El Compás Flamenco: A Phylogenetic Analysis

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Abstract

The *flamenco* music of Andalucia in Southern Spain is characterized by hand clapping patterns in which the underlying meter is manifested through accented claps. A phylogenetic analysis of the five 12/8 time metric timelines used in Flamenco music is presented using two distance measures: the *chronotonic* distance of Gustafson and a new distance measure called the *directed swap distance*. The results support several established musicological tenets. For example, the *fandango* and *soleá* are "centers" of this family of rhythmic patterns. More surprisingly, the chronotonic distance gives the Cuban (Sub-Saharan African) influenced *guajira* a prominent position. Finally, the directed swap distance yields an interesting "ancestral" rhythm.

1   Introduction

Imagine that you are at a concert in Sevilla, after a stunning *flamenco* performance, clapping at a fast uniform pace, much like a heart beat while jogging. Even better, try it out right now, but stop after you reach twelve claps. Then do it again but this time execute the first, third, fifth, eighth, and eleventh claps loudly, and the remaining seven claps softly. Your clapping pattern could then be represented like this: [**1** 2 **3** 4 **5** 6 7 **8** 9 10 **11** 12], where the claps shown in bold face are the ones you clap loudly. It may also be helpful to count aloud the twelve claps in groups as follows: [**1** 2 **1** 2 **1** 2 3 **1** 2 3 **1** 2] and to clap loudly only on the one's. If you repeat this pattern over and over, you will be clapping the rhythm of the *seguiriya* from Andalucia in Southern Spain [13], [21].

The flamenco music of Andalucia uses for the most part a 12/8 time meter that is typically marked by accented claps. To be sure, there also exist flamenco styles that use exclusively binary meters in 2/4 or 4/4 time. These include the *tango* and its variants such as the *tanguillo*, the *rumba*, the *farruca*, the *garrotín*, the *zambra* and the *mariana* [13]. All these binary styles use one and the same meter or clapping pattern given by [. x x x], where "." denotes a soft clap and "x" denotes a loud clap. A popular method for representing flamenco clapping patterns is to use numbers indicating the pulses, with the accented pulses written in bold [8]. Using such a notation the preceeding pattern is expressed as [1 **2 3 4**]. This paper is concerned with the more varied, interesting, and characteristic 12/8 time flamenco metric patterns. We use the term *meter* loosely and refer to it also as rhythm [16].

One of the pioneering, but non-exhaustive, studies of flamenco rhythms is the book by Hipolito Rossy [22] published in 1966. It is well established that the fountain of flamenco music is the *fandango*. In the words of José Manuel Gamboa [13] *"En el fandango está la fuente."* The *fandango*

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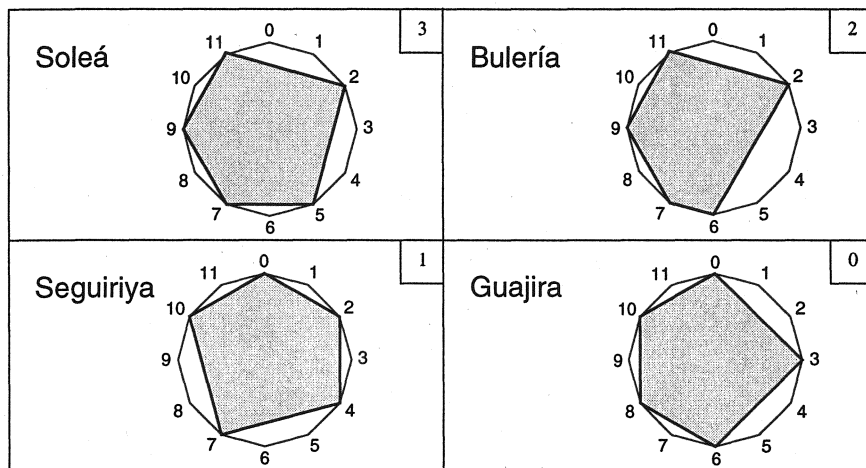[¶]School of Computer Science, McGill University. godfried@cs.mcgill.ca

Figure 1: The four aperiodic 12/8 time flamenco meters.

pattern is given by [x . . x . . x . . x . .]. This rhythm is periodic and repeats the pattern [x . .] four times. There are in addition four aperiodic 12/8 time meters [19], [20], [21]. These are as follows:

$$[. . x . . x . x . x . x] - soleá$$
$$[. . x . . . x x . x . x] - bulería$$
$$[x . x . x . . x . . x .] - seguiriya$$
$$[x . . x . . x . x . x .] - guajira$$

The four patterns are depicted as convex polygons in Figure 1, where the "0" marks the position in time at which the rhythm starts. Note that this may differ from the position at which the rhythm is "launched" for the convenience of dancers. A word is in order concerning the names we have attached to these rhythms. The *soleá* and *bulería* are used in a large variety of flamenco styles. What we refer to as *soleá* is also sometimes called *bulería tradicional*, and what we call *bulería* is sometimes referred to as *bulería moderna*. The *guajira* rhythm is used in fewer styles, but is also most notably used in the *petenera*. These names are in accordance with the classification described by Gamboa [13].

2   Measuring Rhythmic Similarity

To carry out the phylogenetic analysis of the *flamenco* rhythms we first compute the distance (or dissimilarity) between every pair of rhythms. Here two distance measures are used: the *chronotonic* distance and the *directed swap* distance. The chronotonic representation of a rhythm was first proposed in 1987 by Kjell Gustafson, at the Phonetics Laboratory of the University of Oxford for the purpose of displaying speech rhythm [14], [15]. It was later re-discovered by Hofmann-Engl [17] who proposed it for computing a distance measure, and whose psychological experiments demonstrated that this distance agrees with the human perception of rhythmic similarity. The directed swap distance is a generalization of the simpler, more constrained, *swap* distance used in [23] to compare rhythms that are restricted to having the same number of onsets and time spans.
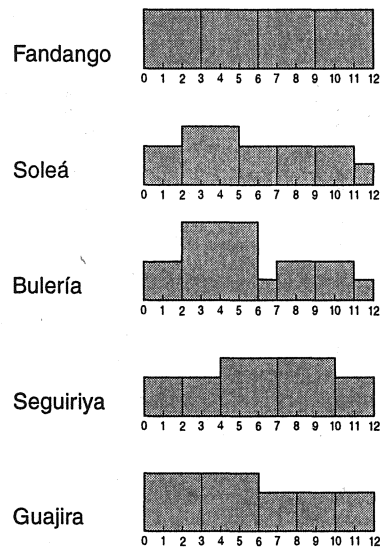
Figure 2: The *chronotonic* representation of the *flamenco* patterns.

A recent comparative study [24] of various distance measures suggests that the swap and chronotonic distance measures are the best for analyzing rhythms.

2.1 The chronotonic distance

Gustafson's idea (first proposed in 1983) is best explained with an example such as the *seguiriya* pattern given by [x . x . x . . x . . x .]. In this representation the relative durations of the intervals are not easily observed. In a *histogram* approach to rhythm visualization the intervals between important events (such as the start, the end, and attack points) are plotted along the y-axis [15], resulting in the *adjacent-interval-spectrum* of the rhythm. In such a representation the relative lengths of the intervals are clearly visible but the temporal information along the x-axis is lost. To obtain a graphical representation that possesses the advantages of both of these methods, Gustafson uses time in both dimensions. The result of this union is illustrated in Figure 2, which shows all five *flamenco* meters in chronotonic notation. Each temporal element between events (interval) is now a box and both the x and y axes represent the length of time of the interval. Gustafson refers to such a display as TEDAS (*Temporal Elements Displayed As Squares*). The unions of the squares depicted in Figure 2 can be viewed as rectilinear monotonic functions of time.

Given the chronotonic representation of two rhythms, there are a variety of ways to measure dissimilarity. In [24] the dissimilarity is measured by the area in between the two functions (curves). We shall use this measure here and refer to it by the name used in [24], *chronotonic* distance. The distance matrix with this distance measure is shown in Figure 3.

2.2 The directed swap distance

Since the *directed swap* distance reduces to the swap distance when the number of onsets is the same, we first describe the simpler swap distance and subsequently its modification. A swap is an interchange of a one and a zero that are adjacent to each other in the binary string. Inter-

Chronotonic Distance Matrix

	Soleá	Bulería	Seguiriya	Guajira	Fandango
Soleá	0	6	8	4	10
Bulería		0	12	8	14
Seguiriya			0	8	6
Guajira				0	6
Fandango					
Σ	28	40	34	26	36

Figure 3: The chronotonic distance matrix of the five rhythms.

changing the position of elements in strings of numbers is a fundamental operation in many sorting algorithms [11]. However, in the sorting literature a swap may interchange non-adjacent elements. When the elements are required to be adjacent, the swap is called a *mini-swap* or *primitive-swap* [2], [3]. Here we use the shorter term *swap* for the interchange of two adjacent elements. The swap distance between two rhythms is the *minimum* number of swaps required to convert one rhythm to the other. For example the rhythm [x . x . x x . x . x . x] can be converted to the rhythm [x . x x . x x . x . x .] by a minimum of four swaps, namely interchanging the third, fifth, sixth, and seventh beats with the corresponding rests preceeding them. The *swap* distance may be viewed as a simplified version of the *fuzzy* Hamming distance [5], [6], that results when only the shift operation is used, and the cost of the shift is equal to its length. The *fuzzy* Hamming distance may be computed using dynamic programming in $O(n^2)$ time.

The swap distance may alternately be viewed as a special case of the more general *earth mover's distance* (also called *transportation distance*) used by Typke et al. [26] to measure melodic similarity. Given two sets of points called supply points and demand points, each assigned a weight of material, the earth movers distance measures the minimum amount of work (weight times distance) required to transport material from the supply points to the demand points. No supply point can supply more weight than it has and no demand point receives more weight than it needs. Typke et al. [26] solve this problem using linear programming, a relatively costly computational method. The swap distance is a one dimensional version of the earth mover's distance with all weights equal to one. Furthermore, in the case where both binary sequences have the same number of "one's" (or onsets), there is a one-to-one correspondence between the indices of the ordered onsets of the sequences. For example, consider again the two sequences X = [x . x . x x . x . x . x] and Y = [x . x x . x x . x . x .], each with seven onsets. The i-th onset of X must travel the necessary distance to reach the position of the i-th onset of Y. For $i = 1$ this distance is zero. For $i = 3$ the distance is one.

The swap distance may of course be computed by actually performing the swaps, but this is inefficient. If X has one's in the first $n/2$ positions and zero's elsewhere, and if Y has one's in the last $n/2$ positions and zero's elsewhere, then at least a quadratic number of swaps would be required. On the other hand, if we compare the distances of the onsets to the origin instead, a much more efficient algorithm results. First scan the binary sequence and store a vector of the x-coordinates at which the k onsets occur. For example, X and Y above yield the vectors $U = (u_1, u_2, ..., u_7) = (1, 3, 5, 6, 8, 10, 12)$ and $V = (v_1, v_2, ..., v_7) = (1, 3, 4, 6, 7, 9, 11)$, respectively. The difference between u_i and v_i is the

Directed-Swap Distance Matrix

	Soleá	Bulería	Seguiriya	Guajira	Fandango
Soleá	0	1	11	7	7
Bulería		0	12	8	8
Seguiriya			0	4	4
Guajira				0	2
Fandango					
Σ	25	29	31	21	21

Figure 4: The directed-swap distance matrix of the five rhythms.

number of swaps that must be performed to bring the two onsets into alignment. Therefore, in general, the swap distance between two onset-coordinate vectors U and V with k onsets is given by:

$$d_{SWAP}(U,V) = \sum_{i=1}^{k} |u_i - v_i| \tag{1}$$

Computing U and V from X and Y is done trivially in $O(n)$ time with a simple scan. Therefore $O(n)$ time suffices to compute $d_{SWAP}(U,V)$, resulting in a large gain over using linear or dynamic programming. The reader may wonder what the fuss is about in reducing the complexity from $O(n^2)$ to $O(n)$ when for the case of the flamenco rhythms analysed here $n = 12$. The reason the complexity difference is important is that these distance measures are also intended to be used in music information retrieval applications involving entire pieces of music where n is very large.

The directed-swap distance is a generalization of the swap distance to handle the comparison of rhythms that do not have the same number of onsets. In our study here one flamenco rhythm, the *fandango*, has four onsets instead of five. Accordingly let P and Q be two binary sequences of length n that represent two rhythms. Assume without loss of generality that P has more "1's" than Q. The directed-swap distance is the minimum number of swaps needed to convert P to Q with the following constraints. We will refer to a position that contains a "1" as occupied.
1. Each "1" in P must move to some occupied position of Q.
2. All occupied positions of Q must receive at least one "1" from P.
3. No "1" may travel across the boundary between the "zero-th" and n-th positions in the cycle.

This distance measure may be computed in $O(n)$ time. The distance matrix with the directed swap distance is shown in Figure 4.

3 Phylogenetic Analysis

Several techniques exist for generating phylogenetic trees from distance matrices [18]. Some of these methods have the desirable property that they produce graphs that are not trees, when the underlying proximity structure is inherently not tree-like. One notable example is *SplitsTree* [12], [18]. Like the more traditional phylogenetic trees, *SplitsTree* 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. However, if the

tree structure does not match the data perfectly then new nodes in the graph may be introduced, as for example in Figure 5, with the goal of obtaining a better fit. Such nodes may suggest implied "ancestral" rhythms from which their "offspring" may sometimes be derived. In addition, edges may be split to form parallelograms, (or more general zonotopes) which are also visible in Figures 5 and 6. The relative sizes of these parallelograms are proportional to an *isolation index* that indicates how significant the clustering relationships inherent in the distance matrix are. *SplitsTree* also computes the *splitability index*, a measure of the goodness-of-fit of the entire splits graph. This *fit* is obtained by dividing the sum of all the approximate distances in the splits graph by the sum of all the original distances in the distance matrix [12], [18]. This index is shown in the upper left-hand corners of the SplitsTree figures.

Some observations are evident from the distance matrices themselves. In particular, let us examine the lowest rows in Figures 3 and 4. These numbers are the sums of the distances from a specified rhythm to all the other rhythms. A relatively small number indicates the rhythm is very similar to all the others, whereas a relatively large number means it is distinct.

For example, the rhythm most similar to the others is the *guajira* according to the chronotonic distance, (with *soleá* a close second) but the *guajira* and *fandango* are tied for this position when the directed-swap distance is used.

The results of computing the SplitsTrees with the preceeding distance matrices are shown in Figures 5 and 6. Note that both distance measures yield an impressive fit of 100%.

Consider first the chronotonic distance SplitsTree of Figure 5. It suggests a clustering into three clusters. One cluster consists of the *fandango* and *seguiriya*. The second cluster consists of the *soleá* and *bulería* rhythms, and the *guajira* is a solitary third cluster. The *soleá* and *bulería* rhythms are the only ones that have anacrusis. The *bulería* is the most distinct from all the others, with a sum-distance of 40. It is interesting to note that of all the five rhythms, the *bulería* is the only one that has the *rhythmic-oddity* property [1], [9], [10]. A rhythm has the rhythmic oddity property if it does not contain two onsets that partition the rhythm drawn on a circle into two half-circles. This property is a good measure of preference in African rhythm [25]. The more obvious difference between the *bulería* and all the other rhythms is that it is the only rhythm that contains intervals of lengths 1, 2, 3, and 4. The other rhythms have intervals of lengths 2 and 3 only.

The *guajira*, often described as having significant Cuban influence [4], [20], is the most similar to all the other rhythms with a sum-distance of 26. It is also the only 5-onset rhythm with an *off-beatness* value of zero. The off-beatness (or syncopation) value of a rhythm is defined as the number of onsets it possesses in positions 1, 5, 7, and 11 [25]. The off-beatness is an even better measure of preference in Sub-Saharan West African rhythm than the rhythmic-oddity property [25]. In Figure 1 the off-beatness value of each rhythm is indicated in the upper right-hand corner of each frame. The second most similar rhythm to all others is the *soleá* with a sum-distance of 28 (almost tied with *guajira*). These results support the tenet that the *soleá* is one of the most paradigmatic and genuine styles of flamenco. In the words of Mercader [20], "*la soleá es uno de los palos más jondos del flamenco.*" It is also worth noting that the *soleá* is very special from the geometric (group-theoretic) point of view since it is the *flamenco* rhythm with the highest value of off-beatness equal to 3.

The SplitsTree of Figure 6 suggests a very similar clustering as that obtained with the chronotonic distance, except that here the *fandango* and *guajira* form a tight cluster of two and the *seguiriya* is away by itself. The *fandango* and *guajira* each have a sum-distance of 21. This result lends support to the musicological tenet that the *fandango* is the fountain from which spring all flamenco rhythms. Indeed, in the genealogical trees that have been constructed for flamenco music the *fandango* is located low and at the center of the main "trunk" of the tree [7]. One should remember that these genealogical trees were constructed with the voice and instrumentation totality
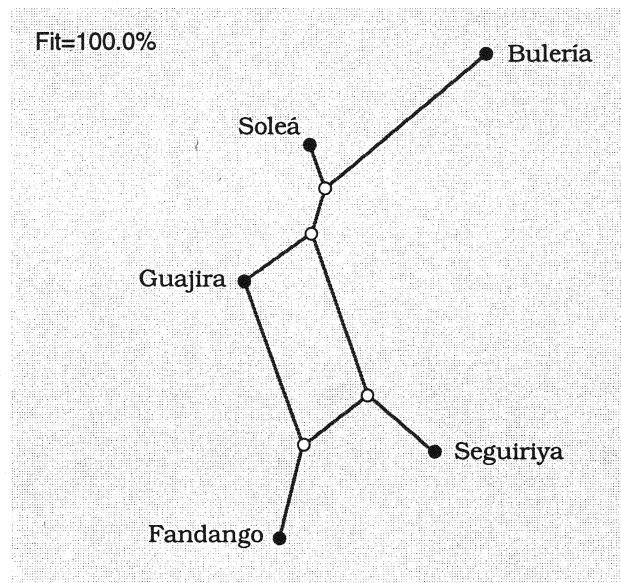
Figure 5: The SplitsTree with the chronotonic distance.

in mind, and not the rhythm in isolation. Finally, it is worth pointing out that the *fandango* and *guajira* are the only rhythms with an off-beatness (syncopation) value of zero.

4 Reconstructing Ancestral Rhythms

At present we do not have algorithms available to automatically reconstruct the "ancestral" rhythms corresponding to the nodes created by the SplitsTree algorithm with our two distance measures. This problem is under investigation. However, with the directed-swap distance this can sometimes be done by hand as follows. One rhythm that we were interested in reconstructing is the ancestral rhythm closest to the "center" of the SplitsGraph. In this case it is the white node incident to the *fandango, guajira,* and *soleá* seen in Figure 6. The output of the SplitsTree program provides the lengths of all the edges in the graph. From these lengths the following graph-distances between the unknown ancestral rhythm and all other rhythms may be inferred:

$$d(ancestor,\ guajira) = 1$$
$$d(ancestor,\ fandango) = 1$$
$$d(ancestor,\ seguiriya) = 5$$
$$d(ancestor,\ soleá) = 6$$
$$d(ancestor,\ bulería) = 7$$

From the distances evident in the graph it is reasonable to suppose that the ancestral rhythm would be quite similar to both the *guajira* and the *fandango*, and would therefore consist of either four or five onsets. Trial and error soon leads to the five-onset rhythm given by [x . . x . . x . . x x .] illustrated as a polygon in Figure 7. The reader may verify that this rhythm satisfies the five distance constraints listed in the preceeding. This five-onset rhythm is the composition of the *fandango* and one additional onset at position 10.

A search of the literature to determine if this "ancestral" rhythm makes an appearence anywhere yielded the following two observations worth noting. Keyser [8] mentions in his book that this pattern is used often in flamenco as a *closure* or *resolution* phrase. Furthermore, it is almost
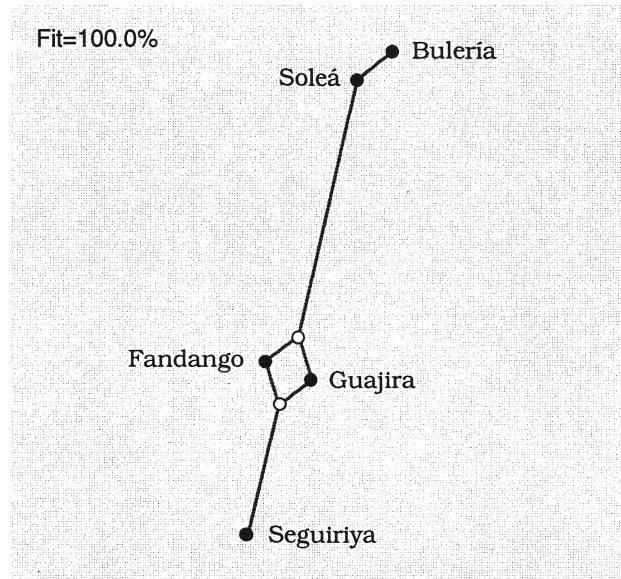
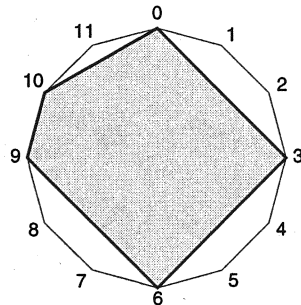Figure 6: The SplitsTree with the directed swap distance.

Figure 7: The "ancestral" rhythm reconstructed with the directed-swap distance.

identical, and has the same feel, as a rhythm Mercader [20] calls the *fandango de Huelva*. This rhythm is the composition of the "ancestral" rhythm of Figure 7 with an additional onset half way betwen the onsets marked 9 and 10. In other words, the *fandango de Huelva* is described in a span of 24 units as: [x . . . . . x . . . . . x . . . . . x x x . . .]. Removing the middle onset from the triplet in the *fandango de Huelva* yields the "ancestral" rhythm.

5   Concluding Remarks

According to Nan Mercader [20], among others [4], the *guajira* was strongly influenced by Cuban music (the rhythm *punto* Cubano) and has the flavor of colonial Spain in the nineteenth century. The rhythm travelled from Cuba to Spain via the Canary Islands where it mixed with some indigenous elements. The name comes from the word *guajiro* for a creole campesino. The fact that the *guajira* appears to be near the "center" of the rhythmic patterns suggests a possible ethnomusicology research project to determine the exact nature of this influence. Of the five *flamenco* rhythms

fandango, guajira, and *soleá* play central roles in the phylogenetic analysis. On the other hand, the directed swap distance places the generated "ancestral" rhythm depicted in Figure 7 even closer to the center of the splits graph, with a sum-distance of 20 when the directed swap distance is used.

Since the *guajira* rhythm has such a marked external influence, it is natural to ask how diferent the phylogenetic analysis of the more authentic flamenco rhythms turns out when the *guajira* is left out of the analysis. When this is done the chronotonic distance identifies the *soleá* as the central rhythm with a sum-distance of 24 to the other three rhythms. With the directed swap distance the *soleá* and *fandango* are tied for center with a sum-distance of 19 for each.

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