A Geometric Evolutionary Search for Melody Composition

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ABSTRACT

In this paper, we present a genetic algorithm using geometric crossover to preserve musically important properties. The length of the chromosome is variable when we use a musical note as a gene. A geometric crossover based on the edit distance was used to combine chromosomes of variable length and succeeded in creating a better child by using a model in which melody pattern is learned. The model can evaluate the score of melody in a specified chord. As a result, we could successfully create a melody preserving parent's good patterns.

CCS CONCEPTS

• DETA - Digital Entertainment Technologies and Arts → Biologically-inspired creativity; Artificial creative agents;

KEYWORDS

Genetic algorithm, automatic composing, geometric crossover

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1 INTRODUCTION

The theory of harmony has been studied a lot. Notes that are considered "good" depend on the musical genre and the type of chord being played. A performer improvising music identifies the scale that fits a chord according to the theory of harmony and aligns a note corresponding to the scale in a musical flow. Therefore, if a computer is able to learn chord-based note sequences, it can select "good" notes. We have developed a model that can learn the chord and melody. This can evaluate the fitness of the melody according to the chord. A genetic algorithm (GA) can use fitness quite well, and explore a good fit if used together with a strong crossover operator. Geometric crossover [1] can be used for a chromosome whose length is variable and the sequence of the genes is important. A melody is a combination of notes with pitch and duration, and their sequence is an element that determines the quality of music. Accordingly, geometric crossover can be very fit for GA-based automatic composition, and we selected it as a crossover operator.

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2 RELATED WORK

GA-based automatic composition was first suggested by Honer et al. [2] and biles created a program called "GenJam," which automatically generates jazz solo melodies [3]. Muñoz et al. [4] created a system that composed a quartet chorus using a memetic algorithm. Moragilio et al. [1] demonstrated that geometric crossover could be used well in biological sequences, and Yoon et al. [5] explained homologous crossover for variable-length sequences by using the mathematical unification of geometric crossovers. A melody has a distance between notes in a musical space. This distance is the actual pitch difference, so suitable musical transformation needs to be done. Accordingly we had done a basic research on melody composition using geometric crossover [6].

3 A GENETIC ALGORITHM

3.1 Representation and Fitness

We set the space where a chromosome is expressed not as a score but as a bar. Each note contain both pitch and duration. Each chromosome's length changes depending on constituting notes' duration, as illustrated in Fig. 1.



Figure 1: Representation of a chromosome.

We used "chord score table", which stores the fit of melody in chord, and "sequence score table," which stores score according to note sequence. The chord score table is the same as the previous study [6] and the sequence score table is designed to be calculated and learned according to the criteria in Fig. 2.



User's rating of this score = 5 (max) \downarrow

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
The number of notes		1	1	1	1	1	1	6	6	1	1	1	1	1	1	1	1
Between high and low	1	1	1	1	6	1	1	1	1	1	6	1	1	1			
The number of inflections	1	6	6	1	1	1	1	1	1	1	1	1	1	1	1		
Pitch difference of notes	26	1	26	6	1	11	1	1	1	1	1	1	1	1			
The number of length		16	41	16	6	1	1	1	1	1	1	1	1	1	1	1	1

Figure 2: Learning process of a sequence score table.

"Between high and low" has a pitch difference between the highest and lowest notes in a bar and "Pitch difference between two notes" means the pitch difference between consecutive notes. The firness of the chromosome is defined as the sum of the elements of the chord score table and the sequence score table. GECCO '18 Companion, July 15-19, 2018, Kyoto, Japan

ALGORITHM	1: Fil	ling w	reighted	edit	distance	table
			erginee a	~~~~	GIOUGILOU	

// <i>T</i> : edit distance table, T_n^{sq} : a score of pitch difference(<i>n</i>)
// Notes ¹ , Notes ² : array of notes
$T_{i,0} \leftarrow 2 \cdot i, \ T_{0,j} \leftarrow 2 \cdot j$
for $i \leftarrow 1$ to <i>Notes</i> ¹ <i>.length</i> $- 1$ do
for $j \leftarrow 1$ to Notes ² .length - 1 do
if $Notes_{i-1}^1 = Notes_{i-1}^2$ then
$T_{i,j} \leftarrow T_{i-1,j-1};$
else if Notes $_{i-1}^1$.pitch = Notes $_{i-1}^2$.pitch then
$T_{i,j} \leftarrow T_{i-1,j-1} + (1 - T_0^{sq});$
else
$min \leftarrow minimum(T_{i-1,j-1}, T_{i-1,j}, T_{i,j-1}) +$
$\left(2-T_{\left Notes_{i-1}^{1}\cdot pitch-Notes_{j-1}^{2}\cdot pitch\right }^{sq}\right);$

3.2 Geometric Crossover

Each gene constituting a chromosome have two elements (pitch and duration). This characteristic adds the concept of a sub-match, which expresses that notes are partially identical, so it must also be determined which element is more important. When good music flows well and gets into inappropriate disharmony, even those who do not know much about music find it odd, but duration is not. Therefore it is highly important to preserve a pitch while it is allowed to change duration a little from time to time. We use a weighted edit distance table to find a more optimal gene using the characteristics of notes with pitch and length. Algorithm 1 shows how to fill this weight distance table, and Fig. 3 shows an example.

	ø	60, 2	57, 3	59, 4	82, 4	65, 1	69, 1	67, 1
ø	0.00	2.00	4.00	6.00	8.00	10.00	12.00	14.00
67, 4	2.00	1.91	3.90	5.87	7.87	8.87	9.87	12.39
57, 3	4.00	3.67	1.91	2.91	4.91	6.87	8.87	10.86
59, 1	6.00	5.18	2.91	2.30	4.30	6.30	8.30	10.26
59, 3	8.00	6.69	3.91	3.30	4.30	6.30	8.30	10.26
83, 2	10.00	8.69	5.91	5.30	4.81	6.30	8.30	10.30
66, 3	12.00	10.69	7.87	7.21	6.81	6.31	8.07	9.57

Figure 3: Weighted edit distance table for notes of parents.

In a row-to-column table, a score table's $T_{i,j}$ is the cost of converting the *i*-th note into the *j*-th note. The cost is 0 if the two values are the same, as they do not need to be converted. However, when the two values are different, a pitch difference of 1 and that of 13 cannot be regarded as equal, so the program has to select the optimal note by using the number even though a pitch was not matched. The number that could be used in the edit distance table is a "pitch difference between two notes" in a sequence score table. Accordingly, an analyzed example result can be described as in Fig. 4. The transcript in Fig. 4 is adjusted a little from an expression used in Moraglio et al.'s study [1]. 'M' is a place holder and must be selected. 'R' is replacement, which is indicated when there is a pitch match, and selects one of the two notes using sequence score table. A gene is preserved in these two cases, and it is not yet selected when it is insertion ('I') or deletion ('D'). When this process was

completed, a selected note table was queried in reverse order, and successfully generated a new chromosome that contains notes.

P_1	-	60, 2	57, 3	59, 4	-	82, 4	-	65, 1	-	69, 1	-	67, 1
P_2	68, 4	-	57, 3	-	59, 1	-	59, 3	-	83, 2	-	66, 3	-
Edit	I	D	М	D	I	D	I	D	I	D	I	D

Figure 4: Edit ipt associated with an alignment.

4 EXPERIMENTS AND DISCUSSION

This study picked 50 songs using "Canon chord progression" to create its learning data. Which songs were selected and what table number changes occurred can be found in the accompanying video (https://youtu.be/VbIY399sHEM). The result of our experiment at the 1,000th generation can be seen in the video found online at (https://youtu.be/VmqeLcEkRbw). The music at the 100th generation was the smoothest to hear and the average fitness exceeded 7. Fig. 5 shows the sum of fitnesses according to the number of generations. This shows that the proposed evolution is successful through our geometric crossover.





However, it showed a limitation in creating better music after convergence. The reason seems that the learning score table is specialized to store scores for basic information, such as the number of notes, rather than characterizing the pattern. Since geometric crossover has been successfully applied to automatic composition, we will further study the patterns that can be collected in a melody and create better melodies.

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