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Cultural heritage education-driven utilization of NSGA algorithms to construct innovative path design for the inheritance of non-heritage music and art

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ABSTRACT
Traditional non-heritage music art is gradually declining, driven by cultural heritage education, this paper studies the future inheritance trend of non-heritage music art. In this paper, the infectious disease dynamics model and complex network propagation theory are used to construct a mathematical model of the inheritance of non-heritage music art, an improved non-dominated sorting genetic algorithm is proposed, and the trend characteristics of the inheritance of non-heritage music art are simulated by solving the parameters of the model through the improved NSGA-Ⅱ algorithm which introduces the congestion calculation method and the crossover strategy. The improved NSGA-Ⅱ algorithm shows better convergence speed of optimization search and uniformity of solution distribution on single peak function and three ZDT functions. Its SP and IGD indexes are much better than the comparison algorithm, with values less than one-half of the comparison algorithm. Taking the heat of non-heritage music and art inheritance in Baidu index for several days as the simulation object, it is found that the simulation of the mathematical model of non-heritage music and art inheritance in this paper has a maximum heat value of 115,000 and the real maximum heat value of 117,241 are not much different from each other, which confirms that this paper's non-heritage music and art inheritance mathematical model has a better fitting effect and reasonableness. The work of this paper has injected new vitality into the innovation of non-heritage music art inheritance.

Keywords: Infectious disease dynamics model, Complex network propagation, Improved NSGA-II algorithm, Non-heritage music art inheritance

1. Introduction

China has a long history, and in this long history many traditional music cultures have been born, which have incomparable valuable values [1-2]. Traditional culture has condensed the wisdom of Chinese

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people from generation to generation, and it is a great mission for people to find a truly suitable inheritance method [3-4]. Music culture is an important branch of traditional culture, and traditional music culture contains many positive spiritual connotations, which promote the practice of socialist core values [5-7]. In the current era, science and technology are advancing, and various communication media have come into people's view, traditional music culture should also seize this opportunity to gain more attention, by considering it as a non-heritage, so as to further develop it [8-11].

The inheritance and innovation of non-heritage music art is to make the traditional music which lacks of system, through the organization of art workers and the use of learned professional knowledge, to make it systematic and without losing the original flavor, and at the same time, to be able to display on the large-scale stage, to meet the public's aesthetic demand [12-15]. Traditional music is an important part of Chinese traditional culture, has a very rich cultural heritage and connotation, in the intangible cultural heritage, music art is an indispensable part, the level of development of non-heritage music culture has an important impact on the cultural heritage education [16-18]. Therefore, in the era of information technology, non-heritage music has been given a new opportunity for development, and it is necessary to take this opportunity to study its innovative development methods, and to find out the development path that is really suitable for it [19].

In this paper, the genetic algorithm is combined with the theory of infectious disease dynamics to construct a mathematical model of the inheritance of non-heritage music art and predict the trend of the inheritance of non-heritage music art. Considering the defects of NSGA2 algorithm such as insufficient congestion distance formula and easy to fall into local optimization, a brand new congestion calculation method and crossover algorithm are introduced, and NSGA2 algorithm is comprehensively optimized through the work of elite retention strategy improvement, congestion improvement and crossover operator improvement. The ZDT series of test functions and SP and IGD indicators are used to evaluate the performance of the improved algorithm, and then the heat value of non-legacy music and art inheritance in Baidu index is used to test the fitting effect of the model.

2. Mathematical model of non-heritage music and art inheritance and its solution

2.1. Establishment of mathematical model for the inheritance of non-heritage music and art

2.1.1. Theories related to modeling infectious disease dynamics. To study the spread of infectious diseases, we need to analyze four characteristics and their three conditions, which are the virus-producing individual, i.e., the pathogen, whether the disease is infectious or not, the epidemiological characteristics of the disease, and whether the individual is immune to the infection or not, and the three conditions are the source of the disease, i.e., organisms carrying the pathogen, the susceptible group, i.e., the individuals who lack specific immunity, and the route of transmission, i.e., how the disease is transmitted to the susceptible group. The three conditions are the source of infection of the disease, i.e., the organism carrying the pathogen, the susceptible population, i.e., the individuals lacking specific immunity, and the transmission route, i.e., how the disease is transmitted to the susceptible population.

To study the dynamics of infectious diseases [20], it is first necessary to analyze the transmission mechanism of infectious diseases and establish a mathematical model that describes the process of disease transmission according to the four basic characteristics and three epidemic conditions mentioned above, and the general flowchart of modeling and analysis is usually used to study the dynamics of infectious diseases by using the steps mentioned above, and also to analyze and judge the global stability of the model, as well as to analyze the sensitivity to the parameter, and the general flowchart of infectious disease modeling and analysis is shown in Fig. 1. The general flow chart for modeling and analysis of infectious diseases is shown in Figure 1.

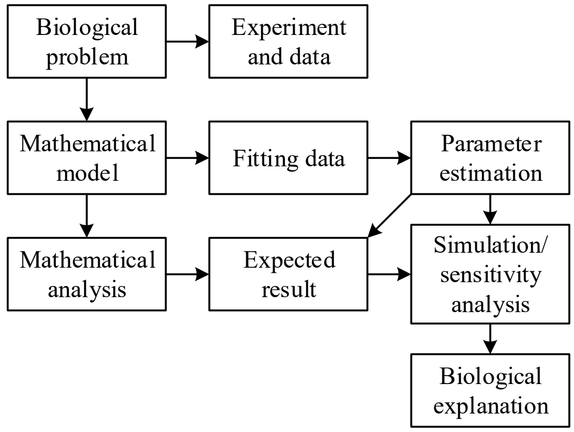

Fig. 1. General flow chart of dynamic modeling and analysis

At present, the dynamics of infectious diseases are basically studied based on SIR models. When an infectious disease is prevalent, the population is divided into three categories, susceptible individuals are currently in a healthy state, but susceptible to infection, and do not have specific immunity, usually denoted by S, infected individuals are currently in an infected state, and can infect susceptible individuals to make them infected individuals, usually denoted by I, recovered individuals are currently in a recovering state and have obtained antibodies, are not likely to be reinfected, and are removed from the dynamic model, usually denoted by R.

A typical SIR$ model is to divide the population into the above three types of individuals, $s(t)$ denotes the proportion of susceptible individuals to the total individuals at the moment of t, $i(t)$ denotes the proportion of infected individuals to the total individuals, and $r(t)$ denotes the proportion of recovered individuals to the total individuals, then there is $s(t)+i(t)+r(t)\equiv 1$, which defines that the susceptible individuals in the model in unit time The probability of being infected in the model is β, and the probability of recovery of infected individuals is γ, then the kinetic equation of the SIR model is as follows:

$$\begin{cases} \dfrac{ds}{dt} = -\beta si \\ \dfrac{di}{dt} = \beta si - \gamma i \\ \dfrac{dr}{dt} = \gamma i \end{cases} \tag{1}$$

2.1.2. Complex network communication theory. With the continuous development of complex network theory, it is found that the connection between the real world can be described by complex networks, and the propagation theory based on the network structure is constantly proposed, one of the important branches is applied in the study of infectious disease propagation behavior, and many models of infectious diseases based on the network structure have been proposed, and common propagation theories can be classified into two kinds: the theory of infectious disease propagation on a homogeneous network and the theory of propagation on a non-homogeneous network. The common transmission theories can be categorized into two: the theory of infectious disease transmission on uniform networks and the theory of transmission on non-uniform networks.

SIS propagation model on homogeneous hybrid networks [21]. The SIS model is typical among infectious disease propagation models and can be easily generalized to other models. Assuming that each node in the network represents an individual, and the states of the nodes are categorized into two kinds: susceptible state (S) and infected state (I), the infectious disease can be spread with the connections between the nodes. If node S is connected to node I, the probability of being infected is β, the probability of node I recovering itself is γ, the ratio of the two probabilities is noted as $\lambda = \beta / \gamma$, the prevalence of the infected individual at the moment t, i.e., the mean density, is noted as $\rho(t)$, the degree distribution in the network is noted as $\langle k \rangle$, describes the SIS model in a homogeneous network:

$$\partial_t \rho(t) = -\rho(t) + \lambda \langle k \rangle \rho(t)[1 - \rho(t)] \tag{2}$$

This yields a propagation threshold of:

$$\beta_c = \frac{\gamma}{\langle k \rangle} \tag{3}$$

If the contagion rate β is greater than the critical value β_c, it indicates that the contagion will continue to expand the contagion eventually stabilizing at a certain value, and vice versa, the infected individuals will gradually decrease to 0, and eventually the contagion disappears.

SIS propagation model on non-uniform mixed networks. For non-uniform complex networks, some nodes have large degrees, the average density of nodes needs to be set in a case-by-case basis, assuming that the total number of nodes in the network is N, the node state is divided into susceptible (S) and infected (I), the probability of node S being infected is β, the probability of node I recovering is γ, and the node I recovering may be re-infected to become a susceptible state again . Remember that the ratio of the two probabilities $\lambda = \beta / \gamma$, the density of node I with k connections at moment t is $\rho_k(t)$, and the infection rate of the SIS model is:

$$\frac{d\rho_k(t)}{dt} = \lambda k[1 - \rho_k(t)]\Theta_k(t) - \rho_k(t), k = 1, 2, \cdots, n. \tag{4}$$

where the propagation rate of node S is $1 - \rho_k(t), \Theta_k(t)$ denotes the probability that a node of degree k connects to an infected node at moment t, which can be expressed by the following equation:

$$\Theta(t) = \frac{\sum_k kP(k)\rho_k(t)}{\langle k \rangle} \tag{5}$$

This yields a propagation threshold of:

$$\beta_c = \frac{\gamma \langle k \rangle}{\langle k^2 \rangle} \tag{6}$$

The basic regeneration number is:

$$R_0 = \frac{\beta \langle k^2 \rangle}{\gamma \langle k \rangle} \tag{7}$$

The epidemiological trend of infectious diseases is analyzed according to the basic regeneration number obtained, if $R_0 < 1$, the disease gradually decreases until it disappears, if $R_0 \geq 1$, the disease will gradually expand the scale of infection and eventually stabilize at a certain value.

2.1.3. Mathematical model of the inheritance of non-heritage music and arts. Since non-heritage music and art is one of the important contents of national culture, this paper combines the SEIA model, does not consider the birth rate and death rate for the time being, takes the existing people who are familiar with the non-heritage music and art culture as the “contagious source”, and introduces the policy reference factor of u_1, u_2, to construct a model of non-heritage music and art inheritance. The model is as follows:

$$\begin{cases} \dfrac{dS(t)}{dt} = -\alpha S(t)E(t) + \beta E(t)u_1 + (1-\nu)I(t)u_2 \\ \dfrac{dE(t)}{dt} = \alpha S(t)E(t) - E(t)u_1 - \eta E(t) \\ \dfrac{dI(t)}{dt} = \eta E(t) - I(t)u_2 \\ \dfrac{dA(t)}{dt} = (1-\beta)E(t)u_1 + \nu I(t)u_2 \end{cases} \tag{8}$$

where: $S(t)$ is the proportion of the national population interested in NRM. $E(t)$ is the proportion of the population familiar with non-heritage music and arts to the national population. $I(t)$ is the proportion of the national population who are inheritors of non-heritage music and arts. $A(t)$ is the number of opponents of cultural preservation as a proportion of the national population. α is the probability of contact between each person who is familiar with the non-heritage music and art and the person who is interested in the non-heritage music and art. β is the probability that a person familiar with NRM is not actively spreading the culture. η for the probability that a person familiar with the art of NRM will become a bearer of the art of NRM. ν is the probability that the bearer of a non-heritage musical art becomes an opponent of cultural preservation. u_1 is a reference factor for people who are familiar with the art of NRM under the State's policy of encouraging people to become inheritors of NRM. u_2 as a reference factor for the demise of non-heritage musical arts under the influence of national policies.
where u_1, u_2 is a randomly assumed value based on existing state support for national culture. α, β, η, ν is unknown, this paper applies genetic algorithms to solve the parameters of the mathematical model of the inheritance of non-heritage music and art.

2.2. Mathematical model solution for the inheritance of non-heritage music and art

2.2.1. NSGA-II Algorithm. The second generation of Non-dominated Sorting Genetic Algorithm (NSGA-II) [22] continuously optimizes the population mainly through the operations of crossover, mutation, and selection, and it excels in dealing with multi-objective optimization problems. The core features of the NSGA-II algorithm include the fast non-dominated sorting, the elite strategy, the tournament selection, the crowding distance, and the key operations of selection, crossover, and mutation. A brief description is given below.

1) Fast Undominated Sorting Approach. Fast non-dominated sorting acts as a sorting technique based on Pareto dominance relations. It mainly sorts each member of the population by evaluating how they are dominated, which can help the NSGA-II algorithm to efficiently mine a diverse batch of Pareto-optimal solutions in a limited time with less computational resources.

2) Congestion distance. The NSGA-II algorithm adopts the fast non-dominated sorting technique to hierarchically sort the members of the population, which guarantees the advantage of approximation among the members of the same level. However, the uneven distribution of members in the solution space may cause the algorithm to easily fall into local optimality at the initial stage. To overcome this problem, NSGA-II introduces the concept of crowding distance. The specific formula for calculating the crowding distance can be expressed as shown in the following equation.

$$i_d = \sum_{j=1}^{m} \left(\frac{|f_j^{k+1} - f_j^{k-1}|}{f_j^{\max} - f_j^{\min}} \right) \tag{9}$$

where f_j^k is the k th value of the j th objective function. $f_j^{\min}$ and $f_j^{\max}$ are the minimum and maximum values of the j th objective function, respectively. m is the number of objective functions.

3) Tournament selection. Using the tournament selection method, a group of individuals are randomly selected from the population, and the iterative process is implemented by first considering those individuals that are ranked higher in the Pareto ranking. For the case of the same ranking, the tendency is to select those individuals with higher crowding for the next iterative operation, and this process is executed repeatedly until a new population is constructed whose size satisfies the pre-set criteria.

4) Elite strategy. Starting from the initial parent population P_t, a new generation of offspring populations Q_i is successfully spawned through the operations of pairing, crossover and mutation. Then, this newborn Q_i population merges with its parent P_i, and together they form the doubled size R_i population. Thereafter, a fast non-dominated sorting method is used, based on Pareto ranks such as 1, 2, 3-. to n to group individuals and prioritize the entry of higher ranked individuals into the next generation of the population. If the addition of individuals of a certain rank may cause the total number to exceed N, the population will be replenished by selecting individuals with larger crowding distances in order to complete the population replenishment until a $t+1$ -generation population is formed that satisfies the size requirement.

5) Selection. The goal of the NSGA-II algorithm in implementing the selection operation is to maximize the retention of high-quality individuals in the population, which requires that the selected individuals not only perform well on the current fitness function, but also ensures that these high-quality individuals are sufficiently differentiated from each other in order to maintain the genetic diversity of the population.The NSGA-II algorithm achieves its goal by combining the strategies of nondominated and crowding ordering, which together ensure that the two sorting methods together ensure that both the performance advantages of individuals are taken into account while maintaining the diversity of the population.

6) Crossover. The crossover operation, as a key genetic operation in genetic algorithms, is an effective strategy in the initial iterative search process. The process consists of selecting parent individuals with excellent performance from the population, and by using specific crossover methods, such as single-point crossover, multipoint crossover, or uniform crossover, a new generation of offspring individuals can be generated. This process ensures that newly generated individuals have a greater likelihood of inheriting superior genes from their parents.

7) Mutation. In genetic algorithms, the variation operator acts as a crucial local search tool, which is executed by modifying the genetic information of an individual in the form of single-point variation and multipoint variation.

The NSGA-II specific algorithm flowchart is shown in Fig. 2.

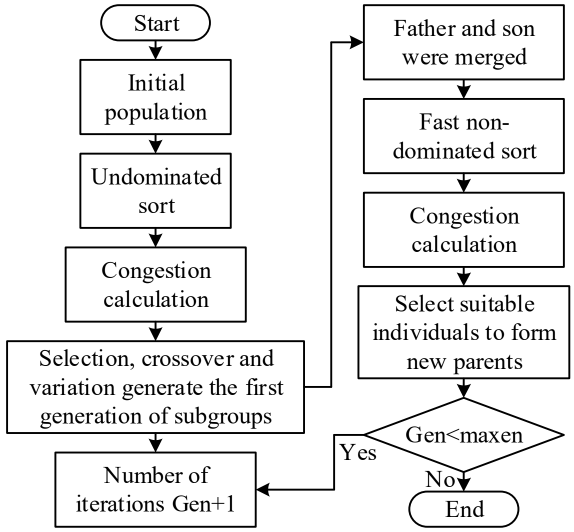

Fig. 2. Flowchart of NSGA- Ⅱ algorithm

The first generation of offspring is generated from the parent population through binary tournament selection, uniform crossover, and a single-point mutation strategy.

2.2.2. Improvement of NSGA-II algorithm. In order to overcome the problems of NSGA-II algorithm in optimization accuracy and uniform distribution of solutions, an improved NSGA-II algorithm is proposed in this paper. The algorithm compensates for the deficiencies in search accuracy and particle uniformity by improving the crossover algorithm in the genetic process and optimizing the congestion calculation method in the non-dominated sorting stage, aiming to improve the search efficiency and enhance the uniformity of the solution distribution. This is achieved by adapting the crossover mechanism and the crowding degree evaluation method in the non-dominated sorting stage during the genetic process.

NSGA-II is a commonly used multi-objective optimization algorithm [23], which has an elite retention strategy, and the elite retention strategy enables the algorithm to obtain a more qualified solution, so as to optimize the decision scheme that best meets the requirements of the decision maker In order to better help the algorithm to select more excellent individuals to form the elite set, this paper proposes the concept of pseudo-fitness value, and the smaller the value indicates that the individual is more excellent. Its calculation formula is shown in the following equation:

$$f = k + 1 - \frac{\sum_{i=1}^{n} D_i}{M} \tag{10}$$

where k is the order of the Pareto front. D denotes the congestion distance. M is the number of objective functions.

The NSGA-II algorithm shows some limitations in coping with multi-objective problems possessing complex Pareto frontiers, multi-dimensional variables, and complex nonlinear characteristics. This shortcoming has the potential to limit the genetic potential of individuals, which in turn affects the uniform distribution of the solution set and the maintenance of diversity. The traditional distance formula is shown in the following equation:

$$i_d = \sum_{j=1}^{m} \left(\frac{| f_j^{k+1} - f_j^{k-1} |}{f_j^{\max} - f_j^{\min}} \right) \tag{11}$$

where f_j^k is the k th value of the j th objective function. $f_j^{\min}$ and $f_j^{\max}$ are the minimum and maximum values of the j th objective function, respectively. m is the number of objective functions.

Therefore, this paper proposes a novel variance-based congestion distance method, which aims to improve the convergence speed and the distribution of the algorithm. Its formula (12) is as follows:

$$i_D = \frac{i_d}{\left\{\frac{1}{m}\sum_{j=1}^{m}\left[\left(\left|f_j^{i+1} - f_j^{i-1}\right|\right) - \frac{i_d}{m}\right]^2\right\}^{-1} + 1} \tag{12}$$

Simulated binary crossover (SBX) operation is a widely used technique in the practice of NSGA-II algorithms, which performs crossover operations on parents encoded in real numbers. It is implemented by randomly selecting the crossover points and subsequently exchanging the gene segments of the parents between these two points. The method works to improve the global search capability of the algorithm and effectively maintains the diversity of the population. To achieve this goal, the crossover operation of NSGA-II is optimized in this paper, and the arithmetic crossover operator is employed to achieve the desired effect.

Let $X_i^{'}$ and $X_j^{'}$ be the real-valued encodings of the corresponding decision variables at the crossover point of the two bodies in the 1st generation, respectively, then the decision variables corresponding to the two bodies after the crossover are shown in the following equation as:

$$\begin{cases} X_i^{t+1} = aX_i^t + (1-a)X_j^t \\ X_j^{t+1} = bX_j^t + (1-b)X_i^t \end{cases} \tag{13}$$

where a, b are uniformly distributed random numbers on [0, 1].

2.2.3. Improvement of NSGA-II algorithm to solve model parameters. This paper takes the population size of the existing non-heritage music art transmitters as the number of the first generation population, takes 50 years as the unit time, and uses genetic algorithms to solve the parameters of the non-heritage music art inheritance model to predict and analyze the trend of the non-heritage music art inheritance.

1) Calculation of fitness. In genetic algorithm, it is crucial to determine the fitness function. In this paper, the functions $\sum_{j=1}^{n}\varphi_j^2 = \sum_{j=1}^{n}(\varphi(i_j) - i_j)^2$ and $\sum_{j=1}^{n}\varphi_j^2 = \sum_{j=1}^{n}(\varphi(a_j) - a_j)^2$ as the fitness function, i.e., the sum of squares of residuals of the estimated number of people familiar with NRM music and art and the actual number of people familiar with NRM music and art, the sum of the residuals of NRM music and art The sum of the squared residuals of the estimated value of the number of opponents of art protection and the actual value of the number of opponents of non-legacy music art protection is used as the fitness function to find the value of the parameter α, β, η, v when the fitness function takes the minimum value.

2) Natural Selection. Selection, also known as replication, is the process of selecting the best individuals in a population to produce a new population. In genetic algorithms, it is realized through selection operators, where individuals with high fitness are inherited into the next generation of the population with a higher probability, and individuals with low fitness are inherited into the next generation of the population with a lower probability, and eventually keep approaching the optimal solution. Commonly used selection operators are: roulette selection, random competitive selection, optimal retention selection, no-playback random selection, optimal preservation strategy and so on.

In this paper, roulette is used as the selection operator. Through the fitness function to calculate the fitness of the individual, according to the size of the fitness on the roulette wheel divided into proportions, each individual is like a sector in the disk, put a pointer on the roulette wheel to randomly select, the greater the fitness of the individual, the greater the chances of being selected, the smaller the fitness, the smaller the chances of being selected.

If the population size is selected too large to affect the algorithm's optimization speed affects the efficiency, if it is too small and will not be conducive to finding the optimal solution. In this paper, we choose the population size of 400, although the running time is a little longer, but it can better find the optimal solution, to avoid the occurrence of precocity phenomenon. The crossover rate in the genetic algorithm is generally between 0.4 and 0.9, this paper takes the crossover rate as 0.6. The variation rate cannot be too large, too large a variation rate will lead to instability of the genetic algorithm, in this paper we take the variation rate as 0.01. The number of iterations is too low which will lead to the failure to search for the optimal solution, and too high which will lead to the growth of the computing time, in this paper we take the number of iterations as 100.

3. Algorithm performance and non-heritage music art inheritance trend analysis

3.1. Performance test of improved NSGA-II algorithm

In order to test the computational efficiency of the improved algorithm proposed in the paper, the traditional ZDT series of test functions and the single-peak function in the standard test of the CEC2005 international competition are used for this test. After the comparison test, the simulation graphs of the original and improved algorithms of the three functions are obtained as shown in Fig. 3-Fig. 5, which record the number of iterations for different functions to find the optimal point under the operation of the two algorithms. From this comparison of the convergence trend graphs of F1, F2 and F3, it can be seen that the improved NSGA-II algorithm has a higher convergence speed, especially in the initial optimization search performance is particularly obvious.

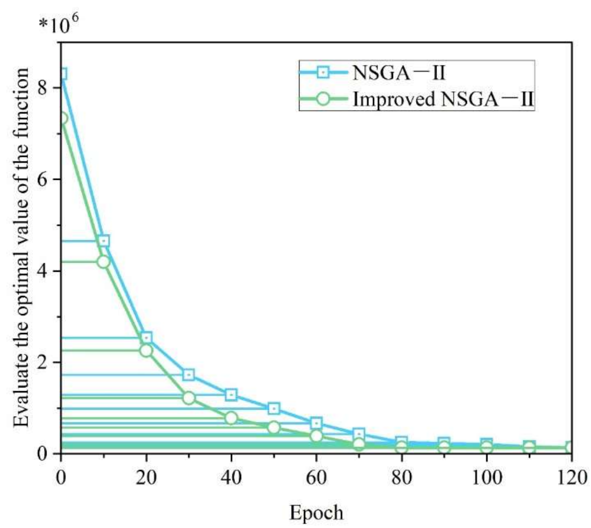

Fig. 3. Formula F1 function convergence curve

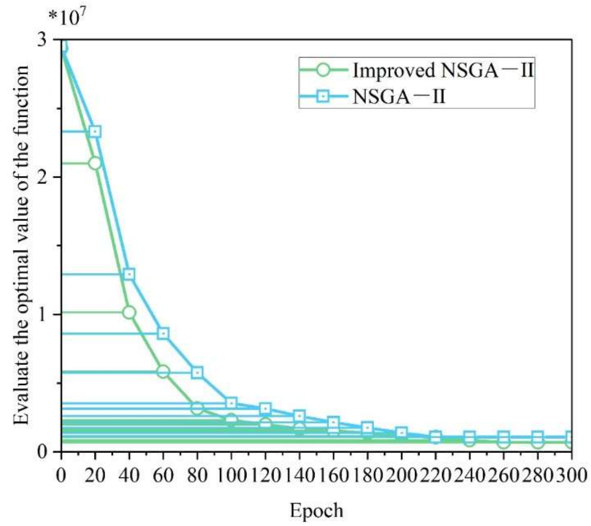

Fig. 4. Formula F2 function convergence curve

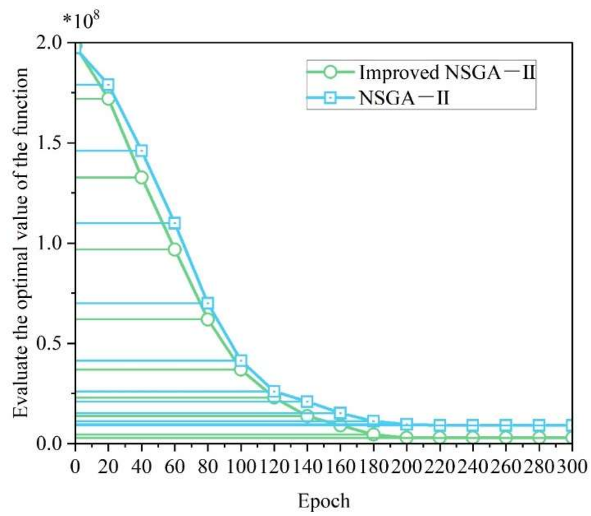

Fig. 5. Formula F3 function convergence curve

Comparison tests are conducted for these three functions of ZDT, and the Pareto frontiers of ZDT1, ZDT1 and ZDT1 problems are shown in Fig. 6-Fig. 11, respectively. The Pareto optimal solution obtained by the improved NSGA-II algorithm is better distributed, while the distribution of the optimal solution frontiers obtained by the NSGA-II algorithm is concentrated somewhere in the region, and the distribution is relatively sparse in the ZDT1 problem when the f1 value is 0.6-0.8, and the crowding of the individuals of the improved NSGA-II algorithm is lower and the density of the individuals is more dispersed in the ZDT2 problem and the distribution is more uniform.

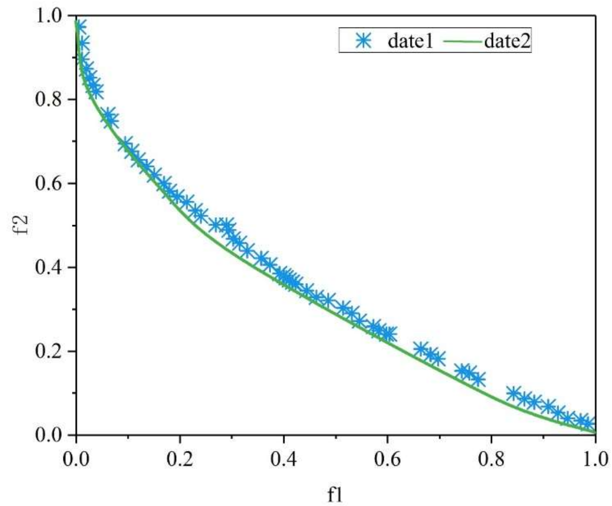

Fig. 6. The ZDT1 problem based on NSGA-Ⅱ-algorithm

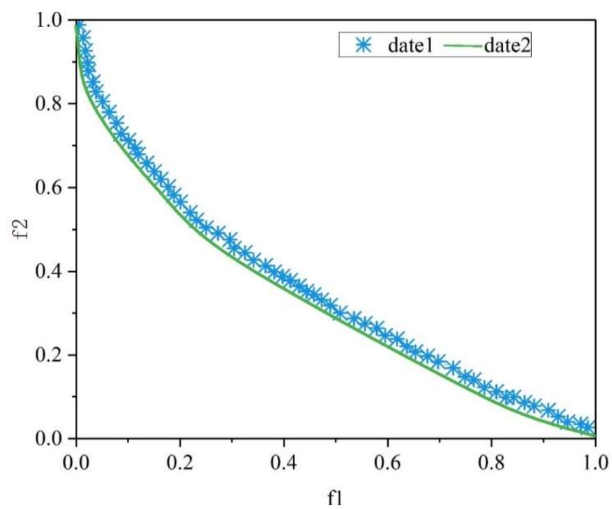

Fig. 7. The ZDT1 problem based on the improved NSGA-Ⅱ-algorithm

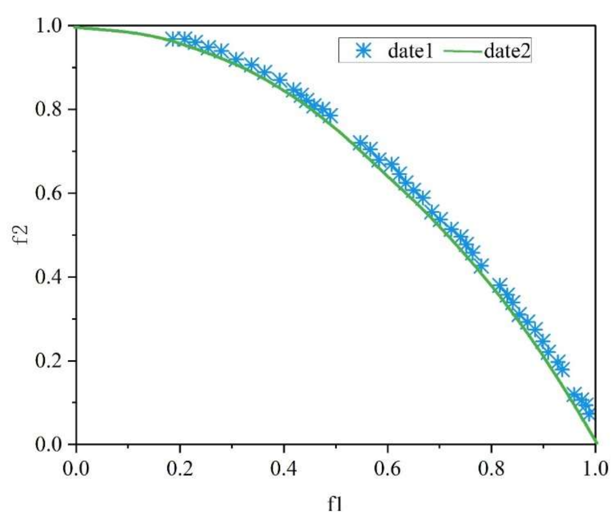

Fig. 8. The ZDT2 problem based on NSGA-Ⅱ-algorithm

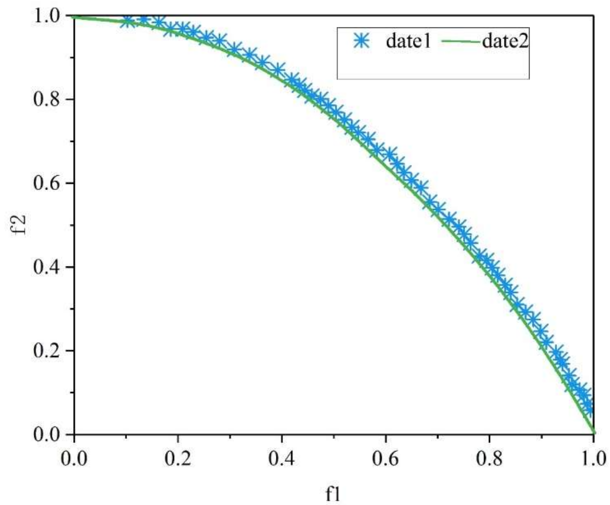

Fig. 9. The ZDT2 problem based on the improved NSGA- Ⅱ -algorithm

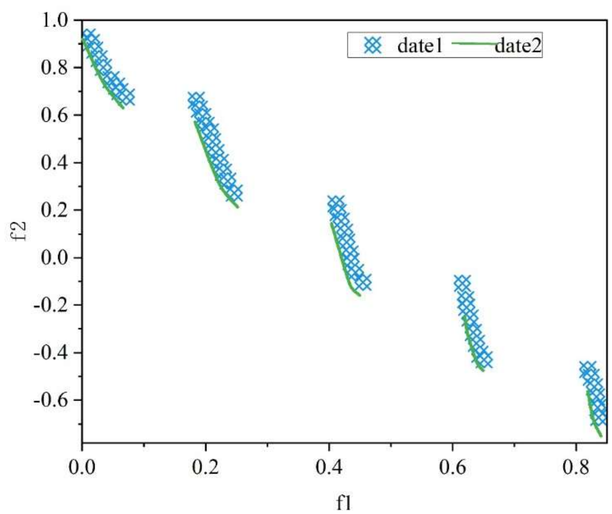

Fig. 10. The ZDT3 problem based on NSGA- Ⅱ -algorithm

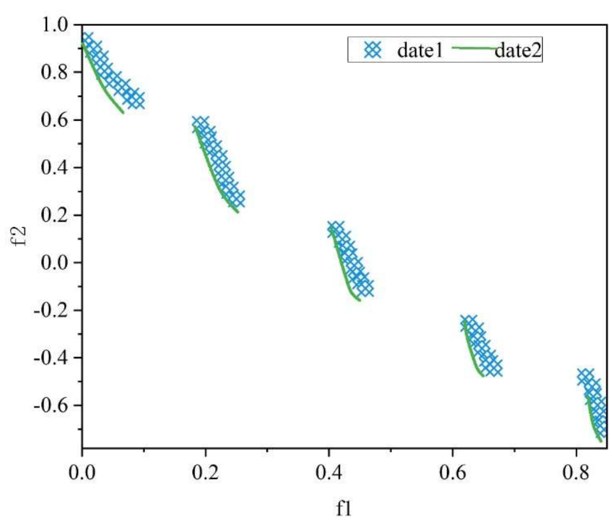

Fig. 11. The ZDT3 problem based on the improved NSGA- Ⅱ -algorithm

The ultimate goal of the multi-objective evolutionary algorithm optimization is to obtain a uniform

Pareto solution set, in order to qualitatively evaluate the algorithm solution results, here we use the spatial evaluation metrics SP. In testing the comprehensive performance of the multi-objective evolutionary method, the inverse generation distance (IGD) is used to evaluate it, the meaning of the IGD indicates that the Pareto optimal solution obtained by individual optimization is the same as the true Pareto frontier approximation.

Based on the definitions of the above two evaluation index functions, we use four algorithms, NSGA-II algorithm, Improved NSGA-II algorithm, MOEA/D-EGO and NMPSO, for comparison. The three selected groups of ZDT functions are calculated independently and the obtained mean values of SP and IGD are shown in Table 1 and Table 2, respectively.

The SP values obtained from the improved NSGA-II algorithm tested in ZDT1 and ZDT2 are significantly lower than the remaining three algorithms. The average value in ZDT3 is slightly lower than the NMPSO algorithm test results, this is because the solution set of ZDT3 has a stepped distribution and has a broken part, in general, from the point of view of improving the distribution of the solution, the improved NSGA-Ⅱ algorithm has a better performance. By comparing and analyzing the IGDs obtained by each algorithm, it can be seen that the improved NSGA-Ⅱ algorithm is significantly better than the other algorithms. From the data in the table, it can be seen that the average value of the IGDs obtained in the two test functions of ZDT1 and ZDT3 is less than 1/2 of the other three algorithms, which indicates that the Pareto optimal solutions obtained by this improved algorithm have a higher degree of convergence.

Table 1. Comparison of SP indicators of different algorithms

Test function	NSGA-Ⅱ	Improved NSGA-Ⅱ	MOEA/D-EGO	NMPSO
ZDT1	0.47584	0.26541	0.38672	0.28034
ZDT2	0.44651	0.41762	0.42181	0.43205
ZDT3	0.59659	0.52135	0.56364	0.52139

Table 2. Average value of IGD

Algorithm	ZDT1	ZDT2	ZDT3
NSGA- Ⅱ	0.035355	0.072392	0.114512
Improved NSGA- Ⅱ	0.021081	0.038416	0.037265
MOEA/D-EGO	0.046182	0.067344	0.092537
NMPSO	0.047262	0.049585	0.074837

3.2. Simulation results of the inheritance trend of non-heritage music and arts

3.2.1. Impact of Opinion Integration Thresholds on Inheritance. The effects of different opinion integration thresholds on susceptible, infected and recovered people in the transmission of online non-heritage music and art are shown in Fig. 12-Fig. 14.

With the continuous inheritance of non-heritage music and art, the density of susceptible people decreases with the inheritance time of non-heritage music and art within a certain time range, and finally tends to stabilize. The density of infected people first rises and reaches the peak value with the inheritance time of non-heritage music and art, and then decreases continuously and finally stabilizes. The density of recovered people rises at a certain point in time and eventually stabilizes with the transmission time of non-legacy music and art. Different opinion integration thresholds d have different effects on the rate of change of the density of susceptible, infected and rehabilitated people. As the opinion fusion threshold d becomes smaller, the rate of decrease in the density of the susceptible becomes smaller, the density at equilibrium becomes smaller, the peak duration becomes longer, and the rate of decrease in the density of the susceptible is greatest when d is 0.9. The rate of increase in the density of susceptibles becomes smaller, and the density at equilibrium becomes smaller. The rate of increase of the density of the rehabilitated becomes smaller, and the density at equilibrium becomes smaller. Through the analysis of simulation results, combined with the non-heritage music art inheritance model of this paper, the following conclusions can be obtained: as the opinion fusion threshold decreases, the scope of information exchange is reduced, the echo chamber effect is enhanced, and the duration of non-heritage music art inheritance is prolonged.

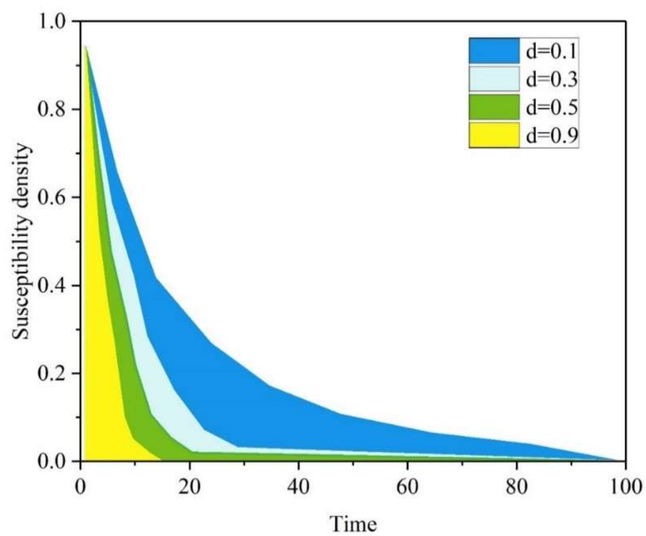

Fig. 12. The density of susceptible people in different opinions

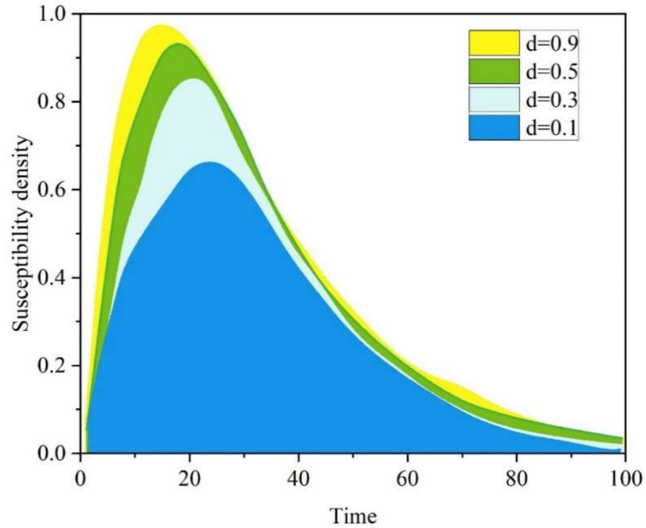

Fig. 13. The density of infected people in different opinions

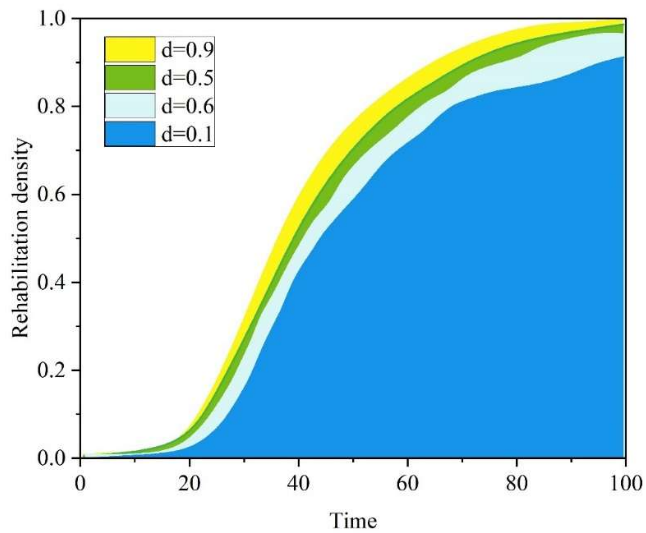

Fig. 14. The density of the confluence of different opinions

3.2.2. Impact of the distribution of users' initial opinion values on inheritance. The distribution rule conforms to the random distribution and normal distribution of the initial opinion values of the nodes, and the evolution process of getting different infected and rehabilitated people is shown in Figs. 15 and 16. When the user's initial opinion value conforms to the normal distribution, the rising rate and peak value of the infected density curve are both higher than that of the infected density curve when the initial opinion value conforms to the random distribution, and the highest infected density under the normal distribution is 0.995, and the highest infected density is only 0.877 when it doesn't conform to the state distribution.At the same time, the rising rate and peak value of the rehabilitated density curve are both higher than that of the infected density curve when the initial opinion value conforms to the the density curve of the rehabilitants when random distribution. Through the analysis of simulation results, combined with the non-heritage music and art inheritance model of this paper, the following conclusions can be obtained: when the distribution of the initial opinion value conforms to the normal distribution, it means that at the initial stage of the non-heritage music and art inheritance, some of the users have strong opinions as well as extreme similarity of opinions, and the opinions of the users will have a certain degree of homogeneity at the initial stage, then under the same opinion threshold, there will be more users accepting information that is similar to their own In the case of the same opinion threshold, more users will accept information similar to their own opinions, i.e., more susceptible people will become communicators.

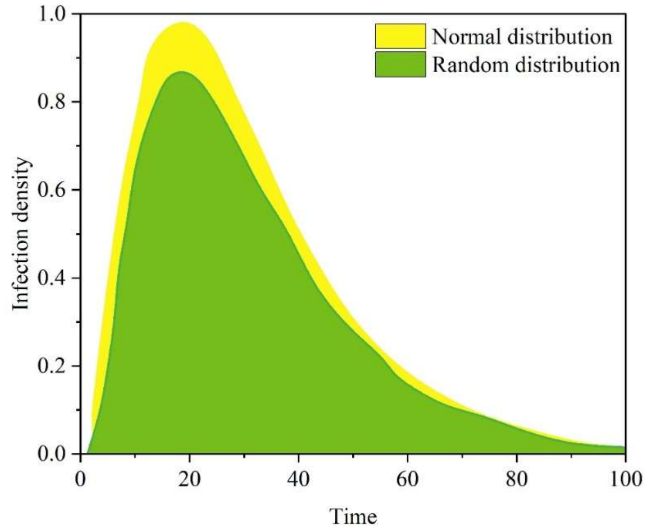

Fig. 15. The density of infected people under different distribution rules

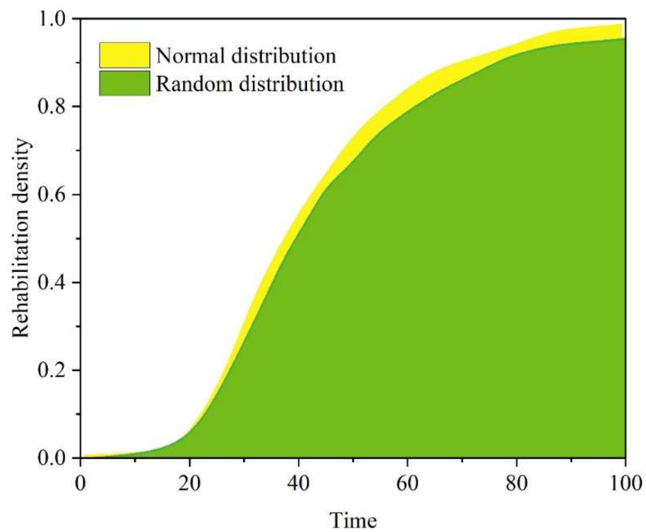

Fig. 16. The density of the concomient under different distribution rules

3.3. Mathematical model fitting effect of non-heritage music and art inheritance

In order to explore the fitting effect of the mathematical model of non-heritage music and art inheritance, the 184-day heat of non-heritage music and art inheritance in Baidu index from November 1, 2023 to May 1, 2024 is taken as the simulation object, and the daily search data values are obtained from Baidu index, and the specific meanings of the different parameters in the practical application are explored through the simulation of multi-variable rate example, and the daily heat propagation trend is shown in Fig. 17 The daily heat propagation trend is shown in Figure 17.

The experimental simulation sets the total number of individuals participating in the topic $N=10^6$, the contagion rate $\beta=0.2$, the individual immunization time h=60h, and runs the experiment 20000 times, and the simulation results are shown in Figure 18.

The simulation results show that the highest infection rate of 1 million individuals is 0.11, indicating that the highest daily hot topic value is about 115,000, which is close to the actual highest hot topic value of 117,241, and the infection is not stopped after 10,000 times of individual interactions, which indicates that the experimental parameters can effectively explain the real situation, and confirms the validity of the establishment of the mathematical model of the inheritance of the non-heritage music and art and the solution algorithm in this paper.

Specifically, the contagion rate of non-heritage music and art inheritance is 0.3 among 1 million network groups, indicating that at most 300,000 people receive the information conveyed by non-heritage music and art during each interaction, and they decide whether to be interested in non-heritage music and art inheritance according to the non-heritage music and art library they are interested in. In addition, the individual immunity time and cross-immunity threshold show that the individual's immunity is low, and the variation rate of the core and auxiliary segments shows that the individual's innovation of the non-heritage music and art inheritance is low, such as the combination of the non-heritage music and art inheritance and the modern popular elements, which retains the original meanings of the non-heritage music and art, so that the non-heritage music and art will survive for a long period of time.

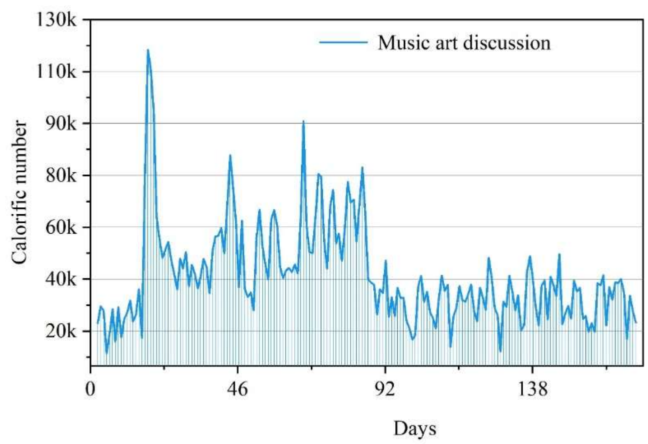

Fig. 17. Non-legacy music art baidu index day search trend

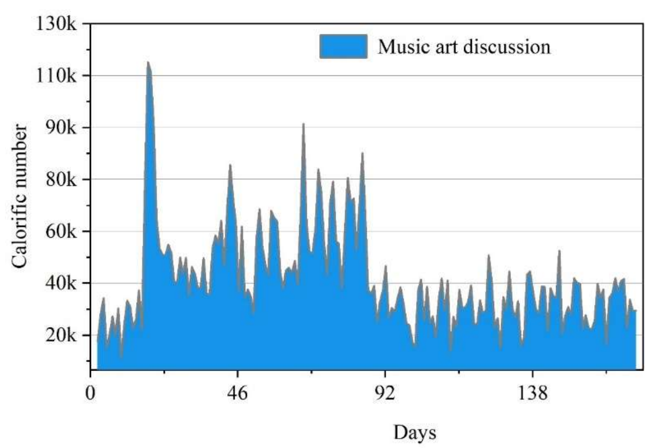

Fig. 18. The highest calorific value simulation of non-relict music art

4. Conclusion

This paper constructs a model of non-heritage music art inheritance, and uses the improved NSGA-Ⅱ algorithm to solve the model parameters to predict the development trend of non-heritage music art inheritance.

In order to test the superiority of the improved NSGA-Ⅱ algorithm in this paper, the single peak function and three ZDT functions are used for testing from the perspectives of convergence speed of algorithm optimization and distribution density of solution. The values of SP and IGD metrics of the improved NSGA-Ⅱ algorithm are lower than those of the comparison algorithm, and most of the values are 50% and less than those of the comparison algorithm, showing good prediction accuracy.

As the opinion threshold decreases, similar information will be aggregated and homogenized, resulting in a longer duration of the inheritance of non-heritage music and art. At the same time, when the initial distribution of opinion values conforms to normal distribution and the opinion threshold is the same, the probability of susceptible people turning into communicators is greater, which is more conducive to the inheritance of non-heritage music art.

The simulation results show that the highest buzz value of non-heritage music and art propagation trend predicted by this paper's model is about 115,000, which is closer to the highest daily buzz value of 117,241 in Baidu index, indicating that this paper's non-heritage music and art inheritance model can explain the real situation effectively, and provide a force for the extensive inheritance of non-heritage music and art.

In conclusion, by predicting the trend of the inheritance of non-heritage music art, we can understand the development direction and potential demand of non-heritage music art in modern society, which provides a direction for the design of innovative paths for the inheritance of non-heritage music art, prompting the inheritors to adopt digital means of dissemination, and combining non-heritage music art and popular elements to enhance the inheritance efficiency.

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