
Metal/Punk
Bachata
Merengue
Bolero
Salsa
Axe
Gaucha
Forro
Pagode
Serteneja

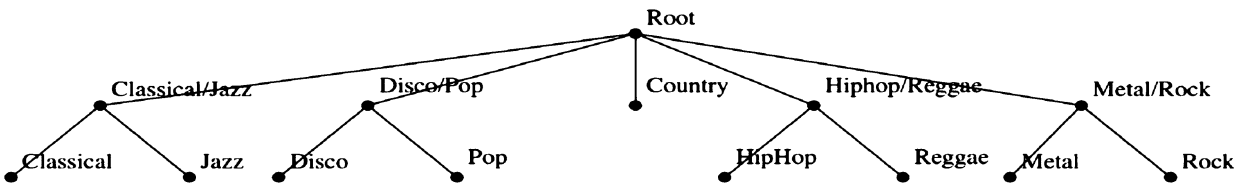
(c)


Music
Classical
Ambient
Electronic
New Age
Rock
Punk
Jazz
Blues
Folk
Ethnic

(d)


Root
Classical
Jazz
Blues
Country
Rock
Reggae
Disco
HipHop
Metal
Pop

(e)


Root
Classical/Jazz
Disco/Pop
Country
Hiphop/Reggae
Metal/Rock
Classical
Jazz
Disco
Pop
HipHop
Reggae
Metal
Rock

(f)

default parameters: K-Nearest Neighbors (KNNs), Naive Bayes (NBs), Multi Layers Perceptrons (MLPs) and SVMs. After a 80–20 % cross-validation, the best accuracy he obtained for his hierarchical classification was 78.82 %.

In [6], Burred performed the hierarchical classification of the 10 genres of the MIREX2005 database (1515 songs, 30 s each) using the manually generated audio taxonomy shown in Fig. 1d. He extracted 15 music descriptors and used Gaussian Mixture Models (GMMs) developed into a M2K framework (using MATLAB integration modules) as classifiers. No cross-validation was realized. The training and the classification phases, respectively, included 66.4 and 33.6 % of the data. He obtained accuracies of 54.12 and 59.22 %, respectively, for the flat and the hierarchical classifiers.

In [7], Hasitha proposed an approach to automatically generate music genres taxonomies. He extracted 13 music descriptors to describe each audio window. Taxonomies were generated for the two following experimental databases: GTZAN presented in Fig. 1e and HBA (15 genres, 500 songs per genre, 30 s each). The PROjected CLUSTering algorithm (*PROCLUS*) [13] executed in a top-down manner was used to generate taxonomies. This algorithm enables the user to control the breadth of the generated taxonomy by setting the number K of desired clusters. They selected the *K-Mediods* method for distance measurement. The algorithm starts with a single cluster containing all the genres as input, then the output clusters are used as input for the next step in a repetitive manner until the generation of clusters containing only one genre. LibSVM, Sequential Minimal Optimization (SMO that is SVMs with polynomial kernel), KNNs, Decision Trees (DTs), Logistic Regression (LOG) and MLPs were combined during the classification phase. At each node of the hierarchy, he selected both the best attribute as proposed in [14] and the suitable classifier to be used. Attribute selection is commonly performed by techniques like Principle Component Analysis (PCA) and Linear Discriminant Analysis (LDA). Most of the widely used attribute selection techniques in music genre classification are described in [14]. The hierarchical classification produced the following results: (1) On GTZAN, the hierarchical classifier obtained 72.9 %, while the corresponding flat classifier produced 70.9 %. (2) On HBA, the hierarchical classifier obtained 78.6 %, while the corresponding flat classifier produced 77.2 %.

In [8], Ulaş used GMMs to model the inter-genre similarities in order to automatically generate the taxonomy presented in Fig. 1f. After the taxonomy generation, these GMMs were later used to perform hierarchical classification. For each audio window, he extracted 7 timbre music descriptors. Experiments were realized on 9 genres all coming from the GTZAN database ('blues' excluded), but only 20 songs were considered per genre. To automatically construct the hierarchy of N genres, he proceeded as follows:

1. Consider each genre as a cluster of size 1.
2. Train one GMM for each cluster using the songs of all the genres belonging to the considered cluster
3. Realize the flat classification of the songs of each cluster considering these models ; this step leads to a confusion matrix $C = \{c_{ij}\}$.
4. Find the two clusters $i*$ and $j*$ having the highest confusion value in C and merge them into a new cluster: $(i*, j*) = \arg\max c_{ij}$ with $(i \neq j)$
5. Repeat steps 2–4 until one single cluster is obtained.

The 90–10 % cross-validation he performed provided accuracies of 63.33 % for the flat classifier and 78 % for the hierarchical classifier.

2.2 Sequential patterns in music genres classification

Many authors have already used sequential pattern mining techniques to perform music genres classification. Conklin [15] modeled the melody of a song as a sequential pattern. He extracted a list of association rules for the two classes of his training database composed of 102 Austrian and 93 Swiss folk song melodies. The classification phase was realized by a decision list method based on these association rules. Lin [16] extracted Significant Repeating Patterns from the rhythm and the melody of music excerpts to build training databases. To realize the classification of a candidate song c, he adopted a dynamic programming approach to measure the similarities between c and the content of the various training databases. In [17, 18], Ren first transformed each music piece into a sequential pattern composed of hidden Markov model indices. The frequent sequential patterns of each genre are then discovered, and their occurrence frequencies are calculated. Finally, *K-NN* (in [17]) and SVMs (in [18]) classifiers are used during the classification phase. The main difference between these work and the proposed approach relies on the semantic of the sequential patterns. Table 1 presents the details of related work on hierarchical music genre classification and on flat music genre classification using sequential pattern mining techniques.

Before describing the methodology of the approach proposed here, basic concepts about sequential patterns and some sequential pattern mining algorithms are first presented. In the following, an *item* is considered as the smallest information that can be found in a sequential pattern database δ. Thus an item can for example be an integer or a character identifying an information. Let $X = \{x_1, x_2, \ldots, x_k\}$ be the set of all the items appearing in δ. A subset of X is called an *itemset*. We assume here that all the items of an itemset are sorted in a

Table 1 Performances of the cited work in hierarchical music genres classification and flat music genres classification using sequential patterns mining techniques

Referenced work	Number of genres	Songs per genre	Taxo. Auto. Generated	Database	Classifiers	Cross valid.	Flat acc.	Hier. acc.	Gain acc.	Year
Brecheisen [2]	11	≈30	**No**	Custom	SVM	Yes	72.01	70.03	**−1.98**	2006
Tao [4]	10	100	**No**	GTZAN	SVM	**No**	72.01	72.69	**+0.68**	2005
Silla [5]	15	[52, 615]	**No**	ISMIR 2005, LMD	KNN, MLP, NB, SVM	Yes	–	78.82	–	2009
Burred [6]	10	>100	**No**	MIREX 2005	GMMs	**No**	54.12	59.22	+5.1	2003
Hasitha [7]	15	500	Yes	HBA	KNN, DT, LOG,	**No**	77.2	78.6	**+1.4**	2012
	10	100	(*PROCLUS*)	GTZAN	SVM, MLP		70.9	72.9	**+2**	
Ulaş [8]	9	20	Yes (*GMMs*)	GTZAN	GMMs	Yes	63.33	78	+14.67	2005
Conklin [15]	2	{93, 102}	–	Essen Folk Song	Decision list, Association rules	Yes	77	–	–	2009
Lin [16]	7	–	–	Custom	Dynamic Programming	**No**	49.18	–	–	2004
Ren [17]	5	[354, 785]	–	Magnatunes, Dortmund	KNN	**No**	74.19	–	–	2010
Ren [18]	10	100	–	GTZAN	SVMs	Yes	74.5	–	–	2011

Bold represents that in these related works: (1) the taxonomies were generated manually, (2) the classification phases were not cross-validated and (3) the accuracy gains were very low

given order, such as alphabetic or numeric order. A sequential pattern $s = \langle s_1, s_2, \ldots, s_m \rangle$ is an ordered list of itemsets $s_i \subseteq X$ with $i \in [1, m]$. The number of itemsets of s denoted $|s|$ is called the *size* of s. The total number of items in s denoted $l(s)$ is called the *length* of s. A sequential pattern $\alpha = \langle a_1, a_2, \ldots, a_m \rangle$ is a *sub-sequence* of another sequential pattern $\beta = \langle b_1, b_2, \ldots, b_n \rangle (\alpha \sqsubseteq \beta)$ if there exist $i_1, i_2, \ldots, i_m$ such that the two following conditions are verified [19]: (1) $1 \leq i_1 < i_2 < \cdots < i_m \leq n$; (2) $a_1 \subseteq b_{i_1}, a_2 \subseteq b_{i_2}, \ldots,$ and $a_m \subseteq b_{i_m}$. When α is a sub-sequence of β, β is called *super-sequence* of α and it can be said that β *contains* α.

A sequential patterns database $\delta = \{s_1, s_2, \ldots, s_n\}$ is a set of sequential patterns and $|\delta|$ is the number of sequential patterns in δ. As described in Eq. 1, the *frequency* of a sequential pattern α in δ denoted $freq(\alpha, \delta)$, is the number of sequential patterns in δ which contain α. The *support* of a sequential pattern α in δ denoted $sup(\alpha, \delta)$ is obtained by dividing the frequency of α by $|\delta|$. Given a minimum support threshold *min_sup*, a sequential pattern α is *frequent* if and only if its support is greater than *min_sup*. More formally, given δ and *min_sup*:

$$\begin{cases} freq(\alpha, \delta) = |\{s | s \in \delta \text{ and } \alpha \sqsubseteq s\}| \\ sup(\alpha, \delta) = \dfrac{freq(\alpha, \delta)}{|\delta|} \\ (\alpha \text{ is frequent}) \Leftrightarrow (sup(\alpha, \delta) \geq min\_sup) \end{cases} \quad (1)$$

For instance, let $X = \{1, 2, \ldots, 8\}$ and $\delta = \{s_1, s_2, s_3, s_4\}$ be the sequential patterns database of Table 2. Consider $\alpha = \langle (6)(27) \rangle$:

Table 2 Database δ

No.	Content
s_1	$\langle (23)(\mathbf{167})(\mathbf{3})(\mathbf{267})(\mathbf{24}) \rangle$
s_2	$\langle (15)(169)(4) \rangle$
s_3	$\langle (\mathbf{56})(\mathbf{2478})(\mathbf{37}) \rangle$
s_4	$\langle (\mathbf{168})(\mathbf{2357}) \rangle$

1. The super-sequences of α in δ are s_1, s_3 and s_4. The corresponding items are written in bold in the table.
2. $freq(\alpha, \delta) = |\{s_1, s_3, s_4\}| = 3$ and $sup(\alpha, \delta) = \frac{3}{4}$
3. for $min\_sup = 0.5$, α is frequent. But for $min\_sup = 0.9$, α is not frequent.

The problem of frequent sequential pattern mining can be specified as follows: given a sequential pattern database δ and a minimum support threshold *min_sup*, one would like to discover all the frequent sub-sequences of the sequential patterns of δ with respect to *min_sup*. The following algorithms have been developed to perform frequent sequential pattern mining: *Apriori* [20], *GSP* [21], *SPADE* [22], *Freespan* [23] and *Prefixspan* [19]. Several other algorithms have been developed and a detailed survey on sequential pattern mining algorithms can be found in [24].

2.3 Problem statement

As presented in Table 1, the existing hierarchical approaches [2, 4, 7] show accuracy gains not greater than 2 %. The taxonomies used in [2, 4–6] are generated by humans and no cross-validation is applied in [4, 6, 7]

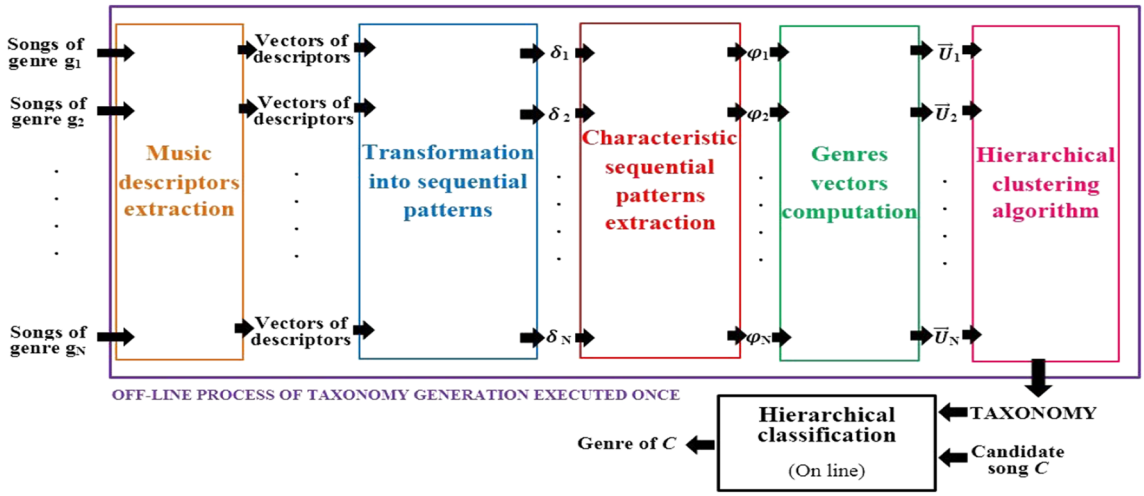


Fig. 2 Methodology of the proposed approach

during the classification step. This is a drawback because a classifier may generate good classification results for particular *training* and *test* sets of the considered database, and exhibit poor classification accuracy after cross-validation. On the other hand, the automatic generation of taxonomies is useful for huge music databases that are difficult or even impossible to handle manually. Another advantage of automatic generation is that a priori knowledge or particular expertise on the genres is not required. The natural clusters existing in the database are automatically detected according to the selected low-level music descriptors. Nevertheless, the experts' contributions may be essential to validate the resulting taxonomy.

This paper aims at providing better classification performances than existing work by proposing an automatic approach for taxonomy generation. Sequential pattern mining techniques are applied to propose new vectorial music genres descriptors. These vectors are later used as input for a hierarchical clustering algorithm to generate the taxonomy. Cross-validation is applied during the classification step. Several commonly used classifiers are used to illustrate the performance gains obtained with the corresponding hierarchical classifiers.

3 The proposed approach

3.1 Main idea

The main idea of this work is based on a fundamental observation about both music samples and genres. When listening to some music excerpts, one has the impression of shifting from one genre to another. This happens when the corresponding genres have strong similarities. For example, a song may seem to belong to *reggae* at its beginning, but transits to *country* for a while before shifting to *blues*.

Let $G = \{g_1, g_2, \ldots, g_N\}$ be a family of genres and let c be a song. The previous remark allows to see c as a sequence of genres of G, each term of the sequence corresponding to a short time interval. In some cases, it is even difficult to assign a particular genre to a short time interval of a music excerpt because it has some characteristics that can be found in several genres. Therefore, the notation presented in Eq. 2 is adopted for a song where $(g_{j1}g_{j2}\ldots g_{jk_j})$ is the set of the possible genres corresponding to the time interval of index j. Such an expression is called a sequential pattern i.e., a sequence of subsets of genres' labels.

$$c = (g_{11}\ldots g_{1k_1})(g_{21}\ldots g_{2k_2})\ldots(g_{w1}\ldots g_{wk_w}) \quad (2)$$

3.2 Methodology

To perform hierarchical classification, the methodology presented in Fig. 2 and proposed in this paper proceeds in 10 steps grouped in the 6 following phases: Music descriptors extraction (steps 1–3), transformation into sequential patterns (steps 4–5), characteristic sequential patterns extraction (steps 6–7), computation of vector descriptors for genres (step 8), hierarchical clustering (step 9) and hierarchical classification (step 10). Details about each step are presented below:

1. Choose the time interval.
2. Choose the features that will be used.
3. Represent each training song c as a sequence $c = v_1v_2\ldots v_w$ of vectors of descriptors.
4. For each genre g_i, apply a clustering algorithm on the collection of vectors of descriptors corresponding to its training songs to obtain k central vectors per genre.
5. Transform each representation $c = v_1v_2\ldots v_w$ into a sequential pattern as indicated by Eq. 2 where

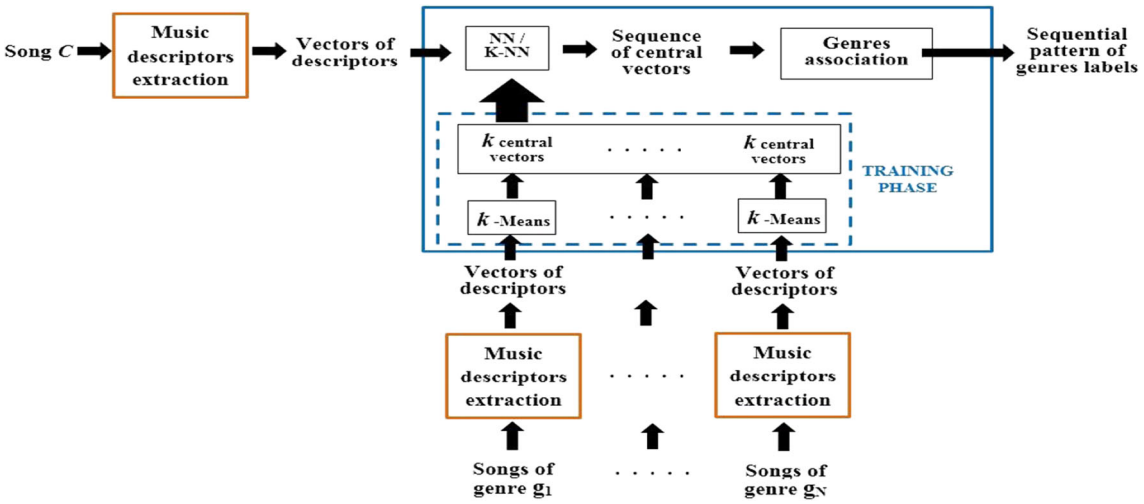


Fig. 3 Transformation of a song into a sequential pattern

$(g_{j1}g_{j2}\ldots g_{jk_j})$ is the set of genres associated with the nearest central vectors of v_j. This generates a database δ_i of sequential patterns for each genre g_i.

6. Apply a sequential pattern mining algorithm on δ_i to compute the set σ_i of frequent patterns of each genre g_i.
7. Extract from σ_i the set φ_i of characteristics frequent patterns corresponding to g_i.
8. Use all the $\varphi_i (1 \leq i \leq N)$ to compute the vector descriptor $\overrightarrow{U_i}$ of genre g_i for $i = 1, \ldots, N$. $\overrightarrow{U_i}$ is a positive N-dimensional real vector with normalized components.
9. Build the taxonomy based on the vector descriptors computed at step 8 by applying a hierarchical clustering algorithm.
10. Perform the hierarchical classification based on the computed taxonomy using an efficient flat classifier.

3.3 Music descriptors extraction

The time interval of the first step of the methodology is set at *one second*. Therefore, music features were extracted from music excerpts within texture windows of one second as it was done in [25]. In a survey proposed in 2010, Mitrović drew a list of 70 highly utilized audio descriptors based on 200 publications [26]. For steps 2 and 3 of the methodology, timbre music descriptors have been adopted to generate a taxonomy. The following wide-spread short term timbre music descriptors to generate the taxonomy are extracted: *Mel Frequency Cepstral Coefficients* (MFCCs), *Spectral centroid*, *Spectral rolloff*, *Spectral flux* and *Zero crossing rate*. Details about the extraction of these music descriptors can be found in [25].

After the taxonomy generation, some rhythm music descriptors were extracted and combined with the previous timbre music descriptors during the classification step. The 4 following rhythm music descriptors were extracted: *bpm* peak values (1), *Rhythm Patterns* (200), *Rhythm Histogram* (60) and *Statistical Spectrum Descriptor* (140). These rhythm music descriptors have been selected because they provided an accuracy of 74.9 % when Lidy made the flat classification of GTZAN in [27]. They were extracted using the online available MATLAB framework [28] developed by Lidy. The selected rhythm music descriptors were not used for the taxonomy generation because they required a considerable amount of data (more than one second) to produce reliable results.

3.4 Transformation of a song into a sequential pattern

As shown in Fig. 3, the global transformation process includes a training step. During the training of each genre of the family G, the collection of vectors of music descriptors (one per second) coming from all its training excerpts was taken into account. The *k-means* method was first applied to cluster the collection of vectors into k clusters. This produces k central vectors per music genre as stated in the 4th step of the methodology. After the training step, the *K-NN* algorithm has been applied to perform the transformation as specified in step 5 of the methodology.

3.4.1 Transformation with the NN algorithm

Let us first present the simple case of the *K-NN* algorithm with $K = 1$. To obtain the sequential pattern of a music excerpt c, its sequence of vectors of music descriptors is first extracted. This produces $c = v_1 v_2 \ldots v_w$. For each

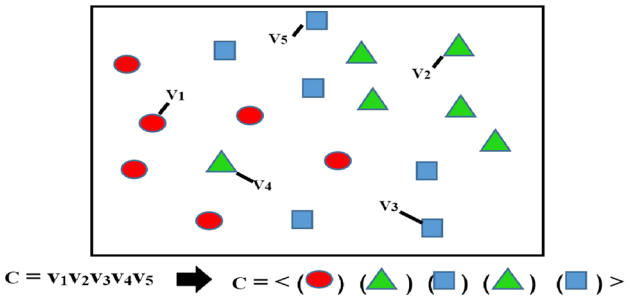


Fig. 4 Transformation of a song with the NN approach. *Squares*, *circles* and *triangles* represent respectively the central vectors of 3 genres g_1, g_2 and g_3

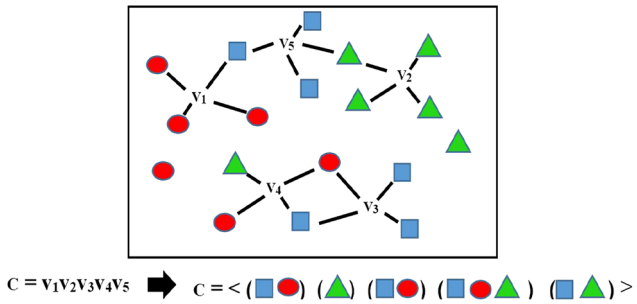


Fig. 5 First transformation of a song with the K-NN approach ($K = 4$). *Squares, circles* and *triangles* represent respectively the central vectors of 3 genres g_1, g_2 and g_3

vector v_j of c, the *Nearest Neighbor* algorithm is applied to determine its nearest central vector among all the central vectors of the N genres. Then v_j is replaced by the genre associated with this central vector. Therefore, c is transformed into the sequential pattern $\langle (g_{i_1})(g_{i_2})\ldots(g_{i_w})\rangle$. As presented in Fig. 4, the resulting representation adheres with the one of Eq. 2.

Consider the song c of Fig. 4 represented as a sequence of 5 vectors. If squares, circles and triangles represent respectively the central vectors of genres *classical*, *jazz* and *blues* then the corresponding sequential pattern is c = $\langle$*(jazz) (blues) (classical) (blues) (classical)* $\rangle$. This means that the first second of c contain characteristics of *jazz*, the next second contains those of *blues*, and so on. When this principle is applied to all the training excerpts of each genre g_i, it outputs one training sequential patterns database δ_i.

3.4.2 First transformation with the K-NN algorithm

With the NN algorithm, one single central vector is considered to determine the genre g_{ij} associated with a vector v_j of a song c. But an information is still unexploited because in the neighborhood of v_j, there may exist several other central vectors associated with other genres. To avoid this situation, the *K-NN* algorithm with $(K > 1)$ is applied. We thus determine the set of all the genres associated with the K nearest central vectors of v_j. Then v_j is replaced by this set of genres which becomes an itemset that may contain more than one genre. c is then transformed into the sequential pattern $\langle s_{i_1}, s_{i_2}, \ldots, s_{i_w}\rangle$ where every s_{i_j} is a set of genres as shown in Fig. 5.

When the 4-NN algorithm is applied in Fig. 5 in similar conditions as those of Fig. 4, the song c is transformed into the sequential pattern c = $\langle$*(classical jazz) (blues) (classical jazz) (classical jazz blues) (classical blues)* $\rangle$. This means that the first second of c contains characteristics of *classical* and *jazz*, the next second contains characteristics of *blues*, and so on. This principle is applied to all the training songs of each genre g_i of G to obtain one training sequential patterns database δ_i.

3.4.3 Second transformation with the K-NN algorithm

The first transformation of a song using the *K-NN* algorithm with $(K > 1)$ is limited for high values of K. Indeed, if the value of K is large, the itemset corresponding to any vector v_j of music descriptors may always be $(g_1, g_2, \ldots, g_N)$ because all the N genres may be found in the neighborhoods of v_j, but not in the same proportions. In such a situation, the same sequential pattern may be generated for each training song. This limitation comes from the fact that the number of central vectors of the genres appearing in the neighborhoods v_j is not considered during the transformation. As shown in Fig. 6, the itemsets associated with vectors v_1 and v_3 are the same (composed of squares and circles) when the first transformation is applied, but they are different with the second transformation. According to this figure, the song c can therefore be seen as a sequence of *Histograms* $(H_1 H_2 \ldots H_w)$. Each histogram H_j is having N bins $\{g_1, g_2, \ldots, g_N\}$ and the height of bin k (namely $H_j(k)$) is the number of central vectors of genre g_k found in the neighborhoods of vector v_j. To avoid the situation where $H_j(k) = 0$ in the histogram, 1 is intentionally added to the number of central vectors of genre g_k found in the neighborhoods the vector v_j. With this last transformation, one will need to mine sequences of frequent histograms to derive the vector of descriptors of each genre.

Histograms (*colour histograms*) are widely used in image and video information retrieval. Surveys on the theory and applications of image and video mining techniques are respectively proposed in [29, 30]. In [31], Fernando performed frequent itemset mining for image classification. In that work, he proposed a simple method to convert a *local colour histogram* of an image into a

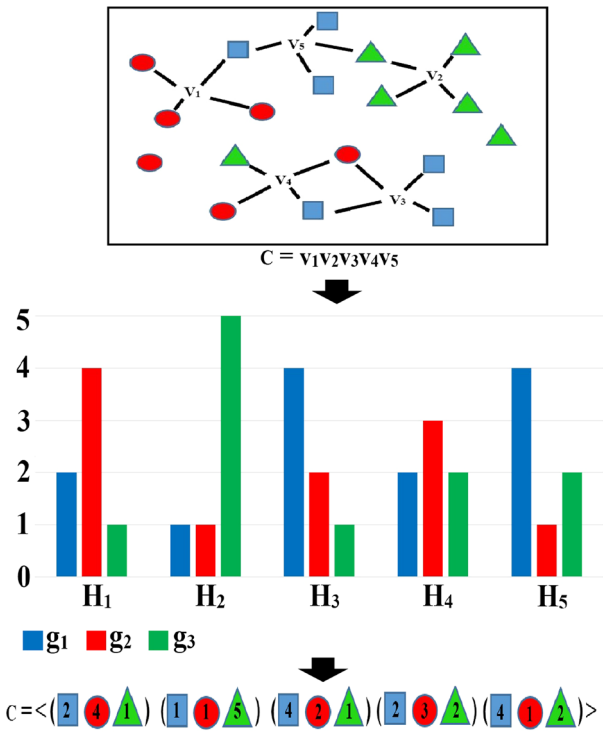


Fig. 6 Second transformation of a song with the *K*-NN approach ($K = 4$). *Squares*, *circles* and *triangles* represent respectively the central vectors of 3 genres g_1, g_2 and g_3. The song c is initially transformed into a sequence of histograms $(H_1 \ldots H_5)$. Finally c becomes a sequential pattern where each item is a pair $(g_k, H_j(k))$

particular type of itemset. A similar method is applied in this paper to convert sequences of histograms into sequential patterns as presented in Fig. 6. This transformation enables to mine frequent sequences of histograms with common sequential pattern mining algorithms. In order to transform the sequence of histograms $(H_1 H_2 \ldots H_w)$ of a song c into a sequential pattern, one can proceed as follows:

1. An *item* is now considered as a pair (g, y), g being a genre label and y a positive integer.
2. The kth bin of histogram H_j is converted into the item $(g_k, H_j(k))$.
3. Histogram H_j becomes the itemset $s_j = \{(g_k, H_j(k))\}$ with $k = 1 \ldots N$.
4. The sequence of histograms $(H_1 H_2 \ldots H_w)$ of c becomes the sequential pattern $\langle (s_1)(s_2) \ldots (s_w) \rangle$ where each s_j is the itemset derived from H_j.

One can observe that with this transformation, the resulting sequential patterns are composed of itemsets containing always exactly N items. This was not the case with the first transformation with the K-NN algorithm ($K > 1$). In these conditions, an itemset s_{j1} is included in another itemset s_{j2} (i.e: $s_{j1} \subseteq s_{j2}$) if $(H_{j1}(k) \leq H_{j2}(k))$ for $k = 1 \ldots N$. The other concepts (*sub-sequence, super-sequence, support, frequent sequence, etc.*) previously defined in Sect. 2.2 remain the same. All the common sequential pattern mining algorithms can be adapted to mine frequent histograms. This can be done by filtering the output of the considered algorithm so that only sequences composed of itemsets containing exactly N items are taken into account. This allows to remain consistent with the methodology because adapted versions of common sequential pattern mining algorithms are finally used to mine frequent sequences of histograms. In the rest of the paper, the first and the second K-NN transformations ($K > 1$) will be, respectively, referenced as the *K-NN approach* and the *histogram approach*.

3.5 Characteristic frequent patterns extraction

Step 6 and 7 of the methodology are applied in this section to extract the characteristic frequent sequential patterns of each genre. For step 6, *Prefixspan* is selected in this work among all the algorithms listed in Sect. 2.2. The problem of genres characteristic frequent sequential patterns mining can be stated as follows: Consider N distinct genres $g_1, g_2, \ldots, g_N$ associated with N training sequential patterns databases $\delta_1, \delta_2, \ldots, \delta_N$. For each genre g_i, one wants to extract the set φ_i of sequential patterns that verify the following properties [32]: (1) They should be frequent with respect to a minimum support threshold, (2) they should characterize the genre g_i, and (3) they should not be redundant. Let α be a sequential pattern. The *confidence* that α can characterize the genre g_i (associated with the sequential patterns database δ_i) denoted $conf(\alpha, \delta_i)$ is given by formula 3. In other words, $conf(\alpha, \delta_i) = 0.9$ means that 90 % of the super-sequences of α found in δ_{all} belong to δ_i.

$$conf(\alpha, \delta_i) = \frac{freq(\alpha, \delta_i)}{freq(\alpha, \delta_{all})} \quad \text{where } \delta_{all} = \bigcup_{i=1}^{N} \delta_i \tag{3}$$

To extract the characteristic frequent sequential patterns of music genres as specified in step 7 of the methodology, the *FeatureMine* algorithm [32] proposed by Lesh and Zaki can be used. Given *min_sup* and a minimum confidence threshold *min_conf*, *FeatureMine* constructs the set φ_i of characteristic frequent sequential patterns of genre g_i that meet the 3 afore-listed properties. Details about this algorithm can be found in [32]. Figure 7 describes this process of genre characteristics extraction from the database δ_i of

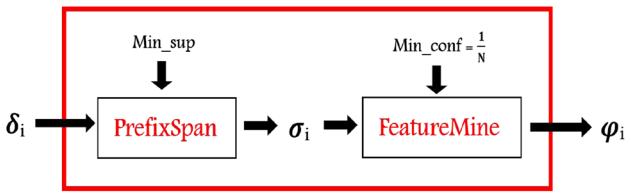


Fig. 7 Characteristics extraction for genre g_i

genre g_i. Generally for N genres, it is advised to set *min_conf* to $\frac{1}{N}$ for each genre [32]. This value is adopted in the rest of this paper.

3.6 Vector associated with a genre

This section details the 8th step of the methodology by computing a new descriptor for each genre. Consider a song c associated with the sequential pattern S_c. Let $\varphi_i = \{f_{i1}, f_{i2}, \ldots, f_{i|\varphi_i|}\}$ be the set of characteristic sequential patterns of g_i output by *FeatureMine*. The song c is represented as the vector $\overrightarrow{c} = (\omega_1(c), \ldots, \omega_N(c))$ where each $\omega_i(c)$ is the percentage of the characteristic frequent sequences of the genre g_i contained in S_c as shown in Eq. 4. For instance, $\overrightarrow{c} = (0.55, 0.67, 0.75)$ means that c contains 55 % of the characteristic sequences of genre g_1, 67 % of the characteristic sequences of genre g_2 and 75 % of the characteristic sequences of genre g_3.

$$\omega_i(c) = \frac{\sum_{j=1}^{|\varphi_i|} y_{ij}(c)}{|\varphi_i|} \quad \text{with} \quad y_{ij}(c) = \begin{cases} 1 \text{ if } f_{ij} \sqsubseteq S_c \\ 0 \text{ otherwise} \end{cases} \tag{4}$$

The proposed descriptor of genre g_i is the vector $\overrightarrow{U_i} = (\theta_1(g_i), \ldots, \theta_N(g_i))$ where each $\theta_j(g_i)$ is the normalized sum of the jth components of the vectors $\overrightarrow{c}$ associated with the songs $c \in \delta_i$ as shown in Eq. 5.

$$\theta_j(g_i) = \frac{100}{|\delta_i|}\left(\sum_{c \in \delta_i} \omega_j(c)\right) \tag{5}$$

According to this representation, $\overrightarrow{U_i} = (40, 75, 55)$ means that genre g_i contains 40 % of the characteristic sequences of genre g_1, 75 % of the characteristic sequences of genre g_2, and 55 % of the characteristic sequences of genre g_3.

3.7 Taxonomies generation

This section is devoted to the taxonomy generation as specified in step 9 of the methodology. To achieve this goal, the similarity between two genres must first be computed. In this work, the similarity between two music genres is considered as the mathematical distance between their associated vectors. The 4 following distances have been selected: *Euclidean distance* d_e, *Manhattan distance* d_m, *Tchebychev distance* d_t and *Cosine distance* d_a extracted from the dot product of their associated vectors. Equation 6 shows how to compute these distances for two vectors $\overrightarrow{U_i} = \{u_{i1}, u_{i2}, \ldots, u_{iN}\}$ and $\overrightarrow{U_j} = \{u_{j1}, u_{j2}, \ldots, u_{jN}\}$, respectively associated with genres g_i and g_j.

$$\begin{aligned}
d_e(\overrightarrow{U_i}, \overrightarrow{U_j}) &= \sqrt{\sum_{k=1}^{N} (u_{ik} - u_{jk})^2} \quad \text{(Euclidean)} \\
d_m(\overrightarrow{U_i}, \overrightarrow{U_j}) &= \sum_{k=1}^{N} |u_{ik} - u_{jk}| \quad \text{(Manhattan)} \\
d_t(\overrightarrow{U_i}, \overrightarrow{U_j}) &= \max_{1 \le k \le N} |u_{ik} - u_{jk}| \quad \text{(Tchebychev)} \\
d_a(\overrightarrow{U_i}, \overrightarrow{U_j}) &= \arccos\left(\frac{\overrightarrow{U_i} . \overrightarrow{U_j}}{|\overrightarrow{U_i}| . |\overrightarrow{U_j}|}\right) \quad \text{(Cosine)}
\end{aligned} \tag{6}$$

The similarity between two genres allows to perform the hierarchical clustering of music genres. The similarity matrix (square and symmetric) between all the genres $g_i \in G$ is first built. This matrix will then enable us to realize the hierarchical clustering of the N genres. This operation can easily be realized by the *AHC* [9] algorithm that outputs a detailed *dendrogram* of the N genres from which the taxonomy can be derived. The principle of this algorithm is as follows: initially, each genre g_i is considered as a cluster of size 1. At each step, the two closest clusters are found and merged into a new cluster. The process is repeated until one single cluster is obtained. AHC involves the existence of a distance measure between two clusters. There exist several possible distances between clusters. The 4 following distances have been considered in this work: the *minimum*, the *centroid*, the *average* and the *maximum* distances.

4 Experimental results

4.1 Experiments on *GTZAN*

The proposed method was experimented on the GTZAN database [25] composed of 10 music genres: *blues, classical, country, disco, hiphop, jazz, metal, pop, reggae* and *rock*. In the rest of the paper, these genres will, respectively, be represented in figures by the acronyms: *bl, cl, co, di, hi, ja, me, po, re* and *ro*. Each genre being represented by 100 '.wav' files (30 s, 22,050 Hz, 32 bits floating point, mono). It is important to note that 7.2 % of the excerpts of GTZAN come from the same recording (including 5 % being exact duplicates) and 10.8 % of the database is mislabelled [33]. The 9 first steps of the methodology have been applied to GTZAN as follows:

Steps 1–3: To compute the music descriptors listed in Sect. 3.3, each music excerpt was split into windows of about 20 ms, each window having 512 samples with an overlap of 50 % between two consecutive windows. The

mean of the music features was calculated for each texture window of one second.

Steps 4–5: To transform a song into a sequential pattern, the *k-means* algorithm was applied to generate k central vectors per genre. Experiments are realized in [34] to select a suitable value of k. In that paper, it was proposed to apply the *k-means* algorithm to transform a music excerpt into a Markov chain of genres. To select the value of k, flat classification experiments on a dataset composed of 10 music genres including 4 Cameroonian genres were performed. Up to 30 different values of k taken between 5 and 150 with a step of 5 were tested. The training was done with 90 songs per genre, and 10 songs were used per genre for the flat classification stage. The highest accuracy value (84 %) was reached for $k = 95$ and $k = 100$. It is according to these experiments that k is set to 100 in this paper.

The *K-NN* approach was applied for $K = 6, 7, 8, 9, 10$, and the histogram approach for $K = 50$ and $K = 100$. This enabled us to analyze the impact of the value of K on the vector descriptor $\overrightarrow{U}$ of genres. After these analysis, only the values $K = 10$ and $K = 50$ were finally selected, respectively, for the K-NN and histogram approaches during the taxonomy generation.

With the simple *NN* approach, each training song of 30 s was then transformed into a sequential pattern. In contrast, the length of the sequential patterns generated with the *K-NN* and the histogram approaches was too large (hundreds of items). Under such conditions, *PrefixSpan* can generate millions of sequences if the whole song is considered. For this reason, every training song of 30 s was split into 6 consecutive songs of 5s each before being converted into a sequential pattern. The maximum length of the generated sequences decreased from 300 to 50 items.

Steps 6–7: Adapted versions of *PrefixSpan* and *FeatureMine* were developed in C language. After setting *min_conf* to $\frac{1}{10}$ (because GTZAN has 10 genres), the process described in Fig. 7 was applied by successively executing the *PrefixSpan* and *FeatureMine* on GTZAN. The minimum support threshold varied from one transformation to another in order to extract a reasonable number of characteristic sequential patterns per genre. Table 3 shows the number of characteristic frequent sequential patterns found for each genre. In this table, the K-NN approach is applied with $K = 10$ and the histogram approach is applied with $K = 50$.

Step 8: The vectors associated with the various genres were later calculated as explained in Sect. 3.6. Each line of Table 4a–h shows the components of the vector associated with the corresponding genre in GTZAN. Table 4a reveals

Table 3 Number of frequent characteristic sequences extracted by *FeatureMine* for the genres of GTZAN

	bl	cl	co	di	hi	ja	me	po	re	ro
NN	146	871	193	301	244	271	198	391	194	243
K-NN	82	487	154	755	274	707	1618	577	170	597
Histo.	96	226	75	74	110	190	119	166	77	42

that with the NN algorithm, in the vector representing a genre g_i, the dominant component is always the ith component. This is a nice coherence property that is not satisfied by the other approaches.

The vector descriptors obtained with the K-NN approach were calculated for $K = 6, \ldots, 10$, and a particular configuration was observed for $K = 7, 9, 10$ respectively as shown in Table 4b–d: the vectors representing *country*, *reggae* and *rock* were dominated by the component corresponding to *blues*. The same situation occurred in the vectors of *disco* and *metal* that were dominated by their components corresponding to *hiphop*. These confusions may be due to the strong timbre similarities existing between these genres. Therefore, it is possible to deduce that these genres may later belong to the same clusters in the resulting taxonomy. This observation led to the selection of the value $K = 10$ during the taxonomy generation.

Similarly, the value $K = 50$ was selected for the histogram approach because in Table 4e–f, the vector descriptors are similar for $K = 50$ and $K = 100$. In these tables, the vectors representing *classical* and *jazz* are dominated by the component corresponding to *country*. Thus, one can guess that these 3 genres may belong to the same cluster and this was later observable in the resulting taxonomy.

Step 9: From the vector representation, the distance matrix between the genres of GTZAN is calculated using the 4 distances described in Sect. 3.7. Finally, the *AHC* clustering algorithm was applied to realize the hierarchical clustering and generate dendrograms from which a taxonomy was extracted. The 4 cluster distances presented in Sect. 3.7 were used to achieve this goal. These pairs of distance measures generated the 6 dendrograms presented in Fig. 8a–f. Table 5a–c specify the dendrogram generated by each pair, respectively, for the NN, the *K-NN* ($K = 10$) and the histogram ($K = 50$) approaches.

The contents of dendrograms DG_1, DG_2 and DG_3 are similar. From these 3 dendrograms generated by the NN and the *K-NN* approaches, the taxonomy T_1 of GTZAN presented in Fig. 9a was derived. The histogram approach generated dendrograms DG_4, DG_5 and DG_6. DG_4 is not similar to DG_5 and DG_6. DG_5 and DG_6 are quite similar, only the location of genre *pop* changes from DG_5 to DG_6.

Table 4 Genres vectors in GTZAN (one vector per line)

	bl	cl	co	di	hi	ja	me	po	re	ro
(a)—Simple NN with min_sup = 0.5										
bl	**59.6**	6.4	51.6	37.4	39.5	26.7	33.1	24.5	46.8	46.2
cl	21.6	**60.1**	28.1	4.9	5.5	56.1	4.3	2.6	18.9	12.0
co	56.8	15.4	**59.3**	33.0	35.6	37.2	33.1	17.3	53.8	48.4
di	41.7	1.8	35.7	**59.2**	57.8	8.5	57.2	43.6	43.8	50.1
hi	40.7	1.8	35.2	54.1	**59.0**	8.8	50.2	44.6	43.0	47.6
ja	38.8	34.8	44.1	14.1	14.1	**59.4**	15.7	5.6	35.1	26.5
me	34.2	0.5	26.9	50.8	50.1	3.9	**59.9**	36.6	36.0	45.0
po	35.0	2.8	26.6	49.4	52.6	7.4	39.2	**58.1**	31.1	36.2
re	51.0	5.1	52.5	37.6	39.8	21.1	38.2	23.4	**59.7**	52.0
ro	52.7	5.3	50.1	45.6	46.5	18.8	47.4	26.8	56.2	**60.1**
(b)—K-NN approach with K = 7 *and min_sup* = 0.75										
bl	**82.7**	53.5	75.6	56.2	63.0	59.5	47.9	45.0	69.6	69.2
cl	56.7	**81.2**	59.9	11.2	14.4	75.6	7.7	5.7	37.7	33.2
co	**82.3**	60.5	81.4	51.4	56.9	66.5	43.8	34.4	75.8	72.5
di	73.3	18.2	62.1	81.1	**82.1**	27.2	75.9	69.8	70.1	71.6
hi	72.3	21.9	59.5	76.8	**81.2**	29.6	70.0	72.1	66.6	68.5
ja	73.5	78.6	77.4	27.7	32.5	**80.8**	22.8	15.7	61.4	55.9
me	71.1	12.7	57.5	81.7	**81.9**	21.3	81.1	69.2	66.2	69.6
po	61.5	17.4	46.4	74.7	79.5	22.4	66.5	**80.4**	54.0	56.5
re	**80.9**	44.1	78.2	62.9	69.0	53.4	55.2	47.8	80.3	77.0
ro	**85.1**	38.4	80.2	68.9	73.4	49.0	63.2	51.0	82.4	81.9
(c)—K-NN approach with K = 9 *and min_sup* = 0.85										
bl	**90.5**	62.4	86.1	63.8	72.4	67.6	53.6	57.0	82.5	75.9
cl	66.7	**88.7**	68.9	15.0	20.9	84.6	9.6	9.1	49.4	40.9
co	**90.1**	71.0	89.4	59.6	67.8	75.0	49.7	47.1	85.3	79.6
di	84.3	25.8	76.9	88.9	**90.9**	35.2	83.2	83.6	83.0	78.1
hi	83.6	29.7	74.8	84.3	**88.9**	36.8	77.7	82.0	80.1	75.1
ja	83.4	87.9	85.3	34.2	43.6	**89.0**	27.6	25.1	73.0	65.4
me	85.2	18.7	76.7	88.8	**91.1**	27.9	89.1	83.3	82.8	78.3
po	74.8	22.4	63.0	82.6	87.3	27.1	76.4	**88.2**	69.8	62.6
re	**89.3**	56.4	87.1	72.8	79.5	64.1	63.6	61.6	88.5	83.6
ro	**93.3**	48.8	91.1	78.2	83.9	58.1	71.5	66.7	92.0	89.3
(d)—K-NN approach with K = 10 *and min_sup* = 0.85										
bl	**90.0**	59.9	85.1	60.6	70.5	65.4	52.2	54.7	81.3	74.4
cl	64.4	**88.8**	68.0	12.9	19.7	83.8	8.5	8.6	45.4	36.5
co	**90.4**	69.8	89.2	56.2	65.9	74.9	47.5	44.9	83.7	77.9
di	85.9	23.6	77.0	88.5	**90.6**	33.4	83.5	83.5	84.9	79.2
hi	85.1	27.2	75.0	83.4	**88.3**	35.0	77.6	81.3	82.2	76.1
ja	82.0	87.7	84.4	31.5	41.3	**88.7**	25.9	23.9	69.5	60.9
me	85.8	16.2	75.4	88.9	**91.0**	25.0	88.6	84.8	84.6	79.3
po	75.4	20.1	62.1	81.0	86.2	25.5	75.8	**87.9**	72.6	62.6
re	**89.4**	53.7	86.2	71.0	78.9	62.5	62.9	60.9	88.6	83.0
ro	**94.0**	45.5	90.1	77.5	83.4	55.6	70.9	66.5	92.2	89.0
(e)—Histogram approach with K = 50 *and min_sup* = 0.005										
bl	**1.34**	0.47	0.99	0.42	0.42	0.59	0.32	0.31	0.33	0.19
cl	1.34	1.74	**2.14**	0.01	0.02	1.59	0.02	0.01	0.18	0.16
co	0.59	0.43	**1.17**	0.20	0.18	0.53	0.12	0.10	0.28	0.30
di	0.24	0.02	0.12	**0.95**	0.55	0.05	0.49	0.41	0.39	0.25
hi	0.33	0.05	0.19	0.73	**0.99**	0.09	0.60	0.58	0.48	0.23

Table 4 continued

	bl	cl	co	di	hi	ja	me	po	re	ro
ja	1.00	0.90	**1.52**	0.10	0.06	1.31	0.10	0.02	0.24	0.37
me	0.23	0.01	0.06	0.69	0.68	0.05	**1.02**	0.55	0.43	0.16
po	0.40	0.06	0.14	0.88	1.38	0.08	1.12	**1.53**	0.68	0.13
re	0.28	0.12	0.29	0.46	0.41	0.20	0.37	0.30	**0.89**	0.43
ro	0.26	0.13	0.35	0.32	0.25	0.23	0.24	0.15	0.38	**0.74**
(f)—Histogram approach with $K = 100$ *and min_sup* $= 0.005$										
bl	**1.42**	0.44	1.31	0.44	0.45	0.61	0.30	0.31	0.29	0.21
cl	1.41	1.82	**2.32**	0.02	0.03	1.79	0.02	0.02	0.13	0.14
co	0.70	0.43	**1.27**	0.21	0.19	0.52	0.12	0.10	0.16	0.19
di	0.30	0.02	0.09	**0.97**	0.62	0.05	0.46	0.42	0.41	0.29
hi	0.40	0.05	0.18	0.78	**1.04**	0.07	0.57	0.59	0.48	0.31
ja	1.02	0.95	**1.63**	0.07	0.05	1.36	0.09	0.01	0.12	0.28
me	0.23	0.01	0.07	0.66	0.72	0.05	**1.01**	0.56	0.55	0.30
po	0.49	0.05	0.15	1.07	1.52	0.06	1.21	**1.54**	0.89	0.12
re	0.25	0.11	0.20	0.41	0.39	0.15	0.35	0.29	**0.83**	0.32
ro	0.25	0.12	0.27	0.32	0.27	0.19	0.24	0.15	0.27	**0.75**

The highest component of each vector is bold

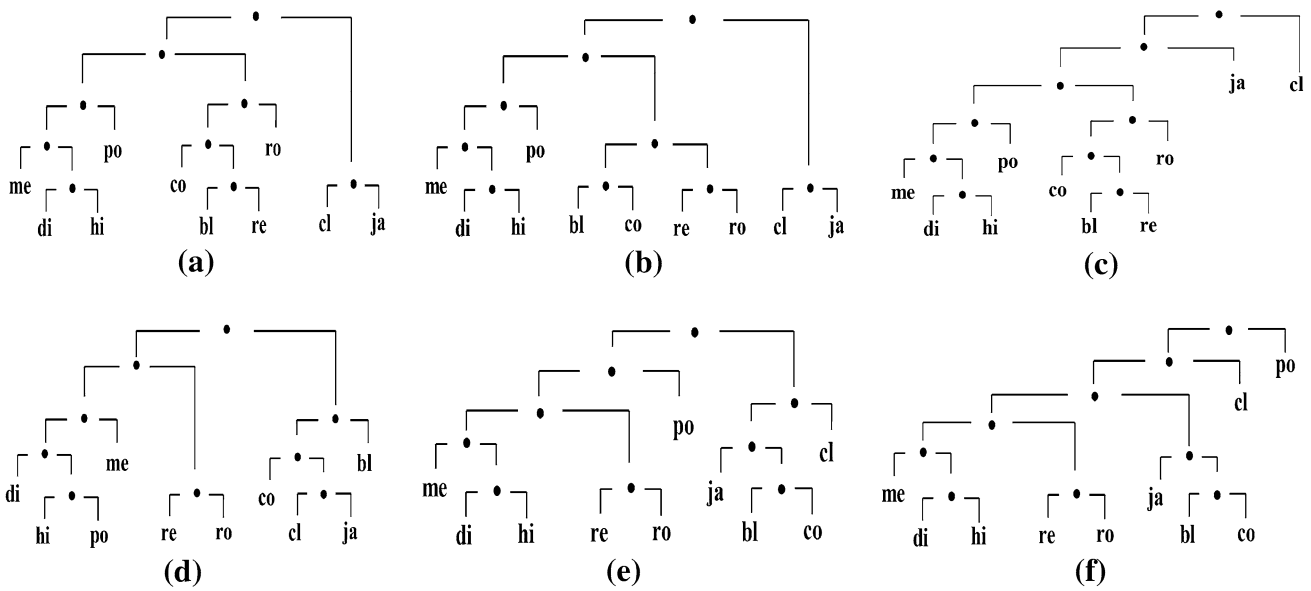


Fig. 8 Automatically generated dendrograms of GTZAN. **a** Dendrogram DG_1. **b** Dendrogram DG_2. **c** Dendrogram DG_3. **d** Dendrogram DG_4. **e** Dendrogram DG_5. **f** Dendrogram DG_6

But this difference cannot be neglected. Thus the 3 taxonomies T_2, T_3 and T_4 of GTZAN presented in Fig. 9b–d are, respectively, derived from dendrograms DG_4, DG_5 and DG_6.

4.2 Experiments on *GTZAN+*

In order to experience the consistency of the proposed method, experiments have been realized on a new database composed of a combination of GTZAN and 5 Afro genres. The proposed name of this new database is *GTZAN+*. The 5 new genres are: *bikutsi, makossa, bamileke, salsa* and *zouk*. In the rest of the paper, these 5 genres will be represented in figures by the acronyms: *bi, ma, ba, sa* and *zo*. Each Afro genre was represented by 100 '.wav' files of 30 s each with the same properties as those of GTZAN. *Zouk* is a French-Caribbean genre and *salsa* is a genre having Cuban origins, but here many

Table 5 Dendrograms generated on GTZAN

	d_e	d_m	d_t	d_a
(a) The NN approach				
Max	DG_2	DG_2	DG_2	DG_2
Ave	DG_2	DG_1	DG_2	DG_2
Cen	DG_1	DG_1	DG_1	DG_1
Min	DG_3	DG_3	DG_3	DG_1
(b) The K-NN approach ($K = 10$)				
Max	DG_2	DG_2	DG_1	DG_2
Ave	DG_2	DG_2	DG_1	DG_2
Cen	DG_2	DG_2	DG_1	DG_2
Min	DG_3	DG_3	DG_3	DG_1
(c) The histogram approach ($K = 50$)				
Max	DG_6	DG_5	DG_5	DG_4
Ave	DG_5	DG_5	DG_6	DG_4
Cen	DG_6	DG_5	DG_6	DG_4
Min	DG_5	DG_5	DG_6	DG_4

salsa samples played by Cameroonian singers have been included. The 3 remaining new genres are Cameroonian genres, and their short descriptions can be found online [35].

The first nine steps of the methodology followed in Sect. 4.1 for GTZAN have been followed for GTZAN+. However, at step 7, *min_conf* was set to $\frac{1}{15}$ for *FeatureMine* because GTZAN+ has 15 genres. As it was done on GTZAN, the associated vectors of each genre were calculated and the *AHC* algorithm was applied to generate dendrograms. Due to space constraints, only the NN and the *K*-NN approaches are presented for GTZAN+. For the same reason, the components of the vectors associated with the genres of GTZAN+ are not presented. The number of characteristic sequences extracted by *FeatureMine* for each genre is presented in Table 6. The 4 dendrograms presented in Fig. 10a–d were obtained for GTZAN+. Table 7 specifies the dendrogram generated by each pair of distance measures for the NN approach. The dendrogram DG'_3 presented in Fig. 10c was generated for all the 16 pairs of distances with the *K*-NN approach ($K = 10$). From the general shapes of these automatically generated dendrograms, the taxonomy T' of GTZAN+ presented in Fig. 11 was derived.

4.3 Properties of the generated taxonomies

The taxonomies of GTZAN generated by the proposed method share some similarities with the existing taxonomies presented in Fig. 1b–f [4, 7, 8]. Additionally, the proposed method generates taxonomies satisfying the following criteria proposed by Pachet in [10]:

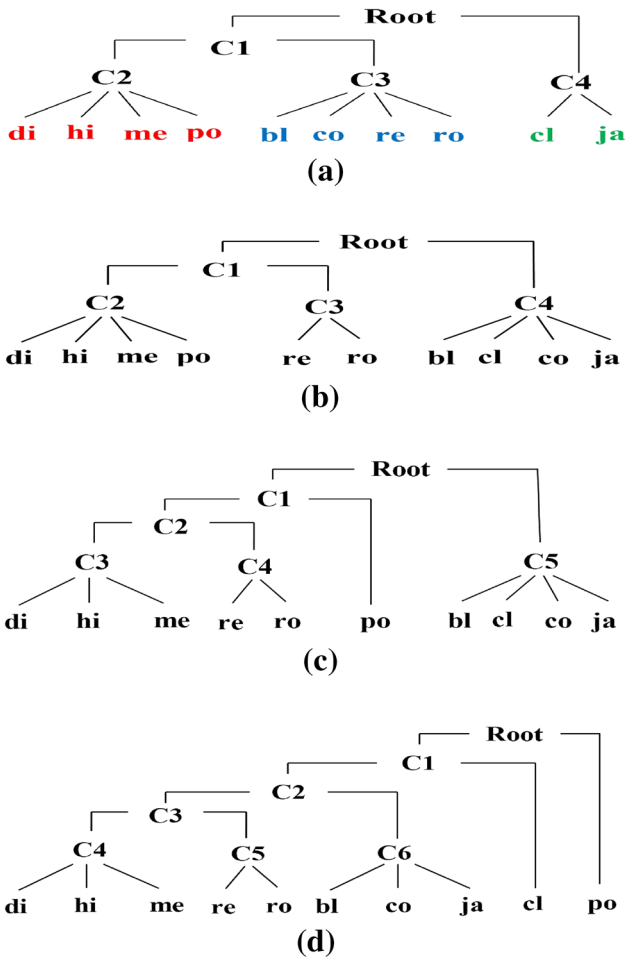


Fig. 9 Proposed taxonomies T_1, T_2, T_3 and T_4 of GTZAN. T_1 is generated by the NN and the *K*-NN approaches. T_2, T_3 and T_4 are generated by the histogram approach. **a** Taxonomy T_1. **b** Taxonomy T_2. **c** Taxonomy T_3. **d** Taxonomy T_4

Table 6 Number of frequent characteristic sequences extracted by *FeatureMine* for the genres of GTZAN+

	bi	bl	cl	co	di	hi	ja	ma
NN	226	39	812	72	96	97	189	82
K-NN	540	10	450	28	53	26	234	46
	me	ba	po	re	ro	sa	zo	
NN	87	192	127	80	68	140	133	
K-NN	82	124	84	22	41	402	542	

1. *Objectivity*: The proposed method generates objective taxonomies because a taxon is a music genre defined as a vector composed of N elements calculated with Eq. 5.
2. *Similarity*: The proposed taxonomies allow search by similarity because if two genres of G belong to the same cluster, their associated vectors are close with respect to the similarity measure.

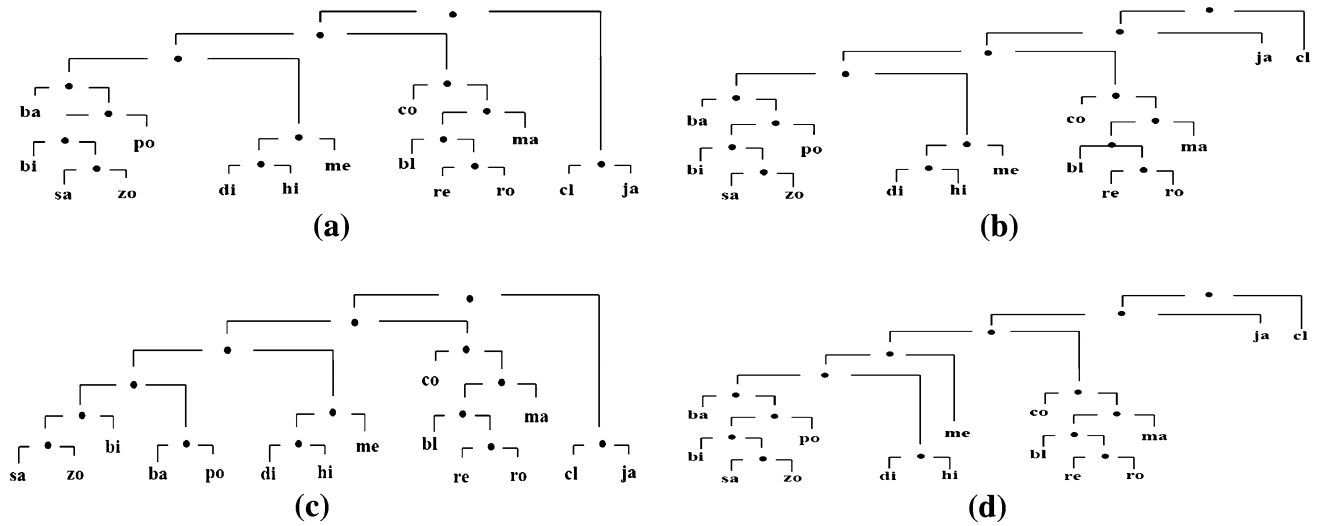


Fig. 10 Automatically generated dendrograms of GTZAN+. **a** Dendrogram DG'_1. **b** Dendrogram DG'_2. **c** Dendrogram DG'_3. **d** Dendrogram DG'_4

Table 7 Dendrograms of GTZAN+ with the NN

	d_e	d_m	d_t	d_a
max	DG'_3	DG'_3	DG'_1	DG'_3
ave	DG'_1	DG'_3	DG'_4	DG'_1
cen	DG'_1	DG'_3	DG'_4	DG'_1
min	DG'_2	DG'_2	DG'_4	DG'_2

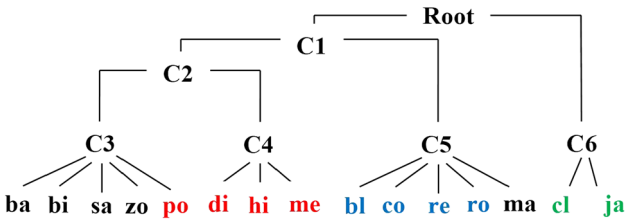


Fig. 11 Proposed taxonomy T' of GTZAN+

3. *Consistency*: The proposed taxonomies are consistent because the semantic of the links remains the same throughout the taxonomies.
4. *Evolutivity*: As it can be observed in Figs. 9a and 11, the taxonomy of GTZAN generated by the NN and the *K*-NN approaches is preserved in the taxonomy of GTZAN+ generated by these approaches. Therefore the proposed method is *experimentally evolutive* because it is capable to cope with new genres.

4.4 Time performance for dendrogram generation

The proposed taxonomies were generated off-line and once on a personal computer having the following properties: (1) Processors: *Intel(R) Core(TM) i7-2670QM CPU @2.2GHz 2.2GHz* (2) RAM: *8 GB*. Table 8 gives details about the maximum time taken to generate a dendrogram.

4.5 Hierarchical genres classification

This section shows how to perform the hierarchical classification which is the last step of the methodology. Experiments on flat and hierarchical classifiers were performed using the MEKA [36] data mining tool. Recently developed in 2014, MEKA is an extension of WEKA [12] that enables multi-label classification. A detailed evaluation and analysis of some of the main multi-label classification methods in MIR can be found in [37]. MEKA was selected because it includes a meta classifier named *HASEL* that enables the user to clearly specify a taxonomy in an '.arff' file. Then the user selects a basic WEKA classifier to be applied with this taxonomy. HASEL partitions labels into subsets based on the defined hierarchy. It assumes that a dot '.' in the attribute name defines hierarchical branches. Figure 12 presents the header of the '.arff' file in which the taxonomy of GTZAN was described.

Several music genres classifiers are presented in [38]. The 4 following basic classifiers have been selected (their WEKA/MEKA corresponding names are in brackets): SVMs with polynomial kernels (*SMO*), Multi Layers Perceptrons (*MLP*), Decision Trees (*J48*) and KNNs (*IBk*). All these classifiers were used with their default settings in MEKA. After a 10-fold cross-validation (90–10 %), the results presented in Table 9a–b were obtained for GTZAN and GTZAN+.

Experimental results show that the hierarchical classifiers based on the proposed taxonomies always outperform the corresponding flat classifiers. The best classification results were obtained with the MLP and SMO classifiers in the two

Table 8 Time performance for dendrogram generation

Step	Max. time	Result
Descriptors extraction	≈5 s/song	1 Sequence of vectors of descriptors/song
k-means	≈2 min/genre	100 central vectors/genre
K-NN	≈1 s/song	1 sequential pattern/song
PrefixSpan	≈(around 15 min)/genre	1 sequential pattern database/genre
FeatureMine	≈(1 h)	Many characteristics for each genre
Genre vector	≈1 s/genre	1 vector/genre
AHC	≈1 s	1 dendrogram

```
@relation 'gtzanHier: -C 10'
@attribute Root.C1.C3.blu {0,1}
@attribute Root.C4.cla {0,1}
@attribute Root.C1.C3.cou {0,1}
@attribute Root.C1.C2.dis {0,1}
@attribute Root.C1.C2.hip {0,1}
@attribute Root.C4.jaz {0,1}
@attribute Root.C1.C2.met {0,1}
@attribute Root.C1.C2.pop {0,1}
@attribute Root.C1.C3.reg {0,1}
@attribute Root.C1.C3.roc {0,1}
@attribute Root {0,1}
@attribute Root.C1 {0,1}
@attribute Root.C1.C2 {0,1}
@attribute Root.C1.C3 {0,1}
@attribute Root.C4 {0,1}
```

Fig. 12 Headers of the 'arff' file describing the proposed taxonomy of GTZAN in MEKA

experimental databases with accuracies greater than 80 %. However, classification with MLP took several hours unlike the other classifiers for which just a couple of seconds was needed. Hierarchical classification based on IBk and SMO always showed minimum accuracy gains close to 10 %. The minimum accuracy gains provided by J48 classifier are always close to 20 % and MLP gave minimum accuracy gains reaching 40 % in GTZAN+. Additionally, the hierarchical classification accuracies are close for GTZAN+ and GTZAN. This can be explained by the fact that the proposed method generated evolutive taxonomies for the NN and the *K*-NN approaches.

In fact, $\frac{4}{5}$ of the new added Afro genres are gathered in the same cluster $C3$ in the taxonomy T' of GTZAN+. Therefore, a single classifier is trained and dedicated to separate them at this level. This reduces considerably the error rate for these 4 new genres. The preservation of the taxonomy T_1 of GTZAN implies that almost all the songs that were accurately classified in GTZAN were also accurately classified in GTZAN+.

4.6 Comparisons with related work

The taxonomy proposed here for GTZAN has been compared with the taxonomies of Fig. 1b, e, f (genre 'blues' excluded) used, respectively, in [4, 7, 8]. The best hierarchical classification performance of this work was compared with those in these three papers. To make comparisons with [8] in which only 9 genres of GTZAN are considered, a new taxonomy T'_1 was generated for the database GTZAN ^{blues} (GTZAN without the genre 'blues') using the NN and the *K*-NN approaches. The resulting taxonomy T'_1 was almost identical to T_1 presented in Fig. 9a with 'blues' removed from cluster $C3$. Table 10 gives details about the hierarchical classification results on GTZAN ^{blues} based on the approach.

As shown in Table 11a, the best performance (85.3 %) obtained by the approach proposed here with MLP clearly improves the best performance (78 %) obtained in [8]. Table 11b shows comparisons for GTZAN. These comparisons show that the hierarchical classifiers proposed in this work outperform with more than 7 % the results presented in [4, 7, 8].

Table 9 Classification results with *I*Bk = KNNs, *SMO* = SVMs with polynomial kernels, *MLP* = Multi Layers Perceptrons, *J48* = Decision Trees

	Flat	T_1	T_2	T_3	T_4	Min Gain
(a) Results in GTZAN						
IBk	63.8	74.2	77.3	81.6	84.4	+10.4
SMO	72.3	81.7	85.5	90.2	91.2	+9.4
MLP	68.4	85	87.4	90.9	**91.6**	+16.6
J48	47.3	67.7	68.5	76.1	79.3	20.4

	Flat	T'	Gain
(b) Results in GTZAN+			
IBk	65.4	77.1	+11.7
SMO	75.5	**85.2**	+9.7
MLP	41.9	82.1	+40.2
J48	47.3	69.5	+22.2

Accuracies are in (%)

5 Conclusion

The new radio prototype based on FPGA technologies developed in [1] is already able to perform the concurrent demodulation of entire broadcast bands. But music genre

Table 10 Classification results in GTZAN^{blues} with *IBk* = KNNs, *SMO* = SVMs with polynomial kernels, *MLP* = Multi Layers Perceptrons, *J48* = Decision Trees

	T_1'
IBk	75.7
SMO	83.7
MLP	**85.3**
J48	69.4

Accuracies are in (%)

The value in bold is the highest accuracy produced by the hierarchical classifier based on the proposed taxonomy of GTZAN, *blues* excluded. This value is later compared with the best accuracy in [8]

Table 11 Comparisons with work cited for hierarchical genre classification

	Ulaş [8]	This work T_1'	
(a) Comparisons in GTZAN ^{blues}			
Accuracy	78	**85.3**	
	Tao [4]	Hasitha [7]	This work T_4
(b) Comparisons in GTZAN			
Accuracy	72.69	72.9	**91.6**

Accuracies are in (%)

The values in bold are the highest accuracies. They are in bold to show that the proposed approach outperforms the state of the art

classification is not yet applicable in that prototype. Several hierarchical classifiers have been developed to improve the efficiency of music recognition systems. The goal of this work was to provide hierarchical classification with better performances than existing work. This has been achieved by the proposal of an automatic approach for taxonomy generation based on sequential pattern mining techniques. The main idea was to transform a song into a sequence where each element represents the proximity between the corresponding music excerpt and the genres under consideration. Three separated approaches were proposed to transform a song into a sequence: the *simple NN* approach, the *K-NN* approach and the *histogram* approach.

Timbre music descriptors were used for the taxonomies generation. They were then combined with rhythm descriptors during the classification phase. Experiments were carried on the GTZAN database composed of 10 genres and on GTZAN+ which extends GTZAN with 5 Afro genres. The hierarchical classifiers based on the taxonomies generated in this work outperformed the corresponding flat classifiers with minimum accuracy gains of 11.7 % for IBk, 9.7 % for SMO, 40.2 % for MLP and 22.2 % for J48. The best classification accuracies were obtained with the hierarchical classifiers based on taxonomies resulting from the histogram approach. The best classification results where obtained with the SMO and the MLP classifiers with accuracies always greater than 80 %. This improves by more than 7 % the performances of the existing hierarchical classifiers. The robustness of the proposed method follows from the fact that the generated taxonomies satisfy *objectivity*, *similarity*, *consistency*. *Evolutivity* is experimentally checked with the simple NN and the *K*-NN approaches.

Future work may focus on the implementation of the proposed method in the radio prototype developed in [1]. In this way, the taxonomy will be integrated in the hardware of the FPGA device and the hierarchical classification will be performed using a selected basic classifier.

References

1. Tietche BH, Romain O, Denby B, De Dieuleveult F (2012) FPGA-based simultaneous multichannel fm broadcast receiver for audio indexing applications in consumer electronics scenarios. IEEE Trans Consum Electron 58(4):1153–1161
2. Brecheisen S, Kriegel H-P, Kunath P, Pryakhin A (2006) Hierarchical genre classification for large music collections. In: Multimedia and expo, 2006 IEEE international conference on, pp 1385–1388
3. Costa E, Lorena A, Carvalho ACPLF, Freitas A (2007) A review of performance evaluation measures for hierarchical classifiers. In: Evaluation methods for machine learning II: papers from the AAAI-2007 workshop, pp 1–6
4. Li T, Ogihara M (2005) Music genre classification with taxonomy. In: Acoustics, speech, and signal processing, 2005. In: Proceedings.(ICASSP'05). IEEE international conference on, vol. 5, pp. v-197
5. Silla Jr CN, Freitas A et al (2009) Novel top-down approaches for hierarchical classification and their application to automatic music genre classification. In: Systems, man and cybernetics, 2009. SMC 2009. IEEE international conference on, pp 3499–3504
6. Burred JJ, Lerch A (2003) A hierarchical approach to automatic musical genre classification. In: Proceedings of the 6th international conference on digital audio effects, pp 8–11
7. Ariyaratne HB, Zhang D (2012) A novel automatic hierarchical approach to music genre classification. In: Multimedia and expo workshops (ICMEW), 2012 IEEE international conference on, pp 564–569
8. Bağcı U, Erzin E (2005) Boosting classifiers for music genre classification. Comput Inf Sci-ISCIS 2005:575–584
9. Shao X, Xu C, Kankanhalli MS (2004) Unsupervised classification of music genre using hidden markov model. In: Multimedia and expo, 2004. ICME'04. 2004 IEEE international conference on, vol 3, pp 2023–2026
10. Pachet F, Cazaly D et al (2000) A taxonomy of musical genres. RIAO, pp 1238–1245
11. http://marsyasweb.appspot.com/download/data_sets/
12. Witten IH, Frank E (2005) Data mining: practical machine learning tools and techniques
13. Aggarwal CC, Wolf JL, Yu PS, Procopiuc C, Park JS (1999) Fast algorithms for projected clustering. ACM SIGMoD Rec 28(2):61–72

14. Doraisamy S, Golzari S, Mohd N, Sulaiman MN, Udzir NI (2008) A study on feature selection and classification techniques for automatic genre classification of traditional malay music. In: ISMIR, pp 331–336
15. Conklin D (2009) Melody classification using patterns. In: Second international workshop on machine learning and music, pp 37-41
16. Lin C-R, Liu N-H, Wu Y-H, Chen ALP (2004) Music classification using significant repeating patterns. Database systems for advanced applications, pp 506–518
17. Ren J-M, Chen Z-S, Jang JSR (2010) On the use of sequential patterns mining as temporal features for music genre classification. In: IEEE international conference on acoustics speech and signal processing (ICASSP), pp 2294–2297
18. Ren J-M, Jang JSR (2011) Time-constrained sequential pattern discovery for music genre classification. In: IEEE international conference on acoustics, speech and signal processing (ICASSP), pp 173–176
19. Pei J, Han J, Mortazavi-Asl B, Pinto H, Chen Q, Dayal U, Hsu M-C (2001) Prefixspan: mining sequential patterns efficiently by prefix-projected pattern growth. ICCCN, pp 02-15
20. Agrawal R, Srikant R (1994) Fast algorithms for mining association rules. In: Proceedings of 20th international conference on very large data bases. VLDB 1215:487–499
21. Srikant R, Agrawal R (1996) Mining quantitative association rules in large relational tables. ACM SIGMOD Rec 25(2):1–12
22. Zaki MJ (2000) Scalable algorithms for association mining. IEEE Trans Knowl Data Eng 12(3):372–390
23. Han J, Pei J, Mortazavi-Asl B, Chen Q, Dayal U, Hsu M-C (2000) FreeSpan: frequent pattern-projected sequential pattern mining. In: Proceedings of the sixth ACM SIGKDD international conference on knowledge discovery and data mining, pp 355–359
24. Rao VCS, Sammulal P (2013) Survey on sequential pattern mining algorithms. Int J Comput Appl 76(12):24–31
25. George T, Georg E, Perry C (2001) Automatic musical genre classification of audio signals. In: Proceedings of the 2nd international symposium on music information retrieval, Indiana
26. Mitrović D, Zeppelzauer M, Breiteneder C (2010) Features for content-based audio retrieval. Adv Comput 78:71–150
27. Lidy T, Rauber A (2005) Evaluation of feature extractors and psycho-acoustic transformations for music genre classification. ISMIR, pp 34-41
28. www.ifs.tuwien.ac.at/mir/muscle/del/audio_extraction_tools.html
29. Sudhir R (2011) A survey on image mining techniques: theory and applications. Comput Eng Intell Syst 2(6):44–53
30. Asghar MN, Hussain F, Manton R (2014) Video indexing: a survey. framework, vol 3(01)
31. Fernando B, Fromont E, Tuytelaars T (2012) Effective use of frequent itemset mining for image classification. In: European conference on computer vision, pp 214–227
32. Lesh N, Zaki MJ, Oglhara M (2000) Scalable feature mining for sequential data. Intell Syst Appl 15(2):48–56
33. Sturm BL (2012) An analysis of the GTZAN music genre dataset. In: Proceedings of the second international ACM workshop on music information retrieval with user-centered and multimodal strategies, pp 7–12
34. Iloga S, Romain O, Bendaouia L, Tchuente M (2014) Musical genres classification using Markov models. In: Audio, language and image processing (ICALIP), 2014 international conference on, pp 701–705
35. http://fr.wikipedia.org/wiki/GenreName
36. http://meka.sourceforge.net/
37. da Silva V, and Winck AT (2014) Multi-label classification of music into genres
38. Nicolas Scaringella, Giorgio Zoia, Daniel Mlynek (2006) Automatic genre classification of music content: a survey. Signal Processing Magazine 23(2):133–141