The Matrix Profile for Motif Discovery in Audio - An Example Application in Carnatic Music

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Abstract. We present here a pipeline for the automated discovery of repeated motifs in audio. Our approach relies on state-of-the-art source separation, predominant pitch extraction and time series motif detection via the matrix profile. Owing to the appropriateness of this approach for the task of motif recognition in the Carnatic musical style of South India, and with access to the recently released Saraga Dataset of Indian Art Music, we provide an example application on a recording of a performance in the Carnatic *rāga*, *Rītigaula*, finding 56 distinct patterns of varying lengths that occur at least 3 times in the recording. The authors include a discussion of the potential musicological significance of this motif finding approach in relation to the particular tradition and beyond.

Keywords: Musical Pattern Discovery, Motif Discovery, Matrix Profile, Predominant Pitch Extraction, Carnatic Music, Indian Art Music

1 Introduction and Related Work

Short, recurring melodic phrases, often referred to as "motifs", are important building blocks in the majority of musical styles across the globe. The automatic identification and annotation of such motifs is a prominent and rapidly developing topic in music information retrieval [1–4], playing a significant role in music analysis [5–7], segmentation [8–10] and development of musical theory [11–13]. No consensus exists on how this is best achieved, and indeed difficulty and differences in evaluation make it hard to contextualize the efficacy of a method outside of the task to which it is applied. A thorough review and comparison of approaches that handle symbolic music representations can be found in [1] and [4] however in this paper we focus on the much more common case of music without notation, extracting repeated motifs from audio.

Difficulty in working with raw audio for this task stems from the incredibly dense amount of information contained in audio signals, simultaneously clouding that which we might be interested in and providing a heavy workload for computational methods. A common method of reducing this complexity is to extract from the raw audio an object or feature set that captures the aspect of the music most relevant to the type of motif desired, and to subsequently compute some self-similarity metric between all subsequence pairs to group or connect similar sections [14, 15]. This could take the form of audio features such as Mel-frequency cepstral coefficients (MFCC) [16, 17]

or chroma [15, 18], rhythmic onsets [19, 20] or monophonic pitch [21, 22]. When performed successfully, it is the latter that provides an abstraction with the most information pertaining to the melody in audio. And with more recent advances in both predominant pitch extraction [23] and time series motif detection [24], we are afforded the opportunity to revisit the approach of predominant pitch extraction/self-similarity in computationally feasible time on relatively large time scales.

Certain musical styles are particularly suitable for this type of analysis: for example, those for which automated transcription is not yet possible, and where the symbolic to sonic gap is such that musically salient units may sometimes be better characterised by segments of continuous time series pitch data than by transcriptions. This is the case in Indian Art Music (IAM), including Hindustani and Carnatic styles. Automated motif detection in these traditions is a limited but active area of research. In the case of Carnatic music, *svaras* (notes) are coarticulated (merged) through *gamakas* (ornaments) [25]. This characteristic provides particular challenges for processes involving automated segmentation, and can even mean that different Carnatic musicians' annotations of the same phrase may vary subtly in places, with different degrees of symbolic detail being possible. This leaves motif detection through time series pitch data as one of the most viable and popular approaches to finding meaningful melodic units in the style [26–28].

In this paper we demonstrate an approach for the automated discovery of repeated motifs in audio: state-of-the-art source separation [31], predominant pitch extraction using the Melodia algorithm [23] and ultra-fast means of time series motif detection via the matrix profile [24]. Owing to the appropriateness of this approach for the task of motif recognition in Carnatic music, and with access to the recently released Saraga Dataset of IAM [32], we provide an example application, applying these existing methods in this tradition. All code is available on GitHub³ with a Jupyter notebook walk through of both the generalized and IAM-specific code.

2 Dataset

We demonstrate our approach on an example recording from the Saraga dataset [32]. Developed within the framework of the CompMusic project⁴ and openly available for research, Saraga comprises two IAM collections, representing the Hindustani and Carnatic traditions. Both collections comprise several hours of music with accompanying time-aligned expert annotations and relevant musical (e.g. $r\bar{a}ga$, $t\bar{a}la$, form) and editorial (e.g. artist, work, concert) metadata. In this work we focus on a performance taken from the Carnatic collection, 168 of which contain separate microphone recordings of: lead vocal, background vocal (if present), violin, mridangam and ghatam (if present). However, since these tracks are recorded from live performance, the multi-track audios in the dataset contain considerable background leakage, i.e., are not completely isolated from the other instruments.

We access and interact with the Saraga dataset through the mirdata library [33]. This tool provides easy and secure access to the canonical version of the dataset, while load-

³ https://github.com/thomasgnuttall/carnatic-motifs-cmmr-2021/

⁴ https://compmusic.upf.edu/

ing and managing the dataset contents (audio, annotations and metadata) to optimize our research pipeline.

3 Methodology

The process consists of two stages (1) the extraction from audio of a vocal pitch track, which consists of a one-dimensional time series representing the main melodic line of the performance and (2) the use of self-similarity euclidean distance to identify likely candidates for repeated motifs in the main melodic line.

3.1 Predominant Pitch Extraction

The quality and consistency of the predominant pitch extraction is paramount. Given the shortage of training data and algorithms to extract the vocal pitch from Carnatic music signals, our raw audio recording is subject to three processing steps to arrive at a one dimensional time series of pitch values representing the main melodic line.

Isolating the Vocal Source Where possible we use the vocal track recording for analysis (still containing leakage from other instruments). If this is not available, the mix is used. For the isolation of voice from the background instruments (both in mixed and vocal tracks), we use Spleeter, which is a deep learning based source separation library which achieves state-of-the-art results on automatically separating vocals from accompaniment [31].

Extracting the Predominant Pitch Curve We use one of the most popular signal processing based algorithms for predominant pitch estimation from polyphonic music signals, the Melodia algorithm [23], applying an equal-loudness filter to the signal beforehand to encourage a perceptually relevant extraction. In the majority of studies attempting this task in IAM, Melodia has achieved consistent and viable results [26,28–30,34]. We use a time-step of 2.9ms for the extraction.

Post-Processing Two post-processing steps are applied to the pitch track. (1) Gap interpolation, linearly interpolating gaps of 250ms or less [36], typically caused by glottal sounds and sudden decrease of pitch salience in *gamakas* and (2) Gaussian smoothing with a sigma of 7, softening the curve and providing a more natural, less noisy shape.

The final extracted pitch track is a time-series of n pitch values, $P = p_1, p_2, ..., p_n$.

3.2 Repeated Motif Discovery

To search P for regions of similar structure we look for groups of subsequences that have a low euclidean distance between them. The subsequence length to search for, m is a user-defined parameter of the process.

Matrix Profile An efficient method of inspecting the euclidean distances between pairwise combinations of subsequences in a time series is the matrix profile [24]. Given a time series, T, and a subsequence length, m, the matrix profile returns for each subsequence in T, the distance to its most similar subsequence in T. The STAMP algorithm computes the matrix profile in impressive time by exploiting the overlap between subsequences using the fast Fourier transform, requiring only one parameter, subsequence length, m [24]. We use the non-z-normalized distance, since we are interested in matching subsequences identical in shape and y-location (i.e. pitch).

The matrix profile is therefore defined as $MP = ed_1, ed_2, ..., ed_{n-m}$ where ed_i is the regular euclidean distance between the subsequence of length m beginning at element i and its nearest neighbour in P.

Exclusion Mask To ensure that only subsequences of interest are considered, a mask of subsequences in P to exclude is computed by applying a series of *exclusion functions* to each subsequence. These exclusion functions are informed by expert understanding of what constitutes a relevant motif in the tradition. Explicitly, the exclusion mask, $EM = em_1, em_0, ..., em_n$ where em_i is either 1 or 0, yes or no, does the subsequence satisfy any of the following:

- *Too silent* more than 5% percent of the subsequence is 0 (i.e. silence)
- Minimum gap subsequence contains a silence gap of 250ms or more
- *Too stable* in more than 63% of cases for a rolling window of 100, the average deviation of pitch from the average is more than 5 Hz. This step is designed to exclude subsequences with too many long held notes although musically relevant, not interesting from a motific perspective. A similar approach is taken in [26]

Subsequences that correspond to a mask value of 1 are not considered valid and not returned.

Identifying Motif Groups The search for groups of repeated motifs begins by looking for a *parent* subsequence; those in P that have the lowest euclidean distance to another subsequence i.e. minimas in MP. The assumption being that if these subsequences have one very near neighbour, i.e. they are repeated once, then they are more likely to occur multiple times; a similar approach is used in [27].

For a candidate parent motif, we use the MASS similarity search algorithm [24] to calculate the non-normalised euclidean distance to every other subsequence in the pitch track, returning those that satisfy the requirements set by the parameters; topN, maxOcc, minOcc and thresh. Algorithms 1 and 2 describe the process and parameters.

Output The returned motif groups are arrays of start indices in P. The number of groups and occurrences in each is influenced by the topN, minOcc and maxOcc parameters.

Algorithm 1 Identify groups of motifs with low inter-group euclidean distance

```
1: procedure GETMOTIFGROUPS
        MP \leftarrow \text{matrix profile array from } \textit{Matrix Profile}
 2:
 3:
        P \leftarrow \text{pitch sequence array from } Predominant Pitch Extraction
 4:
        EM \leftarrow exclusion mask array from Exclusion Mask
 5:
        m \leftarrow pattern length
 6:
        topN \leftarrow maximum number of groups to return
 7:
        maxOcc \leftarrow maximum number of occurrences per group
 8:
        minOcc \leftarrow minimum number of occurrences per group
9:
        thresh \leftarrow maximum length-normalised distance of occurrence to parent
10:
11:
        MP[\text{where}(EM == 1)] \leftarrow \infty
12:
        nGroups \leftarrow 0
13:
        allMotifs \leftarrow array()
14:
        while nGroups < topN
15:
            ix \leftarrow argmin(MP)
                                                                                 ⊳ get parent index
16:
            if MP[ix] == \infty
                                                                        17:
                 break
18:
            motifs \leftarrow GetOccurrences(ix, P, m, maxOcc, thresh, EM)
19:
            if Length(motifs) < minOcc
                                                         20:
                 continue
21:
            for mtf in motifs
                                                                     ⊳ motifs is an array of indices
22:
                 MP[mtf - m : mtf + m] \leftarrow \infty

    ▷ clear part of array to avoid future discovery

23:
            nGroups \leftarrow nGroups + 1
            allMotifs \leftarrow \mathbf{append}\ motifs
24:
25:
        return allMotifs
                               > array of motif groups, each motif group an array of start indices
26: end procedure
```

Algorithm 2 Identify other occurrences of parent motif in P using MASS

```
1: procedure GETOCCURRENCES
 2:
        ix \leftarrow index of parent sequence to query
 3:
        P \leftarrow \text{pitch sequence array from Predominant Pitch Extraction}
 4:
        m \leftarrow \text{pattern length}
 5:
        maxOcc \leftarrow maximum number of occurrences to return
 6:
        thresh \leftarrow maximum length-normalised distance of occurrence to parent
 7:
        EM \leftarrow exclusion mask array from Exclusion Mask
 8:
9:
        parent \leftarrow P[ix : ix + m]
10:
        stmass \leftarrow MASS(parent, P) \Rightarrow array of distances between parent and all subsequences
11:
        stmass[where(EM == 1)] \leftarrow \infty
12:
        nOccs \leftarrow 0
13:
        allOccs \leftarrow array()
14:
         while nOccs < maxOcc
15:
             ix \leftarrow argmin(stmass)
16:
             if stmass[ix]/m > thresh
                                                                          ⊳ length normalised distance
17:
                  break
                                                        ⊳ cease search, no significant patterns remain
18:
             stmass[ix - m : ix + m] \leftarrow \infty
19:
        allOccs \leftarrow append ix
20:
         return allOccs
                                                    > array of occurrence start indices for this parent
21: end procedure
```

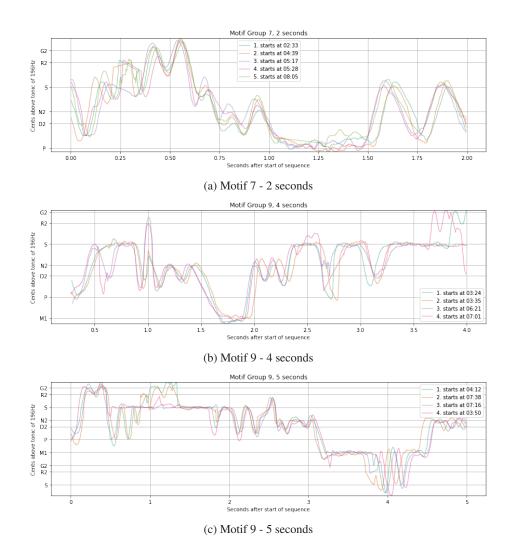


Fig. 1: Overlaid pitch contour plots of three returned motif groups. The y-axis of each figure represents cents above the tonic (S) of 196Hz, divided into the discrete pitch positions defined in Carnatic music theory for this $r\bar{a}ga$ - S, R2, G2, M1, P, D2, N2 [35]. R2 is two semitones (200 cents) above the tonic, S, and G2 is one semitone (100 cents) above R2, and so on. The oscillatory melodic movement that can be seen cutting across these theoretical pitch positions is typical of the style, illustrating the challenges of locating individual 'notes', either through expert annotations or automatically.

4 Results

We include the results of our process applied to a performance by the Akkarai Sisters of a composition titled Koti Janmani⁵, by the composer Oottukkadu Venkata Kavi, which

⁵ https://musicbrainz.org/recording/5fa0bcfd-c71e-4d6f-940e-0cef6fbc2a32

is set in the Carnatic $r\bar{a}ga$, $R\bar{t}igaula$. The process is run for pattern lengths of 2,3,4, 5 and 6 seconds using parameters; topN=15, minOcc=3, maxOcc=20. The parameter thresh is selected by subjective evaluation of the patterns returned in one motif group, choosing a value beyond which consistency is lost.

The number of significant motif groups found for 2, 3, 4, 5 and 6 second runs is 15, 15, 11, 11 and 4 respectively. For the code and full results we refer the reader to the GitHub repository. Fig. 1a, 1b and 1c present the pitch plots associated with the top 5 occurrences of an example pattern in the 2, 4 and 5 seconds groups respectively.

5 Discussion

Due to the current lack of complete (i.e., saturated) ground truth annotations in the Saraga dataset, it is difficult to evaluate our application systematically. Creation of such annotations are ongoing as part of this project. In the meantime, however, the nature of the task and size of the results allow us to reflect on the coherency between patterns and their significance within the tradition.

The high degree of similarity between patterns returned within groups is obvious even to listeners who have no experience of the style, and can be appreciated from both the audio and pitch plots. This similarity is unsurprising, we choose a modest euclidean distance threshold and the process returns motifs that correspond to areas of pitch that are very similar by this measure. It is however a testament to the quality and consistency of the pitch extraction process and audio in the Saraga dataset [32], both resources not yet available in previous works. And more impressive still, also unseen in other works, is that these results can be achieved relatively quickly on a personal machine requiring little user input: pattern length, m and euclidean distance threshold, thresh (easily tuned in negligible time). This is due to the efficiency of the STAMP and MASS algorithms in computing the all pairs self-similarity [24].

Of course, we are more interested in whether the consistent results identified by a process like ours have the potential to contribute to ongoing musicological endeavours of pattern recognition, documentation and music analysis in the Carnatic tradition. Initial evaluation by the third author, who has expertise in the tradition [25], suggests that that there is a high degree of musical similarity across the returned patterns in each group. At least the first few matches, and often all of the patterns, in each group would be considered by experts in the style to consist of the same motifs, or motif fragments. Some of the returned groups contain whole motifs that are particularly important for this $r\bar{a}ga$; $R\bar{t}igaula$ is one of the Carnatic $r\bar{a}gas$ that is expressed through a number of characteristic motifs, sometimes referred to as pidi (catch-phrases), $sa\bar{n}c\bar{a}ras$ or prayo-gas [35].

Two examples of particularly musically significant motifs returned can be seen in Fig. 1a and Fig. 1b. Fig. 1a shows a frequently recurring phrase in this composition that includes the motif "npnn" (expressed here in *sargam* notation, which is used by practitioners to represent Carnatic *svaras*). The fact that 11 results are returned for this pattern (only five of these are illustrated for the sake of visual clarity) points to both the significance of the phrase in this composition, and also the importance of the motif "npnn" in the $r\bar{a}ga$ [35]. Fig. 1b consists of another recurring characteristic phrase

"ssndmmnns", which is amongst the annotations of characteristic phrases identified by Carnatic musicians for the Saraga dataset [32].

The musicological applications of this process as it stands are limited to some extent by the fact that some of the matches returned are not full motifs, but rather are partial: for example, including part of one motif and then part of another (e.g., 5-second motif 0) or not returning the full motif (e.g., 5-second motif 1).⁶ Segmentation at musically meaningful junctures such as silences or articulation of consonants should improve this. Another problem is that the process currently often returns multiples of the same motif, but with different top matches (e.g., 5-second motif groups 9 and 10). Lastly, it is clear that we need to evaluate the results against comprehensive annotations of all motifs in the performance,⁷ to discover whether the process returns a good number of the total number of occurrences.

One interesting feature is that the process, in addition to returning precise matches of motifs, also identifies those that are similar but not identical. This could be particularly useful in a style such as Carnatic music which often employs a theme and variation structure, where phrases are repeated many times but with various elaborations. We can see an example of this returning of non-identical, but musically closely-related motifs in Fig. 1c where 4 motifs are returned, with two of them including a variation in the period between 0.5-1.5 seconds. Any process used to identify motifs in Carnatic music for musicological purposes would ideally show this degree of flexibility, in order to provide useful and meaningful results. Finally, considering the significance of recurring motifs in the vast majority of musical styles, it seems likely that this process would be musically relevant beyond the specific case of Carnatic music.

6 Further Work

Close scrutiny of the results offers potential lines of improvements; variable length motif detection could help capture full motifs rather than partial motifs, so too could more tradition-specific exclusion rules such as consonant onset detection, which should aid in further constraining the search to whole motifs due to the fact that the style is melismatic, with several *svaras* often sung to one syllable. An essential next step for the continuation of this work is the development of a more empirical evaluation framework of comprehensive ground truth motifs created in collaboration with expert performers of the tradition. We also recognize that to facilitate inter-recording discovery, a dynamic time warping distance measure or tempo normalisation might be necessary.

7 Conclusion

We hope to have demonstrated the effectiveness of predominant pitch extraction and matrix profile/self-similarity for the task of repeated motif identification and annotation in audio. We highlight its potential for these tasks in Carnatic music, a tradition where

⁶ Please refer to the Github repository for results not plotted here.

⁷ Although some motifs are annotated in the Saraga dataset, these annotations are not complete. Such annotating is extremely time consuming and must be done by practitioners of the style.

transcriptions into symbolic representation can show variance, and so where working directly with time series pitch data from audio is a more promising approach to motif identification. Alongside this document we provide the code and full results for the application to this tradition as well as to example audio from other musical styles.

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