# A Comparative Phylogenetic-Tree Analysis of African *Timelines* and North Indian *Talas*

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# Abstract

North Indian *talas* (rhythmic *timelines* or *ostinatos*) are compared to Afro-American and African *timelines*, using several measures of rhythm dissimilarity with the goal of determining which measures are the best for use in phylogenetic algorithms. Such algorithms can be used for music information retrieval applications, culture-based musical rhythm classification, and determining a phylogeny of world rhythms. The results show that the dissimilarity measures proposed by Irfan et al. do not perform as well as previously suggested. However, this work also shows that their *angle-distance* measure produces equivalent results to the chronotonic-distance, which correlates well with human perception of rhythm dissimilarity. Thus this study adds validity to the angle-distance measure.

### 1 Introduction

This paper is concerned with a comparative analysis of rhythmic features in North Indian and Sub-Saharan African music. Time is probably the most important and fundamental feature of music. Indeed, according to H. A. Clarke, "the first and the fundamental law of music is rhythm" [3]. Yet, musicology has tended to overlook the study of rhythm, compared to some of music's other features [4]. Work has been done comparing Indian with Western music [7, 9], and even rhythm in particular [5], but comparisons of Indian rhythm with African rhythm are almost nonexistent. A notable exception is the work of Irfan et al. [16] which proposes three different measures for comparing musical rhythms. Using their measures together with phylogenetic-tree analysis, they compared seven North Indian talas (rhythmic timelines or ostinatos) with six Afro-American and African timelines. They concluded that these two families of rhythms from very different geographical areas and cultures, could be well separated (clustered) with these computational tools. The measures they used are new to the computational music literature, and the size of their data set is small (11 rhythms in total). These authors did not explore measures of rhythm dissimilarity that are favoured by the computational music community, or measures that music psychologists have shown to be correlated with human judgements of rhythm dissimilarity. Neither did they compare their new measures to the latter. Furthermore, their measures compare rhythms with unequal numbers of sounded pulses in a rather ad-hoc manner that appears to depend heavily on the difference of the cardinalities of the sounded pulses in each rhythm. Indeed, in the data set they used in their experiments, the Indian talas may be perfectly separated from the African timelines by merely counting the number of sounded pulses in each rhythm: the African timelines all have five sounded pulses, whereas the North Indian talas all (but one) have three sounded pulses, and the exceptional one has four. In this paper we report on several experiments to address these deficiencies. We compare the measures of Irfan et al. [16] with the well-known and favoured *edit-distance* [17, 19, 20], as well as the psychologically tested and validated chronotonic-distance [24]. Furthermore, we use much larger groups of rhythms from both cultures (38 rhythms in total).

### 2 Rhythm Dissimilarity Measures

In this work, we use symbolic input. Therefore, it is sufficient for us to define a rhythm as a cyclic binary sequence of *n* pulses. The pulses are either sounded (called *onsets*) or silent.

Geometric representation. A rhythm with n pulses and k onsets may be represented by n points evenly spaced on a circular lattice as in Figure 1(a). The k onsets may also be connected to form a convex polygon.



Figure 1: The clave son rhythm.

**Angle-distance, length-distance, and ratio-distance**. With this geometric representation of rhythms we now describe the measures used by Irfan et al. [16]. They present three distance measures, referred to here as the *angle-distance*, *length-distance*, and *ratio-distance*. The angle-distance and the length-distance are described in the following, and the ratio-distance is defined as the former divided by the latter.

The angle-distance is computed in four steps. Let *A* and *B* be polygon representations of rhythms. Compute the set of angles  $A(\theta) = \{A(\theta_1), A(\theta_2), \dots, A(\theta_\ell)\}$  and  $B(\theta) = \{B(\theta_1), B(\theta_2), \dots, B(\theta_m)\}$  for each polygon, where *A* and *B* have  $\ell$  and *m* angles and edges, respectively. Each  $\theta_i$  is the angle found by computing its value from the turning function [1, 2, 16]. Consider Figure 1(b) to illustrate the turning function. We see that each  $\theta_i$  will be the amount by which each ray in the figure must be turned clockwise about its starting vertex such that the ray meets edge *i*. Each ray is constructed at an angle to extend the previous edge in the polygon. Once each angle is found we compute the distance  $D_{ANGLE(A,B)}$  between *A* and *B* (see Equation 1) using the starting point of each edge of *B* as a reference point. This means that *B* is rotated for each edge by an amount corresponding to the arc-length (duration) of the edge, and the computation is performed *m* times. Finally, we take the minimum of the *m* computations to be the angle-distance between polygons *A* and *B* [16].

$$D_{ANGLE(A,B)} = \begin{cases} \sum_{p=1}^{\ell} |A(\theta_p) - B(\theta_p)| & \text{if } \ell = m \\ \sum_{p=1}^{\ell} |A(\theta_p) - B(\theta_p)| + \sum_{q=\ell+1}^{m} B(\theta_q) & \text{if } \ell < m \\ \sum_{p=1}^{m} |A(\theta_p) - B(\theta_p)| + \sum_{q=m+1}^{\ell} A(\theta_q) & \text{if } \ell > m \end{cases}$$
(1)

The length-distance is computed using the same four steps as in the case of the the angle-distance, except that the computation of angles is replaced by measurement of the lengths of the edges of the polygon. As

seen in Figure 1(a), the length of an edge corresponds to the distance of the line segment between adjacent onsets. We follow Irfan et al. in our implementation; see [16] for details.

**Edit-distance**. Rhythms can be notated in many different ways [23, 24]. The most common is western music notation, but other forms include box notation, binary strings, and interval strings. In order to measure the distance between two binary strings, we may transform one string into the other keeping track of the number of edits used in doing so. This is the well-known *edit-distance* (or Levenshtein-distance) which assumes one string is a corrupted version of the other, which contains errors in the form of deletions, insertions, and substitutions [17]. The edit-distance counts each such "error" as an operation. For example, take the clave son to be 1001001000101000 in binary notation, and the shiko to be 1000101000101000. Moreover, index each rhythm starting from zero. We see that two substitutions are required to transform the clave son into the shiko. In the clave son, if we substitute the 1 at pulse (bit) 3 with a 0 and substitute the 0 at pulse (bit) 4 with a 1, then we arrive at the shiko for an edit-distance of 2. Alternately, we could transform the son to the shiko with one insertion and one deletion, namely, insert a 0 after the 1 at pulse 0, and delete a 0 after the 1 originally at pulse 3. Several variants of the edit-distance have been used extensively in the computational music field [19, 20]. The edit-distance used here is defined as the minimum number of operations (insertions, deletions, and substitutions) needed to transform one rhythm to another.

**Chronotonic-distance**. Consider the clave son rhythm in box notation,  $[x \dots x \dots x \dots x \dots x]$ . To increase visualization, Kjell Gustafson proposed a representation to display a rhythm by using time along both the *x*- and *y*-axes [12]. Gustafson refers to this representation as Temporal Elements Displayed As Squares, or TEDAS for short [8, 23]. Figure 2 depicts the TEDAS representation for the clave son and shiko rhythms with the clave son overlayed on the shiko. Each square has its dimensions corresponding to the interval between the onsets. The union of the squares forms a monotonic function of time [8].

We want to use the TEDAS representation to measure distance between two rhythms. Viewing each representation as a piece-wise linear function, reveals many possible distance functions. Following work by Toussaint [24], we shall use the Kolmogorov variational distance [22] to compute the chronotonic-distance between two rhythms with TEDAS representation functions  $f_1(x)$  and  $f_2(x)$  [8, 23, 24]. This is given by  $K = \int |f_1(x) - f_2(x)| dx$ . The chronotonic-distance measure was rediscovered by Hofmann-Engl [14] who established with psychological experiments that it correlates well with human perceptual judgements. It was also used as a measure of melodic similarity for the case where a melody is represented as an orthogonal polygonal function of time, as is common in *piano-roll* notation [1, 18].



Figure 2: Chronotonic-distance between the clave son and shiko rhythms.

As a final remark, it should be noted here that the edit- and chronotonic- distances are computed with the given rhythms in a fixed position in time, unlike the measures used by Irfan et al. [16], which are minimized over all onset starting points (rotations).

### **3** Experimental Results

The distance measures described in the preceding were implemented in MATLAB [21]. We used a previous implementation of the edit-distance [11, 13], and developed code for the angle-distance, length-distance, ratio-distance, and chronotonic-distance. Regarding the angle-distance, length-distance, and ratio-distance, when using the geometric representation to calculate the lengths of the sides of the rhythm polygon, the circle's radius was fixed at 1. For the chronotonic-distance, the timespan of each rhythm was scaled to the range 0 to 1 (inclusive), so as to normalize for rhythms with different numbers of pulses.

**Rhythm data**. Each distance measure was used to calculate a phylogenetic-tree for each of the two rhythm data sets by calculating distances between all pairs of rhythms in each data set. The first data set consisted of the rhythms studied by Irfan et al. [16] reproduced in Table 1 marked by †. The second data set consisted of the rhythms studied by Irfan et al. [16], all the *talas* (clapping patterns) obtained from the detailed and scholarly book of Martin Clayton [6], and an exhaustive set of African and Afro-American *timelines* collected from various papers; these are shown in Table 1. The 26 African *timelines* selected for use in this study correspond to the most well known and documented *timelines* in the literature that have at most five onsets.

Afro-American and African timelines		п	k	North-Indian talas		п	k
Akan	xxx.x	12	4	AdaCautal	x.xxx	14	4
Ashanti	xx.xx	12	4	AditalTintal <sup>†</sup>	xxx	16	3
BembeSubOne	x.xx	12	3	Brahmatal	x.xx.xxx.xxxx.	14	10
BembeSubThree	xxx.x.	12	4	CautalEktal <sup>†</sup>	xxx.x.	12	4
BembeSubTwo	x.xx.x.	12	4	Dhamartal <sup>†</sup>	xxx	14	3
BossaNova <sup>†</sup>	xxxxx	16	5	Jhaptal <sup>†</sup>	x.xx	10	3
CentralCuba	x.x.xxx	12	5	JhumratalDeepchandital <sup>†</sup>	xxx	14	3
Columbia	x.xx.x.x.	12	5	Mattatal	x.xx.xxx.	9	6
Domba	x.xxxx	16	5	PancamSavarital	xxx	15	3
FourBeat	xxxx	12	4	Rupaktal	xx.x.	7	3
FumeFume	x.x.xx	12	5	Savarital	xx	11	2
Ga	x.x.x.xx.	12	5	Sultal	xx.x	10	3
Gahu <sup>†</sup>	xxxxx.	12	5				
GuajiraClap	xxx.x	12	5				
Kpatsa	xxxx	16	5				
Kromanti	x.xxx.x	16	5				
NandomBawaa	xxx	16	3				
Rumba <sup>†</sup>	xxxxx.	16	5				
Shiko <sup>†</sup>	xx.xx.x	16	5				
Son <sup>†</sup>	xxxx.x.	16	5				
Soukous <sup>†</sup>	xxxxx	16	5				
ThreeBeat	xxx	12	3				
Timini	x.xx.xx	16	5				
TresilloOne	xxx	16	3				
TresilloTwo	xxx	16	3				
Tuareg	xx.x.xx	16	5				

Table 1: Thirty-eight Afro-American and African timelines and North-Indian talas.

**Results**. Several techniques exist for generating phylogenetic trees from distance matrices obtained from data. The method we used computes a plane graph embedding with the property that the distance in the drawing between any two nodes reflects (as closely as possible) the true distance between the corresponding two rhythms in the distance matrix.

For every pair of rhythms in both data sets, all the distance measures were computed, yielding distance matrices. Then phylogenetic trees using the BioNJ algorithm [10] in the program SplitsTree [15] were computed for all the distance matrices. Of the three distance measures proposed by Irfan et al. [16], the

angle-distance yielded the best performance. Therefore, here we compare only this measure with the editand chronotonic- distances. The resulting phylogenetic trees are pictured in Figures 3, 4, and 5.



Figure 3: Phylogenetic trees.

# 4 Discussion and Conclusion

Consider first the phylogenetic trees for the 11-rhythm data set depicted in Figure 3, where the dashed lines indicate the best separation of the two families of rhythms. The African rhythms are identified with black disks, whereas the Indian *talas* are shown with unfilled squares. The angle-distance and chronotonic-distance both separate this data perfectly well at first glance. This result appears to add validity to the angle-distance as a measure of dissimilarity that correlates with human perception. We also tested the edit-distance, length-distance, and ratio-distance. However, they did not perform as well as the two shown, thus we leave out their phylogenetic trees due to space limitations.

Turning to the 38-rhythm data set, we also compared the angle-distance with the chronotonic-distance. The phylogenetic tree using the angle-distance is shown in Figure 4. The measure yields eight misclassifications: *ada-cautal, brahmatal, mattatal*, and *cautal-ektal* are lumped in with the African rhythms, and four African rhythms are present in the Indian cluster, namely, *tresillo-two, three-beat, bembe-sub-one*, and *nandom-bawaa*. The phylogenetic tree using the chronotonic-distance shown in Figure 5, also yields eight misclassifications: *ada-cautal, brahmatal*, and *mattatal* are lumped in with African rhythms, and the same four African rhythms are present in the Indian cluster, with the addition of *tresillo-one*. This result shows that the angle-distance, which had the best performance in our experimentation, does not perform as well as suggested by Irfan et al. [16] when more rhythms are introduced. Moreover, the chronotonic-distance and the angle-distance measures yield almost identical trees.





Figure 4: Phylogenetic tree for the angle-distance.

Another observation apparent from the phylogenetic trees is a general trend of an increasing number of onsets in the rhythms as one travels upwards along the tree. In Figures 4 and 5 the boxes (in dotted-lines) show the clustering of rhythms with a similar number of onsets in the trees. Each box is labeled with the number of onsets (k) that its rhythms contain. If a rhythm is not inside a box, then the label of the rhythm has a suffix that indicates the number of onsets it contains (e.g. *savarital-2*). Also, for the chronotonic-distance in Figure 5, note that *mattatal-6* is present in the box for k = 5 onsets since there is no easy way to separate this rhythm from the 5 onset cluster. However, from this separation, we can see that the number of onsets is an important aspect of each distance measure. Moreover, note that the angle-distance depicts a more distinct clustering with respect to the number of onsets. The reason for this is perhaps due to the distance function defined by Irfan et al. [16]. Refering to Equation 1, one can see that if the number of onsets in one rhythm is greater than the number of onsets a large distance between rhythms which have a large difference in the number of onsets, e.g., in Figure 4, *brahmattal* with 10 onsets is very far from *savarital* with 2 (c.f., their distance in the tree for the chronotonic-distance).

This observation can also be seen in the results using 11 rhythms, in Figure 3. The separation is clear: the rhythms which have 3 onsets are at the bottom of the tree, *cautal-ektal* with 4 onsets is right in the middle, and the rhythms with 5 onsets are at the top of the tree. This means that the same separation can be obtained trivially by counting the number of onsets, which suggests that the study by Irfan et. al. [16] did

#### Chronotonic-Distance, BioNJ LF Fitness 98.62



Figure 5: *Phylogenetic tree for the chronotonic-distance*.

not adequately test the performance of the measures they proposed. Furthermore, if we restrict ourselves to the 11 rhythms with, for example, three onsets, the best separation yields 4 errors. This casts doubt on their claim that "the proposed classification system [angle, length, and ratio -distance measures] has been able to grasp the difference between rhythms of North India and other regions [Africa]" [16].

In conclusion, the angle-distance proposed by Irfan et al. [16], although very different in design from the chronotonic-distance, appears to work in a similar way, in spite of the fact that the angle-distance is rotationally invariant, whereas the chronotonic-distance is not. Recall from Figure 5 that the chronotonic distance measure, like the angle-distance measure, also tends to sort the rhythms along the tree by the cardinalities of their onsets, in spite of the fact that the measure is normalized to offset the variable number of pulses. This is probably due to the fact that the area of the TEDAS boxes varies as the square of the inter-onset durations. Thus having fewer onsets inflates the area and the resulting distance, introducing greater dependence on the number of onsets a rhythm contains. This suggests that these two distance measures should be scrutinized in more detail to fully understand the reasons for such behaviour.

The classification results with the 38-rhythm data set indicate that both measures do a fair job at separating North Indian *talas* from African *timelines*. However, note that in both Figures 4 and 5 we can obtain the same results by classifying all rhythms with 4 or more onsets as African. These results suggest that although rhythms with a different number of onsets can appear to be quite similar from a perceptual point of view, the number of onsets is nevertheless an important feature for discrimination. Furthermore, this research suggests that to penetrate deeper into the difficult problem of designing successful measures of rhythm dissimilarity, one should also test the measures on rhythms that have the same number of onsets.

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