

**TOPOLOGY AND DIMENSIONAL SYNTHESIS OF
LINKAGE MECHANISM BASED ON THE CONSTRAINED
SUPERPOSITION METHOD**

by

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ABSTRACT OF THE THESIS

Topology and Dimensional Synthesis of Linkage Mechanism

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Mechanism design consists of two parts: kinematic synthesis and kinematic analysis. The classical kinematic analysis based on graphical method or analytical method is hard to implement into computer program and have accuracy issue. In this work, a novel analysis method called the Constrained Superposition Method (CSM) is presented base on Finite Element Method (FEM). The new method is based on the penalty formulation on constrained boundaries in the finite element analysis and then applies superposition to two constrained systems for linkage analysis. Genetic Algorithm (GA) is combined with this new analysis method to solve mechanism synthesis problem. To further improve the efficiency of evolutionary optimization process, two feasibility checks are introduced to ensure the connectivity and mobility. Design examples generated from this approach will be presented.

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Dedications

This thesis is dedicated to my dear parents and sister.

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Chapter 1.

Introduction

1.1. Mechanism Design Problem

A mechanical system consists of two parts: a power source and a mechanism that control the use of this power. Solid mechanics is one of the ways to analyze the conversion of energy from the power source to the output of the mechanism. Three major branches of solid mechanics are kinematics, static and kinetics[1, 2]. Kinematics is the study of relative motion, static is the study of forces and moments on the bodies with out motion and kinetic deals with the force acted on the bodies. The main concern of this paper is to determine the mechanical constraints that provided a desired movement. This falls into the category of kinematics design.

Kinematics design can be separated into two parts: kinematics analysis and kinematics synthesis. In kinematics analysis, a specific given mechanism is analyzed based on the geometry of the mechanism and the other possible characteristics such as input angle. On the contrary, kinematics synthesis is the process of designing a mechanism to accomplish a desired task which is also the main goal of our work. To design a mechanism to fit a specific objective, two steps have to be taken which are type synthesis and dimensional synthesis. Type synthesis is the process of determining the type of mechanism and the number of joints and links. The decision made in type synthesis is mainly based on the requirement of the objective. Experienced-guess or

system modification is often used in this step since there is no method that can guarantee the user of finding the best mechanism. The dimensional synthesis calculates the proper or optimum set of dimensions for the mechanism parts that optimize the performance of the selected mechanism type.

1.2. Review of Kinematics Synthesis

Different techniques have been used for kinematics synthesis of mechanisms over the century. One approach to solve the synthesis problem is by setting precision points to be reached by the coupler point of the mechanism[3-5]. However, the number of precision point is limited in order to allow the solution of the mathematical system to be closed. Problem will be caused with wrong sequence of precision points.

As the computational power grows, many numerical methods have been developed to solve optimization problem. Khade et al., Kwong et al. and Hall is one of the first to come up with the idea of optimal design for kinematics synthesis[6-8]. Han, Kramer, Sandor, Sohoni and Haug optimized the error between the points tracked by the coupler and its desired trajectory for mechanism design[9-11] . The problem setup of the optimal design problem using numerical method mainly consists of three parts: mechanism generation including the generation of link, joint and joint type of the mechanism, mechanism analysis which gives us the performance of the mechanism and the optimization process procedure.

Mechanism generation can be viewed as type synthesis of the mechanism which can also be called topological synthesis. Topology optimization is the technique that finds the optimal layout of the structure or the mechanism within a specified design domain. Two approach for structural topology optimization has been proposed by Bendsoe and Sigmund [12]. These two methods are continuous element approach and discrete element approach. In continuous element approach, one of the most established methods is the homogenization approach proposed by Bendsoe and Kikuchi[13]. This approach provides a systematic way to seek the optimal material distribution in a predefined design domain by using the stiffness-density relation obtained by the homogenization of the properties in a microstructure. Each element is assumed to contain infinite number of microscopic cells that can either represent solid or void. The ratio of solid/void in the base cell is used as the design variable and is associated with each element. The optimal value of the design variable and the value associated with each element are calculated using gradient based search method. If the ratio of solid/void in the base cell is an intermediate value, filters or penalty function will be used to avoid the ambiguity of the structure topology. In discrete element approach, the elements in the mechanism are represented with binary numbers, 1 or 0. Evolutionary approaches are often used to programming discrete element approach due to the binary characteristic. In this paper, discrete element approach is used to determine the type of the mechanism.

1.3. Review of Kinematics Analysis

Initially, people use graphical techniques to perform analysis of mechanism. The basic technique of graphical method was used until the use of an atlas of coupler curves been proposed by Hrones and Nelson[14]. They have developed the atlas of four-bar mechanisms with almost 10,000 curves. These graphical methods are easy to use but often with low precision cause by human effects. Since the introduction of computers, analytical method has been introduced[15, 16]. The analytical method is much more useful than the graphical method when analyzing a number of positions and/or a number of different mechanisms since the expression of the analytical method can easily be programmed for automatic computation. Another method is proposed using total potential energy method to analyze the performance of the mechanism[17]. Unlike the analytical method, the total potential method can be applied to various mechanism types without any modification. However, the accuracy of this method is based on random search which will not always perform well. Finite element method is often used for structural analysis and some specific mechanism called compliant mechanism. A compliant mechanism is a mechanism that gains some or all of its mobility from the flexibility of its components[18]. Thus, compliant mechanism can easily be analyzed by finite element, but not for general mechanisms.

In order to analyze the performance of general mechanisms while applying analysis method into evolutionary optimization process, a new method is presented based on the concept of finite element analysis in the paper.

1.4. Review of Optimization Techniques

The optimization problem of finding the best mechanism to perform the desired motion is a very complex problem and cannot be solved by classical gradient-based optimization methods. In the recent years, a number of successful heuristic algorithms have been created and developed to solve optimization problems. Nature-inspired methods do not need information about the gradient. Among them the most famous of nature-inspired methods are Simulated Annealing(SA) proposed by Kirkpatrick et al[19], Ant Colony Optimization (ACO) [20] and Genetic Algorithm(GA). SA is inspired by the annealing of metal to increase the size of its crystals and reduce the defects by controlling the cooling process. ACO is inspired in the behavior of real ants and their communication scheme by using pheromone trail. GA mimics the evolution of a species based on Darwin's principle of survival of the fittest. The advantages of these methods include the robustness, the efficiency and the tendency of finding the global or near the global solution.

The optimization method chosen for mechanism synthesis is Genetic Algorithm. Holland is the first person to introduce Genetic Algorithm[21]. Genetic Algorithms have been applied to different optimization problems successfully and extensively. Cabrera, Simon and Prado have applied Genetic Algorithm to optimize a specific type of mechanism for trajectory following[22]. Chedmail and Ramstein applied Genetic Algorithm to optimize the type of robot and its performance[23]. A typical Genetic Algorithm requires two things to be defined: a genetic representation of the solution domain and a fitness function to evaluate the solution domain. Genetic Algorithm does

not require a full knowledge of the design domain and is very easy to implement into computer program.

1.5. Research Contributions

In previous works, almost all the kinematics analysis method have failed to work on problems that viewed the connected joint number as a variable. This phenomenon is due to the various characteristic of the mechanisms with different joint number. Total potential energy method can solve problems with different joint number, but the performance of the total potential energy method is not always consistence. A new kinematics analysis method called Constrained Superposition Method is presented here. Constrained Superposition Method is based on Finite Element Analysis (FEM) which is well developed in structure analysis..

One drawback of GA is that it cannot guarantee the feasibility of the chromosome produced by reproduction. In order to improve computational efficiency for linkage synthesis, two additional feasibility checks is introduced: connectivity check and mobility check. After applying Constrained Superposition Method into the Genetic Algorithm, we can find different types of mechanism that are feasible and provide the users with multiple solutions.

1.6. Thesis Outline

The thesis outline is organized in the following manner:

Chapter 2 introduces different methods of analysis for kinematics mechanism. Three existing analysis method are introduced in this chapter. They are graphical method, analytical method and total potential energy method. A new method called Constrained Superposition Method based on finite element analysis is presented here. For validation purpose, the method is applied on a simple problem and compared with the other method mentioned before.

In chapter 3, mechanism design using Genetic Algorithm is introduced. The paragraph starts with the explanation of the general Genetic Algorithm with its definition of three genetic operators, and then it shows how the mechanism been encoded to take the advantage of Genetic Algorithm. Two important feasibility checks are also introduced in this chapter.

Chapter 4 shows two different kinds of applications of the method presented. The first section shows the importance of boundary condition and how it affects the final result when searching for mechanisms that can give us the maximum output distance. The second section of this chapter will demonstrate the feasibility of this method when applied on a predefined output distance problem.

In chapter 5, we will give a conclusion of our work and discuss the work that can be done in the future.

Chapter 2.

Review of Mechanism Analysis

2.1. Kinematics Analysis Method

The result of an analysis of mechanism is the indicator of performance in optimization algorithm. Without proper mechanism analysis, it is impossible to do kinematics synthesis. The most commonly known methods are the graphical method and the analytical method. For mechanism synthesis using optimization, implemental possibility is an important issue when choosing the method to analysis the performance of the mechanism. Both of the methods have its difficulties to be implemented into computers. In order to solve this problem, a method is been proposed by Kwon[17] called potential energy method. In this chapter, a new kinematics analysis method is presented and compared with these three methods.

2.1.1. Graphical Method for Kinematics Analysis

Graphical method used the physical characteristic of mechanism to solve the relative position of the joints. However, it is really hard to scale down the real size mechanism without compromise the accuracy of the result and it is almost impossible to be implemented into computer programs. The procedure of graphical method for a four-bar linkage with a rotational input on link AB will be stated as the following.

1. Draw an arc about joint A with radius AB, Draw another arc about joint D with radius CD.
2. Place joint B at the defined position B'
3. Draw an arc about B' and place C' at the intersection of two arcs.
4. Connect link AB', B'C' and C'D. The graphical analysis is complete.

Figure 2.1 shows the four step of graphical method.

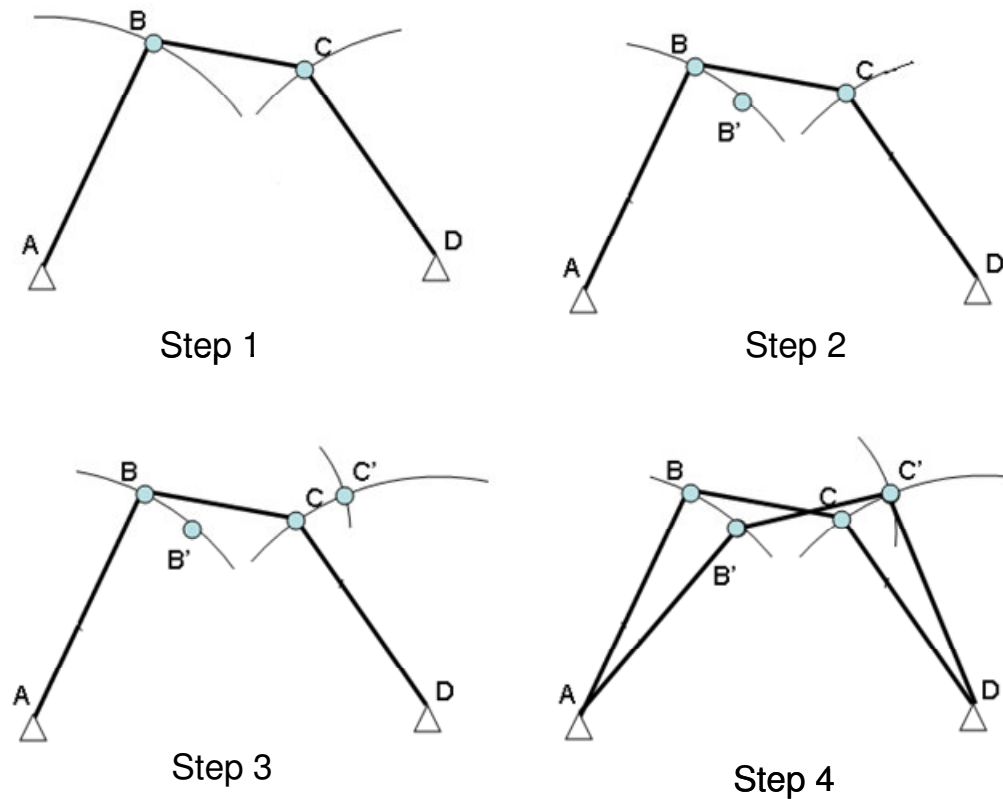


Figure 2.1 Demonstration of Graphical Method

2.1.2. Analytical Method for Kinematics Analysis

Analytical method can always provided the user an exact solution. To get the solution with the analytical method, a vector notation expressed by polar vector notion form is used to describe the motion of a rigid body[17]. Figure 2.2 shows a four bar linkage with parameters required to solve the mechanism analysis.

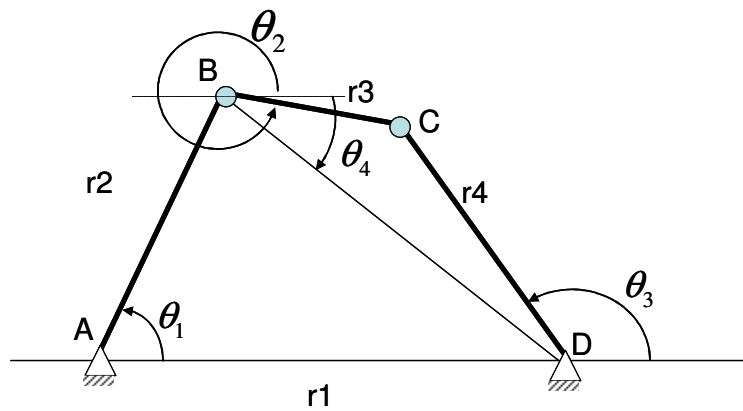


Figure 2.2 Demonstration of Analytical Method

In [17], Kwon stated that a four bar mechanism such as shown in Figure 2.2 can be solved by using the method of “independent position equations” by Raven[24]. For the four bar mechanism, the equation for analytical method can be written as

$$\theta_4 = \tan^{-1} \left(\frac{-r_2}{r_1 - r_2 \cos \theta_1} \right) \quad (1.1)$$

$$\theta_3 = \cos^{-1} \left(\frac{r_3^2 + d^2 - r_4^2}{2r_3 d} \right) + \theta_4 \quad (1.2)$$

$$\theta_2 = \sin^{-1} \left(\frac{r_3 \sin \theta_3 - d \sin \theta_4}{r_4} \right) \quad (1.3)$$

So if θ_1 is known, the configuration of the whole mechanism will be known.

However, this method is rarely used for mechanism synthesis. The reason for that is that

for different types of mechanisms, the equations of the analytical method will change. For mechanism synthesis, the type of the mechanism is not predefined so the equations can not be derived to fit the problem and new method must be created to suit the need for kinematics mechanism design.

2.1.3. Total Potential Energy Method for Kinematics Analysis

Total potential energy method is proposed by Kwon[17]. Total potential energy method is more general the analytical method, it can be applied on many different types of mechanism without modification. Another advantage of total potential energy is that it is really easy to implement. However, the downside of this method is that it can not provide the same solution of the mechanism analysis if applied more than once. The principle of the total potential energy method is to search the design that satisfies the minimum potential energy by the iterative process. This method is proved to be effective on approximating mechanism behavior. Total potential energy method used random search technique to find a design in the trust region that satisfies the minimum potential energy equation(1.4).

$$\Pi(u) = \sum_i^N \left(\frac{1}{2} K_i u_i^2 - F_i u_i \right) \quad (1.4)$$

where K is the stiffness matrix and F is the axial force. However, the final result of total potential energy method will vary due to the characteristic of random search. The procedure for kinematics analysis with total potential energy method is shown as following.

1. Assign sample points inside the trust region.
2. Calculate the total potential energy of the sample points.
3. Find the sample point with minimum total potential energy.
4. Check if the current total potential energy is smaller than the previous one, if not, reduce the trust region and search for new sample points again
5. Check the termination criteria. If satisfied, the iteration process stops. Otherwise execute the process again.

A flowchart for the total potential energy method is shown in Figure 2.3.

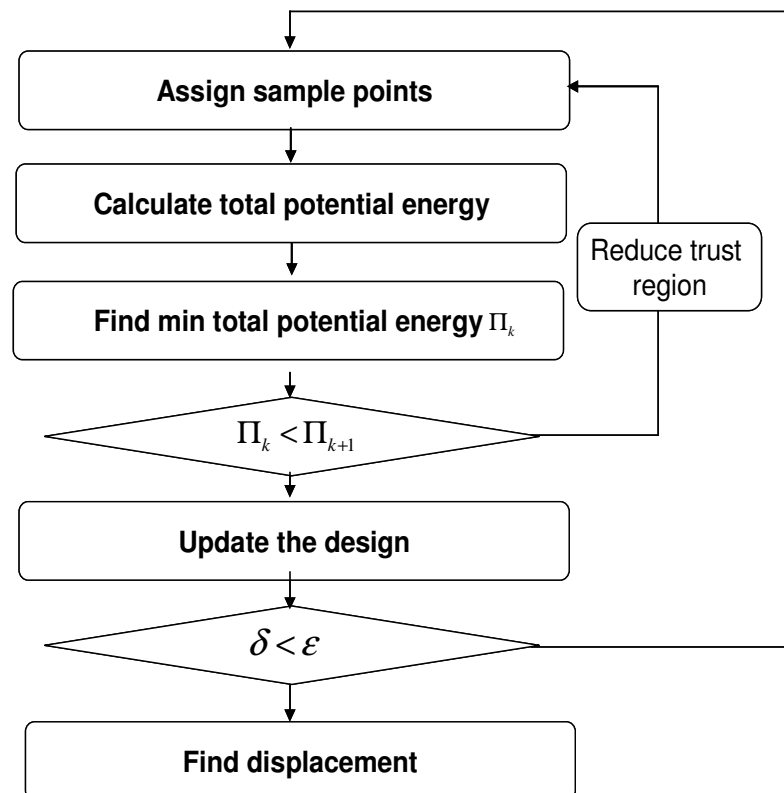


Figure 2.3[17] Flow Chart of Total Potential Energy Method.

Chapter 3.

Constrained Superposition Method

3.1. Constrained Superposition Method (CSM) for Kinematics Analysis

The method presented here is based on finite element method. The advantage of this method is that it is really easy to implement into optimization. CSM can be applied to various types of mechanisms and at the same time provide a consistent solution. Finite element method is largely used in structure analysis. It is based on matrix algebra and can easily be implemented into computers. A truss is an engineering structure consisting of straight members connected at their ends by means of bolts, rivets, pins or welding. For a truss structure, the displacement q caused by external force F can be easily calculated using Eqn. (2.1).

$$Kq = F \tag{2.1}$$

where K is the global stiffness matrix of the truss. The global stiffness matrix is computed according to the position and orientation of the links inside of the truss. The stiffness matrix of a mechanism can be calculated in the same way. However, the displacement of a mechanism can not be calculated by Eqn. (2.1) due to the mobility of the mechanism. Since Eqn. (2.1) is based on the assumption that the structure is in equilibrium condition, a mechanism can be viewed as a structure that can never reach equilibrium. The new analysis method called Constrained Superposition Method is

developed to compensate the deficiency of the boundary condition of the mechanism. In order to formulate the Constrained Superposition Method, a basic knowledge of finite element method is required. In the first part of this section, the finite element method is reviewed.

3.1.1.1. Review of Finite Element Analysis

Finite element method is a numerical procedure that can be applied to obtain solutions to a variety of problems in engineering. In this paper, we are focusing on the plane truss analysis with finite element method. In the following analysis, several important assumptions are made. We assumed that all loads must be applied at the joint of the truss. This assumption is true for most cases since the trusses are designed in a manner such that the majority of the load is applied at the joints. The second assumption is that the trusses are light-weight trusses so that the weights of the trusses are negligible. The last assumption is that the internal force only act in equal and opposite direction along the link.

Let us first consider the deflection of a single link when it is subjected to a force F as shown in Figure 3.1.

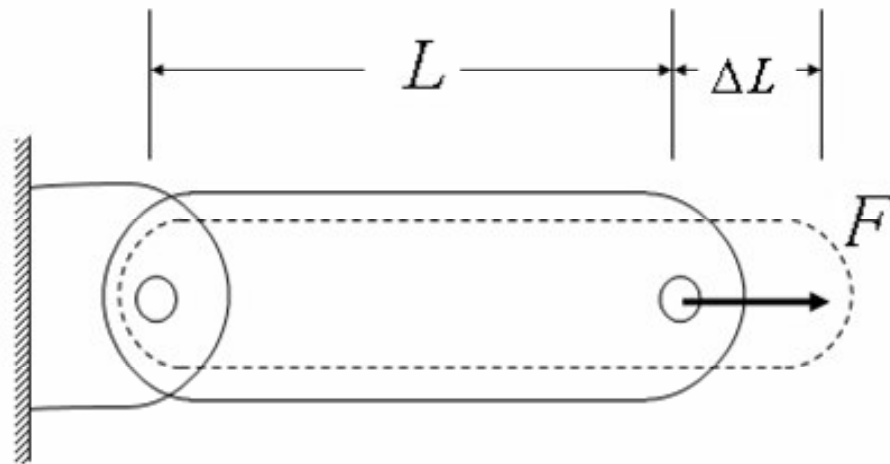


Figure 3.1 A Link Subjected to a Force F

Recall that the average stresses are given as

$$\sigma = \frac{F}{A} \quad (2.2)$$

where A is the cross section of the link and is always set to be a constant in this paper. The average strain of the link can be expressed by

$$\varepsilon = \frac{\Delta L}{L} \quad (2.3)$$

In the elastic region, the stress and the strain are related by Hooke's law[25]

$$\sigma = E\varepsilon \quad (2.4)$$

E is the young's module of the link. Combining Eqn. (2.2), Eqn. (2.3)and Eqn. (2.4), we can obtain Eqn. (2.5).

$$F = \left(\frac{AE}{L}\right)\Delta L \quad (2.5)$$

From observation, Eqn. (2.5) is similar to the equation of a linear spring. Therefore, the link can be viewed as a spring with an equivalent stiffness of

$$k_{eq} = \frac{AE}{L} \quad (2.6)$$

Global and local coordinate are required when describing truss problems. The global coordinate (X, Y) is fixed and used to keep track of the orientation of each link in the truss while the local coordinate (x, y) moves with the link and is used to describe the behavior of each individual link as shown in. Figure 3.2.

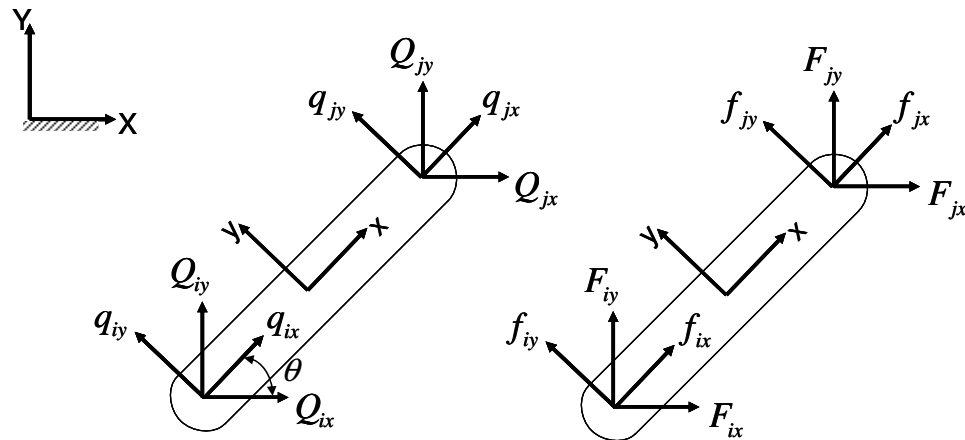


Figure 3.2 Relationship Between Global and Local Coordinates.

The relationship between the global and local coordinates can be expressed in the following equations.

$$Q_{ix} = u_{ix} \cos \theta - u_{iy} \sin \theta \quad (2.7)$$

$$Q_{iy} = u_{ix} \sin \theta + u_{iy} \cos \theta \quad (2.8)$$

$$Q_{jx} = u_{jx} \cos \theta - u_{jy} \sin \theta \quad (2.9)$$

$$Q_{jy} = u_{jx} \sin \theta + u_{jy} \cos \theta \quad (2.10)$$

Eqn. (2.7) can also be written in matrix form as follow.

$$\{Q\} = [L]\{q\} \quad (2.11)$$

where

$$\{Q\} = \begin{Bmatrix} Q_{ix} \\ Q_{iy} \\ Q_{jx} \\ Q_{jy} \end{Bmatrix}, [L] = \begin{bmatrix} \cos \theta & -\sin \theta & 0 & 0 \\ \sin \theta & \cos \theta & 0 & 0 \\ 0 & 0 & \cos \theta & -\sin \theta \\ 0 & 0 & \sin \theta & \cos \theta \end{bmatrix}, \text{ and } \{q\} = \begin{Bmatrix} q_{ix} \\ q_{iy} \\ q_{jx} \\ q_{jy} \end{Bmatrix}$$

L is the transformation matrix that transfers the local displacement into global displacement. The same relation can also be applied to the force transformation and the equation can be written as

$$\{F\} = [L]\{f\} \quad (2.12)$$

Base on the assumption that the internal forces will only act in equal or opposite directions along the link, the internal force will only be affected by the displacement in the x-direction as shown in Figure 3.3 .

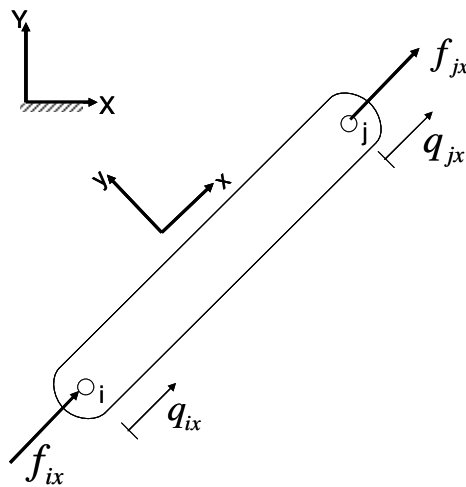


Figure 3.3 Relationship Between the Internal Force and the Local Displacement

The relationship between the internal force and the displacement can be illustrated in the following equation.

$$\begin{aligned}
 f_{ix} &= k_{eq} (q_{ix} - q_{jx}) \\
 f_{iy} &= 0 \\
 f_{jx} &= k_{eq} (q_{jx} - q_{ix}) = -k_{eq} (q_{ix} - q_{jx}) \\
 f_{jy} &= 0
 \end{aligned} \tag{2.13}$$

Eqn. (2.13) can also be written in matrix form.

$$\{f\} = [K]\{q\} \tag{2.14}$$

where

$$\{f\} = \begin{Bmatrix} f_{ix} \\ f_{iy} \\ f_{jx} \\ f_{jy} \end{Bmatrix}, [K] = \begin{bmatrix} k_{eq} & 0 & -k_{eq} & 0 \\ 0 & 0 & 0 & 0 \\ -k_{eq} & 0 & k_{eq} & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

After substituting Eqn. (2.11) and Eqn. (2.12) into Eqn. (2.14), we have

$$\{F\} = [L][K][L]^{-1}\{Q\} \tag{2.15}$$

According to Eqn.(2.15), $[L][K][L]^{-1}$ can be viewed as the global link stiffness matrix $[K]_{gl}$. By substitute the values of these matrixes into Eqn.(2.15), the global link stiffness matrix can be expressed as

$$[K]_{gl} = \frac{AE}{L} \begin{bmatrix} \cos^2 \theta & \sin \theta \cos \theta & -\cos^2 \theta & -\sin \theta \cos \theta \\ \sin \theta \cos \theta & \sin^2 \theta & -\sin \theta \cos \theta & -\sin^2 \theta \\ -\cos^2 \theta & -\sin \theta \cos \theta & \cos^2 \theta & \sin \theta \cos \theta \\ -\sin \theta \cos \theta & -\sin^2 \theta & \sin \theta \cos \theta & \sin^2 \theta \end{bmatrix} \tag{2.16}$$

The global truss stiffness matrix can be assembled by the sum of the global link stiffness matrix of all the links due to superposition principle[26].

3.1.1.2. Constrained Superposition Method

The Constrained Superposition Method used the basic concept of finite element method to solve a mechanism analysis problem. To demonstrate the concept of the Constrained Superposition Method, a structure with a given input displacement is shown in Figure 3.4. The system is denoted by System SD for demonstration convenience. Joint A of system SD is moved with the given displacement Δ and caused joint B to move from point B to B'.

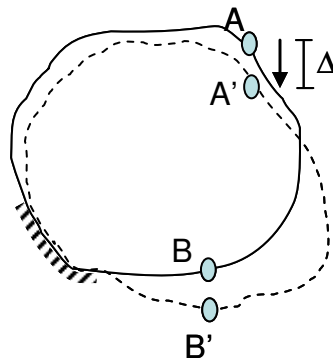


Figure 3.4 System SD Structure with a Given Displacement

Instead of analyzing the displacements of the points in system SD caused by moving joint A with a given displacement directly, another system is introduced to simplify the calculation. A stiff spring with stiffness value of C is placed at joint A as shown in Figure 3.5. The appropriate value of C will be discussed later in the text. The grounded end of the spring is moved with the same given displacement Δ and caused joint A to move with a displacement q_1 . Since the displacement q_1 of joint A will almost

be equal to Δ due to the small resistance of the structure compared to the spring, the displacement of joint B and all the other nodes will almost be the same between the systems in Figure 3.4 and Figure 3.5 . In other words, we can obtain the displacement of all the nodes in system SD by calculating the displacement of the system in Figure 3.5.

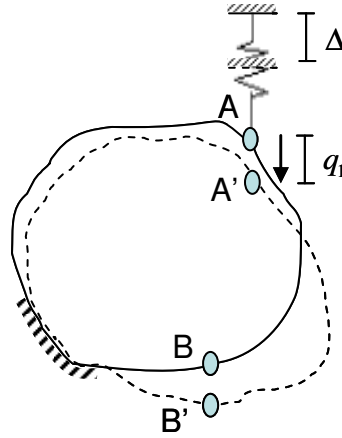


Figure 3.5 Penalty Approach of the System

The extension of the spring in Figure 3.5 can be calculated as $q_1 - \Delta$. The total potential energy of the system can therefore be expressed as

$$\Pi = \frac{1}{2} Q^T K Q + \frac{1}{2} C (q_1 - \Delta)^2 + Q^T F \quad (1.1)$$

Since the system will tend to move to the position where the potential energy is minimized, by setting $\frac{\partial \Pi}{\partial q_i} = 0, i = 1, 2, \dots, N$, the minimization of Π will be obtain. The results of the derivation are shown in the following equation.

$$\begin{bmatrix} (k_{11} + C) & k_{12} & \cdots & k_{1N} \\ k_{21} & k_{22} & \cdots & k_{2N} \\ \vdots & \vdots & & \vdots \\ k_{N1} & k_{N2} & \cdots & k_{NN} \end{bmatrix} \begin{Bmatrix} q_1 \\ q_2 \\ \vdots \\ q_N \end{Bmatrix} = \begin{Bmatrix} f_1 + C\Delta \\ f_2 \\ \vdots \\ f_{10} \end{Bmatrix} \quad (1.2)$$

It is clear that in order to satisfy the given displacement; a large number is added on to the diagonal term with $C\Delta$ added on to the force term of the input point. This method is called penalty approach [27, 28]. The magnitude of C is often chosen by the following equation.

$$C = \max |k_{ij}| \times 10^4 \quad (1.3)$$

$$1 \leq i \leq N, 1 \leq j \leq N$$

The nodes of system SD in Figure 3.4 can be separated into four categories: The input node, the output node, the nodes with constraints and the free nodes. Since a fixed joint can be viewed as a joint with a desired displacement of zero, penalty can also be applied on the constrained joint. By applying penalty approach to system SD, we get

$$\left(\begin{bmatrix} k_{S_{Dii}} & k_{S_{Doi}} & k_{S_{Dci}} & k_{S_{Dri}} \\ k_{S_{Dio}} & k_{S_{Doo}} & k_{S_{Dco}} & k_{S_{Dro}} \\ k_{S_{Dic}} & k_{S_{Doc}} & k_{S_{Dcc}} & k_{S_{Drc}} \\ k_{S_{Dir}} & k_{S_{Dor}} & k_{S_{Der}} & k_{S_{Drr}} \end{bmatrix} + \begin{bmatrix} P & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & P & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{Bmatrix} q_{S_{Di}} \\ q_{S_{Do}} \\ q_{S_{Dc}} \\ q_{S_{Dr}} \end{Bmatrix} = \begin{Bmatrix} P\Delta \\ 0 \\ 0 \\ 0 \end{Bmatrix} \quad (1.4)$$

Where $q_{S_{Di}}$ represents the displacement array of the input node, $q_{S_{Do}}$ represents the displacement array of the output node, $q_{S_{Dc}}$ represents the displacement array of the constrained nodes in their constrained direction and $q_{S_{Dr}}$ represents the displacement array of the rest of the nodes. P is an identity matrix multiplied by the large stiffness C . With some rearranging, we have

$$\begin{bmatrix} k_{S_{Dii}} & k_{S_{Doi}} & k_{S_{Dci}} & k_{S_{Dri}} \\ k_{S_{Dio}} & k_{S_{Doo}} & k_{S_{Dco}} & k_{S_{Dro}} \\ k_{S_{Dic}} & k_{S_{Doc}} & k_{S_{Dcc}} & k_{S_{Drc}} \\ k_{S_{Dir}} & k_{S_{Dor}} & k_{S_{Dcr}} & k_{S_{Drr}} \end{bmatrix} \begin{Bmatrix} q_{S_{Di}} \\ q_{S_{Do}} \\ q_{S_{Dc}} \\ q_{S_{Dr}} \end{Bmatrix} = \begin{Bmatrix} P\Delta \\ 0 \\ 0 \\ 0 \end{Bmatrix} - \begin{bmatrix} P & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & P & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{Bmatrix} q_{S_{Di}} \\ q_{S_{Do}} \\ q_{S_{Dc}} \\ q_{S_{Dr}} \end{Bmatrix} \quad (1.5)$$

Above, we can see that on the left hand side, the stiffness matrix is the original stiffness matrix without the penalty terms. We can simplify Eqn. (1.5) with the following equation.

$$\left[K_{S_d} \right] \{ Q_{S_d} \} = \begin{Bmatrix} P\Delta - Pq_{S_{Di}} \\ 0 \\ -Pq_{S_{Dc}} \\ 0 \end{Bmatrix} \quad (1.6)$$

where $\left[K_{S_d} \right]$ is the original stiffness matrix without penalty terms. Except obtaining the displacement of all the nodes by applying penalty approach to system SD, we can also obtain the displacement of all the nodes by separating system SD into two systems. The first system has a fix constraint placed at joint B and a given displacement as shown in Figure 3.6 and is denoted by system CD. The second system has a fix constraint placed at joint A after joint A be moved to point A' and a force applied on joint B as shown in Figure 3.7 and is denoted by system CF. The displacement of system SD will be equal to the sum of the displacements of system CD and system CF which will be proved later in the text.

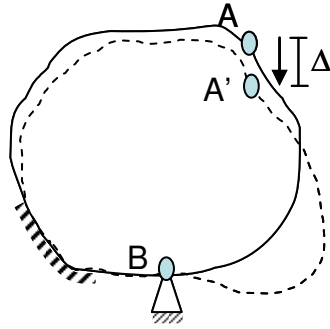


Figure 3.6 System CD Structure with a Desired Displacement and a Fixed Constraint

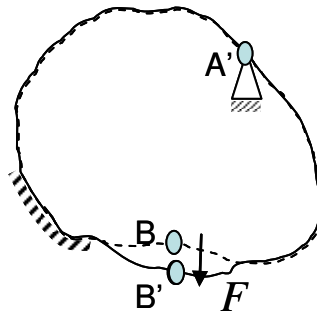


Figure 3.7 System CF Structure with Input Point Fixed at Its Desired Position with an External Force

Since point B is viewed as the output joint of the systems, the force equilibrium equation of system CD in Figure 3.6 will be express as the following equation where all the nodes except the free nodes are penalized.

$$\left(\begin{bmatrix} k_{C_{Dii}} & k_{C_{Doi}} & k_{C_{Dci}} & k_{C_{Dri}} \\ k_{C_{Dio}} & k_{C_{Doo}} & k_{C_{Dco}} & k_{C_{Dro}} \\ k_{C_{Dic}} & k_{C_{Doc}} & k_{C_{Dcc}} & k_{C_{Drc}} \\ k_{C_{Dir}} & k_{C_{Dor}} & k_{C_{Dcr}} & k_{C_{Drr}} \end{bmatrix} + \begin{bmatrix} P & 0 & 0 & 0 \\ 0 & P & 0 & 0 \\ 0 & 0 & P & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{Bmatrix} q_{C_{Di}} \\ q_{C_{Do}} \\ q_{C_{Dc}} \\ q_{C_{Dr}} \end{Bmatrix} = \begin{Bmatrix} P\Delta \\ 0 \\ 0 \\ 0 \end{Bmatrix} \quad (1.7)$$

Where q_{b_i} represents the displacement array of the input node, q_{b_o} represents the displacement array of the output node, q_{b_c} represents the displacement array of the constrained nodes in their constrained direction and q_{b_r} represents the displacement array of the rest of the nodes. By rearranging Eqn. (1.7), we have

$$\begin{bmatrix} k_{C_{Dii}} & k_{C_{Doi}} & k_{C_{Dci}} & k_{C_{Dri}} \\ k_{C_{Dio}} & k_{C_{Doo}} & k_{C_{Dco}} & k_{C_{Dro}} \\ k_{C_{Dic}} & k_{C_{Doc}} & k_{C_{Dcc}} & k_{C_{Drc}} \\ k_{C_{Dir}} & k_{C_{Dor}} & k_{C_{Dcr}} & k_{C_{Drr}} \end{bmatrix} \begin{Bmatrix} q_{C_{Di}} \\ q_{C_{Do}} \\ q_{C_{Dc}} \\ q_{C_{Dr}} \end{Bmatrix} = \begin{Bmatrix} P\Delta \\ 0 \\ 0 \\ 0 \end{Bmatrix} - \begin{bmatrix} P & 0 & 0 & 0 \\ 0 & P & 0 & 0 \\ 0 & 0 & P & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{Bmatrix} q_{C_{Di}} \\ q_{C_{Do}} \\ q_{C_{Dc}} \\ q_{C_{Dr}} \end{Bmatrix} \quad (1.8)$$

Same with Eqn. (1.5), the stiffness matrix of the left hand side is the original stiffness matrix of system (b). Therefore, Eqn. (1.8) can be simplified into the following equation.

$$[K_{C_D}] \{Q_{C_D}\} = \begin{Bmatrix} P\Delta - Pq_{C_{Di}} \\ -Pq_{C_{Do}} \\ -Pq_{C_{Dc}} \\ 0 \end{Bmatrix} \quad (1.9)$$

where $[K_{C_D}]$ is the original stiffness matrix without penalty term. System CF can also be analyzed in the same fashion. By penalizing the constrained joints, the force equilibrium equation of system CF can be expressed as

$$\begin{bmatrix} k_{C_{Fii}} & k_{C_{Foi}} & k_{C_{Fci}} & k_{C_{Fri}} \\ k_{C_{Fio}} & k_{C_{Foo}} & k_{C_{Fco}} & k_{C_{Fro}} \\ k_{C_{Fic}} & k_{C_{Foc}} & k_{C_{Fcc}} & k_{C_{Frc}} \\ k_{C_{Fir}} & k_{C_{For}} & k_{C_{Fcr}} & k_{C_{Frr}} \end{bmatrix} + \begin{bmatrix} P & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & P & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{Bmatrix} q_{C_{Fi}} \\ q_{C_{Fo}} \\ q_{C_{Fc}} \\ q_{C_{Fr}} \end{Bmatrix} = \begin{Bmatrix} 0 \\ F \\ 0 \\ 0 \end{Bmatrix} \quad (1.10)$$

The notation follows the same pattern in system (a) and system (b). With some rearrangement, Eqn. (1.10) can be expressed as

$$\begin{bmatrix} k_{C_{Fii}} & k_{C_{Foi}} & k_{C_{Fci}} & k_{C_{Fri}} \\ k_{C_{Fio}} & k_{C_{Foo}} & k_{C_{Fco}} & k_{C_{Fro}} \\ k_{C_{Fic}} & k_{C_{Foc}} & k_{C_{Fcc}} & k_{C_{Frc}} \\ k_{C_{Fir}} & k_{C_{For}} & k_{C_{Fcr}} & k_{C_{Frr}} \end{bmatrix} \begin{Bmatrix} q_{C_{Fi}} \\ q_{C_{Fo}} \\ q_{C_{Fc}} \\ q_{C_{Fr}} \end{Bmatrix} = \begin{Bmatrix} 0 \\ F \\ 0 \\ 0 \end{Bmatrix} - \begin{bmatrix} P & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & P & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{Bmatrix} q_{C_{Fi}} \\ q_{C_{Fo}} \\ q_{C_{Fc}} \\ q_{C_{Fr}} \end{Bmatrix} \quad (1.11)$$

Since the left hand side represents the original stiffness matrix multiplied by the global displacement of the system, Eqn. (1.11) can be denoted as

$$[K_{C_F}]\{Q_{C_F}\} = \begin{Bmatrix} -Pq_{C_{Fi}} \\ F \\ -Pq_{C_{Fc}} \\ 0 \end{Bmatrix} \quad (1.12)$$

All the systems discussed previously are considered as linear systems. Hence, the force equilibrium equations of system (b) and system (c) can be summed up as follow.

$$[K_{C_D}]\{Q_{C_D}\} + [K_{C_F}]\{Q_{C_F}\} = \begin{Bmatrix} P\Delta - Pq_{C_{Di}} \\ -Pq_{C_{Do}} \\ -Pq_{C_{Dc}} \\ 0 \end{Bmatrix} + \begin{Bmatrix} -Pq_{C_{Fi}} \\ F \\ -Pq_{C_{Fc}} \\ 0 \end{Bmatrix} = \begin{Bmatrix} P\Delta - Pq_{C_{Di}} - Pq_{C_{Fi}} \\ -Pq_{C_{Do}} + F \\ -Pq_{C_{Dc}} - Pq_{C_{Fc}} \\ 0 \end{Bmatrix} \quad (1.13)$$

The first component in Eqn. (1.13) consists of three terms. Since point A is fixed in case (c), $q_{C_{Fi}}$ is closed to zero. Compared to the other terms in the equation, the last term of the first component is too small and can be viewed as zero. Given that $q_{S_{Di}} \cong \Delta, q_{C_{Di}} \cong \Delta$, we can say that $q_{S_{Di}} \cong q_{C_{Di}}$. Therefore, the first component in Eqn. (1.13) can be rewrite as $P\Delta - Pq_{S_{Di}}$ which is exactly the same with the first component in Eqn. (1.6)

Consider the second component of Eqn.(1.13), $q_{C_{Do}}$ is close to zero since point B is fixed in system CD. However, $q_{C_{Do}}$ has been multiplied by a very large number P , the order of this term might still be large and can not be viewed as zero. Under the assumption that $F = Pq_{C_{Do}}$, the second component of Eqn. (1.13) will be zero and is the

same with the second component of Eqn.(1.6). Both terms in the third component of Eqn. (1.13) are the displacements of the constrained nodes multiplied by a large number P . Since $q_{S_{Dc}}, q_{C_{Dc}}, q_{C_{Fc}}$ are all close to zero, the third component of Eqn. (1.13) and Eqn. (1.6) will be the same. The last components of Eqn. (1.13) and Eqn. (1.6) are both zero and equal to each other. According to the discussion above, the relationship between the three systems can be expressed as

$$\left[K_{S_D} \right] \{ Q_{S_D} \} = \left[K_{C_D} \right] \{ Q_{C_D} \} + \left[K_{C_F} \right] \{ Q_{C_F} \} \quad (1.14)$$

The relationship above is true only when the following assumption is true.

$$F = Cq_{C_{Dc}} \quad (1.15)$$

Since the original shapes of system SD and system CD are the same as shown in Figure 3.4 and Figure 3.6. The stiffness matrixes of both of them will also be the same. For small deformation, the stiffness matrix can be viewed as a constant as shown below.

$$\left[K_{S_D} \right] = \left[K_{C_D} \right] \cong \left[K_{C_F} \right] \quad (1.16)$$

By replacing $\left[K_{C_D} \right]$ and $\left[K_{C_F} \right]$ with $\left[K_{S_D} \right]$ in Eqn. (1.14), Eqn. (1.14) can then be rewrite as

$$\left[K_{S_D} \right] (\{ Q_{S_D} \} - \{ Q_{C_D} \} - \{ Q_{C_F} \}) \cong 0 \quad (1.17)$$

Since $\left[K_a \right]$ is not zero, $\{ Q_a \} - \{ Q_b \} - \{ Q_c \}$ must be close to zero and can be expressed as follow.

$$\{ Q_{S_D} \} \cong \{ Q_{C_D} \} + \{ Q_{C_F} \} \quad (1.18)$$

Eqn. (1.18) shows that by calculating the displacements of two of the three systems shown previously, the displacement of the third system will be known.

As discussed previously, the mechanism can be viewed as a truss that lacks one boundary condition. To verify that Eqn. (1.18) can also be applied to truss systems, the displacement of a truss with a specific input distance is decomposed into two systems according to Eqn.(1.18) as shown in Figure 3.8.

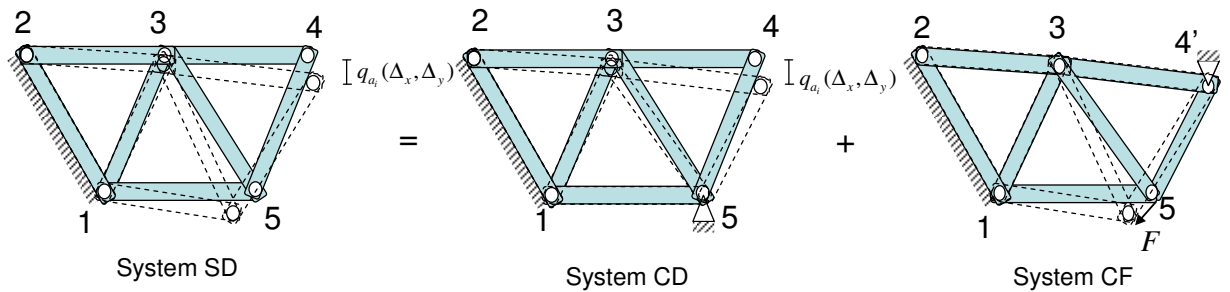


Figure 3.8 Decomposition of the Deformation of a Truss

System SD is a truss with one specified moving distance for point 3. The displacement of system SD can be calculated by penalty approach in the following equation.

$$\begin{bmatrix} k_{S_D11} & k_{S_D12} & \cdots & k_{S_D110} \\ k_{S_D21} & k_{S_D22} & \cdots & k_{S_D210} \\ \vdots & \vdots & & \vdots \\ k_{S_D101} & k_{S_D102} & \cdots & k_{S_D1010} \end{bmatrix} \begin{Bmatrix} q_{S_D1} \\ q_{S_D2} \\ \vdots \\ q_{S_D10} \end{Bmatrix} = \begin{Bmatrix} -Cq_{S_D1} \\ -Cq_{S_D2} \\ -Cq_{S_D3} \\ -Cq_{S_D4} \\ 0 \\ 0 \\ C\Delta_x - Cq_{S_D7} \\ C\Delta_y - Cq_{S_D8} \\ 0 \\ 0 \end{Bmatrix} \quad (1.19)$$

System CD is a truss with a specified input distance and a fixed constraint at its output joint which is point 5 in this case. The displacement of every joints can be calculated with penalty approach too as shown in Eqn. (1.20).

$$\begin{bmatrix} k_{C_D11} & k_{C_D12} & \cdots & k_{C_D110} \\ k_{C_D21} & k_{C_D22} & \cdots & k_{C_D210} \\ \vdots & \vdots & & \vdots \\ k_{C_D101} & k_{C_D102} & \cdots & k_{C_D1010} \end{bmatrix} \begin{Bmatrix} q_{C_D1} \\ q_{C_D2} \\ \vdots \\ q_{C_D10} \end{Bmatrix} = \begin{Bmatrix} -Cq_{C_D1} \\ -Cq_{C_D2} \\ -Cq_{C_D3} \\ -Cq_{C_D4} \\ 0 \\ 0 \\ C\Delta_x - Cq_{C_D7} \\ C\Delta_y - Cq_{C_D8} \\ -Cq_{C_D9} \\ -Cq_{C_D10} \end{Bmatrix} \quad (1.20)$$

System CF is a truss with the input joint fixed, which in this case point 4 fixed, and a force applied onto the output joint. The force in the x direction and y direction is denoted as f_x and f_y . The displacement is calculated as the following equation.

$$\begin{bmatrix} k_{C_F11} & k_{C_F12} & \cdots & k_{C_F110} \\ k_{C_F21} & k_{C_F22} & \cdots & k_{C_F210} \\ \vdots & \vdots & & \vdots \\ k_{C_F101} & k_{C_F102} & \cdots & k_{C_F1010} \end{bmatrix} \begin{Bmatrix} q_{C_F1} \\ q_{C_F2} \\ \vdots \\ q_{C_F10} \end{Bmatrix} = \begin{Bmatrix} -Cq_{C_F1} \\ -Cq_{C_F2} \\ -Cq_{C_F3} \\ -Cq_{C_F4} \\ 0 \\ 0 \\ -Cq_{C_F7} \\ -Cq_{C_F8} \\ f_x \\ f_y \end{Bmatrix} \quad (1.21)$$

Since the truss is assumed to be a linear system, Eqn. (1.20) and Eqn. (1.21) are added up as shown below.

$$\begin{aligned}
 [K_{C_D}]\{Q_{C_D}\} + [K_{C_F}]\{Q_{C_F}\} = & \begin{Bmatrix} -Cq_{C_D,1} \\ -Cq_{C_D,2} \\ -Cq_{C_D,3} \\ -Cq_{C_D,4} \\ 0 \\ 0 \\ C\Delta_x - Cq_{C_D,7} \\ C\Delta_y - Cq_{C_D,8} \\ -Cq_{C_D,9} \\ -Cq_{C_D,10} \end{Bmatrix} + \begin{Bmatrix} -Cq_{C_F,1} \\ -Cq_{C_F,2} \\ -Cq_{C_F,3} \\ -Cq_{C_F,4} \\ 0 \\ 0 \\ -Cq_{C_F,7} \\ -Cq_{C_F,8} \\ f_x \\ f_y \end{Bmatrix} = \begin{Bmatrix} -Cq_{C_D,1} - Cq_{C_F,1} \\ -Cq_{C_D,2} - Cq_{C_F,2} \\ -Cq_{C_D,3} - Cq_{C_F,3} \\ -Cq_{C_D,4} - Cq_{C_F,4} \\ 0 \\ 0 \\ C\Delta_x - Cq_{C_D,7} - Cq_{C_F,7} \\ C\Delta_y - Cq_{C_D,8} - Cq_{C_F,8} \\ -Cq_{C_D,9} + f_x \\ -Cq_{C_D,10} + f_y \end{Bmatrix} \quad (1.22)
 \end{aligned}$$

The first four terms of Eqn.(1.22) can be viewed as the constrained points of which can be represented by the third term of Eqn. (1.13). The fifth and the sixth terms of Eqn. (1.22) represent the free node of the truss, and have the same characteristic with the fourth term in Eqn. (1.13). The seventh and the eighth terms in Eqn. (1.22) represent the input point with a specified input distance, and will have the same characteristic of the first term in Eqn.(1.13). The last two terms of Eqn. (1.22) represent the force act on the output point, and will have the same characteristic of the second term of Eqn. (1.13). Due to this quality, it is clear that Eqn. (1.16) can also be applied to truss systems.

Again, we have mentioned that a mechanism can be viewed as a truss that lacks some boundary conditions and can not be analyzed by FEM. In this paper, we mainly focused on mechanism with one degree of freedom. A mechanism with one degree of freedom can be viewed as a truss that lacks only one boundary condition. By taking one link away from the truss describe above as shown in Figure. 3.9, the truss becomes a

mechanism with one degree of freedom. The positions of the joints in the system are also shown in Figure. 3.9.

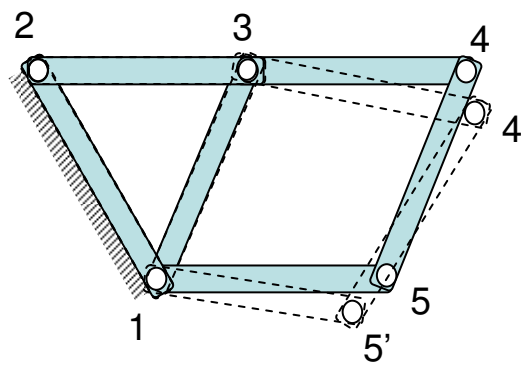


Figure. 3.9 Typical mechanism with one degree of freedom

The displacement of the mechanism in Figure. 3.9 are impossible to calculate directly by FEM due to the insufficiency of boundary condition. By applying Eqn. (1.18), the movement of a mechanism with one degree of freedom can be analyzed by obtaining the displacement of the two trusses shown in Figure. 3.10.

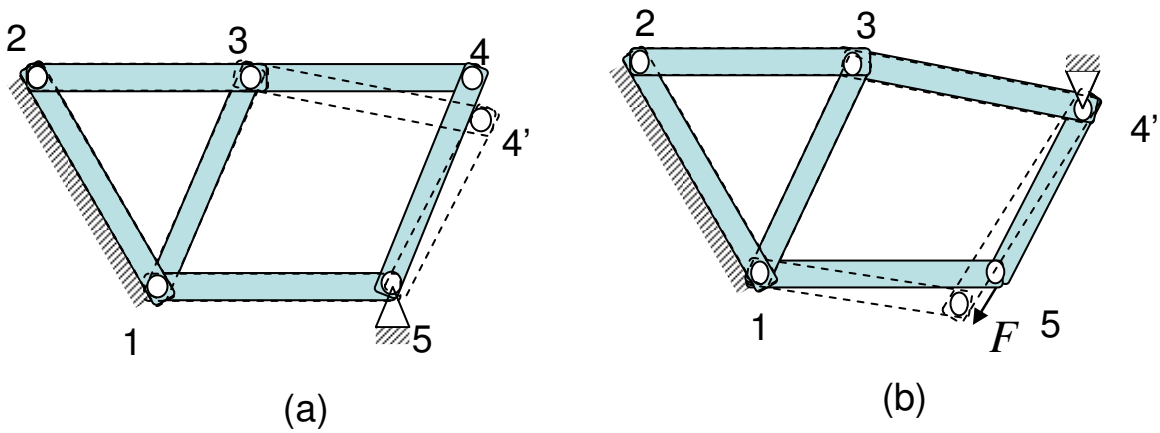


Figure. 3.10 Constrained Superposition Trusses (a) system CD (b) system CF

To analyze the performance of the mechanism in Figure. 3.9, the global displacement with the input link 34 rotate 0.2 degrees CW is defined as follow according to Eqn. (1.18).

$$\{Q_{S_d}\} = \{Q_{C_d}\} + \{Q_{C_f}\} \quad (1.23)$$

$\{Q_{C_d}\}$ is the displacement of the system in Figure. 3.10(a) caused by moving joint 4 to point 4' and $\{Q_{C_f}\}$ is the displacement of the system in Figure. 3.10(b) caused by applying force at joint 5. By fixing the input joint to its target position as shown in Figure. 3.10(a) and fixing the output joint at its original position as shown in Figure. 3.10 (b), the insufficiency of the boundary condition will be compensated and the mechanism can be viewed as a truss. Note that the new location of the input joint has to be feasible. In other words, the given displacement can not cause the input link to deform.

Initially, the global stiffness of the mechanism $[K_{C_d}]$ is calculated by the initial positions of all the joints. To move the input joint to its target position, Penalty terms are add to the diagonal terms of the fixed joints and the joints with predefined displacement and formed a new stiffness matrix $[K_{C_d}]_p$. The displacements of each joint on the mechanism in Figure. 3.10(a) when the input link moves 0.001 degrees CW can be calculated as

$$\{Q_{C_D}\} = [K_{C_D}]_p^{-1} \{F_{C_D}\} = \begin{Bmatrix} -0.0000000000000001 \\ -0 \\ 0.0000000000000004 \\ 0 \\ 0.000000000904833 \\ -0.000000000452417 \\ 0.000000001809661 \\ -0.000174532352035 \\ -0.000000000286576 \\ -0.000000000573156 \end{Bmatrix} \quad (1.24)$$

Recall from Eqn. (1.15), the force acted on system CF can be calculated with the displacement value of point 5 in system CD. We can calculate the force that was applied on joint 5 in Figure. 3.10(b) as follow

$$\{F_{C_F}\} = \begin{Bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ Cq_{p_9} \\ Cq_{p_{10}} \end{Bmatrix} \quad (1.25)$$

After adding penalty terms in the stiffness matrix $[K_{C_F}]$, the stiffness matrix becomes $[K_{C_F}]_p$. The displacement of the system in Figure. 3.10 (b) caused by applying force $\{F_{C_F}\}$ at joint 5 can be calculated by the following equation.

$$\{Q_{C_F}\} = [K_{C_F}]_p^{-1} \{F_{C_F}\} = \begin{Bmatrix} 0.0000000000000006 \\ 0 \\ -0.0000000000000001 \\ -0 \\ -0.000000000143286 \\ 0.00000000007165 \\ -0.000000000286582 \\ -0.000000000573156 \\ 0.0000000013764 \\ -0.00017453091693 \end{Bmatrix} \quad (1.26)$$

With Eqn. (1.24) and Eqn. (1.26), $\{Q_{S_D}\}$ can easily be calculated according to Eqn. (1.23) as shown below.

$$\{Q_{S_D}\} = \{Q_{C_D}\} + \{Q_{C_F}\} = \begin{Bmatrix} 0.0000000000000005 \\ 0 \\ 0.0000000000000003 \\ -0 \\ 0.000000000761546 \\ -0.000000000380767 \\ 0.000000001523079 \\ -0.000174532925191 \\ 0.000000001089824 \\ -0.000174531490086 \end{Bmatrix} \quad (1.27)$$

After updating the joint positions with Eqn.(1.27), the equilibrium of the mechanism is reached. The solution is verified by Working Model (WM) published by Design Simulation Technologies, Inc. WM applies Newton's law with joint constraints and external forces to calculate the internal forces and acceleration of each rigid body. The velocity and position of each body can be calculated using numerical integration[29]. The results of the mechanism analyzed by using Constrained Superposition Method

(CSM) iteratively and WM are shown as below along with the results calculated by analytical method when link 34 rotates 0.2 degrees.

	CSM	WM	Analytical Method
Q_{s_D} (mm)	$\begin{Bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ -0.000000151896199 \\ 0.000000076315993 \\ -0.000060926711561 \\ -0.034907660521652 \\ -0.000060623311398 \\ -0.0349078122217287 \end{Bmatrix}$	$\begin{Bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ -0.00006 \\ -0.035 \\ 0 \\ -0.0352 \end{Bmatrix}$	$\begin{Bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ -0.00006092342209 \\ -0.03490651415224 \\ -0.00006092342209 \\ -0.03490651415224 \end{Bmatrix}$

Table 3.1 The Result of Mechanism with CSM, WM and Analytical Method

From Table 3.1, it is clear CSM and WM can both provide acceptable solution with negligible errors. Note that CSM is only suitable for small deformation. In order to make sure that the displacement is small enough for accurate approximation, the input joint will be move to the target point iteratively if the given displacement is too large. By doing so, the computational power of this method will be higher compared to WM or analytical method. However, analytical method and WM are hard to implement into computers to do mechanism synthesis due to the calculation complexity.

As mentioned before, the mechanism can not have any deformation during the moving process and its strain energy should always be zero. If the strain energy of the

mechanism suddenly goes up, it means that the mechanism reaches its singularity point and starts to deform. The iteration will be stopped if the strain energy of the mechanism is greater than a really small number set by the user.

The procedure of Constrained Superposition Method will be written as follows.

1. Calculate the global stiffness value of the mechanism $[K_{C_d}]$.
2. Penalized the stiffness matrix $[K_{C_d}]_p$ and calculate $\{Q_{C_d}\}$ with the predefined displacement of the input joint.
3. Calculate $\{F_{C_f}\}$ and $[K_{C_f}]$
4. Penalized the stiffness matrix $[K_{C_f}]_p$ and calculate $\{Q_{C_f}\}$
5. Calculate $\{Q_{S_d}\}$ and update the mechanism with it
6. Check if strain energy of the mechanism (Π) is greater than criteria set by the user (ε). If it is, stop the iteration, otherwise, go back to step 1

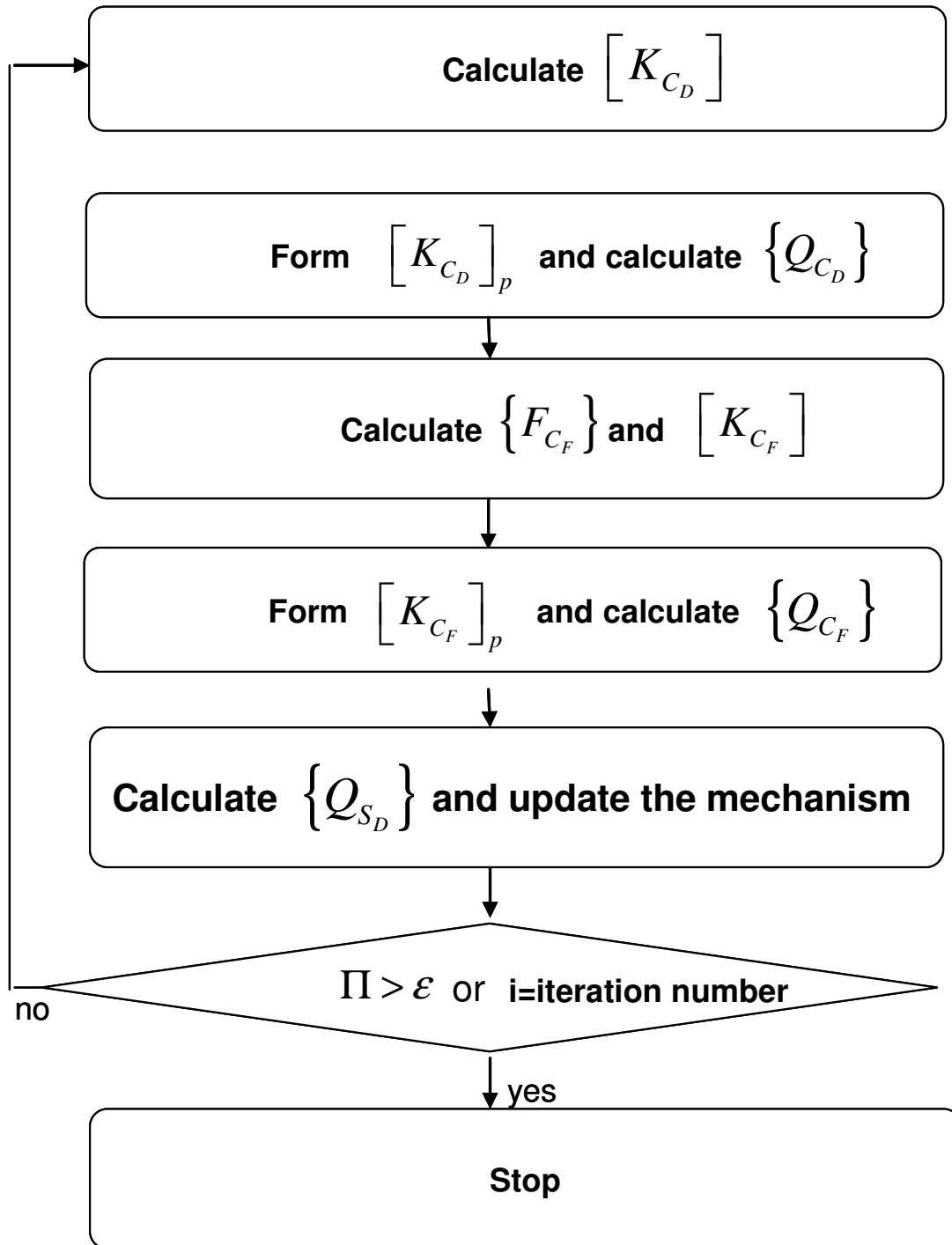


Figure. 3.11 Flow chart of Constrained Superposition Method

3.2. Conclusion

In Kwon's work[17], he had compared the result of graphical method, analytical method and total potential energy method by a four-bar linkage mechanism. The initial position of four joints are A (0, 0), B (6, 0), C (1, 2) and D (7, 5). In order to apply Constrained Superposition Method onto this problem, the iteration number is set to be 200. With iteration number set to be 200, the input joint will be moved 0.1 degree in each iteration. The result of Constrained Superposition Method will be shown in Table 3.2.

		Graphical method	Analytical method	Total potential energy method	Constrained Superposition Method
B	X position	0.2	0.2558	0.2630	0.2595
	Y position	2.20	2.2213	2.2214	2.2210
C	X position	6.4	6.3193	6.3296	6.3237
	Y position	5.1	5.0890	5.0872	5.0890

Table 3.2 The Result of Four-bar Linkage Mechanism with Graphical, Analytical, Total Potential Energy and Constrained Superposition Method

From the result, we can see that the graphical method can not provide a solution as accurate as the ones provided by the other methods base on the human errors. The analytical method will provide us with the most accurate solution of all since it is directly derived by the geometry of the mechanism. However, analytical method is really hard to implement into an optimization problem. The total potential energy method also gives us a quite accurate solution, but if we apply the total potential energy on the same problem

again, it will give us a different answer. In the optimization process of this paper, it is possible that we will eliminate the best design due this phenomenon. On the other hand, the Constrained Superposition Method will also provide an accurate solution with any variation. CSM is also really easy to implement into the optimization process in this paper, which will be introduced in the next chapter.

Chapter 4.

Genetic Algorithm

4.1. Definition of Genetic Algorithm (GA)

Kinematics synthesis of mechanism can not be formulated into a continuous equation. For traditional optimization method, it is almost impossible or inefficient to solve a problem with discontinuous characteristic since all the methods requires the gradient of the objective function. Even if the traditional optimization method solved the problem successfully, there is a great chance that the local optimum is found in stead of the global optimum. Due to the lack of robustness in traditional optimization algorithms, Genetic Algorithm is chosen as the optimization method in this work. Genetic Algorithm is a stochastic optimization method based on the principles of the natural selection and genetics. Genetic Algorithm emulates the evolution of the ecological system, which the driving force of the improvement of the performance comes from the mechanics of natural selection. Natural selection is proved to be highly probabilistic and gives Genetic Algorithm a highly probabilistic characteristic. Genetic Algorithm does not require the gradient of the objective function so that it can apply to any discrete problem as long as the variable can be properly encoded into the chromosomes. Furthermore, since Genetic Algorithm search for a population of points in stead of a single point, all the points are considered in parallel, thus avoiding local optimums.

4.1.1. Genetic Reproduction Operator

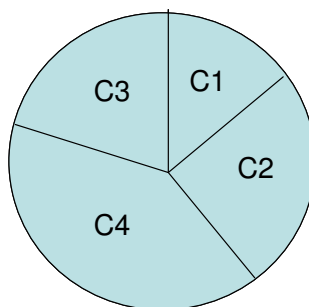
Genetic Algorithm consists of two major operations: creation of initial population and reproduction results in a new population. Three reproduction operators are used in reproduction process: selection, crossover and mutation.

4.1.1.1. Selection

Parents selecting is one of the most important parts of the Genetic Algorithm. The survival of one single chromosome is determined by its fitness value. The fitness value is usually obtained from the value of objective function. There are many different ways to do parents selecting. There is no definite answer to which of the method is the most useful. Roulette Wheel Parent-Selection Procedure is one of the most popular selection methods. Roulette Wheel Parent-Selection Procedure divides a fortune wheel into several slots weighted in proportion to the fitness values of the chromosomes. The possibility of a chromosome to be chosen can then be calculated by Eqn. (2.1).

$$P_i = \frac{U_{i(x)}}{\sum_{k=1}^n U_k(x)} \quad (2.1)$$

where U_i is the fitness value of i th chromosome. In Figure 4.1, an example of parents selecting is presented. Four chromosomes C1,C2,C3 and C4 each have a fitness value of 15,30,25 and 50, respectively. By using Eqn. (2.1), the probability of the chromosomes can be calculated.



Chromosome	C1	C2	C3	C4
Fitness value $U(x)$	15	30	25	50
Probability P_i	0.125	0.25	0.208	0.416

Figure 4.1 Example of Roulette Wheel Parent-Selection Procedure.

4.1.1.2. Crossover

After selecting the parents, the chromosomes are randomly paired up. A crossover rate must be set in order to perform the crossover, in the ecological system, the crossover rate is often really high and normally been set in the range of 0.6~0.9. After the crossover rate is set, a random number between zero and one is generated for each pair of chromosomes, and if the random number is smaller than or equal to the crossover rate, crossover will be performed. Once sure the crossover will be performed. Another random number between zero and one is generated in order to determine the crossover site. The random number will be multiplied by the length of the chromosome minus one rounded off. The value obtained by previous step will be considered as the crossover site. Every gene behind the crossover site has to be crossed over. An example is shown in Figure 4.2. A random number 0.76 is generated for the parent to determine the site to perform crossover. For a chromosome with six genes on it, there will be five sites that can perform crossover. By round off the product of the random number and the number of

sites, the crossover site is determined. Another random number is then generated to determine whether the chromosome should crossover or not. If the number is smaller than the predefined crossover rate, the crossover will be performed.

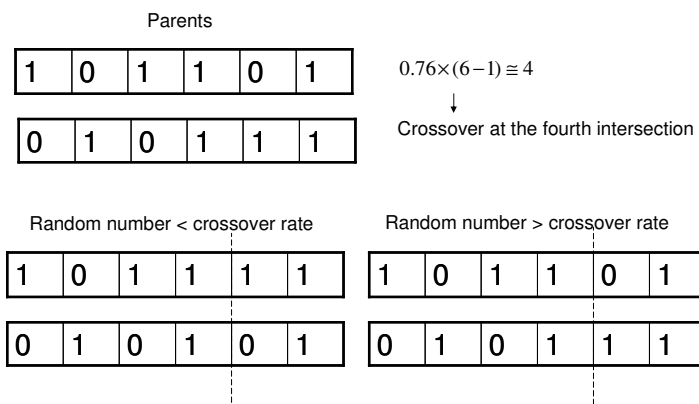


Figure 4.2 Example of Crossover.

4.1.1.3. Mutation

It is necessary to have a mutation process to give the population some offspring so the solution will not converge to a local minimum. Similar to the crossover, before processing any mutation, a mutation rate must be chosen. In the natural world, the product of mutation can be really undesirable. So the normal range of the mutation rate is between 0.01~0.1. After the mutation rate is set, a random number between zero and one is generated for each gene on the chromosome. If the random number is smaller or equal to the mutation rate, mutation will be performed. That is, if the gene is one, flip it to zero and vice versa. Figure 4.3 showed an example of mutation. As shown in the example, if we have a chromosome with six genes on it, six random number will be generate (R1~R6). Each random number represent a gene on the chromosome, if the random number is smaller than the predefined mutation rate, the gene will mutate.

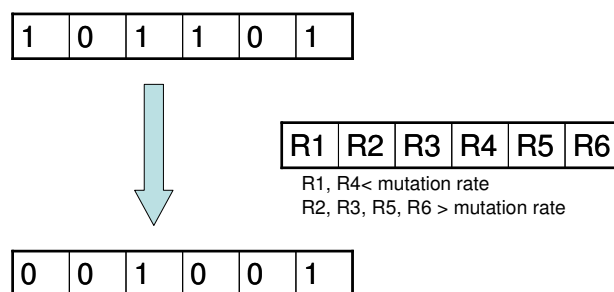


Figure 4.3 Example of Mutation.

4.1.1.4. Elitism

After Mutation, a new generation of population is obtained. However, we can not guarantee that the best in the new population pool is better than the one in the previous population pool. In order to preserve the good quality of the best chromosomes in the previous population pool, the best one or two chromosomes of the current population will automatically be moved to the next generation before the reproduction process started. This method is called elitism.

The process of selection, crossover and mutation will be used on the newly generated population to find another new population over and over again until it reaches the maximum generation number or the convergence criteria set by the user.

4.2. Modified Genetic Algorithm for Mechanism Optimization

In order to introduce Genetic Algorithm in the mechanism synthesis, some modification must be made with Genetic Algorithm. In this section, the changed made and the flowcharts of the modified Genetic Algorithm are shown.

4.2.1. Encoding of Chromosomes

Design representation is essential to Genetic Algorithm process (GA). In Genetic Algorithm, the chromosomal form is binary digits, which is a chain of 1 and 0. There are three types of features in a mechanism which are the topology of the mechanism, the constraints on the joints and the position of the joints of the mechanism. These three features can define a mechanism and have to be encoded into the chromosomes in order to perform Genetic Algorithm. In this section, the method to encode these three types of feature is discussed.

4.2.1.1. Mechanism Topology Representation in chromosomes

The topology of a mechanism contains the essential information about which joint is connected to which other joint and can be expressed in several different ways. The representation of the mechanism can be categorized in to two groups, which is graph-based representation and matrix-based representation. Graph-based representation includes functional schematic representation, structural representation and graph representation which are mentioned In [30]. Graph-based representation is very good for display the main feature of the mechanism. However, for convenience of computer programming, graph-based representation is really hard to implement. In order to represent mechanism in the computer program, Yi Liu and John Mcphee [30] expressed the mechanism in a matrix form. In the paper, they formed a $n \times n$ matrix LAM for a n links mechanism, whenever link i is adjacent to link j , LAM_{ij} equals one, otherwise LAM_{ij} equals zero. This is a very powerful representation and is able to shown

some sufficient information about the topology of the mechanism. However, if this matrix is used to create the chromosome in Genetic Algorithm, it is possible that the operator will generate something that is impossible to decode. To guarantee that the chromosome is decodable, we present another method to represent the topology of the mechanism. The possible linkage number L_n can be calculated if the joint number of the mechanism m is known.

$$L_n = \frac{m \times (m-1)}{2} \quad (2.2)$$

After knowing the possible linkage number, a script can be generated that include all the linkages. Figure 4.4 shows an example of the script for a mechanism with four joint numbers where the first column represent the link number and the second and the third column represent the joint number of the joint connected by the link.

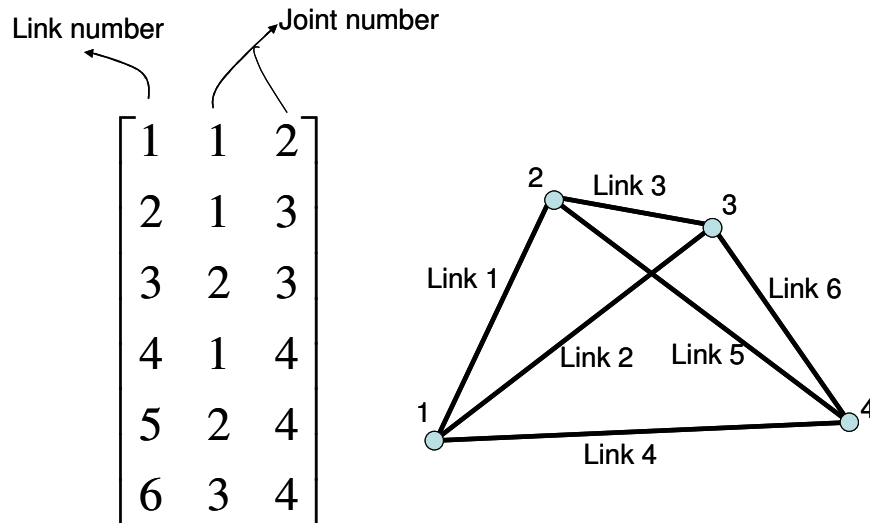


Figure 4.4 Example of Link Script

L_n numbers of ones and zeros can then be generated to represent the mechanism.

$$S_{L_i} = \begin{cases} 1 & \text{if link } i \text{ exist} \\ 0 & \text{otherwise} \end{cases} \quad (2.3)$$

Where $i = 1, \dots, L_n$. S_{L_i} can be viewed as the first part of the chromosome. Figure 4.5 shows one possible S_L for four-joint mechanism and the topology it represent.

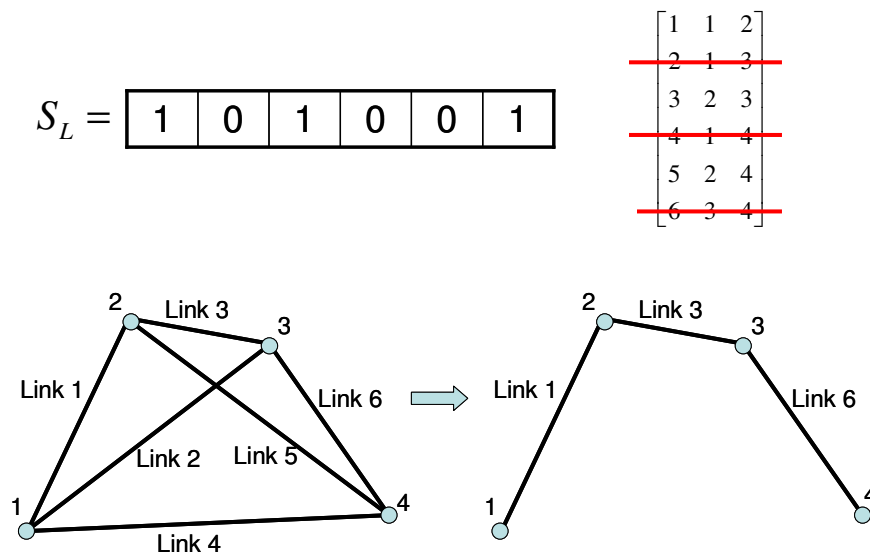


Figure 4.5 Example of Link Representation

4.2.1.2. Constraint Representation in Chromosomes

The constraint of the mechanism force the mechanism to stay steady, without proper constraints, the mechanism will have multi degrees of freedom and the motion of each joint will be unpredictable. In this paper, there are three types of constraints which are the fixed constraints, x-slide constraints and the y-slide constraints. For each joint, it will have two degrees of freedom in the plane, both in the x direction and the y direction. The x-slide constraints take away the degrees of freedom in y direction so the joint will move only in the x direction; the y-slide constraints take away degrees of freedom in the x direction so the joint will move only in the y direction and the fixed constraints take the

degrees of freedom in both directions away so the joint will stay at its initial position and can be viewed as a fixed joint. To encode the constraint into the chromosome is simple; two digits are generated onto the chromosome. The first digit represents the degree of freedom in the x direction and the second digit represents the degree of freedom in the y direction. If the value of the digit is one, the joint is free in the direction it represents. In other words, if the value of the digit is zero, the joint is confined in that direction. After generating $2 \times m$ ones and zeros, the constraint of the mechanism is defined. m is the number of joints. Figure 4.6 shows one possible constraint condition of a four joint mechanism. The first two digits represent the constraint acted on joint 1. Since both number are zero, there is no degree of freedom on joint 1. Hence, joint 1 is constrained by a fixed constraint. The third and the fourth digits of the string represent the constraint acted on joint 2. Since both of them are one, this joint has two degree of freedom and can be viewed as a free node. The fifth and the sixth digits represent the constraint acted on joint 3. The sixth digit is one means the joint has one degree of freedom in y-direction and can be viewed as a y-directional slide. The last two digits represent the constraints acted on joint 4 and since the seventh digit is one, the joint can be viewed as being constrained by an x-directional slide.

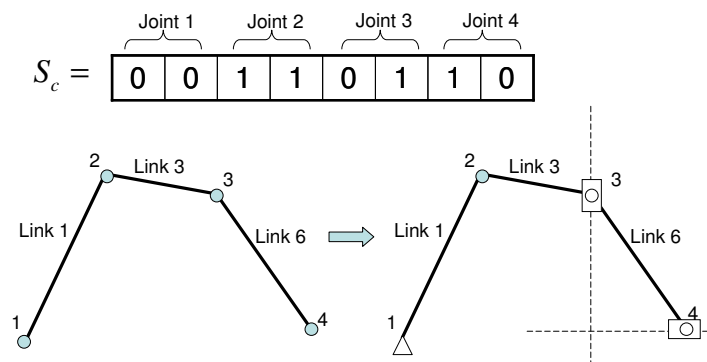


Figure 4.6 Example of Constraint Representation

4.2.1.3. Position Representation in Chromosomes

The type of the mechanism can be determined by the topology and the constraint of the joints of the mechanism. However, the initial position of the joints is essential to determine the initial position and link length of the mechanism. The position consist the x coordinate and y coordinate of the joint. In this paper, each component is represented by ten binary digits. If the binary string is given as:

$$S = S_{10}S_9S_8S_7S_6S_5S_4S_3S_2S_1 \quad (2.4)$$

Then the numbers in decimal digits can be obtained by the formula as follow:

$$x' = \sum_{i=1}^{10} 2^{i-1} S_i \quad (2.5)$$

Since S is a string of ones and zeros, the value obtained using (2.5) will fall into the region $[0,1023]$. However, the real position of the joint should always falls in a design domain $[x_l, x_u]$, where the subscripts represent lower and upper limits of the component that are set by the user. x' must be mapped to the range of the design variables using (2.6) in order to obtain the component of the position

$$x = x_l + \frac{x_u - x_l}{2^{10} - 1} x' \quad (2.6)$$

These procedures enable us to simply generate a $2 \times m$ binary digit string to represent the position of the mechanism and decode them when needed.

Now, all three types of features have been encoded into binary system and formed into a chromosome. Genetic Algorithm can easily be applied for mechanism optimization.

4.2.2. Feasibility of the Mechanism

One disadvantage of Genetic Algorithm is that it can not guarantee the feasibility of the chromosome produced by reproduction. In order to save the computational time to generate the fitness value of infeasible chromosomes, two feasibility checks is proposed in this paper: the connectivity check and mobility check.

4.2.2.1. Connectivity Check

To ensure the feasibility of the mechanism, there are four kinds of situation need to be avoided.

1. The assigned input joint is not connected to the mechanism.
2. The assigned output joint is not connected to the mechanism.
3. The predefined constrained joints are not connected to the mechanism.
4. Existence of unconnected floating links.

In order to identify these four situations, a tree-structured path script is generated according to the link script obtained by decoding the link part of the chromosome. The procedure of creating the path script can be described into four steps:

1. Identify the input joint as the starting point of the tree-structure path script.
2. Find out all the links that are connected to the starting joint and import them into the path script.

3. Eliminate the connected links from the link script.
4. Update the starting point of the path script to the joints that is connected to the previous starting point and repeat step 2.
5. Stop when there is no link left in the link script or if there is no link connected to the starting point.

After the script is generated, the first three situations can be check by checking if the points they are referring to is in the path script. If not, the mechanism represented by the chromosome is an in feasible mechanism. For the last situation, we can simply check if there is any link left in the link script. If there are some links left in the link script, the mechanism is infeasible.

4.2.2.2. Mobility Check

The mechanisms discussed in here will only be applied with one input mechanism. In order for the mechanism to have a unique output with one input, the degree of freedom of the whole mechanism has to be one. In order to calculate the degrees of freedom of the mechanism, Gruebler's equation is introduced in[1]. Gruebler's equation will determine the degrees of freedom of a p-link chain connected by f_1 pin joints, with ground considered as one of the links:

$$DoF = 3 \times (p - 1) - 2 \times f_1 \quad (2.7)$$

Before the constraints are applied onto the mechanism, there is no such thing as a ground link in the system. With the number of links in the link script l , we can modify the Gruebler's equation into Eqn. (2.8)

$$DoF = 3 \times l - 2 \times f_1 \quad (2.8)$$

The degree of freedom will be really high if the constraints are not added into the system. To add a fixed constraint onto a joint, it is like take 2 degree of freedom off of the whole system and can be viewed as adding one joint onto the system according to Eqn. (2.8); Adding a slide constraint in either direction will results in reducing one degrees of freedom of the mechanism. The same effect will happen if we add two joint and one link onto the system. For a mechanism that has C_f fixed constraints and C_s slide constraints, the degree of freedom can be calculated as

$$DoF = 3 \times (l + C_s) - 2 \times (f_1 + 2 \times C_s + C_f) \quad (2.9)$$

In most cases, if the degree of freedom is one, the mechanism is feasible. However, there is some exception to this statement. In Figure 4.7, two mechanisms that have one degree of freedom but are infeasible for analysis are shown.

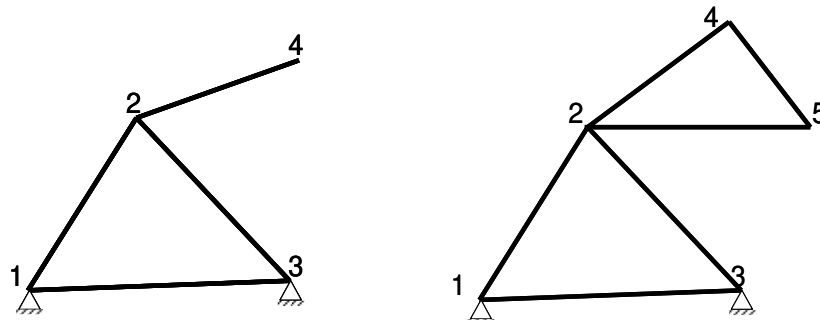


Figure 4.7 Exceptions of Mobility Check

These two mechanisms all have one degree of freedom, but if we use joint 2 as our input point, the mechanism will be stuck. This indicates that the stated input joint have to be able to move. To prevent this mechanism passing the check, the links that connect the input joint and the constrained joint are picked out as shown in Figure 4.8. If the linkages picked out have a zero degrees of freedom, this mechanism is set to be infeasible. Some exception will start to show up as the joint number of the linkage increases. However, these exceptions will not be picked out in this check and will be analyzed by the Constrained Superposition Method. This kind of mechanism will be picked out in the mechanism analysis since for those unmovable mechanisms, the determinants of their stiffness matrixes are zero. Once the determinant is zero, the analysis process will stop and assign the chromosome with a large fitness value.

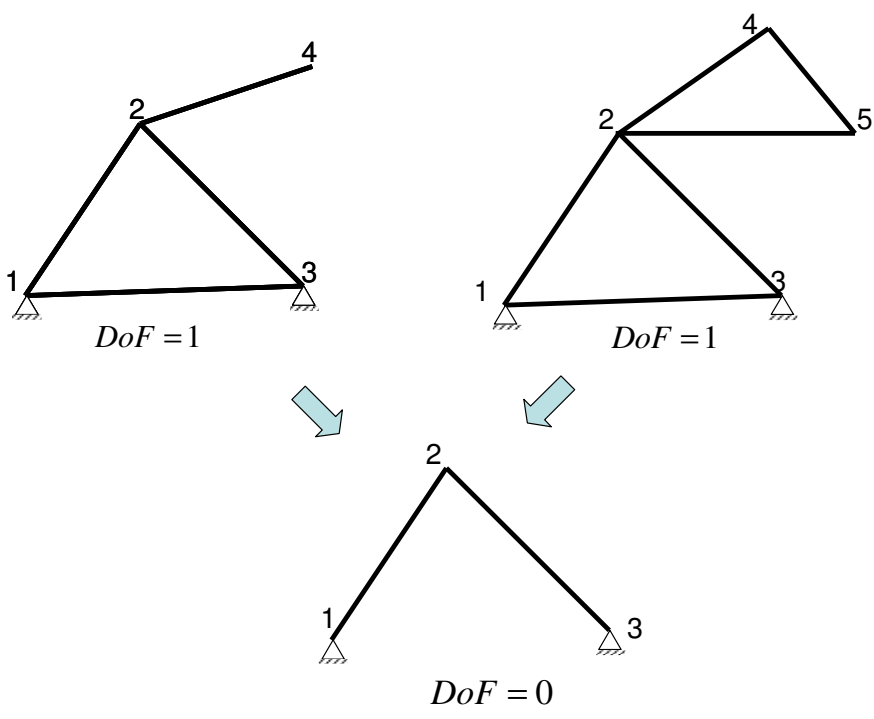


Figure 4.8 Solutions to the Exceptions

4.2.3. Application of Genetic Reproduction Operator

Several traditional genetic reproduction operators had to be modified due to the physical meaning of the problem.

4.2.3.1. Fitness Value

In this paper, we mainly focus on two different types of problem. One is to find a mechanism that maximizes the output distance and the other is to find the most suitable mechanism to fit the given output distance. The fitness value will be different in different types of problem. For the first type of problem, our objective is to maximize the geometry advantage-That is, the output distance divided by the input distance. Since the input distance is set to be a constant in the problem setting, the geometry advantage can be represented by the output distance alone. The fitness value of the first type of problem will then be written as

$$\text{fitness value} = -\| \text{final output position} - \text{initial output position} \| \quad (2.10)$$

Most of the optimization process is a minimization process, a negative sign is added to turn the problem into a minimization problem. For the second type of the problem, our objective is to minimize the distance between the final position and the target position when given the same input distance or angle. The fitness value can then be written as

$$\text{fitness value} = \| \text{final output position} - \text{desired output position} \| \quad (2.11)$$

Since this is already a minimization problem, there is no need to change the sign of the fitness value.

4.2.3.2. Modification of Genetic Reproduction Operator

In this paper, Roulette Wheel Parent-Selection Procedure is chosen as the parents-selecting procedure. However, from the physics of the fitness value, it is possible that the order of fitness value of the chromosome is changeful. In other words, the chromosomes with higher order will have an almost hundred percent chance of being chosen as the parents of next generation. The problem will rapidly converge to a local minimum due to this effect. To avoid this effect, instead of using the fitness value to calculate the probability of being chosen, we use the ranking of the chromosome to calculate it. The new population of chromosomes is ranked in ascending according to the fitness value. The highest-ranking chromosome will have a hundred times more chance to be picked as the parents of the next generation if the population size is a hundred. The method can guarantee that every chromosome has a chance of being picked.

Crossover and mutation are almost the same with the traditional Genetic Algorithm. The crossover rate and the mutation rate are set to be 0.6 and 0.01, respectively. The elitism is also applied in this paper. The best two chromosomes of the current population will be moved to the next population before the reproduction process.

The flow chart of Modified Genetic Algorithm is shown in Figure 4.9, where ps is the population size and tps is the total population size predefined by the user.

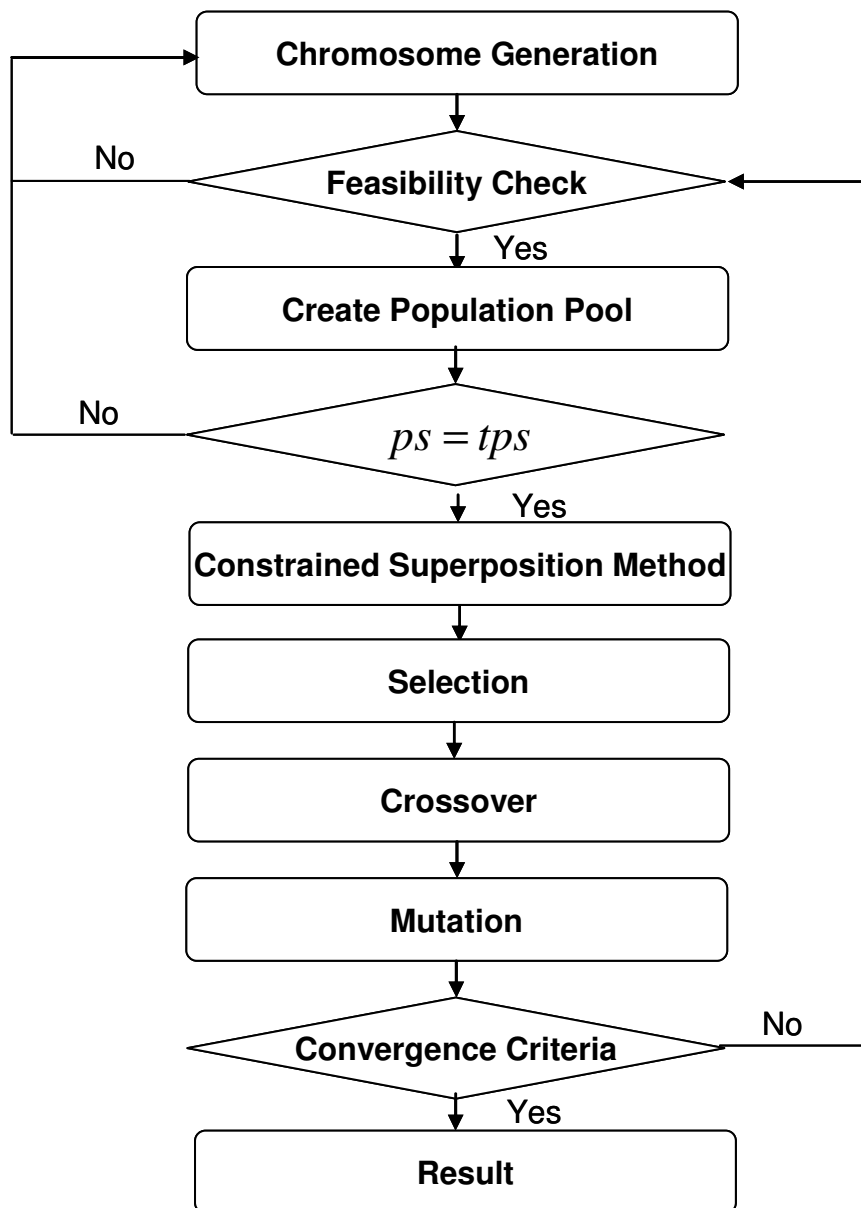


Figure 4.9 Flow Chart of Modified Genetic Algorithm

Chapter 5.

Mechanism Design

5.1. Mechanism Design for Maximum Output Distance

With the same input value, people intend to maximize the output of the mechanism in order to improve the efficiency. In order to obtain the maximum output distance, the fitness value in this section is formulated according to Eqn. (2.11).

5.1.1. Toggle-press Design for Maximum Output Distance

A toggle press is design to press or stake light gauge stock. A general toggle press is shown in Figure 5.1.

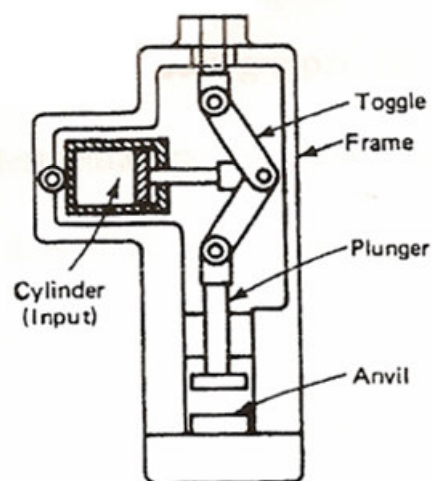


Figure 5.1[17] Model of Toggle-press

This example is used by Kwon in [17]. We now use the same setup to maximize the depth that the plunger of the toggle-press can reach. The problem setup including the predefined constraints, the size of design domain and the positions of the input and output joint are shown in Figure 5.2.

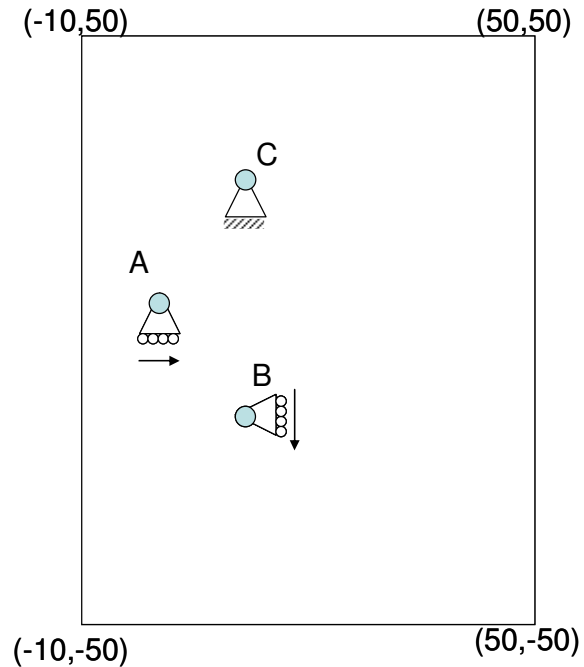


Figure 5.2 Problem Setup for Toggle Design for Maximum Output Distance

In this design problem, Joint A is the input joint and joint B is the output joint. Joint A can only move in the x direction and joint B can only move in the y direction while joint C is fixed. The positions of joint A, joint B and joint C are (0, 0), (10, -10) and (10, 10), respectively. The input distance is set to be 4 units and our objective is to maximize the distance between the initial position and the final position of joint B.

For the optimization process, the population size is 50 and the iteration number is 100. The crossover rate is 0.6 and the mutation rate is 0.02. Figure 5.3 shows the best-to-date fitness value of Genetic Algorithm throughout the optimization process.

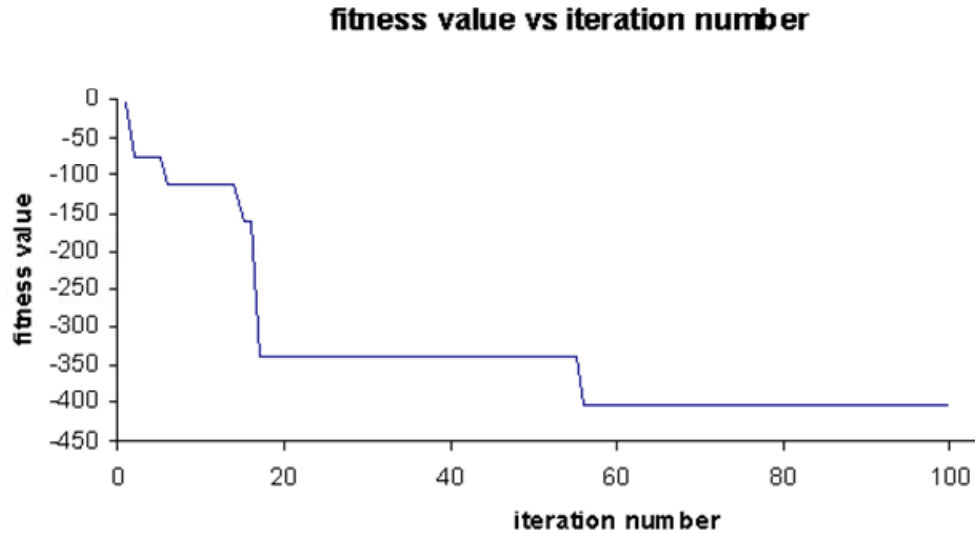


Figure 5.3 Fitness Value throughout Optimization Process for Maximizing Output Distance.

The best-to-date mechanisms correspond to the fitness value above are shown in Figure 5.4. Figure 5.4 (f) is the final solution for toggle synthesis. The red joint represents a fixed joint; the green joint represents the joint that can only move toward x-direction and the gray joint represents a joint that can only move in the y direction. It is clear that Figure 5.4 (d)(e)(f) are very similar with each other with a slice difference of the last position.

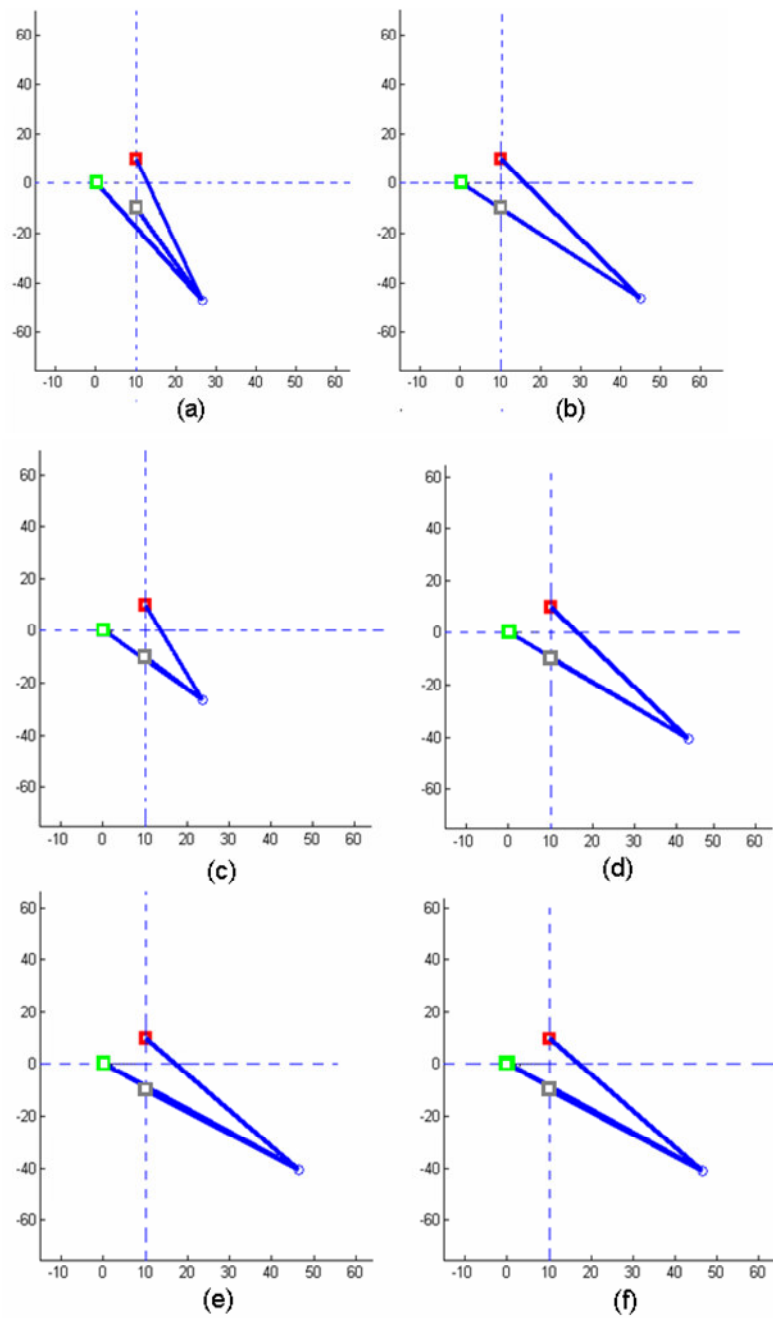


Figure 5.4 Mechanisms Corresponding to the Change of Best-to-date Fitness Values for Toggle Problem. (a) 1st iteration (b) 5th iteration (c) 14th iteration (d) 15th iteration (e) 17th iteration (f) 56th iteration

5.1.2. Toggle-press Design for Maximum Output Distance without Boundary Condition

In previous section, we have designed a mechanism to maximize the output distance for toggle-press according to the initial setup of the example proposed by Kwon. However, the boundary condition might eliminate some possible mechanism. In order to see if the solution will still converge to the same result, the fix boundary condition is been taken off. The problem setup can then be shown in Figure 5.5.

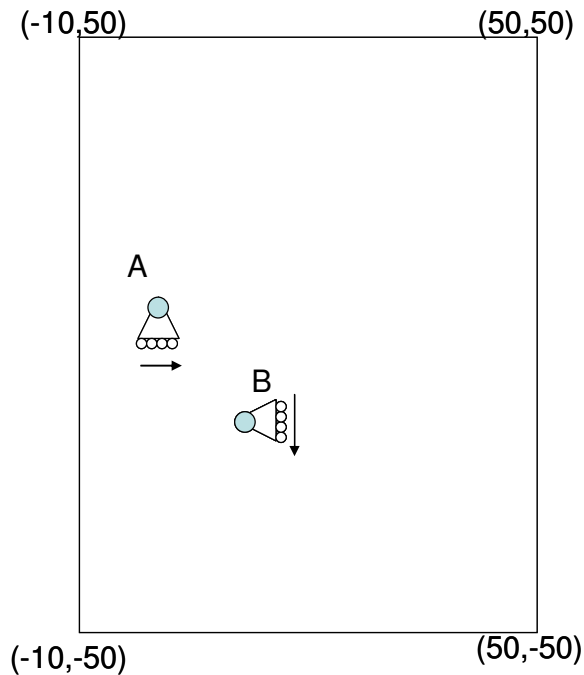


Figure 5.5 Problem Setup for Toggle Design without Boundary Condition

Similar to the previous problem setup, joint A is the input joint and joint B is the output joint with the same boundary condition as in 5.1.1. The positions of joint A and joint B are $(0, 0)$ and $(10, -10)$, respectively. The input distance is set to be 4 units and

our objective is to maximize the distance between the initial position and the final position of joint B.

For the optimization process, the population size is 50 and the iteration number is 100. The crossover rate is 0.6 and the mutation rate is 0.02. Figure 5.6 shows the best-to-date fitness value of Genetic Algorithm throughout the optimization process.

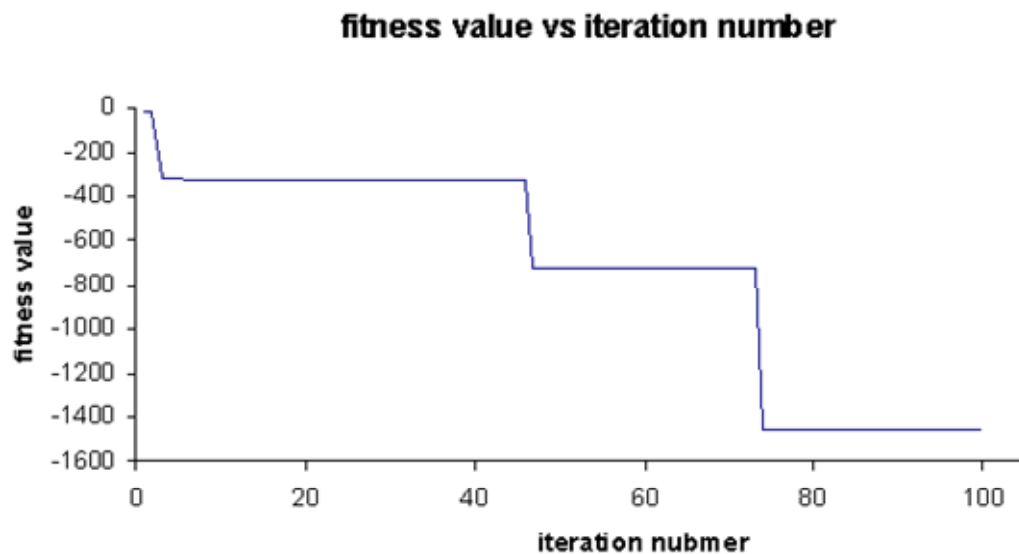


Figure 5.6 Fitness Value throughout Optimization Process for Maximizing Output Distance without Boundary Condition.

The result shows that the mechanism does not converge to the same result as in section Toggle-press Design for Maximum Output Distance5.1.1. The fitness value of the final design in the section is much better than the one in the previous section. We can conclude that the more boundary conditions are given, the less the feasible mechanisms exist.

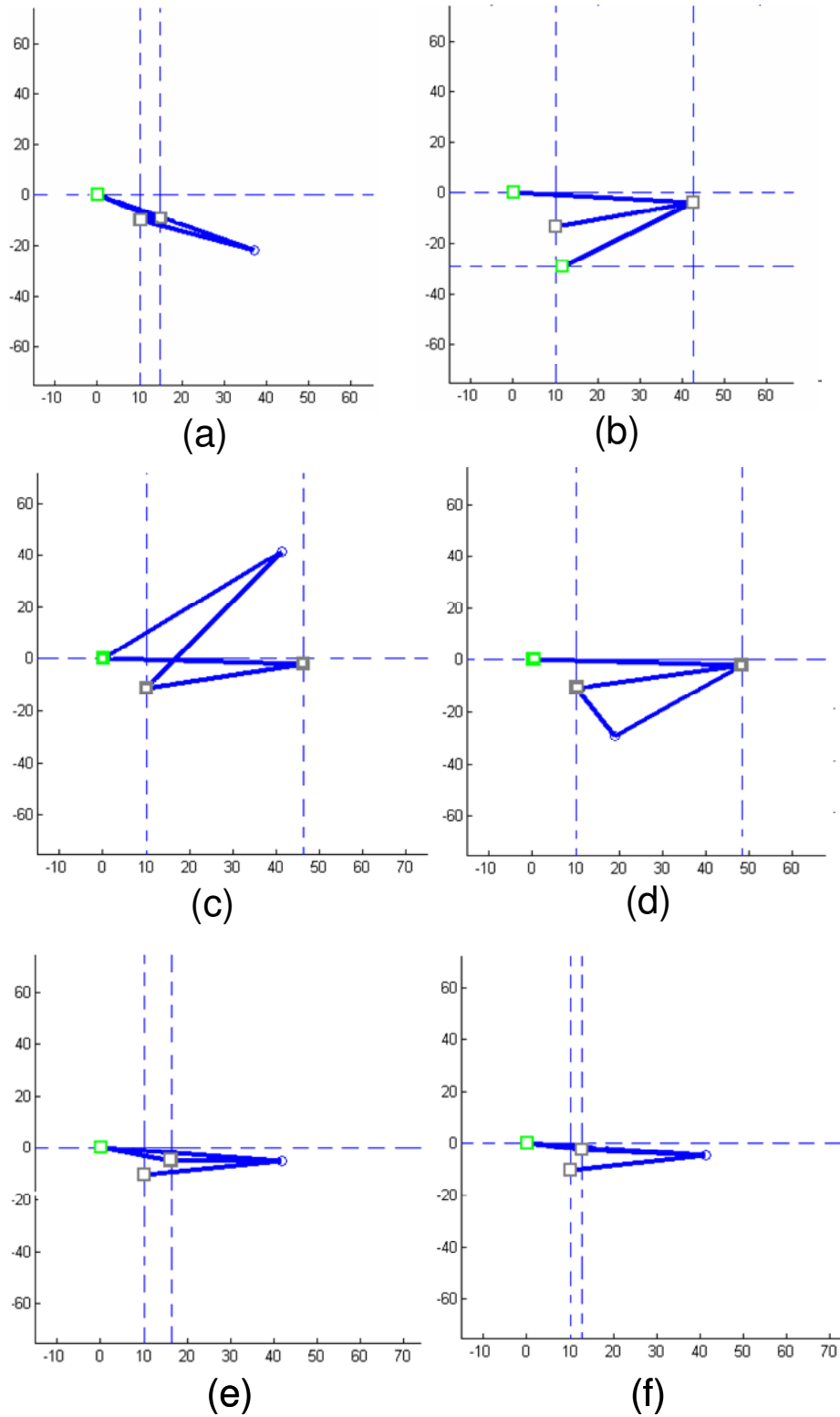


Figure 5.7 Mechanisms Corresponding to the Change of Best-to-date Fitness Values for Toggle Problem without Boundary Condition (a) 1st iteration (b) 3rd iteration (c) 5th iteration (d) 33rd iteration (e) 46th iteration (f) 73rd iteration

5.2. Mechanism Design for Predefined Output Distance

In the industrial world, engineers often try to design mechanism that can reach certain target location instead of just maximizing the output distance. When designing for a mechanism that will reach the goal with a given input, the formulation of the fitness value becomes the distance between the final output joint position and the initial output joint position as mentioned in Eqn. (2.11).

5.2.1. Mechanism Design for One Predefined Output Distance

Any mechanism with one degree of freedom will provide a unique output with a certain input. In this section, a specific four-bar mechanism as shown in Figure 5.8 is used to obtain the initial values of the problem setup.

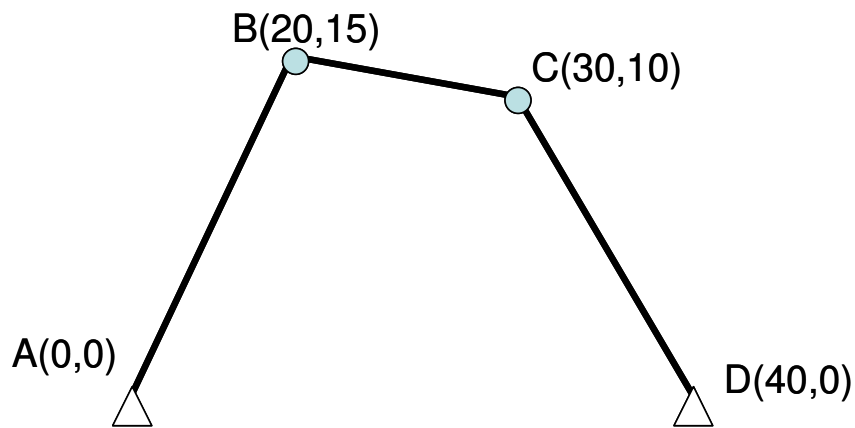


Figure 5.8 Four-bar Linkage for Problem Setup

First, we set link AB to be the input bar that rotates five degree clockwise, and then record the final position of joint C as our predefined output target point. The

problem setup can then be established with design domain predefined as shown in Figure 5.9.

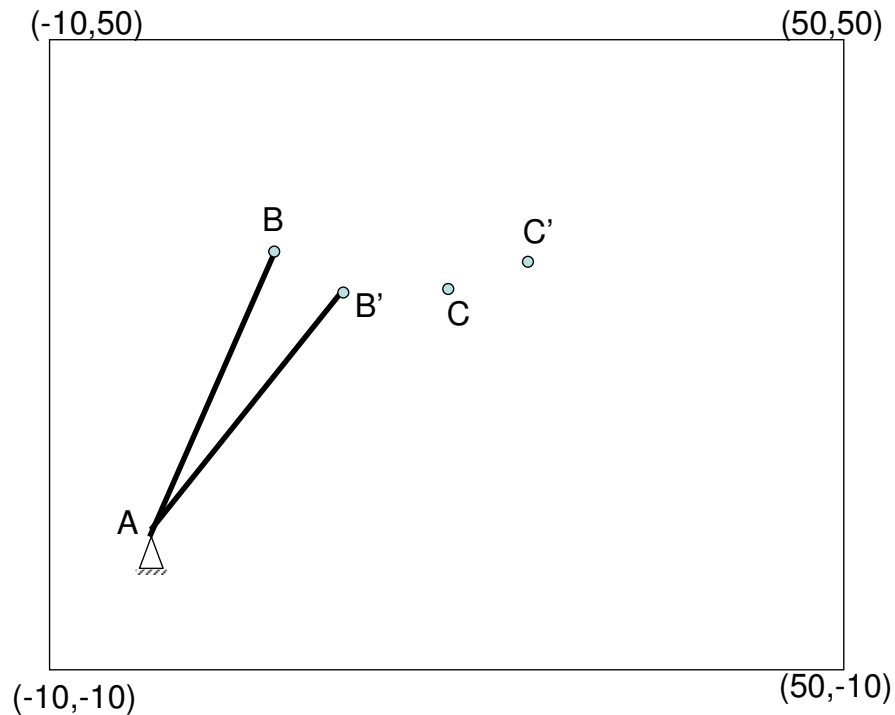


Figure 5.9 Problem Setup of Mechanism Design for One Predefined Output Distance

The main purpose of this mechanism synthesis is to find a mechanism that can move its joint C from point C to point C' while moving its joint B from point B to point B'. As shown in Figure 5.9, the given parameter includes the initial position of joint A (0, 0), joint B (15, 20), joint C (30, 10), fixed constraint on A, input angle, design domain and the target point C' (33.691, 12.662). In the optimization process, the population size is 50 and the number of iteration is 100. The crossover rate and mutation rate are 0.6 and 0.02, respectively.

Figure 5.10 shows the change of the fitness value of the best chromosomes through out the optimization process. The fitness value is converted into its logarithm to the base 10 for display purpose.

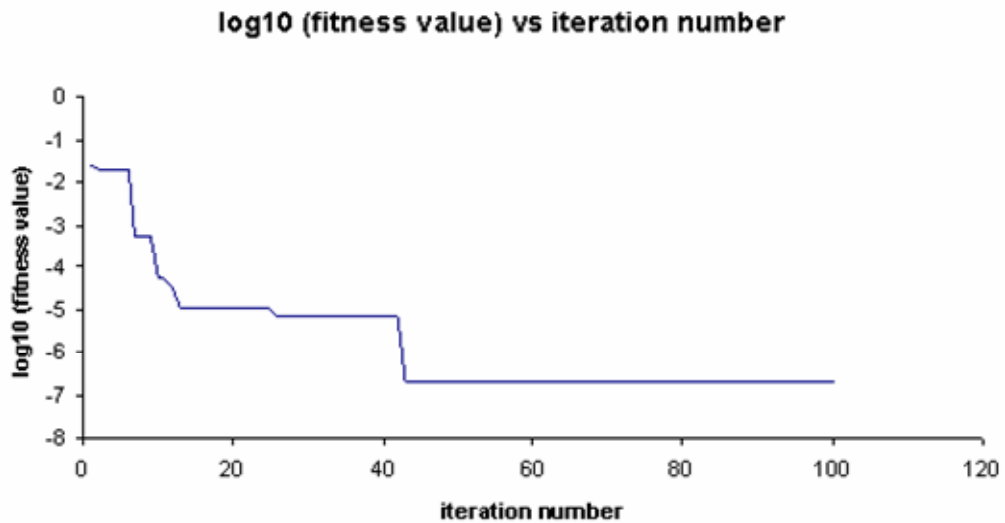


Figure 5.10 Fitness Value throughout Optimization Process for One Predefined Output Distance Mechanism Design.

Figure 5.11 (b) shows the final result of the GA optimization, and Figure 5.11 (b) is the original design of the problem.

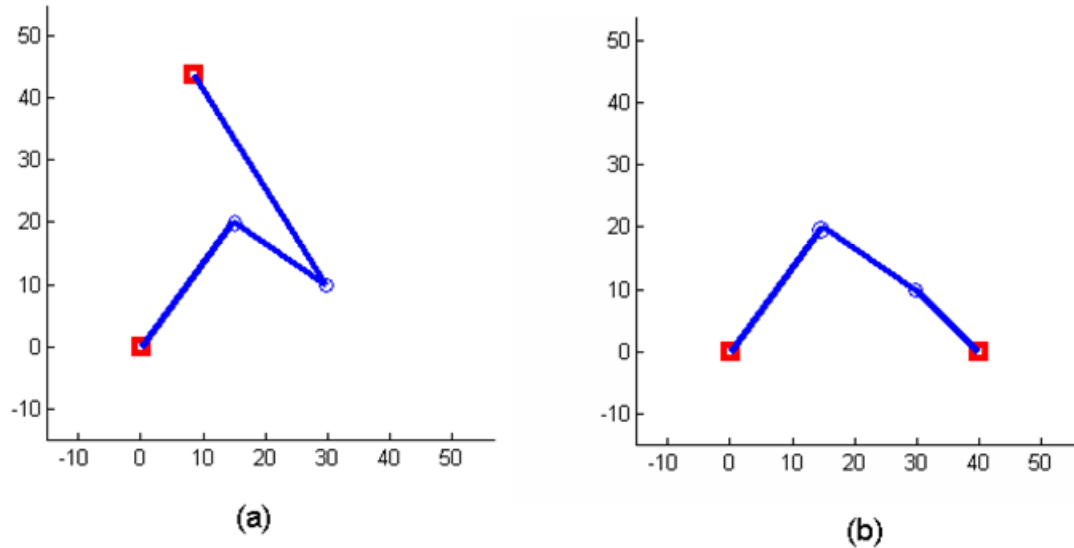


Figure 5.11 Comparison between the Final Result and the Original Design

Compare the result between the best design after 100 iterations and the original design; it is clear that they are not the same. The reason for that can be easily explained by graphical method. Figure 5.12 shows the process of solving the problem with graphical method. First, we have to connect point C and C', then draw a perpendicular bisector as shown in Figure 5.12 (a) (b). According to the definition of perpendicular bisector, any point on the perpendicular bisector will have an equal distance between point C and C'. Hence, the forth joint can locate at any place on the perpendicular bisector. Figure 5.12 (c) (d) shows two sets of the possible cases. It is easy to tell that Figure 5.12 (c) is the solution got from the optimization process and Figure 5.12(d) is the original design. To sum up, since the problem has multi-solutions, all of the solutions are true.

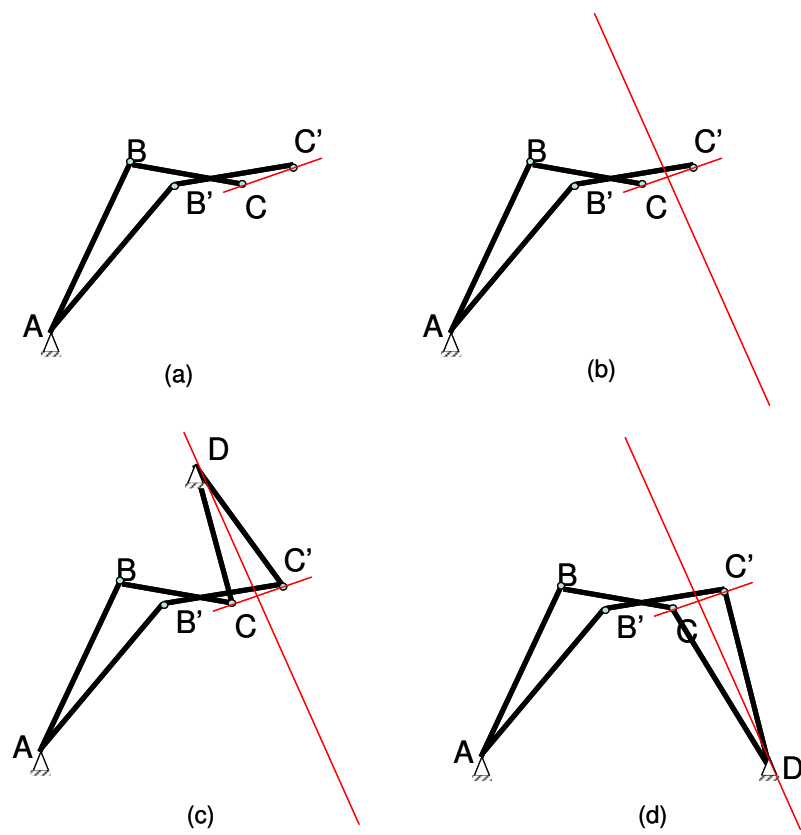


Figure 5.12 Solution of Graphical Method for One Predefined Output Distance Problem.

5.2.2. Mechanism Design for Two Predefined Output Distance

Now we have proved that the algorithm works on designing mechanism for one predefined output distance, we will move on to see the performance of the algorithm with two predefined output distance. The same four-bar linkage mechanism in Figure 5.8 is used in this problem as well; the problem setup of mechanism design for two predefined output distance will be shown in Figure 5.13.

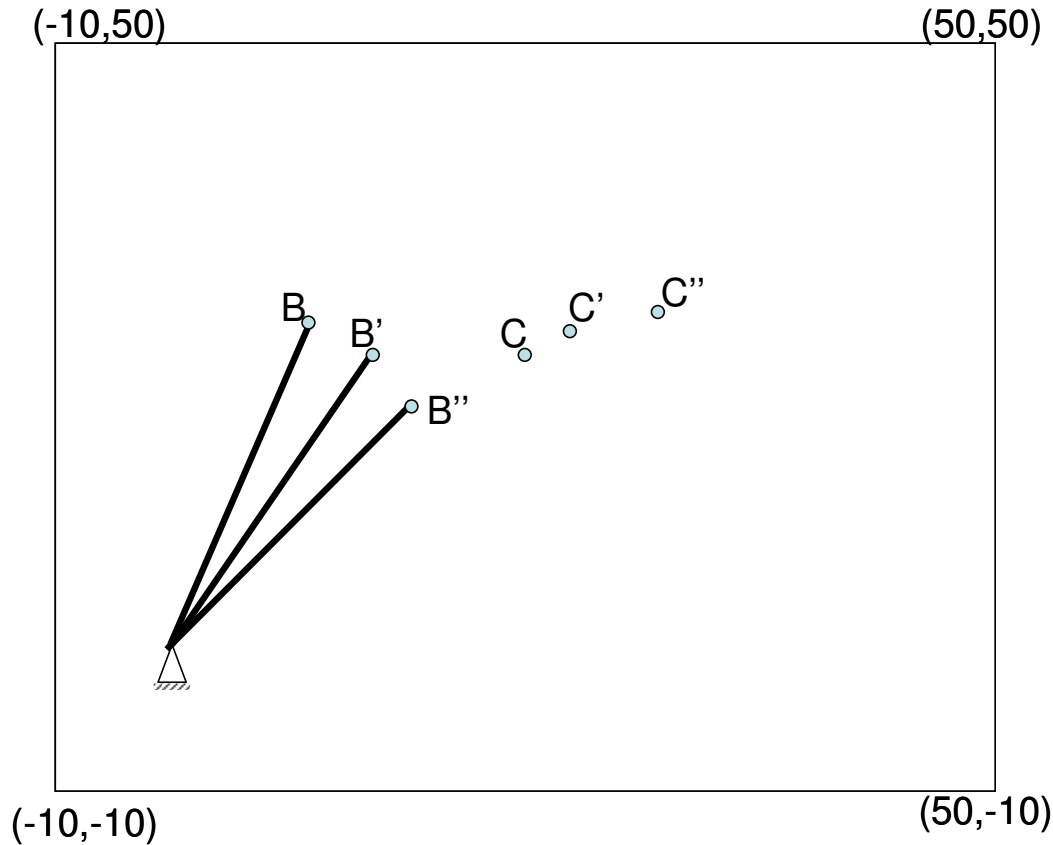


Figure 5.13 Problem Setup of Mechanism Design for Two Predefined Output Distance

Mechanism design for two predefined output distance is not much different from design for one predefined output distance. The only difference is that joint C of the desired mechanism in this section not only has to reach C' while joint B reaches B', it has to reach C'' while joint B reaches B''. As shown in Figure 5.13, the given parameters are almost the same with the ones in the previous section with the second target point C'' (35.902, 13.541) and the second input angle which is also five degrees. The parameters in the optimization process are exactly the same with the previous section.

Figure 5.14 shows the change of the fitness value of the best chromosomes through the optimization process. The fitness value is converted into its logarithm to the base 10 for display purpose.

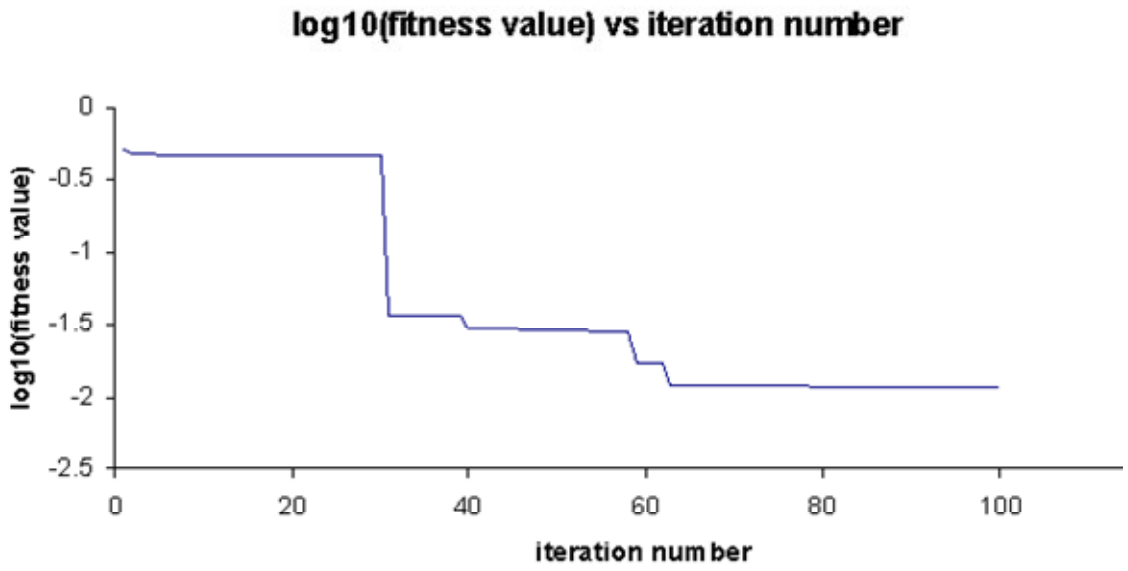


Figure 5.14 Fitness Value throughout Optimization Process for Two Predefined Output Distance Mechanism Design.

Figure 5.15 (a) shows the final result of the GA optimization, and Figure 5.15 (b) is the original design of the problem.

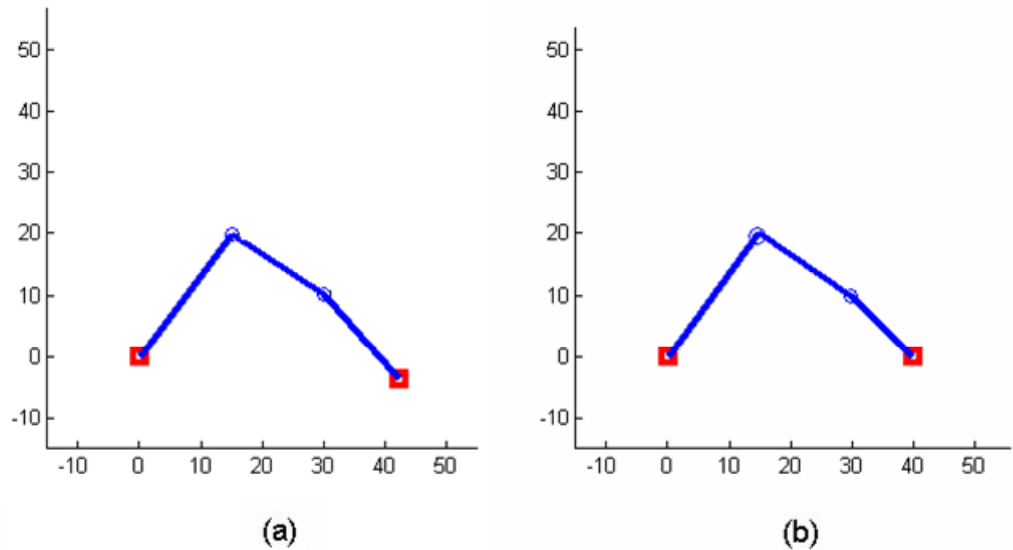


Figure 5.15 Comparison between the Final Result and the Original Design of Two Predefined Output Distance Problem

The result of mechanism design for two output distance is almost the same with the original design. The reason that the solution will converge to the original design can also be explained by graphical method. As describe before, the first step of graphical method is to connect point C to C' and C' to C'', then draw the perpendicular bisector of both lines as shown in Figure 5.16 (a) (b). However, unlike one predefined output distance problem, we can not use random point on the bisectors as our forth point; there is only one intersection of these two perpendicular bisectors. In order to follow both restrictions, only the intersection point can be chosen as the forth joint position. In other words, the solution is unique. Therefore, the result of the algorithm has to converge to the original design.

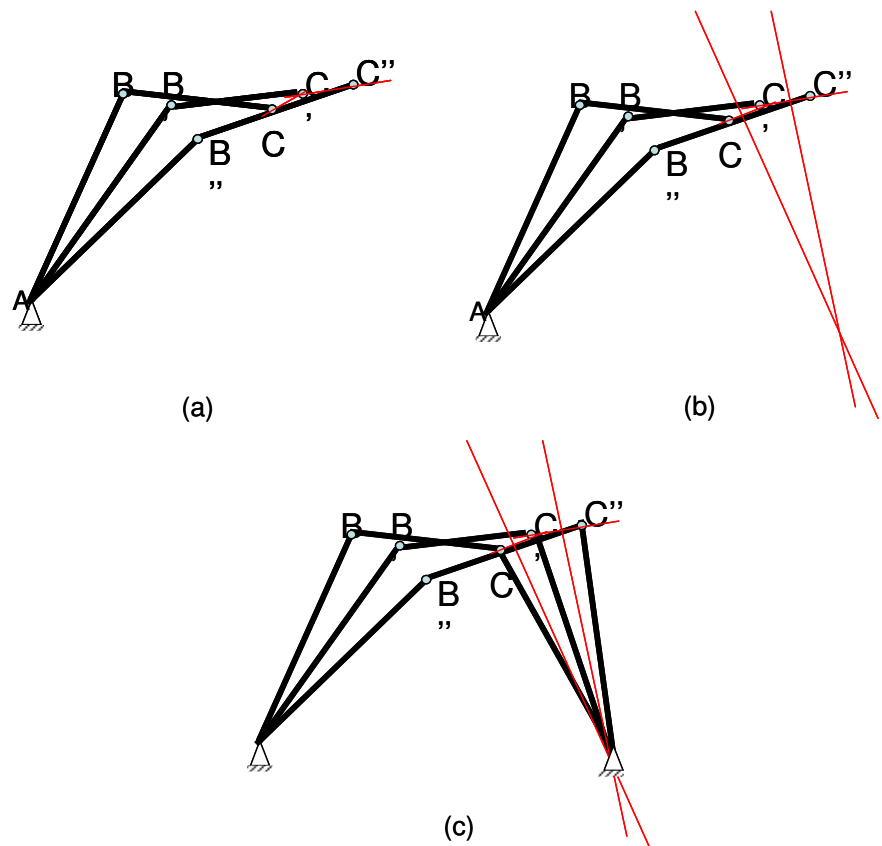


Figure 5.16 Solution of Graphical Method for Two Predefined Output Distance Problem.

5.2.3. Toggle-press Design for One Predefined Output Distance

The toggle-press we have designed in section 5.2.1 and 5.1.2 provide us with the maximum output distance. However, in reality, a toggle press is designed to press a light gauge stock. As shown in Figure 5.1, the plunger can not pass through the anvil and a target destination must be set for toggle-press design problem to avoid collision.

According to the model shown in Figure 5.1Figure 2.1, the toggle-press design problem can be setup within a proper design domain as shown in Figure 5.17. The position of point A, point B and point C are exactly the same with the setup in section 0 and the position of point B' will be set at (10, -20).

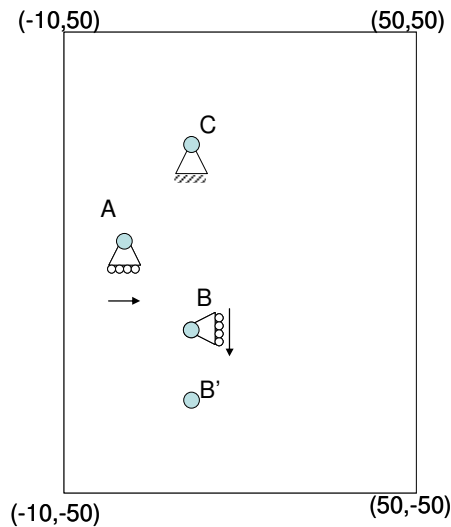


Figure 5.17 Problem Setup for Toggle Design with One Predefined Output Distance

Like the other cases, the input displacement for joint A is four units in the positive x direction while the output joint B tries to reach to point B'. The iteration number for Constrained Superposition Method and Genetic Algorithm are 200 and 100, respectively. The population size is 50, the crossover rate is 0.6 and mutation is 0.02. Figure 5.18

shows the change of the fitness value of the best chromosomes throughout the optimization process. The fitness value is converted into its logarithm to the base 10 for display purpose.

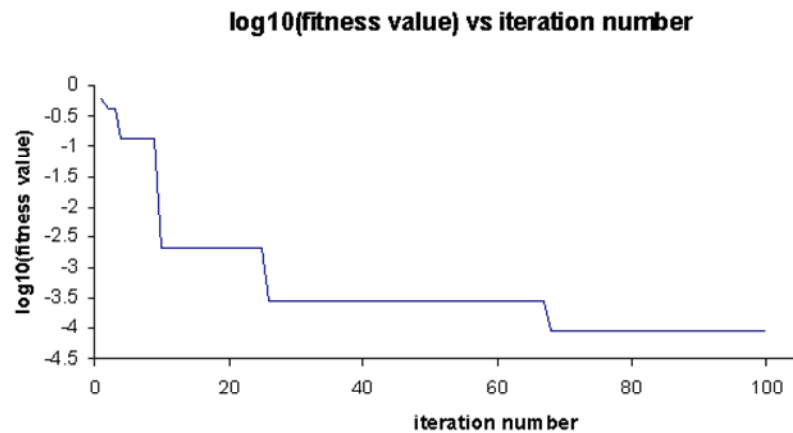


Figure 5.18 Fitness Value throughout Optimization Process for Toggle Design with One Predefined Output Distance.

The result of the optimization process is shown in Figure 5.19. Figure 5.19 (a) shows the mechanism at its initial position and Figure 5.19 shows the mechanism at its final position. It is clear that the mechanism fit the purpose almost perfectly.

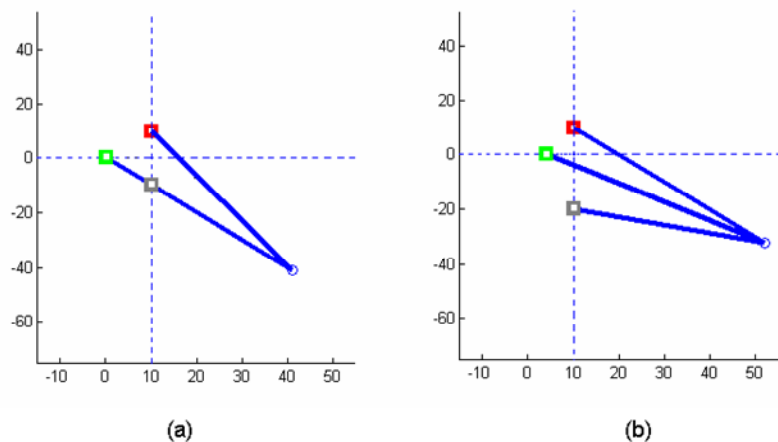


Figure 5.19 Result of Toggle-press Design with One Predefined Output Distance. (a) Initial Position. (b) Final Position.

5.2.4. Gripper Design for One Predefined Output Distance

There are many kinds of mechanical gripper designed for different purpose. However, they all have one thing in common. Mechanical grippers are almost always symmetrical. Hence, we can get the whole design by designing half of the design.

In this work, we tried to find a design similar to the one shown in Figure 5.20(a). Figure 5.20(b) shows the kinematic diagram of half of the gripper above the symmetric line.

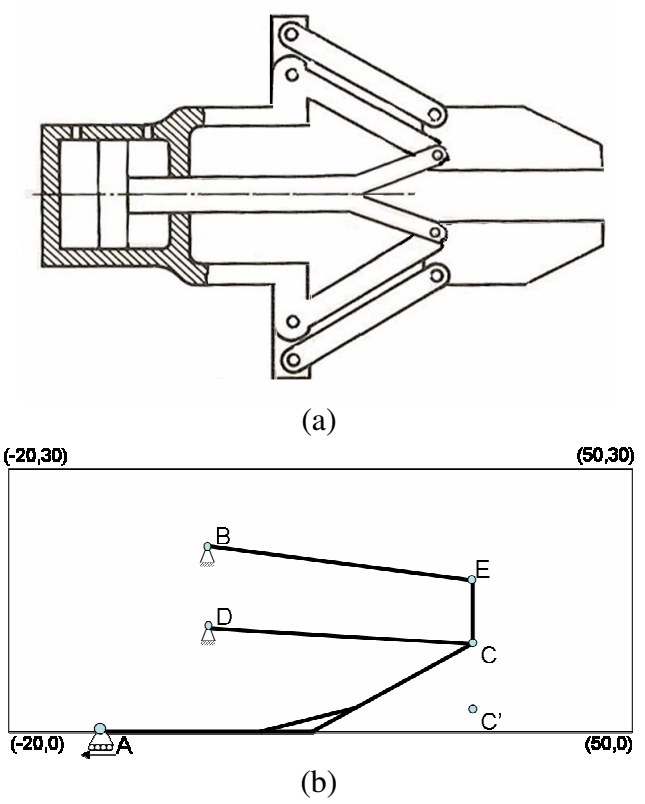


Figure 5.20[1] (a) Model of Gripper (b) Kinematic Diagrams of the Model

The mechanical synthesis problem of this kind of mechanical gripper can then be set up within a proper design domain as shown in Figure 5.21.

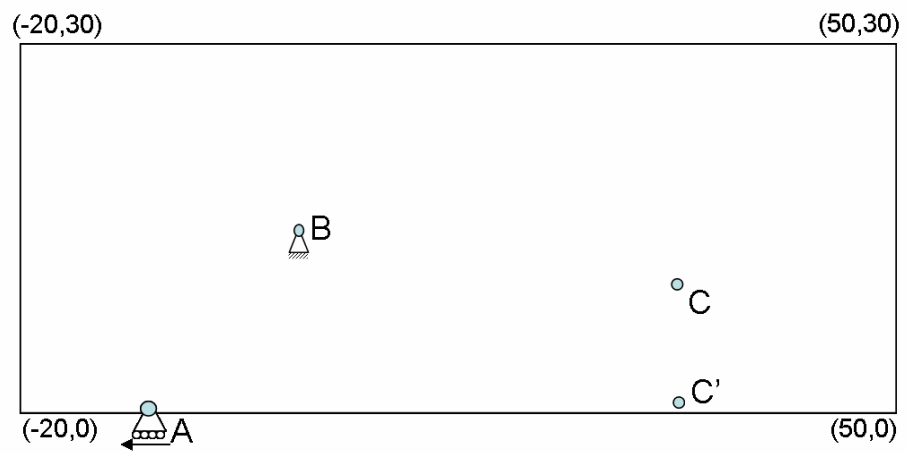


Figure 5.21 Setup of Mechanism Design for Mechanical Gripper

The position of point A B and C are (0, 0), (15, 15) and (40, 10), respectively. The input point is A which goes in the negative y direction for four units. The output point is C and is destined to reach point C'. The maximum allowed joint number is six and the other parameters of GA operators are the same with the previous examples. Figure 5.22 shows the change of the fitness value of the best chromosomes throughout the optimization process. The fitness value is converted into its logarithm to the base 10 for display purpose. The initial and final positions of the optimized design are shown in Figure 5.23

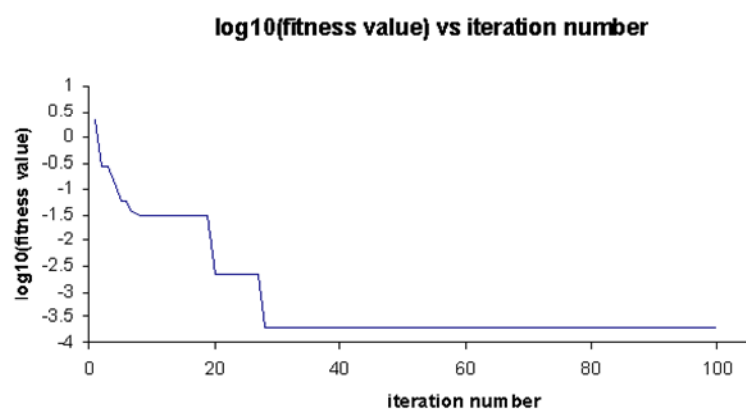
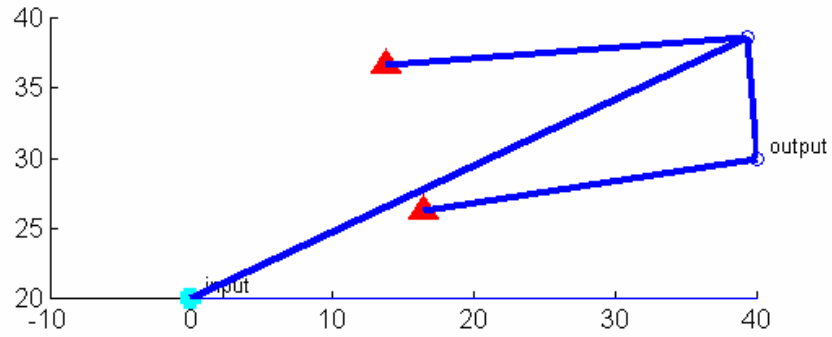
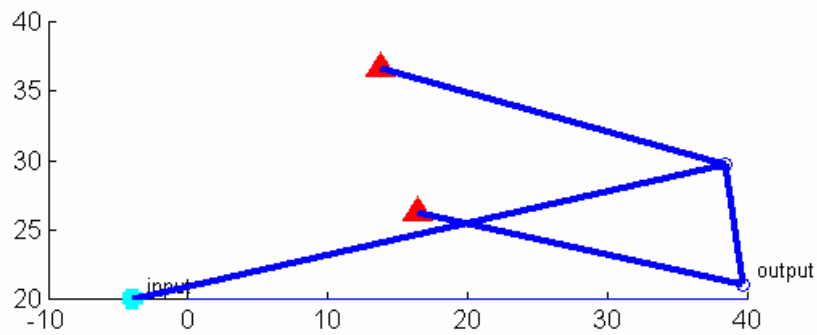


Figure 5.22 Fitness Value throughout Optimization Process for Gripper Design with One Predefined Output Distance.



(a)



(b)

Figure 5.23 Best design of the gripper (a) initial position, (b) final position.

5.2.5. Displacement Inverter Design for One Predefined Output

Distance

A displacement inverter is a mechanism used for the purpose of changing the direction of actuating displacement. The boundary condition and specification required in the design domain are shown in Figure 5.24. Since the symmetric characteristic of the setup, only the upper half of the design domain will be shown.

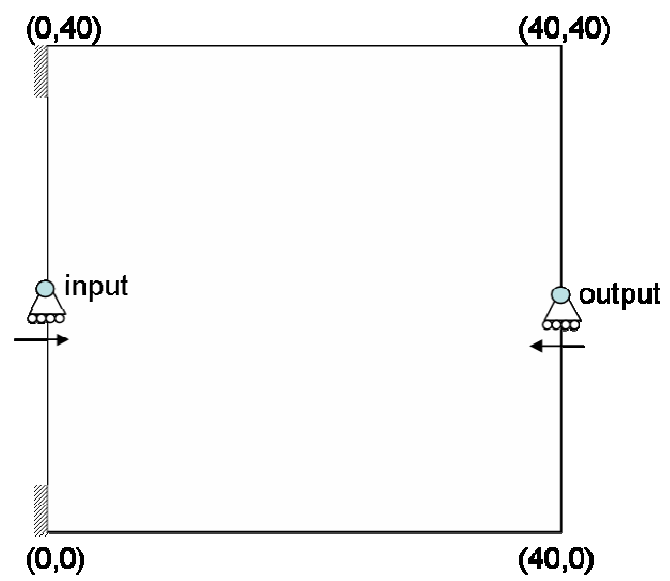


Figure 5.24 Setup of Mechanism Design for Displacement Inverter

The position of the input joint is (0, 20) and the position of the output joint is (40, 20). The input joint goes in the positive y direction for four units. The goal of displacement inverter design is to maximize the displacement of the output joint towards the opposite direction of the input displacement. The maximum allowed joint number is six and the other parameters of GA operators are the same with the previous examples. The initial and final position of the optimized design without redundant links is shown in Figure 5.25.

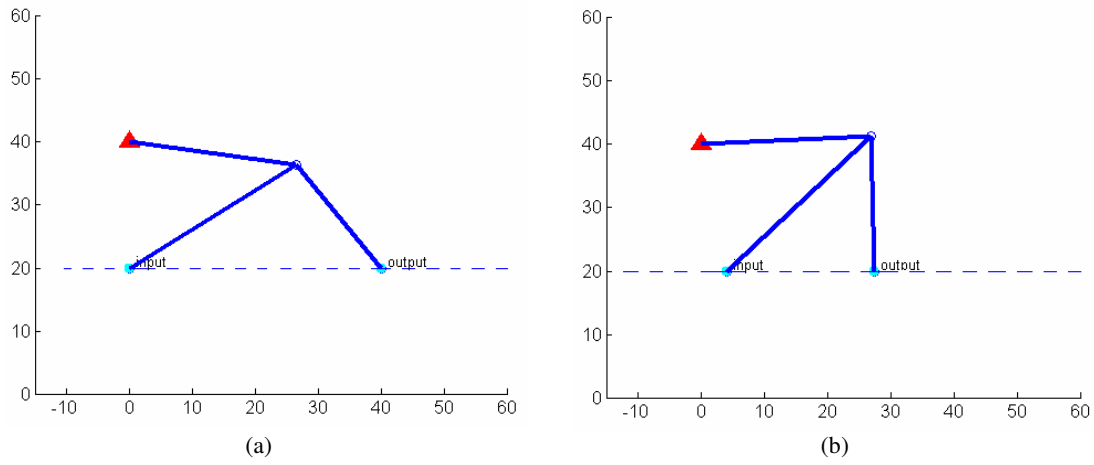


Figure 5.25 Best design of the Inverter (a) initial position, (b) final position.

Chapter 6.

Conclusion and Future Work

6.1. Conclusions

Constrained Superposition Method and Genetic Algorithm are introduced to solve kinematics synthesis problem in the design domain. Due to the limitation of the previous mechanism analysis methods such as the disability of dealing with different type of mechanism without modification, Constrained Superposition Method is formulated for mechanism analysis. The concept of Constrained Superposition Method is similar to truss analysis, which applies the finite element method (FEM) to predict the deformation of the truss when applying an external force on the truss. The mechanism can be decomposed into two subsystems and analyzed by FEM to solve the displacement of each node on the mechanism. Compare to the total potential energy method, the solution of Constrained Superposition Method will be consistent for the same mechanism without any deviation. Even though this method is still an approximation method base on the nonlinearity of the truss deformation[31], the accuracy of Constrained Superposition Method will increase if the iteration number for pre-stained method increases. Constrained Superposition Method can be easily implemented into Genetic Algorithm optimization to evaluate the performance of mechanisms.

This paper provides a systematic method to encode the feature of the mechanism into chromosomes. The connectivity check and the mobility check are used to save the

computational power of Constrained Superposition Method and to maintain the feasibility of the mechanism design. For some special cases, the mechanism will not be feasible but still pass the feasibility check, those mechanisms will be evaluate though Constrained Superposition Method as mentioned previously.

There are two kinds of application for the work in this paper; one is to find a mechanism that can provides the maximum output distance for a pre-described input value, the other is to find a mechanism that will reach the pre-defined output target with a pre-defined input value. Both applications are proven to be useful. As the design problem becomes more and more complicated, the possible mechanism number will increase greatly and the classical mechanism synthesis will be really time-consuming. The advantage of our method is that it can save a lot of computational time, and provide the users with multiple designs at the same time.

6.2. Future Work

In our work, we only focus on planar mechanisms; this method will not be useful if it can not be used to design three dimensional mechanisms, by changing some chromosome definition and the formula of mobility check, we can modify this method into a three dimensional mechanism synthesis tool.

For mechanism design for pre-defined output distance, we have already proven the feasibility of the method. If we increase the amount of the pre-defined output targets, we can then modify our method to solve a path following problem.

As you can see in the examples, there is a possibility for the redundant linkage to exist on the mechanism. Even though these redundant linkages will not affect the performances of the mechanism, it is undesirable to have redundant linkages on the mechanism in an economic point of view.

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