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Precise Pose Alignment through the Combined Method of Differential Evolution and Simplex Algorithm

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Abstract

In reverse engineering applications, there is a problem of precise alignment from measured data to a CAD model. This paper presents a new method where the measurement points can be precisely aligned with its corresponding CAD model. Initially, the measured data is aligned approximately through a least-square method with the minimum distance principle. Based on this initial alignment result, the precise alignment is completed through the Differential Evolution (DE) algorithm and the Simplex method. The experimental results show that the alignment algorithm proposed in this paper possesses an accuracy of 0.055□m and spending less processing time than the genetic algorithm. Therefore, the proposed method is effective for the measured data alignment to the original surface model.

Keywords*: Pose Alignment, Measurement points, Differential Evolution, Original surface model*

1. Introduction

Surface alignment technology plays an important role in the evaluation of surface quality, machining error and measurement error. The iterative closest point (ICP) algorithm is the most commonly used method for data alignment among the existing alignment algorithms, which has the characteristics of simple objective function, fast convergence, and is suitable for many geometric parts [1]. However, ICP algorithm may lead to an alignment failure because of local convergence or due to the presence of a large deformation locally on the free-form surface.

At present, a lot of research focuses on free-form surface alignment [2- 5]. Liu [4] proposed a two-step alignment method where initially the surfaces are approximately aligned and then precisely aligned based on a genetic algorithm. These methods possess a strong adaptability and stability, but are time consuming when used in practice. Xu [6, 7] proposes an alignment method based on a curved surface feature, getting the initial transform matrix according to the curvature of three feature points, which is simple and easy to calculate, but it is difficult to ensure the alignment accuracy because of small random errors in the measured data. Ko et al [8, 9] studied recently the surface alignment problem, based on the intrinsic geometric properties of the surfaces. Compared to the iterative alignment method, it does not need to calculate the initial transformation matrix. Compared with the curvature-based alignment method, the method reduces the influence caused by measurement position and data density, however, it will inevitably generate multi-constraint relationships when applied to complex surfaces consisting of many similar surface patches, which may result in an alignment failure.

In this paper a new algorithm is presented, in order to meet the higher accuracy, stability and faster convergence rate requirements. This paper proposed an alignment method that approximately fits the surfaces using a least squares technique and then uses a combination of two precise alignment techniques, the differential evolution (DE) algorithm and then the Simplex Method. There are only three feature points used in the initial alignment to get the initial transformation matrix, which simplify the algorithms. The comparative experiment results verify that the proposed algorithm is a faster and more accurate method for the surface alignment problem.

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2. Alignment Method

2.1. Initial Alignment through Least Square Method

There are two data sets in the initial alignment, the measured points denoted by Pi (i = 1,2, ..., n); and the other points belong to the CAD model surface denoted by Qi (i = 1,2, ..., n), The key to the alignment process is to find a geometric transformation matrix T. By the transformation of P′= P ·T, the measured points should include the CAD model surface as much as possible.

Suppose the geometric transformation matrix T is

$$\mathbf{T}=\begin{bmatrix}\mathbf{R} & 0\\ \mathbf{P} & 1\end{bmatrix},\quad \mathbf{P}\in R^3,\ \ \mathbf{R}\in O(3) \tag{1}$$

where O(3) is an orthogonal matrix where the determinant equals 1; P or R are matrices that describe the position between the measured data and the CAD model:

$$\mathbf{R}=\begin{bmatrix}\cos\alpha\cos\beta & \cos\beta\sin\alpha & -\sin\beta\\ \sin\alpha\sin\beta\cos\gamma-\cos\alpha\sin\gamma & \sin\alpha\sin\beta\sin\gamma-\cos\alpha\cos\gamma & \sin\alpha\cos\beta\\ \cos\alpha\sin\beta\cos\gamma+\sin\alpha\sin\gamma & \cos\alpha\sin\beta\sin\gamma-\sin\alpha\cos\gamma & \cos\alpha\cos\beta\end{bmatrix}$$

$$\mathbf{P}=[P_x,P_y,P_z]$$

here, [Px,Py,Pz]are translational components, and α, β, γ are the rotational components about the X, Y, Z axes respectively.

Firstly, three feature points denoted by Qi (i = 0, 1, 2) were taken on the CAD model surface, then find the closest corresponding measured points denoted by Pi (i = 0, 1, 2). Finally, structure two groups of unit vectors as following according to the three pairs of points shown in Figure 1.

$$e_1=\frac{P_1-P_0}{|P_1-P_0|},\ e_3=e_1\times\frac{P_2-P_0}{|P_2-P_0|},\ e_2=e_3\times e_1 \tag{2}$$

$$e_1^{'}=\frac{Q_1-Q_0}{|Q_1-Q_0|},\ e_3^{'}=e_1^{'}\times\frac{Q_2-P_0}{|Q_2-P_0|},\ e_2^{'}=e_3^{'}\times e_1^{'} \tag{3}$$

Then set P_0, Q_0 as origin point, and set the unit vectors e1, e2, e3 and e1′, e2′,e3′ as axes, creating two local coordinate systems denoted by Q_0-XYZ and P_0-XYZ respectively. Suppose that the two local coordinate systems overlap perfectly after transformation in Eq.1, it must have

$$[e_1\quad e_2\quad e_3]^T\bullet\mathbf{R}=\left[e_1^{'}\quad e_2^{'}\quad e_3^{'}\right]^T$$

Because of the unit vectors e1, e2, e3, we have

$$\left([e_1,e_2e_3]^T\right)^{-1}=[e_1,e_2e_3]$$

So we can get that

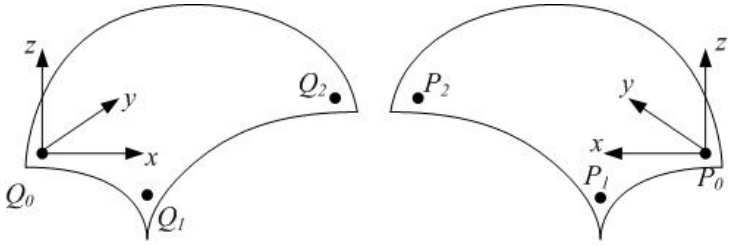
$$\mathbf{R}=[e_1\quad e_2\quad e_3]\bullet\left[e_1^{'}\quad e_2^{'}\quad e_3^{'}\right]^T$$

Solving Eq. 3, we get that

$$\alpha=\arctan\frac{R_{23}}{R_{33}},\quad \beta=\arctan\frac{-R_{13}}{\sqrt{R_{23}^2+R_{33}^2}},\quad \gamma=\arctan\frac{R_{12}}{R_{11}} \tag{4}$$

Finally, the translational components Px, Py, Pz can be calculated by the expression of R:

$$P = P_0 \cdot R - Q_0 \quad (5)$$



a)Target points b) Measured points

Figure 1. Relation between the two local coordinate systems

After the initial alignment mentioned above, the six parameters of geometric transformation matrix (three translational components [Px, Py ,Pz], and three rotational components [α , β , γ] can be approximately determined, then the general orientation of the measured data is known.

2.2. Precise Alignment through the Combined Method

Although the measured data is aligned to the curved surface after the initial alignment, it may not satisfy the accuracy requirements. In order to improve the accuracy of the alignment, this paper proposes a combined two-step alignment method including a Differential Evolution (DE) algorithm and then Simplex Method, which is used to carry out the optimization of the geometric transformation matrix.

First of all, the objective function was constructed on the basis of least-square method with minimum condition principle, the optimum function can be described as:

$$F(\alpha,\beta,\gamma,P_x,P_y,P_z) = \min\sum_{i=0}^{n} \| P_i \bullet \mathrm{T} - Q_i \| \quad (6)$$

where i =0, 1, ..., n; n is the number of measure points; Qi is the points on CAD model surface; Pi is the closest measured point corresponding to the point Qi.

2.3. First Step of the Precise Alignment through a Differential Evolution Algorithm

The differential evolution algorithm, presented by Storn and Price [10,11], is a global optimization algorithm for population evolution. The DE algorithm has been proved to be effective, convergent and robust in the searching process and is applied to solve the alignment problem in this paper. The DE algorithm searches directly for the best solution and it solves the problem in a practical way with few control variables in the evolution process, together with a fine adjustment function in mutation operation, which the genetic algorithm does not have.

The DE algorithm, begins with a random initial values, calculates iteratively following certain rules such as mutation, crossover and selection. Finally, the optimal values will be retained while the inferior values will be eliminated according to each value's fitness, thus the search process can be guided to the optimal solution. The implementation of the DE algorithm is described as follows:

(1) Initialization

In order to get the initial value to start the optimal search, the population must be initialized. Generally the initial population is expressed as S = {X1, X2, ⋯, Xn} and the ith individual defined as Xi = {Xi,1,Xi,2,⋯,Xi,D}, where D is the solution of the space dimension.

The initial population is chosen randomly from the given constraint boundary [lb, ub], and it should cover the entire parameter range, we can refer to the six values of the matrix calculated from the initial alignment (three translational components [Px, Py, Pz] and three rotational components [a， β， γ]), so the variable range (from lb to ub) of independent variables can be set as follow:

$$\begin{aligned} lb[i] &= P_i - C_{1i}, ub[i] = P_i + C_{1i} \\ lb[j] &= R_j - C_{2j}, ub[j] = R_j + C_{2j} \end{aligned} \quad (7)$$

where i and j=1,2,3; P_i represents respectively three translational components as Px, Py, Pz; Rj represents respectively three rotational components a, β , γ ; C1i and C2i represent constants, which can be set respectively corresponding to the values of three translational components and three rotation components.

(2) Individual evaluation

Eq. 6 is used to calculate each individual value denoted by F (Xi). The distance of one single point Pi to the curved surface can be refer to the Quick Iteration method [12].

(3) Variation ---discrepancy

For each parameter vector Xi (i = 1, 2, ... , n) of the gth population, its variate vector can be calculated by the expression:

$$V_{i,g+1} = X_{r_1,g} + F(X_{r_2,g} - X_{r_3.g}) \quad (8)$$

where, r1, r2, r3∈(1, 2, ⋯ ,n), and satisfy: r1 ≠ r2 ≠ r3; F∈[0, 2] is a real and a constant, which modify the variable of, and controls its effect.

(4) Cross-breeding

In order to maintain the diversity of the population, the cross-breeding is introduced to get a candidate vector Ui = [U1i, U2i, ⋯, Uni], which derive from the target vector Xi and the variation vector Vi, and the Uji is:

$$U_{ji,g+1} = \begin{cases} V_{ji,g+1} & if\,(randb(j) \le PC) \,\|\, j = r(i) \\ X_{ji,g} & if\,(randb(j) > PC) \,\|\, j \ne r(i) \end{cases} \quad (9)$$

where i and j = l, 2, ⋯, n; r(i)∈[1,n], is a integer sequence selected randomly, ensuring Uji,g+1 to obtain a parameter from Vi,g+1; randb(j)∈[0,1] is a random constant; cross--breeding factor PC, a parameter of DE algorithm, controls the probability of the current individual replaced by the mutational individual and PC∈[0,1].

(5) Selection

Compare the objective function values, corresponding independent-variables is the target vector Xi of the current population and the candidate's vector Ui, Xi will be replaced by the Ui if the corresponding objective function value is more optimized, otherwise original Xi is kept in the next iterative process. As a consequence, individuals of successive generations will be increasingly more optimal than previous generations.

$$X_{i,(g+1)} = \begin{cases} U_{i(g)} & if\,(f(U_{i(g)}) \le f(X_{i(g)})) \\ X_{i(g)} & otherwise \end{cases} \quad (10)$$

(6) Replacement of the objective function

When the objective function values of optimal individuals has not changed for 20 generations, the objective function in Eq. 6 should be optimized and then go to step (3); otherwise, turn to step (7).

(7) Terminate test

If the solution Xi(g+1) satisfies the terminating condition (< a user define value), Xi(g+1) will be the optimal solution and then exit, otherwise turn to step (2).

The flow chart of DE algorithm is shown in Figure. 2. When the search is terminated, the accuracy of the six transformation parameters will be a great improvement on the least squares alignment method.

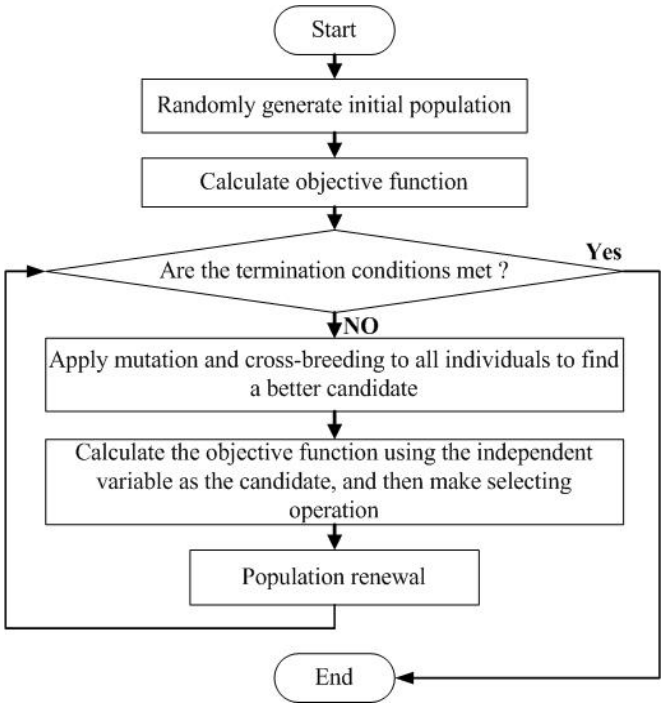


Figure 2. Flowchart of DE algorithm

2.4. Second Step of the Precise Alignment through the Simplex Method

In order to further improve the accuracy of the alignment for the application of precision machining and measurement, the Simplex method is used to further optimize the geometric transformation matrix, where the initial value XG of the method will be assigned with the optimal value from the previous DE algorithm.

Simplex method is a direct search method that does not need to calculate the function gradient, it will converge to the optimal value automatically, the process described as follows:

(1) Calculate and compare the function value Fi = F(Xi) (i = 0,1, ..., n), where the initial population is expressed as Xi =[**α**, **β**, **γ**, Px, Py, Pz] (i = 0,1, ..., n). So we will get the maximum and minimum value denote by F_R and F_L:

$$F_R = F(X_R) = \max_{0 \le i \le n} F_i$$
$$F_L = F(X_L) = \max_{0 \le i \le n} F_i \quad (11)$$

where, FR is the maximum value of Fi, FL is the minimun value of Fi.

(2) Calculate the symmetrical value of the worst point X_R, which is denoted by X_N,

$X_N = 2X_F - X_R$ and $X_F = \frac{1}{n}\sum_{i=0}^{n}(X_i - X_R)$

(3) If $F(X_N) \ge F_R$, then X_N will be replaced by X_M, which is expressed as：

$X_M = (1-\lambda)X_R + \lambda X_N$

If $F(X_M) \geq F(X_0)$ then XR = XM ; otherwise, $X_i = \frac{X_i + X_L}{2}$,and iterated again.

(4) If $F(X_N) < F_R$, then X_N is be replaced by X_E, which is defined as:

$$X_E = (1-\mu)X_R + \mu X_N \quad (\mu > 1)$$

meanwhile, if $F(X_M) < F(X_0)$ then $X_R = X_E$; otherwise, $X_R = X_G$.

(5) when $F_R - F_L < \varepsilon |F_L|$ whereεis a very small positive integer, then the program ends.

A higher degree of accuracy is achieved between the two surfaces after the second precise alignment based on the Simplex algorithm. However, during the optimization process, the transformational components Px, Py, Pz and the rotational components a, β , γ are dimensionally consistent, but they are different from each other. When a unit increment is applied to all the six parameters at the same time a slower convergence is achieved. This may be eliminated by applying six different incremental variables to the values Px, Py, Pz, a, β , γ .

Generally these six variables should be made scale transformation, after the transformation, all variables become dimensionless, same-magnitude and closer variation range. The scale transformation formula is

$$X_i = k_i \bullet X_i^{'}(i = 0,1,...,n-1) \;\; k_i = X_i^{(0)}(i = 0,1,...,n-1) \tag{12}$$

where, n is the number of the variables; X'_i is a variable that has not been transformed; $X_{i'}$ is a variable that has been transformed; k_i is a scale transformation coefficient, $X_i^{(0)}$ is an initial value of the optimizing algorithm.

Through the combined precise alignment method, the virtual measured data are aligned with the CAD model which is shown in Figure.3. The transformation matrices are generated and expressed in Table 1. If these two data sets align perfectly, the transformation matrix T should be the reverse of the original transformation theoretically. Table 1 shows the initial alignment matrix after rough alignment, in which the three measured points have been added some random error to simulate real measurement data.

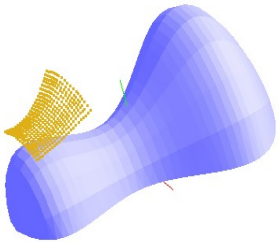


Figure 3a.The initialization state of measure points and CAD model surface

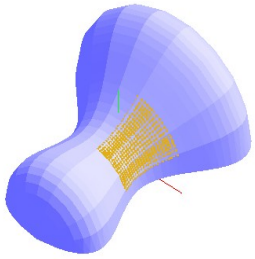


Figure 3b. Aligned points through the proposed method

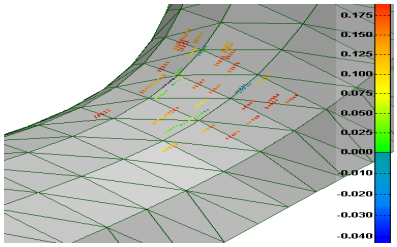


Figure 3c. Alignment Error map of the measured points

3. Experimental Verification

This section provides a numerical experiment of surface alignment between measured data and CAD model surface. First of all, 200 virtual points were generated on a local area of the free-form surface CAD model. This surface is then rotated (α = 0.1, β = 0.2, γ = 0.3) and translated (Px = 10, Py = 20, Pz = 30). This displaced surface is the aligned to the CAD model using double precision alignment algorithm described in this paper.

The algorithm was run on the personal computer with a Pentium 4 1.8GHz CPU and 512MB of RAM. The parameters of DE algorithm were set as follows: the maximum evolution generation Gen = 200, the crossover probability Pc = 0.75, population size N = 100.

To compare the efficiency of this algorithm, this paper calculates an alignment matrix based on the genetic algorithm and the CPU processing time used to calculate the result,

shown in Table 1. Through the comparison, it can be seen that the alignment algorithm proposed in this paper has a higher accuracy and faster calculation time than that of the genetic algorithm based method.

Table 2 shows the alignment errors of a number of selected points on the surface model with their corresponding points, which are processed first and then aligned through the proposed method. From the Table 2 , we can see that the average alignment error between virtual measured data and the surface model is 0.055μm, and the variance of the errors is 0.071μm, demonstrating that this method proposed can achieve a high accuracy for the data processing in precise measurement and quality evaluation.

Table 1. Alignment matrix and its comparison with the theoretical transforming matrix

Alignment method	Transforming matrix		Compared results	
	Rotational matrix	Translational matrix	Error in Rotational matrix	Error in Translational matrix
Theoretical Matrix	$\begin{bmatrix} 0.93629 & 0.31299 & -0.15935 \\ -0.28963 & 0.9447 & 0.15379 \\ 0.19867 & -0.09784 & 0.97517 \end{bmatrix}$	$\begin{bmatrix} -10 \\ -20 \\ -30 \end{bmatrix}$	---	---
Through the proposed Initial alignment	$\begin{bmatrix} 0.8116 & 0.32134 & -0.25531 \\ -0.12323 & 1.04519 & 0.09 \\ 0.30612 & -0.19125 & 1.17414 \end{bmatrix}$	$\begin{bmatrix} -7.5568 \\ -21.1974 \\ -28.1456 \end{bmatrix}$	$\begin{bmatrix} 0.12469 & -0.00835 & 0.09596 \\ -0.1664 & -0.10049 & 0.06379 \\ -0.10745 & 0.09345 & -0.19897 \end{bmatrix}$	$\begin{bmatrix} -2.4432 \\ 1.1974 \\ 1.8544 \end{bmatrix}$
Through the proposed precise alignment method	$\begin{bmatrix} 0.93629 & 0.31297 & -0.15936 \\ -0.28961 & 0.94471 & 0.15377 \\ 0.19868 & -0.09781 & 0.97517 \end{bmatrix}$	$\begin{bmatrix} -9.99981 \\ -20.00011 \\ -30.00022 \end{bmatrix}$	$\begin{bmatrix} 0 & 0.00002 & 0.00001 \\ -0.00002 & -0.00001 & 0.00002 \\ -0.00001 & -0.00003 & 0 \end{bmatrix}$	$\begin{bmatrix} -0.00019 \\ 0.00011 \\ 0.00022 \end{bmatrix}$
Through the Genetic algorithm	$\begin{bmatrix} 0.93634 & 0.31291 & -0.1593 \\ -0.28969 & 0.94471 & 0.15371 \\ 0.19871 & -0.09781 & 0.97518 \end{bmatrix}$	$\begin{bmatrix} -9.99873 \\ -20.00139 \\ -30.00151 \end{bmatrix}$	$\begin{bmatrix} -0.00005 & 0.00007 & -0.00005 \\ -0.00006 & -0.00001 & 0.00008 \\ -0.00004 & -0.00003 & -0.00001 \end{bmatrix}$	$\begin{bmatrix} -0.00127 \\ 0.00139 \\ 0.00151 \end{bmatrix}$

Table 2. Alignment error between measured points and surface model

No.	Points on surface model [mm]	Aligned corresponding points [mm]	Alignment error [mm]		
	P(x,y,z)	P'(x',y',z')	Error	Mean Error	Variance Error
1	(14.0215, 13.5324,-0.11555)	(14.0259, 13.5314, -0.11059)	0.00006989		
2	(11.3928, 20.6641, -5.83346)	(11.3909, 20.6684, -5.83005)	0.00003376		
3	(9.84968, 13.7041, 5.89973)	(9.84666, 13.7047, 5.89584)	0.00003982		
4	(13.0561, 13.4097, 1.24933)	(13.054, 13.4114, 1.24039)	0.00008724	0.000055	0.000071
5	(12.7095, 10.8738, 14.0892)	(12.7054, 10.8699, 14.0897)	0.00005625		
6	(13.5519, 10.3542, 15.7081)	(13.5476, 10.3577, 15.7151)	0.00003844		
7	(4.11283, 21.4939, -3.73232)	(4.11291, 21.4941, -3.7262)	0.00004096		
8	(12.9409, 17.6111, -3.68366)	(12.9429, 17.6018, -3.68615)	0.00009584		
9	(10.0577, 13.389, 6.41912)	(10.0582, 13.3871, 6.415254)	0.00002773		
10	(11.7059, 14.5873, 1.23544)	(11.7063, 14.5885, 1.22579)	0.00006480		

Another experiment was carried out on a twisted blade. Figure.4a shows a number of virtual measured points P on the local area of the blade. The data P is transformed to the P' through the translation and rotation matrix M as the measured points, which has a different coordinate system as the original blade model. Through the process of the proposed alignment method, the measured points P' are aligned with the original model. The alignment error can be obtained by the comparison of the aligned points with the original model, which is shown in Figure.4b. From the comparison result, we can find that the mean error is 0.001mm and the STD deviation is 0.003mm. Through the two examples, it can be proven that the proposed alignment method is effective and accurate for the alignment. Further work is being carried out to demonstrate the robustness of the proposed method.

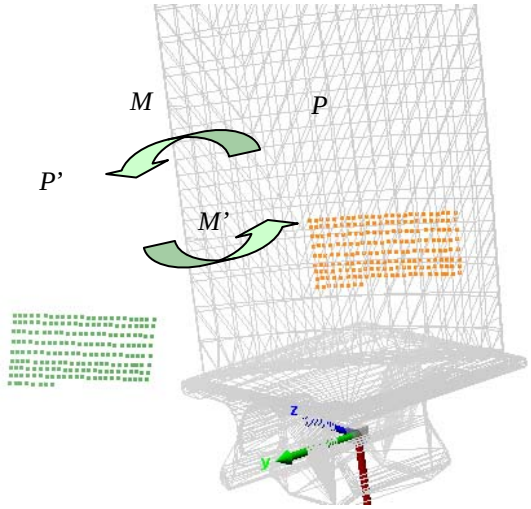


Figure 4a. The initialization state of the measure points and CAD model

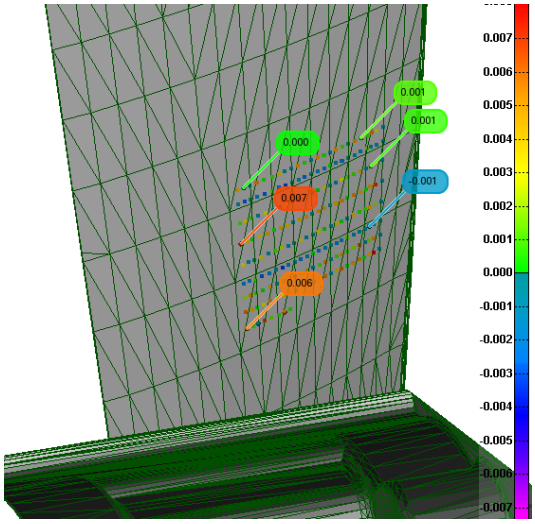


Figure 4b. Alignment error comparison (Mean error=0.001mm, STD Dev =0.003mm)

4. Conclusion

Considering the problems existing on inaccurate alignment between the measured points data to the original free-form surface model, this paper proposed a combined precise alignment method to find the optimal alignment which consisting of a rough alignment and a two-step precision alignment. The objective function is constructed by combining least-squares method with the minimum conditions principle, and then the DE algorithm and the Simplex Method algorithm were used to get the best transformation matrix of the two data sets. From the experiment results, we find that the alignment method presented in this paper possesses a accurate alignment result.

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