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A kinematic calibration method and its application to eva spacesuit mobility measuring mechanical arm

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ABSTRACT

A space suit mobility measuring mechanical arm was developed to test astronauts' capabilities in space-suited extravehicular activity (EVA). The equipment is based on combined coordinate measuring mechanical arm (CCMMA) to measure the space region coordinate of astronauts' reach envelope and work envelope. For improving measurement precision, the distance error model of CCMMA was set up on the basis of Modified Denavit-Hartenberg (MDH). A kinematic calibration method was presented on the basis of Genetic Simulated Annealing Algorithm (GSAA). Calibration experiments were carried on using the method. Results prove the effectiveness of the method and the improvement of accuracy to the equipment.

KEYWORDS

Mobility measurement; Improved genetic algorithm; Combined coordinate measuring mechanical arm; Kinematic libration.



INTRODUCTION

The space suit is the life support and safety protection system for astronauts during EVA. Currently, most manufacturing technology of space suit is pressurized fabric structure, which makes maintaining life support pressure and keeping on a high level of mobility to be a contradiction^[1]. Evaluation and measurement of EVA spacesuit mobility are mainly from three major aspects: view envelope, reach envelope and operational envelope. Therefore, a special measurement instrument based on combined coordinate measuring mechanical arm (CCMMA) is developed to measure astronauts' motion region characteristics (range of motion, reachable region) and biomechanics characteristics (forces, torques) simultaneously. Compared with traditional coordinate measurement machine, CCMMA is more difficult to calibrate, due to many factors such as self-weight increase, elastic deformation, etc.

CCMMA is similar to the robot arms in mechanical structure and kinematic model. Despite different function and driving mode between them, many study methods of robot are also used for CCMMA. As one of the most important ways to improve the accuracy of CCMMA, kinematic calibration attracts many studies^[2-5]. A simple and feasible calibration method is presented in this article. Distance error model based on MDH of CCMMA is set up. Using the model, a method with GSA algorithm is presented to calibrate kinematic parameters. Then the method is applied to calibration experiment of CCMMA to test the efficiency of the calibration method.

THE KINEMATICS MODEL OF CCMMA

Mechanical structure

The mechanical structure of the test equipment of EVA spacesuit operational ability includes 4 rotational mechanical arms in a horizontal plate, an elevation device and a mechanics sensor unit at the end of the arms. The whole equipment is installed on a pillar of the laboratory, shown as Figure 1.

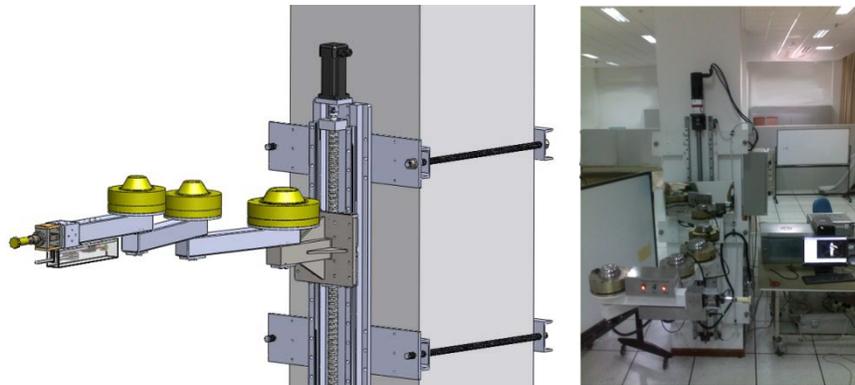


Figure 1 : Model and photo of CCMMA

Articulated coordinate measurement arm is applied in the mechanical structure of the equipment. The astronaut holds the handle to move as far as he can to accomplish reachable region tests, with the angle sensors in each joint measuring the angles to calculate and record the space coordinate of the handle and the reachable region real-timely. Similarly other tests are conducted on the operational region. Differently, in the tests of the operational region, the brake devices lock each joint when astronauts apply force on the measurement handle in the designated positions, so as to detect the operational ability including thrust force, grip strength and torques.

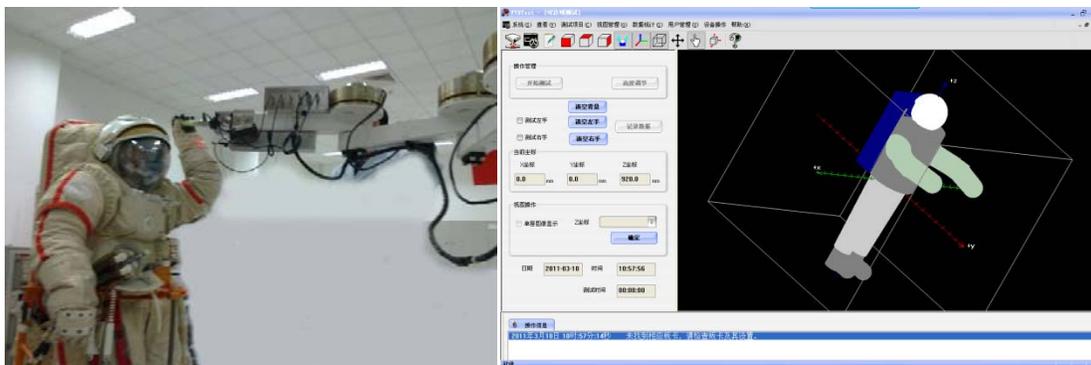


Figure 2 : CCMMA and software for astronaut operation test

Kinematic Model

The Denavit-Hartenberg (D-H) model is the most frequently used kinematic mathematics model for studying robot kinematics. In the model, there are 4 independent structure parameters ($l_i, \alpha_i, d_i, \theta_i$) is devoted to describe the relationship of adjacent linkages. Despite many obvious advantages of the D-H model, there are still some problems in this application. A small error in two theoretically-parallel linkages will lead to considerable error in the test result. Many scholars have studied modified D-H (MD-H) model to solve this problem.

As is demonstrated, the 3D mechanical structure of CMMs in the Figure 3 and Coordinate System of CCMMA in the Figure 4, due to manufacturing tolerance, assembling accuracy and deformation of linkages, the first, second and third joints which are theoretically mutually parallel. But in fact, there will inevitably have minor errors between each other. These minor errors will be magnified through the length of linkages when calculating the position and gesture of the end of CCMMA by the D-H model. Since the traditional D-H model is based on the absolutely parallel linkages, it has to be modified to study the linkages with adjacent parallel joints mentioned above. In this paper, MD-H model of five parameters is applied, which is shown in Tab. 1.

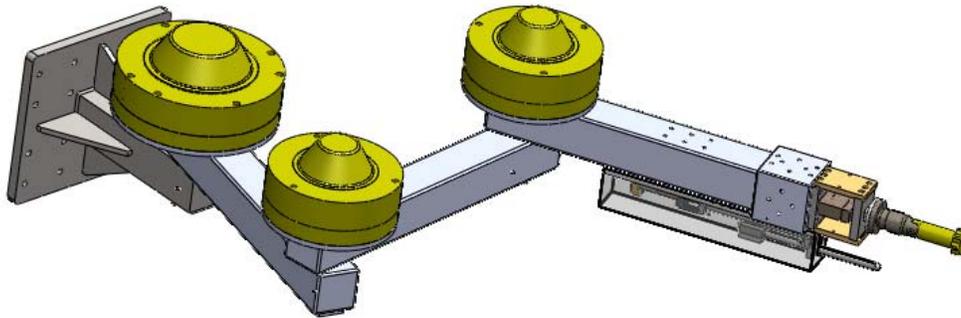


Figure 3 : Three dimension mechanical structure of CCMMA

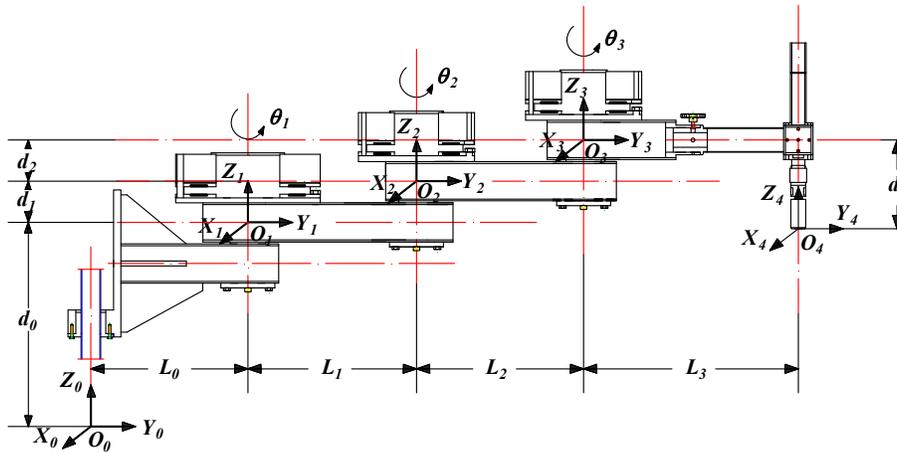


Figure 4 : Coordinate system of CCMMA

TABLE 1 : Designed structure parameters of the mechanical arms

joint i	length of arm l_i (mm)	deviation of joints d_i (mm)	angle of the arm α_i (Deg.)	rotate of the arm β_i (Deg.)	rotate angle of the joint θ_i (Deg.)
1	L_0	z_1	0	0	0
2	L_1	40	0	0	θ_1
3	L_2	40	0	0	θ_2
4	L_3	-40	0	0	θ_3

In the MD-H model, the homogeneous transform matrix between adjacent coordinate systems $\{x_i, y_i, z_i\}$ and $\{x_{i-1}, y_{i-1}, z_{i-1}\}$ is shown as follow.

$$T_{i-1}^i = \text{rot}(z, \theta_i) \text{trans}(z, d_i) \text{trans}(x, a_i) \text{rot}(x, \alpha_i) \text{rot}(y, \beta_i) = \begin{bmatrix} C\theta_i C\beta_i - S\theta_i S\alpha_i S\beta_i & -S\theta_i C\alpha_i & C\theta_i S\beta_i + S\theta_i S\alpha_i C\beta_i & L_i C\theta_i \\ S\theta_i C\beta_i + C\theta_i S\alpha_i S\beta_i & C\theta_i C\alpha_i & S\theta_i S\beta_i - C\theta_i S\alpha_i C\beta_i & L_i S\theta_i \\ -C\alpha_i S\beta_i & S\alpha_i & C\alpha_i C\beta_i & d_i \\ 0 & 0 & 0 & 1 \end{bmatrix} \tag{1}$$

Where $C\theta_i$ represents $\cos \theta_i$, $S\theta_i$ represents $\sin \theta_i$.

The kinematics model of CCMMA can be obtained by the Eq. (1) as follow:

$$T_0^4 = T_0^1 T_1^2 T_2^3 T_3^4 \tag{2}$$

Restricted by mechanical structure, the first joint is a shifting joint, moving along the driving screw vertically. The others are revolute joints, with rotational ranges of θ_2 $[-145^\circ, 145^\circ]$, θ_3 $[-145^\circ, 145^\circ]$, θ_4 $[-145^\circ, 145^\circ]$ respectively.

KINEMATICS CALIBRATION METHOD

Distance error model

CCMMA is similar to robot arm in mechanical structure. Calibration methods of robot arm are also used for CCMMA. Different from calibration of robot, there are no problems of posture error in calibration of CMMs, without getting involved in the problem of command distance. From Eq. (2), ending positions of CCMMA can be obtained by acquisition angle of each joints and the real-time calculation with designed structure parameters. However, the actual structure parameters is not equal to the designed, because of error influence during machining and assembling processing.

As shown in Tab. 1, the deviation between designed values and actual value is described as error vector $\Delta q = (\Delta\theta_i, \Delta\alpha_i, \Delta\beta_i, \sum d_i, \Delta L_i)$. The distance between test coordinate value and actual value of position can be described as:

$$d_i = \sqrt{(x_i - x_0)^2 + (y_i - y_0)^2 + (z_i - z_0)^2} = f(\theta_i, \Delta q_i) \tag{3}$$

(x_0, y_0, z_0) and (x_i, y_i, z_i) represent actual value and test coordinate value of position respectively. θ_i represents joints' angle. Δq_i represents structure parameters error. Simultaneous equations are established by Eq. (2) and Eq. (4) with distance errors set zero. If enough outcomes are measured, the real value or its approximation of Δq can be obtained by solving simultaneous equations. a distance error model instead of position error model is adopted as:

$$D_{ij} = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2 + (z_i - z_j)^2} = g(\theta_i, \theta_j, \Delta q_i) \tag{4}$$

(x_i, y_i, z_i) and (x_j, y_j, z_j) represent test coordinate value of different test points, D_{ij} represents the distance of between two test points. θ_i, θ_j represents joints angle of test points.

In order to simplify the operation of identification, take the square of Eq. (4) as objective function. The identification in essence is a processing to find structure parameters making the distance error reduce to or approach zero. Obviously it is a parameter estimation of nonlinear model. So it is fitting and proper to solve equation using Genetic Algorithm.

GENETIC SIMULATED ANNEALING ALGORITHM(GSAA)

Genetic algorithm is a random search algorithm that simulates natural selection and evolution. It searches through the total solution space and can find the optimal solution globally over a domain. Simple Genetic algorithm can easily get local minimization. Annealing algorithm can easily avoid local optima, but it has the problem of slow convergence to reach the global optima. It is effective to combine the two algorithms. Such as in GSAA, a simulated annealing algorithm is used to alleviate the selection pressure of the genetic algorithm, and enhance the global convergence of GSAA.

In GSAA, the genetic algorithm is served as the main flow of the new algorithm for global search; simulated annealing algorithm adjusts the optimization population to avoid trapping in the local optimum.

In the process of evolution, the adaptive crossover probability p_c and mutation probability p_m are adopted. The value of p_c and p_m is calculated by Eq. (5).

$$p = \text{random}(0,1) \times \frac{f_{\max} - f(x)}{f_{\max} - f_{\min}} \tag{5}$$

The Metropolis criterion is adopted to judge the population in new generation can be accepted or not. If $\Delta E < 0$, the individual with the best fitness in current population would be accepted as the optimal solution, otherwise, update the population with probability of $p = \exp(\Delta E / t)$, t is current temperature.

In cooling process, $t_{k+1} = \alpha t_k$, wherein coefficient of temperature drop is labeled as $\alpha \in (0,1)$.

According to principles mentioned above, the flow chart for the GSAA is shown in Figure 5.

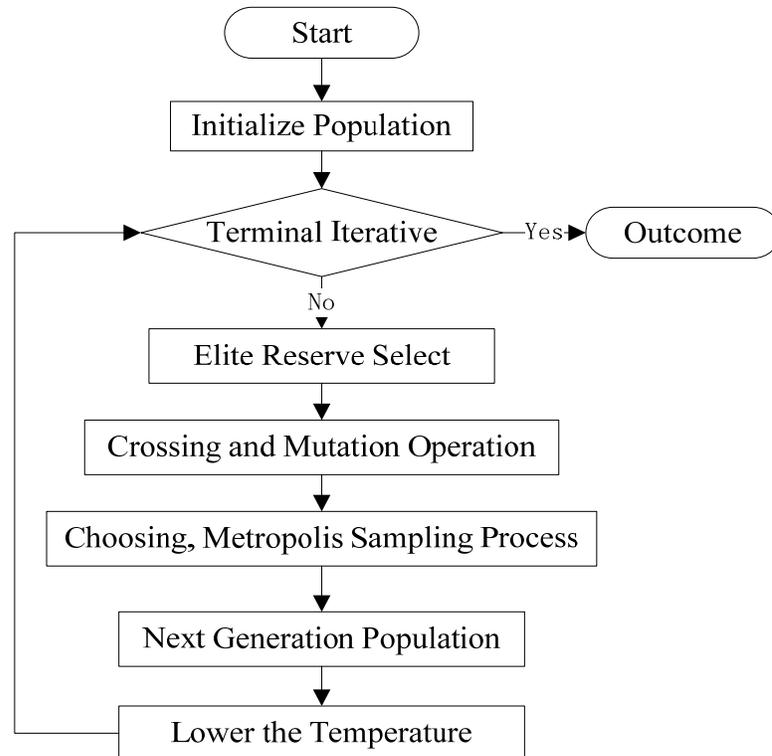


Figure 5 : Flow chart of the GSAA

EXPERIMENTAL

Calibration experiments

A calibration board with 10 holes of 100mm standard distance is used in the experiment. A needle at the end of the handle fixed in a hole of calibration board, and linkages of the arm moved with different gestures, a great number of the coordinate values are tested at the same measuring point. There are 10 points tested by this way. A routine is developed based on GSAA to find the minimum value of fitness.

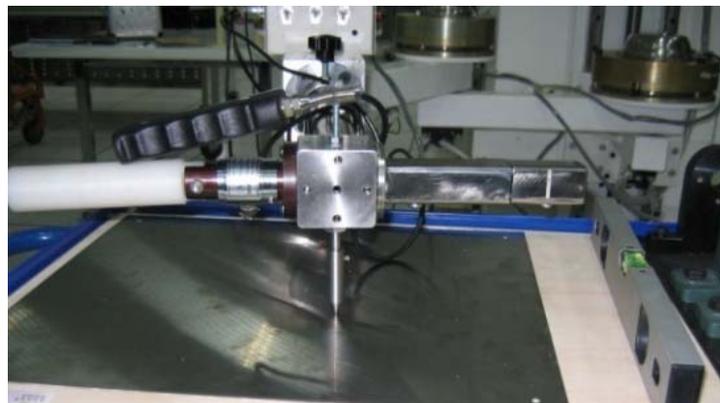


Figure 6 : Photo of calibration system

Structure parameters of the mechanical arms estimated by the experiment. The results of calibration experiment are shown in TABLE 2.

TABLE 2 : Indentified errors of structure parameters

joint <i>i</i>	length of arm $\Delta l/mm$	deviation of joints $\Delta d/mm$	angle of the arm $\Delta \alpha/rad$	rotate of the arm $\Delta \beta/rad$	rotate angle of the joint $\Delta \theta/rad$
1	0.0231	0	0	0	0
2	0.1623	0.023743	0.003054	0.001032	-0.002481
3	-0.0037	0.131200	0.001529	-0.000021	-0.000232
4	0.3299	0.014059	0.000133	-0.000735	0.001801

Verification of identification results

In order to verify effectiveness of the identification results, angle value of the viewpoints with original structure parameters and identification parameters are used separately to calculate the coordinate values and distance values. The calibration results are compared with original values, which are shown in Figure 7 and Figure 8.

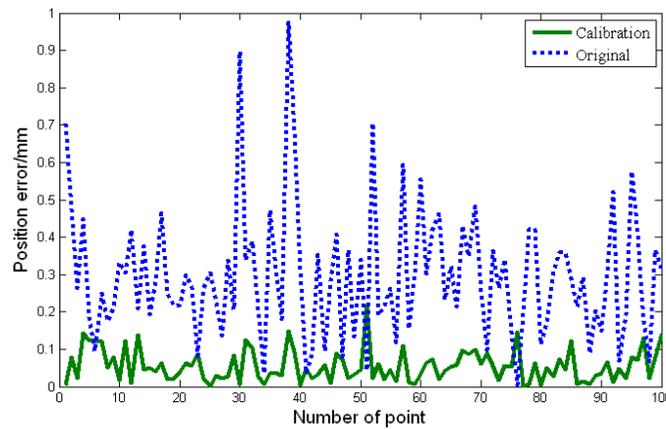


Figure 7 : Positon errors of CCMMA after identification

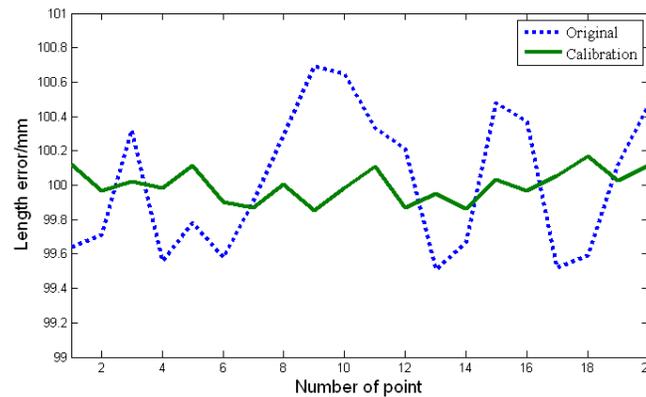


Figure 8 : Length errors of CCMMA after identification

As is indicated in Figure 4, when using designed structure parameters to calculate coordinate values, the maximum error is 0.9746, the average error is 0.2959, and the standard error is 0.1743; while using identified structure parameters to calculate, they are 0.1130, 0.0371, and 0.0332 respectively. Compared with original values, the average of the position repetitive error is improved by 7.97 times.

Also can be found in Figure 5, the length repetitive error with identified structure parameters, the maximum error is 0.1930, compared with 0.6900 in original value, the average error is 0.0637, compared with 0.3730, and the standard error is 0.0435, compared with 0.1532. Using maximum error as evaluation, the length repetitive error is improved by 3.58 times.

CONCLUSION

According to the characteristics of mechanical measurement arm for EVA spacesuit, a calibration method based on modified Denavit-Hartenberg is applied to establish kinematic model and length model repetitively, and the Genetic

Simulated Annealing Algorithm is used to identify structure parameters. Calibration experiment is carried out to verify the effectiveness of the method. Using such method can simplify the calibration process. In addition, this method based on MDH, applying improved genetic algorithm, is also applicable to calibrate other coordinate measurement machines.

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