

Choreogenetics: the Generation of Choreographic Variants Through Genetic Mutations and Selection

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ABSTRACT

In this paper, a genetic algorithm is introduced to generate variants of a choreographic sequence, which are then selected using different criteria. The mutation phase of the algorithm applies six types of mutations on single sequences, as well as four types of mutations on multiple sequences. Six different selection criteria are also distinguishable to assess the fitness of the sequences. An application of *Choreogenetics* is presented to illustrate the performance of the method for the generation of an aesthetic choreography.

Categories and Subject Descriptors

J.5 [Arts and Humanities]: Performing arts (dance)

General Terms

Algorithms, Experimentation.

Keywords

Aesthetics, choreography, dance, information theory, mutation models, sequence evolution, simulation.

1. INTRODUCTION

On several occasions, contemporary arts have been influenced by the field of genetics [7, 12], and probabilistic models have been used since the beginning of time to generate artistic pieces [17]. Indeed, modern choreographers and composers, such as Merce Cunningham and John Cage, have often applied permutations and chance operations in their creative process. However, in spite of the relationship between DNA and the combinatorial methods that Cunningham employed to produce random dances [16], genetic algorithms have never been used by choreographers to create variations in movement sequences. In this paper, I present a computer algorithm that generates choreographic variants through genetic mutations and selection. The *Choreogenetics* algorithm is then applied to simulate the evolution of a sequence of dance movements.

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2. THE ALGORITHM

The *Choreogenetics* algorithm takes as input a choreographic sequence representing independent movements, and transforms it into a new sequence through different types of genetic mutations (the mutation phase). The new sequence is then compared to the previous sequence using different criteria, and the sequence with the best fitness value is selected (the selection phase). The process is repeated for a fixed number of generations, or until a choreographic sequence meeting a given aesthetic criterion is obtained.

2.1 The Mutation Phase

The input choreographic sequence is associated to an alphabet of letters representing independent movements. This sequence could be generated at random by sampling n movements with replacement from a fixed alphabet of m letters, or be provided by the choreographer. Based on parameters set by the user, several types of mutations, with different probabilities, are distinguishable to create movement sequence variations from one sequence to the next. These types of operations are similar to those currently applied by choreographers to modify movement sequences, or combine sequences together.

2.1.1 Mutations on single sequences

The algorithm distinguishes six types of mutations at each generation to make modifications from a single *mother* sequence to a single *daughter* sequence: substitution, insertion/deletion, inversion, translocation, repetition and conversion.

Substitutions are obtained by replacing at random one or more movements from the mother sequence in the daughter sequence, whereas insertions and deletions are obtained by adding or eliminating movements at random to create a daughter sequence with less or more movements than the mother sequence. The probability of replacing a given movement by another is provided by a substitution matrix, which can take the form of any substitution matrix model used in molecular biology [6, 8]. The new movements (substituted or inserted) are sampled from the original alphabet with equal probabilities, or with respect to the frequency distribution of movements in the mother sequence. The relative probabilities of substitutions, insertions and deletions with respect to the other types of mutations are set respectively by the parameter p_s , p_i and p_d .

The other types of mutations on single sequences are generated by first selecting a segment of random length t (with $t < n$) from the mother sequence. Inversions, translocations and repetitions are then obtained by either inverting that segment, moving the

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segment to a different position, or repeating the segment a given number of times in the daughter sequence. The breaking points of inversions, positions of the regions to be deleted from the mother sequence and inserted in the daughter sequence and number of repetitions are set at random, or fixed by the user (e.g. only allowing tandem repeats). The relative probabilities of inversions, translocations and repetitions with respect to the other types of mutations are set respectively by the parameters p_v , p_t and p_r .

Finally, conversions are obtained by selecting one movement, or a segment of random length t (with $t < n$) from the mother sequence, and replacing it by new movement(s) in the daughter sequence. This type of mutation differs from substitution in that movements that were not in the original alphabet are introduced in the daughter sequence. The relative probability of a conversion is set by the parameter p_c .

2.1.2 Mutations on multiple sequences

To deal with more than a single movement sequence at a time (more than one dancer), four other types of operations are also used in the mutation phase of the algorithm to create additional daughter sequences and generate interactions among dancers: duplication, extinction, horizontal transfer, and hybridization

To create a single (or multiple) duplication event(s), the entire mother sequence is duplicated (or replicated), thus generating two (or more) identical daughter sequences to be performed by different dancers. On the other hand, an extinction event is obtained by eliminating one of the mother sequences at random to reduce the number of dancers. The relative probabilities of duplications and extinctions with respect to the other types of mutations are set by the parameters p_l and p_e respectively

When multiple sequences are available, other types of mutations can be used to combine mother sequences with one another. Horizontal transfers are obtained by sampling movements from a single mother sequence to insert them in a new daughter sequence, whereas hybridization events are generated by sampling movements from a pair of mother sequences to create a hybrid daughter sequence. The positions of the regions sampled from the mother sequence(s) and copied into the daughter sequence are selected at random. The relative probabilities of horizontal transfers and hybridizations are set respectively by the parameters p_h and p_z .

2.2 The Selection Phase

Once a choreographic mutant (the daughter sequence) is generated, this new sequence is compared to the previous sequence (the mother sequence) to assess which one has the best fitness. If the daughter is the fittest of the two, the mother sequence is deleted. On the contrary, if the mother is the fittest, the daughter sequence is deleted and a new mutant is generated at the next generation. Thus, the algorithm only proceeds by comparing pairs of mother-daughter sequences, keeping in turn the one that maximizes the value of the selection criterion. When multiple mother sequences are available, each one is considered independently and compared with its corresponding daughter sequence.

2.2.1 Selection criteria

The algorithm implements five different selection criteria that are used to determine which of the mother or the daughter sequence has the best fitness value: the neutral model, user-defined and audience-mediated selection, information theory, aesthetics and coevolution.

Under the neutral (or pan-neutral) model of evolution, the mutations are not selected and all daughter sequences have equal fitness. This implies that the mutation will accumulate constantly with generations and that daughter sequences will always replace the mother sequences, without selection. In visual arts and music, the majority of genetic algorithms rely instead on the user to select the best solution among possible outcomes [4, 11, 14]. This particular type of interactive genetic algorithm (IGA) could also be mediated by a critic or mentor who assesses at each generation whether the mother or the daughter sequence is more pleasing. The result is thus influenced by subjective taste or personal aesthetics. However, this problem is avoided by replacing a single critic by a group of critics, namely the audience [1]. Obviously, this approach can be difficult to implement for the selection of choreographic variants in real time, but an audience-mediated IGA may be used as a training algorithm to modify the probabilities of the mutation model.

The information, entropy and complexity of a sequence of movements can be computed using the same methods as those employed for DNA sequences [15]. The mother and daughter sequences can then be compared with respect to these measures to select the fittest of the two. It is generally accepted that more complex and informative structures are more pleasing to the eye, and this rule applies to dance composition [5]. In his books on the mathematics of aesthetics [2], Birkhoff formally introduced a quantitative measure of beauty (B), defined as the O/C ratio, where O and C respectively represent order and complexity. Whereas complexity measures information content, order is a function of symmetry, repetition, or balance [9]. More recently, a neurological basis of aesthetics have also been proposed [13], and these criteria (e.g. peak shift, contrast) could also be used in the algorithm, assuming that we can quantify them. Using such measures, the daughter sequence will be selected only if it bears more information or is aesthetically more pleasing than its mother.

With a coevolution criterion, a daughter sequence can be selected over its mother sequence with respect to its similarity to a third sequence. This type of selection is used to match sequences and create (partial) unison among dancers interpreting different movements. The basis for choosing the daughter sequence over its mother is the score of the alignment of the competing sequences with respect to a target sequence, which could be provided by the user, or selected among other mother sequences.

2.2.2 Stopping Rules

The *Choreogenetics* algorithm can run forever unless some rules are defined to stop the generative process. One simple way of doing so is to fix a priori the number of generations. Another option is to let the user decide when the sequence meets certain aesthetic criteria. Finally, a quantitative optimum (maximum fitness) may be set to stop the program when this value is reached. Obviously, different solutions will be obtained using different stopping rules and optimality criteria.

3. APPLICATION

The input sequence of five movements represented in Figure 1a was used to create choreographic variants with the *Choreogenetics* algorithm. This original sequence was generated at random from an alphabet of four letters {A, T, C, G}. At the first generation, a repetition of the movements CG was generated (Figure 1b). Then, AT was translocated from the beginning of the sequence to the end of the sequence (Figure 1c). Finally, the last A was transformed by conversion to a U, a new movement that was not included in the original alphabet of four letters (Figure 1d). At each step, the daughter sequence was selected over the mother sequence, with a user-defined aesthetic criterion. Interestingly, complexity also increased from one generation to the next.

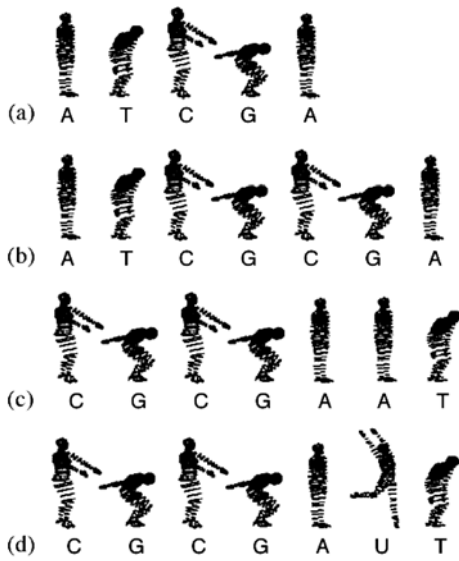


Figure 1: The (a) input sequence and variants of the *Choreogenetics* algorithm, generated by (b) repetition, (c) translocation, and (d) conversion (original movements from [3]). The sequences were selected based on aesthetic criteria.

4. DISCUSSION

The *Choreogenetics* algorithm proceeds by iteratively creating movements sequence variants at each generation, using a defined mutation model. Depending on the relative probabilities of the different types of mutations, multiple solutions are equally likely. However, the selection of variants by objective (or subjective) criteria determines which sequences are to be eliminated or selected. Contrary to most genetic algorithms, the proposed method does not rely on a large population of organisms (sequences) that reproduce sexually to create variation. On the contrary, a simple sequence transmitted asexually from the mother to its daughter is employed, and mutations represent the only source of variation at each generation.

The proposed genetic algorithm could easily be modified to investigate different aspects of the choreographic process. For one, a grammar-based genetic programming system may be defined to encode the rules of a particular type of dance. Also, the use of automated fitness functions would improve the performance of the algorithm, namely by the determination of metrics that correlate to aesthetically pleasing dance sequences.

Finally, the idea of continuity of motion from one movement to the next could be taken into account by using a transition matrix representing the probabilities that each movement is followed by any other movement. Under the current model, every movement is equally likely to occur anywhere in the sequence, but some constraints could be set to avoid certain combinations.

For the time being, this very simple algorithm is appropriate for the generation and selection of movement sequences, because it essentially mimics the creative process of choreographers. As such, it also differs from purely random [10] or chaotic [3] models that have been proposed to create choreographic variants. Indeed, a genetic algorithm not only generates new movement sequences, it also selects among possible outcomes those that maximize the value of the selection criterion. When a choreographer is used for fitness determination, the *Choreogenetics* algorithm is nothing more than a tool for generating new movement sequences. However, when objective aesthetic or information-theoretic criteria are used, the role of the choreographer is entirely assumed by the genetic algorithm and the result is affected only by the parameters of the mutation model. The final sequences may then be assembled to create a full dance, or be used as mother sequences to produce further variants, using different models and/or selection criteria.

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