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Circularity Error Evaluation Using Genetic Algorithm

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Abstract: A genetic algorithm based method for form evaluation of a circle is proposed. Firstly, after an introduction to the background of the form error evaluation method and that of the genetic algorithm, a mathematical model of circularity error together with a fitness (evaluation) function is given in terms of the Mathematical Definition of Dimensional and Tolerancing Principles[1], which corresponds to the minimum zone definition and is easy for interpretation and computer implementation. Then, with the least square solution as the initial value, the whole implementation process of the genetic algorithm in the circularity evaluation is dwelt on. Finally, the simulation results of a quoted example are analyzed and a brief conclusion is given. The example simulation indicates that genetic optimization algorithm has such distinctive advantages as solving nonlinear and large space problems, converging to global optimum solution and convenience of implementation, etc., and it is quite suitable for the form error assessment.

Key words: circularity; genetic algorithm; error evaluation
CLC number: TP23

1 Introduction

The automation, standardization and integration of modern manufacturing demands for the machined parts must satisfy the changeability at the assembly line and the equality of the functionality[2]. For the above demands, the parts have been designed with some tolerance. To verify the validity of the parts, some inspection schemes need to be determined and the sampling data must be processed through some algorithms. The computation based evaluation and inspection algorithm must not only be highly efficient and robust, but also based on proved mathematical principles and tolerance regulations[3-4].

The least square method is relatively mature currently, which is broadly utilized and generally used as the initial value of other algorithms[2,5]. The least square method (LSM) is based on sound mathematical principles that minimize the sum of the squared deviations of the measured points from the fitted feature. This method is robust, but it does not follow the standard intently so that it cannot guarantee the minimum zone solution specified in the standard, which may lead to rejection of good parts.

Therefore, the minimum zone based algorithms have been developed and improved without interruption. Computation geometry based evaluation algorithm was proposed by Lai and Wang[6].

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The 2-dimensional straightness obtained by this method corresponds to the condition of the minimum zone. Its principle is to search the minimum zone that contains the convexes of all sampling data. Jyunping Huang gave the convex-based mathematical model of the 3-dimensional straightness[7]. This method shows that the 3-dimensioal straightness is determined only by the data at the vertexes of the convex, and the cylindrical axis of the minimum zone is parallel to a side of the convex. G.L. Samuel and M.S. Shunmugam realized the straightness and flatness evaluation by the computation geometry technique[3]. Mark J and K. Krishna proposed a minimum zone based algorithm that expressed the functions of straightness and flatness in the geometric form[8].

The rapid development of modern advanced technology demands a high quality of the precision machining so that the inspection abilities of such instruments as CMM[9-12] must be strengthened and the inspection algorithm must be improved at the same time. With all kinds of optimization techniques and computer technology development, some new methods have appeared. The paper has proposed a novel algorithm for the evaluation of form error of a circle that is based on the evolutionary algorithm-genetic algorithm. The rest parts of the paper are arranged as follows. At first, the genetic algorithm is introduced. Then the mathematical model of the problem is given and the process of the implementation of genetic algorithm is depicted in detail. Finally, the simulation results are analyzed and a conclusion is reached.

2 Introduction to genetic algorithm[13-14]

The genetic algorithm is an adaptive and probabilistic searching algorithm with an iterative procedure that simulates the evolution process of the nature. The algorithm starts with an initial approximate solution around which a fixed number of solutions are randomly produced as the candidate individuals. These individuals are encoded as chromosomes which constitute the initial population of the problem. The population evolves from generation to generation to obtain better offspring. By means of the principle of "struggle for existence" or "natural selection", the superior chromosomes are preserved in the population of next generation and the inferior ones are rejected according to their fitness degree. There are such genetic operators as selection, mutation, crossover etc. in the evolution process. The control parameters for a genetic algorithm include the population size, the probability of crossover, the probability of mutation, and the maximum generations of evolution and so on.

Compared with the traditional approaches, the genetic algorithm has its own distinctive characteristics. It deals with the codes of a set of solutions, not the set of solutions itself. The searching process of the algorithm starts with a population of the solution, not a single solution. It just uses the fitness function, not the derivative or other auxiliary information; It utilizes probable but not deterministic state transformation rules. In terms of the above striking differences, the genetic algorithm has such good qualities as solving non-linear, large space optimization problems and converging to a global optimum solution, etc.

3 Mathematical model of the circularity error

3.1 Mathematical definition

According to the Mathematical Definition of Dimensional and Tolerancing Principles[1], a circularity zone at a given cross-section is an annular area consisting of all points $\boldsymbol{P}$ satisfying the conditions:

$$\begin{cases} \hat{T}(\boldsymbol{P}-\boldsymbol{A}) = 0 \\ |\boldsymbol{P}-\boldsymbol{A}|-r| \leqslant \frac{t}{2} \end{cases} \tag{1}$$

where

$\hat{T}$ = for a cylinder or cone, a unit vector that is tangent to the spine at $\boldsymbol{A}$. For a sphere, $\hat{T}$ is a unit vector that points radially in all directions at $\boldsymbol{A}$.

$\boldsymbol{A}$ = a position vector locating a point on the spine

r = a radial distance (which may vary between circular elements) from the spine to the center of the circularity zone (r> 0 for all circular elements)

t = the size of the circular zone

Figure 1 illustrates a circularity zone for a circular element of a cylinder or conical feature.

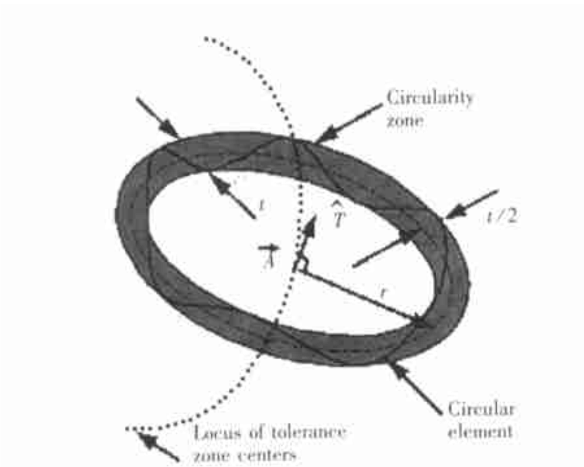

Fig. 1 Illustration of circularity tolerance zone for a cylindrical or conical feature.

3.2 Mathematical equations of A and r[15-19]

According to the mathematical definition, the evaluation of the form error of a circle is to determine the values of $\boldsymbol{A}$ and r under the condition of minimizing the value of $||\boldsymbol{P}-\boldsymbol{A}|-r|$. To verify the validity of the genetic algorithm in the field of form error evaluation, the sampling data provided in the literature 15 are quoted for simulation, see appendix A.

In case of a plane, $\boldsymbol{A}$ can be expressed as $\boldsymbol{A}(a+\Delta a_i(T), b+\Delta b_i(T))$, where a and b are the initial values of the center, T is the generation, $\Delta a_i(T)$ and $\Delta b_i(T)$ are the random variables between $(-k, k)$ which is the variable range determined by the practical problem. Then the distance between the jth point and the center $\boldsymbol{A}(a+\Delta a_i(T), b+\Delta b_i(T))$ can be expressed as:

$$r_{ji}=\sqrt{\{x_j-[a+\Delta a_i(T)]\}^2+\{y_j-[b+\Delta b_i(T)]\}^2}=r_{ji}(\overline{a_i}, \overline{b_i}) \quad (2)$$

According to the minimum zone condition (1), we define the objective function as:

$$G_i(\Delta a_i(T), \Delta b_i(T))=\min[\max r_{ji}(\overline{a_i}, \overline{b_i})-\min r_{ji}(\overline{a_i}, \overline{b_i})] \quad (3)$$

The fitness function then can be expressed as:

$$\text{fitness}(\Delta a_i(T), \Delta b_i(T))=G_i(\Delta a_i(T), \Delta b_i(T))^{-1} \quad (4)$$

If the operation runs at generation of T_0 and the i_0th variable $(\Delta a_{i0}(T_0), \Delta b_{i0}(T_0))$ is selected, the accuracy is up to demand, the $\boldsymbol{A}$ and r can be obtained:

$$\begin{cases}\boldsymbol{A}=(a+\Delta a_{i_0}(T_0), b+\Delta b_{i0}(T_0)) \\ r=\dfrac{r_{\max}+r_{\min}}{2}\end{cases} \quad (5)$$

Where $r_{\max}$ and $r_{\min}$ are the maximum and minimum radii of the concentric circles satisfying the minimum zone condition.

4 Implementation of genetic algorithm [14, 20-23]

The whole process of the proposed algorithm mainly consists of the following steps:

(1) Chromosome representation

For the stability of the population and the accuracy and suitability for large space searching as well, the real numbers are used to represent the genes of the chromosomes. Let $v_i=[\Delta a_i, \Delta b_i]$, where v_i represents the ith chromosome which comprises two genes which are the variables mentioned above.

(2) Initializing population

POP-SIZE is the size of the population of candidate solutions. Randomly select POP-SIZE groups of data $v_i=[\Delta a_i, \Delta b_i], (i=1, 2, \cdots, \text{POP-SIZE})$ between $(-k, k)$.

(3) Evaluation

The values of a and b can be obtained by the least square method. Then compute the fitness value. Evaluation function is given as: $\text{eval}(v_i)=\text{fitness}(\Delta a_i, \Delta b_i)$, $i=1, 2, \cdots, \text{POP-SIZE}$.

(4) Selection

The scheme of roulette wheel selection is chosen to select the superior individuals as the next generation individuals. It is made up of the following four steps.

①Compute the fitness value of every chromosome v_k:

$$\text{eval}(v_k) = \text{fitness}(\Delta a_k, \Delta b_k),$$
$$k = 1, 2, \cdots, \text{POP-SIZE} \quad (6)$$

② Compute the sum of fitness values of all chromosomes:

$$F = \sum_{k=1}^{POP-SIZE} \text{eval}(v_k) \quad (7)$$

③ Compute selection probability p_k of every chromosome v_k:

$$p_k = \text{eval}(v_k)/F, k = 1, 2, \cdots, \text{POP-SIZE} \quad (8)$$

Compute cumulative probability q_k of every chromosome v_k:

$$q_k = \sum_{i=1}^{k} p_i, k = 1, 2, \cdots, \text{POP-SIZE} \quad (9)$$

The process of selection is to rotate the wheel POP-SIZE times and select one chromosome to construct the new population as the following scheme every time.

selection process:

step 1: randomly produce a uniform distribution number r between (0, 1);

step 2: if $r_1 \leqslant q_1$, select the first chromosome v_1; else, select the kth chromosome v_k ($2 \leqslant k \leqslant$ POP-SIZE), make $q_{k-1} < r_1 \leqslant q_k$.

(5) Crossover

The paper uses the scheme of arithmetic crossover. It produces new chromosomes by the two complementary linear combinations of the parents. Produce a uniform distribution number r between (0,1) randomly. If $r <$ PCROSSOVER(i = 1, 2, …, POP-SIZE/2, PCROSSOVER is the crossover probability of the selected individuals), randomly select two chromosomes v_i and v_j for crossover operation.

Let $v_i = [\Delta a_i, \Delta b_i]$, $v_j = [\Delta a_j, \Delta b_j]$ (i, j = 1, 2, …, POP-SIZE), then the produced chromosomes $v'_i = [\Delta a'_i, \Delta b'_i]$, $v'_j = [\Delta a'_j, \Delta b'_j]$.

where:

$$\begin{cases} \Delta a'_i = r\Delta a_i + (1-r)\Delta a_j \\ \Delta b'_i = r\Delta b_i + (1-r)\Delta b_j \end{cases} \quad (10)$$

and

$$\begin{cases} \Delta a'_j = (1-r)\Delta a_i + r\Delta a_j \\ \Delta b'_j = (1-r)\Delta b_i + r\Delta b_j \end{cases} \quad (11)$$

The crossover process is illustrated by figure 2.

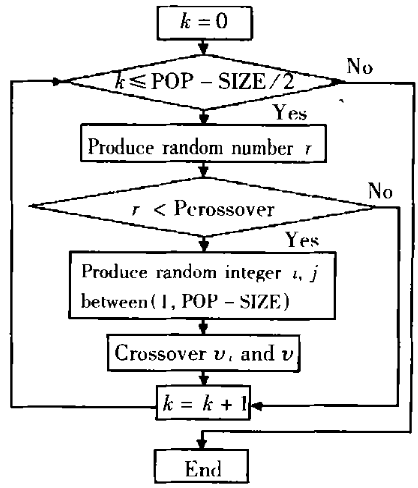

Fig. 2 Implementation of crossover process.

(6) Mutation

Mutation is to change one or more genes of the chromosome by mutation probability. If the binary representation is utilized, the gene of the mutation bit will be replaced with the opposite value, namely if 0, it will be replaced with 1 and vice versa. In the paper, as the chromosome is represented by real values, the mutation bit will be replaced by a new random real number between $(-k, k)$. If the second gene (left gene) Δa_i is selected to mutate, then produce a random number $\Delta a'_i$ to replace it. $v_i[\Delta a_i, \Delta b_i]$ will become $v_i[\Delta a'_i, \Delta b'_i]$.

If the mutation probability PMUTATION is equal to 0.06[24], 6 percent of genes in the population will mutate. In the paper the number of the whole genes is 2×POP-SIZE so that (2×POP-SIZE×6%) genes will mutate in every generation. To give every gene the same opportunity to mutate, produce a series of random numbers r_k(k = 1, 2, …, 2×POP-SIZE×6%). If $r_k <$ PMUTATION, the kth gene is selected to mutate.

To date, one generation of the genetic algorithm has been completed. If the solution is not satisfied, then continue steps (4)-(6) until the desired solution appears.

5 Example verification and simulation result analysis

The example in the literature 15 is quoted to verify the validity of the proposed approach (see appendix A). If let POP - SIZE = 30, PCROSSOVER = 0.35, PMUTATION = 0.06 (the definitions of POP - SIZE, PCROSSOVER and PMUTATION are shown in part 4), the simulation process has ended at the twentieth generation and the best chromosome v^* appeared at the eighteenth generation. v^* = [0.000015157580 38, 0.00067093147337], $\boldsymbol{A} = (a + \Delta a^*, b + \Delta b^*) = (0.0000151575 8038, -0.05292906852663)$, $r^* = 1.00022536885910$.

Table 1, figure 3 and figure 4 show the simulation results.

Table 1 Simulation results

	Fitted radius r^*	Maximum radius radius r_{max}	Minimum radius r_{min}	Circularity Δr
Least square solution	1.0005	1.00514	0.995878	0.009263
Minimum zone solution of literature 15				0.0085
Minimum zone solution of the paper	1.00022536885	1.00449436739	0.99595637032	0.00853799707

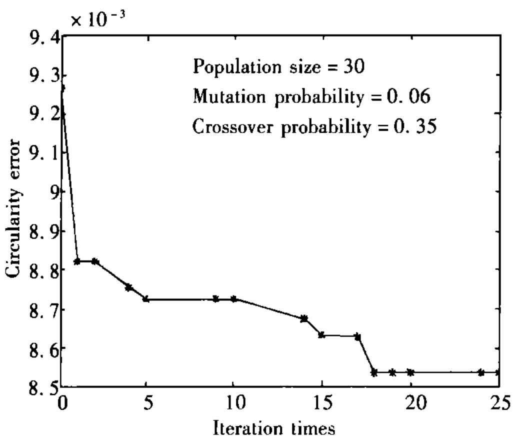

Fig. 3 Relationship between iteration times and circularity error.

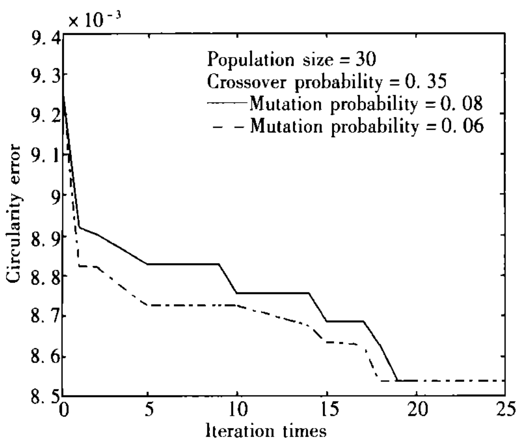

Fig. 4 Comparison of circularity for different mutation probability.

The simulation results indicate that the accuracy obtained by the proposed method is higher than the least square method (see table 1). Because of the features of parallel searching of the genetic algorithm, the obtained solution could be assured a global one to a largest extent. As is seen in figure 4, a smaller mutation probability could converge to the optimum solution rapidly.

6 Conclusion

The genetic algorithm has simulated such principles of the nature as "struggle for life" or "survival of the fittest". It has been used in a wide range of engineering practice, especially in nonlinear optimization problems. The circularity error assessment is just a nonlinear problem, which has some difficulty in implementation through existing methods. The paper successfully evaluates the form error of a circle by a genetic algorithm based approach. The simulation results show that the proposed algorithm can solve the problem with a relative high quality and efficiency. Undoubtedly, it is very significant for this technology to improve the inspection quality in modern manufacturing industry and its future is very bright.

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Appendix A. The sampling data on the $x - y$ coordinate system[15]

No.	X	Y	No.	X	Y
1	1.0249	0.0863	21	− 0.5795	− 0.8424
2	0.9991	0.2226	22	− 0.9618	0.0170
3	0.5974	0.7736	23	− 0.9454	− 0.2605
4	0.4731	0.8485	24	− 0.9077	− 0.3956
5	0.8803	0.4794	25	− 0.8443	− 0.5203
6	0.8017	0.5899	26	− 0.7764	− 0.6394
7	0.9527	0.3551	27	− 0.4635	− 0.9195
8	0.7047	0.6884	28	0.4736	− 0.9507
9	0.2101	0.9295	29	0.5942	− 0.8781
10	0.0708	0.9483	30	− 0.2059	− 1.0269
11	− 0.0683	0.9382	31	0.9950	− 0.3272
12	− 0.8432	0.4157	32	1.0218	− 0.1921
13	− 0.9022	0.2890	33	− 0.0686	− 1.0512
14	− 0.9394	0.1561	34	0.0710	− 1.0568
15	− 0.2071	0.9218	35	0.2087	− 1.0377
16	− 0.3381	0.8782	36	0.3445	− 1.0078
17	− 0.4643	0.8132	37	0.7082	− 0.7982
18	− 0.5771	0.7369	38	0.8873	− 0.5832
19	− 0.7763	0.5367	39	0.9510	− 0.457
20	− 0.6838	− 0.7485			

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基于遗传算法的圆度误差评估

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摘要: 将遗传算法应用于圆度误差的评定。首先简介了误差评定背景和遗传算法及其特点。然后根据尺寸和公差的数学定义[1]给出满足最小区域条件的圆度公差评定的数学模型和适应度函数。接着, 以最小二乘解作为初始值, 对圆度误差的遗传优化过程进行了详细的论述。最后用实例对算法进行验证。优化过程和实验结果显示了遗传算法在解决形状公差的评定这类非线性问题的优越性, 通过并行搜索能最大限度地保证解的全局最优, 计算精度高、效率高, 且易于理解和实现。

关　键　词: 圆度; 遗传算法; 误差评定

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