

UDC 004.8

IMPROVED GENETIC METHOD OF MELODIES HARMONIZATION WITH THE HELP OF PEAK VALUES OF ERROR SMOOTHING

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ANNOTATION. A modification of the genetic method of melodies harmonizing by splitting the duration of melody notes in places of peak values of the error function and adding a new chord is suggested. The performed calculations showed the effectiveness of the proposed modification.

Introduction. One of the most important components of the process of writing music is the harmonization of the melody. The combination of the sounds composing the melody should fully satisfy the numerous rules of the theory of musical harmony [1]. The most promising for automatic harmonization of melodies is the genetic method [2,3]. However, the task of simultaneously satisfying a large number of dissimilar rules of the musical theory is extremely complicated. Therefore, the development of new modifications of genetic algorithms that make it possible to reduce the total error of satisfying the rules of musical harmony is urgent.

Purpose of the work. The aim of the work is to increase the efficiency of the genetic method of harmonization by searching and smoothing the peak error values for combinations of chords by splitting the length of the melody notes and adding a new chord in these places.

The main part of the work. The method considers a musical composition as a sequence of chords, each of which is associated with one note of the melody. Harmony rules regulate a consistent combination of chords with each other.

Under the error of harmony it is understood the fact of violation of the rules of harmony. Each rule, depending on the significance, is correlated with some number, the magnitude of the error. The error e of the chord progression is the ratio of the sum of the errors that occur to the sum of all possible errors for all the rules used:

$$e_c = \frac{\sum_{\varepsilon \in E(c)} q(\varepsilon)}{\sum_{\varepsilon \in E} q(\varepsilon)}, \quad (1)$$

where c – chord progression, ε – error, q – error size function, $q : E \rightarrow \mathbb{R}$, E – set of all possible errors of harmony rules for sequence c , $E(c)$ – set of errors for sequence c .

In the generated composition, after the genetic algorithm is harmonized according to the procedure of [3], errors are usually distributed unevenly. Their number depends heavily on the nature of the notes combined in the melody. An example of a possible distribution of errors is shown in Figure 1. As a solution to this problem, we suggest introducing an additional, connecting chord of short duration between the two chords in question, which will allow smoothing the transition. To do this, a note of a small duration is inserted into the melody, the height value of which is averaged relative to the two neighboring ones. In this case, the duration of one of the note-neighbors should be decreased by the duration of the added note, so as not to destroy the structure of the bars. The duration of notes does not affect the harmony, but it is important to keep the rhythmic pattern of the composition. For simplicity, we can assume that the right note is always reduced, and exactly half, which is the duration of the added note.

In the course of the genetic method, we perform this operation several times, after a specified number of steps. The melody changes unambiguously for the whole generation. The place of introduction of the connecting chord is estimated by the best representative of the generation: we find a

pair of chords with the highest error value.

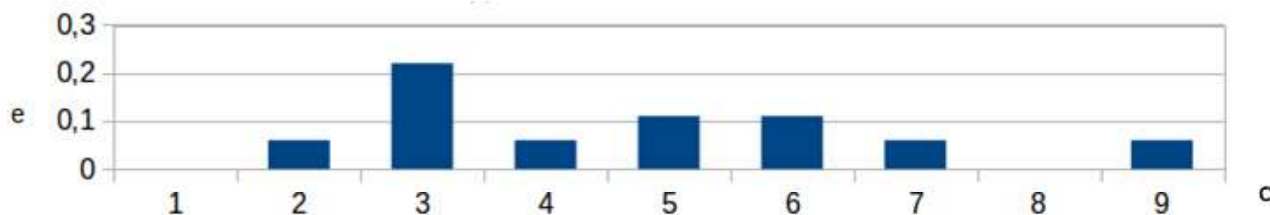


Fig. 1. Errors of each pair of chords of an arbitrary composition of 10 chords after 75 steps of the method [3]. The peak value of the error occurs in the combination of the third and fourth chords.

After this transformation, the entered chord is not yet harmonized with the neighboring chords, so the population of the changed compositions must undergo a sufficient number of iterations n_p of the method, so that the notes of the chord occupy the optimal positions. Accordingly, the more iterations are allocated to the establishment of a new position and the more the peaks p are processed, the error will decrease (Fig. 2a).

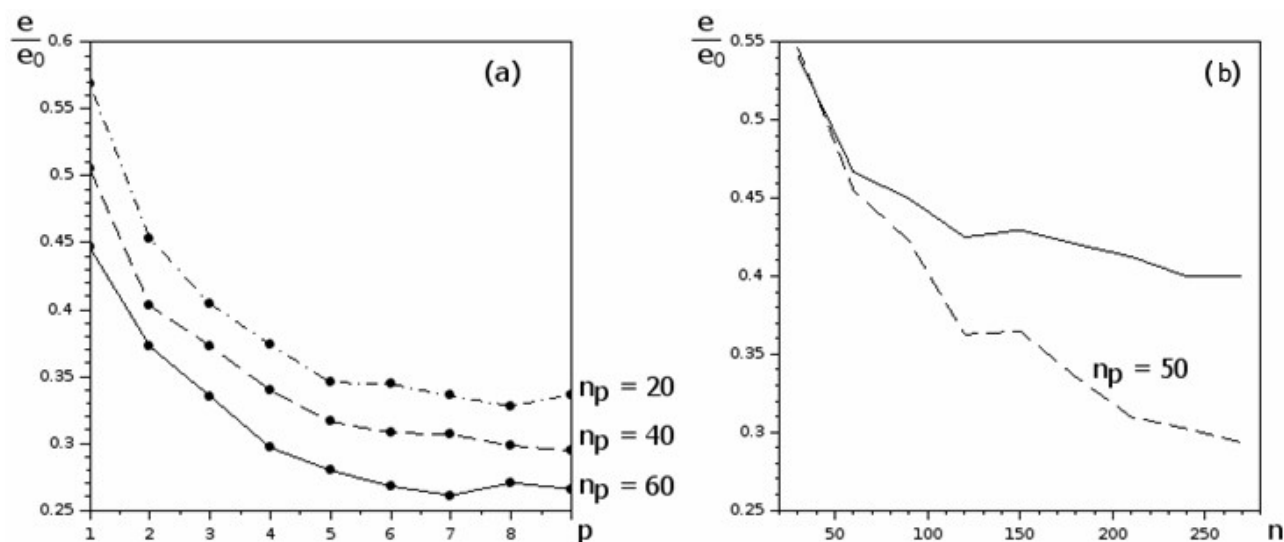


Fig. 2. Dependence of the effectiveness of the method on the number of iterations between the search for peaks and the number of smoothed peaks (a) and comparison with the original method (b).

In Fig. 2b there are shown the results of comparison of the proposed method (dotted line) with the original (solid line) [3]. To smooth out the peaks, a step of 50 iterations was chosen.

Both graphs in Figure 2 were obtained by averaging over an ensemble of 50 randomly generated melodies. The comparison is based on the value of the error e with respect to the level of error in the first generation e_0 .

Conclusions. A new modification of the use of the genetic approach for the melodies harmonization is proposed. The main idea is to iterate into the melody of new intermediate chords in the places of the greatest harmonic errors between neighboring chords and subsequent optimization by the genetic method. The carried out numerical experiments showed an almost twofold decrease in the resulting harmonic error as a result of the application of the proposed modification.

REFERENCES

1. Дубовский И., Евсеев С., Способин И., Соколов В. Учебник гармонии // М.: Музыка. 1965. 436 с.
2. Somnuk Phon-Amnuaisuk, Tuson A., Wiggins G. Evolving musical harmonisation, // Proceedings of the Fourth International Conference on Artificial Neural Networks and Genetic Algorithms (ICANNGA-99), 1999.
3. Jacob B. Composing With Genetic Algorithms // Proc. International Computer Music Conference (ICMC '95), Banff Alberta, September 1995. P. 452-455.