# Mechanism synthesis using a multi-objective optimization bio-inspired technique

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Abstract. Four-bar linkage mechanis is one of the most widely used because its flexibility in generating trajectories, functions and movements. This paper deals with position-velocity mixed synthesis of these mechanisms that involves finding the optimal structural parameters that allow a coupler point in the mechanism to trace a path defined by some precision points at a required velocity. The mixed synthesis is handled as a multi-objective optimization problem in which the objective functions to be simultaneously minimized are the position and velocity errors. As an alternative to graphical and analytical techniques, the bio-inspired optimization technique based on bacterial chemotaxis BCMOA, was in this work used to find the optimal solutions. As a result of the optimization process, several optimal solutions that represent a trade-off between the objective functions were found.

Keywords: Four-bar linkage, multi-objective optimization, mechanism synthesis, bacterial chemotaxis

# **1. INTRODUCTION**

The four-bar mechanism is one of the most widely used because of its extreme flexibility in generation of paths, functions and movements. An important concept in mechanism design is the synthesis, which is the process of selecting and organizing some dimensional variables values such that generate a desired solution. Dimensional synthesis can be classified in three categories (Erdman and Sandor, 1998): i) motion generation, ii) function generation and iii) path generation. The last category, which is the problem to be treated in this work, attempts to find the suitable configuration that allows a coupler point in the mechanism to trace a trajectory defined by a set of precision points.

Graphical and classical analytical methods applied in dimensional synthesis, limit the potential of the four-bar mechanism flexibility to the case of five specific precision points (Sandor and Erdman, 1984) and some predefined coupler positions (Norton, 2008), however the possible existence of singular points make impossible to ensure the mechanism mobility. Alternately, several computational methods which focus the dimensional synthesis as an optimization problem have been proposed. The first approach of dimensional synthesis as the minimization of an error function resulting from the differences between the areas under the actual and the desired curve traced by the coupler was proposed by Fox and Willmert (1967). Subsequent works proposed modifications in the objective function (Bakthavachalam and Kimbrell, 1975), (Youssef, 1975). Kramer and Sandor (1975) relax the problem by specifying a tolerance zone on matching points, concept that was taken up by Krishnamurthi (1993), which applies fuzzy logic for the problem solution. The emergence of non gradient-based optimization methods resulted in the implementation of meta-heuristic optimization techniques for which, besides it is not necessary a great knowledge on the search space, the starting point is not relevant and computational cost is lower. Among these methods, genetic algorithms and neural networks have been successfully applied in dimensional synthesis of mechanisms by finding a global optimum or reducing the computational cost (Fang, 1994), (Mundo et al., 2006), (Cabrera et al., 2002), (Quintero et al., 2004), (Vasiliu and Yannou, 2001), (Hoskins and Kramer, 1993), (Bagci and Burke, 1993), (Sánchez and Pérez, 2003) (Bulatovic and Djordjevic, 2004). Comparatively, there are few works concerning the kinematic synthesis of four-bar mechanism as an optimization problem, among which may be mentioned the works of Fox and Willmert (1967), Conte (1975), Guj (1981), Chang (2001), Yan and Soong (2001) and Galeano et al. (2009).

In this work, the optimal dimensional design for position and velocity synthesis of a four-bar mechanism is solved as a multi-objective optimization problem by implementing a new bio-inspired technique based on chemotactical behavior of bacteria E. coli. This technique was presented and validated in Guzman et al. (2010), and has been applied in the size optimization of mechanical elements with very promising results (Guzman et. al, 2010a).

## 2. Kinematic model for four-bar linkage mechanism

A four-bar mechanism is shown in Fig. 1. The kinematic model for this mechanism can be written as (Norton, 2008):

Any position vector of the coupler point with coordinates  $X_p$ ,  $Y_p$ , follows the equation Eq. (1):

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$$\vec{r}_2 + \vec{r}_3 = \vec{r}_1 + \vec{r}_4$$

(1)

Where  $\vec{r_1}$ ,  $\vec{r_2}$ ,  $\vec{r_3}$  y  $\vec{r_4}$  are position vectors associated to each link.



Figure 1. Four-bar linkage mechanism in a global coordinates system.

This expression can be handled so the unknown angles  $\theta_3$ ,  $\theta_4$  can be solved for input angle  $\theta_2$  as:

$$\theta_3 = 2 \arctan\left(\frac{-E \pm \sqrt{D^2 + E^2 - F^2}}{F - D}\right)$$
(2)

$$\theta_4 = 2\arctan\left(\frac{-B \pm \sqrt{A^2 + B^2 - C}}{C - A}\right)$$
(3)

where A, B, C, D, F are defined by Eqs. (4-9):

Y

 $A = 2r_4[r_1Cos(\theta_1) - r_2Cos(\theta_2)] \tag{4}$ 

 $B = 2r_4[r_1Sin(\theta_1) - r_2Sin(\theta_2)]$ (5)

 $C = r_1^2 + r_2^2 - r_3^2 + r_4^2 - 2r_1 r_2 Cos(\theta_1 - \theta_2)$ (6)

$$D = 2r_3(r_2Cos(\theta_2) - r_1Cos(\theta_1))$$
<sup>(7)</sup>

$$E = 2r_3(r_2Sin(\theta_2) - r_1Sin(\theta_1))$$
(8)

$$F = r_1^2 + r_2^2 + r_3^2 - r_4^2 - 2r_1r_2Cos(\theta_2 - \theta_1)$$
(9)

Thus, the position of a point P in the coupler with coordinates (  $X_p, Y_p$  ) is:

$$X_p = a + r_2 Cos(\theta_2) + r_p Cos(\theta_3 + \alpha_p)$$
<sup>(10)</sup>

$$Y_p = b + r_2 Sin(\theta_2) + r_p Sin(\theta_3 + \alpha_p)$$
<sup>(11)</sup>

Differentiating Eq. (1) respect to time, an expression for coupler angular velocity  $\omega_3$  can be written as Eq.(12):

$$\omega_3 = \frac{\omega_2 r_2 Sin(\theta_4 - \theta_2)}{r_3 Sin(\theta_3 - \theta_4)} \tag{12}$$

Finally, the velocity of point P can be evaluated in rectangular components using the following equations:

$$V_{px} = -\omega_2 r_2 Sin(\theta_2) - \omega_3 r_p Sin(\theta_3 + \alpha_p)$$
<sup>(13)</sup>

$$V_{py} = \omega_2 r_2 Cos(\theta_2) + \omega_3 r_p Cos(\theta_3 + \alpha_p)$$
<sup>(14)</sup>

#### 3.1. Optimization Problem Formulation

Most real-world optimization problems require making decisions involving two or more objectives that must be simultaneously satisfied. In this work, the optimization problem is to find the variable optimal values that simultaneously minimize position and velocity errors. As the problem solution involves achieving two different goals, this is a typical case of a Multi-objective Optimization Problem (MOP). For MOPs, there is not a single solution representing the global optimum; however there is a set of optimal solutions called the Pareto Optimal Front. Each optimal solution from the Pareto Optimal set represents a trade-off between the objective functions.

The kinematic synthesis of mechanisms can be defined as the search for a set of geometric and kinematics variables that allow a point P, located in the coupler link, to reach a path defined for an ordered set of *n* precision points and simultaneously satisfy in certain moments (defined by the angle  $\theta_2$  associated with each precision point), some velocity requirements. According to Fig. 1, the design variables to be optimized are: bar dimensions  $(r_1, r_2, r_3, r_4)$ , inclination angle  $(\theta_1)$ ,  $\alpha_p$  and  $r_p$  which define the relative position of P, dimensions *a* and *b*, and the input angles  $(\theta_{2,1}, \theta_{2,2}, ..., \theta_{2,n})$ , associated to each precision point. Table 1 shows variable feasible values for this problem.

Variable	
$r_1, r_2, r_3, r_4$	[1, 60]
$\theta_1, \alpha_p$	$[0,\pi]$
a, b	[-60, 60]
r <sub>p</sub>	[0, 60]
ω <sub>2</sub>	[0, 10]
$\theta_{2,1}, \theta_{2,2},, \theta_{2,n}$	$[0, 2\pi]$

Table 1. Variable ranges of the problem

The mixed synthesis of mechanisms as Multi-objective Optimization Problem can be defined as follows:

Minimize:

$$f_1(x) = \sum_{i=1}^n \sqrt{\left(\frac{(X_p)_i - X_i}{X_i}\right)^2 + \left(\frac{(Y_p)_i - Y_i}{Y_i}\right)^2}$$

Position error (15)

$$f_2(x) = \sum_{i=1}^n \sqrt{\left(\frac{(V_{px})_i - (V_x)_i}{(V_x)_i}\right)^2} + \sqrt{\left(\frac{(V_{py})_i - (V_y)_i}{(V_y)_i}\right)^2}$$
 Velocity error (16)

Where  $x = (r_1, r_2, r_3, r_4, \theta_1, a, b, r_p, \alpha_p, \theta_2^1, \theta_2^2, \theta_2^3, \theta_2^4, \theta_2^5, \theta_2^6)$ 

Subject to:

$$g_1(x) = 2\max(r_1, r_2, r_3, r_4) + 2\min(r_1, r_2, r_3, r_4) - \sum_{i=1}^4 r_i \le 0$$
 Grashof Conditions (17)

Equation (15), computes the position error as the sum of the distances between each precision point (X, Y) and the corresponding point  $(X_p, Y_p)$  reached by the mechanism. Equation (16) computes the difference between the required velocity  $(V_x, V_y)$  in the precision points and the velocities reached by the coupler.

#### 3. Bacterial Chemotaxis Multi-objective Optimization Algorithm - BCMOA

Bio-inspired multi-objective optimization techniques are numerical methods that emulate life and natural processes to develop search techniques to find global optimum in complex search spaces. In last two decades, helped by the increased computational power, these methods have become very popular for solving a wide range of optimization problems. Bacterial chemotaxis is a directed movement applied by some bacteria in response to certain chemical concentrations in their environment. In the case of E. coli, two movement types are basically verified: swim and tumble. These movement types are sufficient to develop a survival strategy that allows bacteria to find food and avoid hazardous environments. Bacterial Chemotaxis Multi-Objective Optimization Algorithm - BCMOA (Guzman et al., 2010), is a population-based method to solve multi-objective optimization problems that applies simple rules for a virtual bacterial colony, whose members explore and exploit the search space by basic movements. As other multi-objective algorithms, for BCMOA the goals to be achieved are (Deb, 1999): (1) Guide the search towards the Global Pareto Optimal region and (2) Maintain the population diversity in the Pareto Optimal Front. For this, BCMOA algorithm implements a movement strategy that can be summarized as follows:

Bacteria navigate the space of variables, in which bacterial locations represent candidate solutions to the problem. After the evaluation of the objective functions for all bacterial location, the bacterial colony members are classified in two sets: the Strong Bacteria or non-dominated solutions (Deb et. al., 2002) and the Weak Bacteria or dominated solutions. For Strong Bacteria, the chemotactic strategy emulates tumbling natural movement by comparing their current location with previous by non-domination concept. If previous or current location dominates the other, bacterium moves to the non-dominated location and, from there, takes a very small tumble in a random direction. On the contrary, if no location dominates the other from its current position, bacterium takes a bigger tumble in a random direction. In chemotactic strategy for Weak Bacteria, the information exchange between the colony members plays an important role. Every Weak Bacterium moves to a location near the strong selected bacterium. With the new location for all bacteria, a new cycle of classification begins. A typical representation of chemotactic strategy for strong and weak bacteria in the variables space is shown in Fig. 2. A detailed explanation of BCMOA can be found in Guzman et al. (2010), where the efficiency of the algorithm regarding convergence and population diversity is compared with other optimization techniques.



Figure 2. Bacterial chemotactic strategy in BCMOA

# 4. EXPERIMENTS AND RESULTS

The optimization problem solved involves the position and velocity synthesis for a four-bar linkage mechanism. Therefore, BCMOA algorithm is applied to find the optimal values for the variable vector  $x = (r_1, r_2, r_3, r_4, \theta_1, a, b, r_p, \alpha_p, \theta_2^1, \theta_2^2, \theta_2^3, \theta_2^4, \theta_2^5, \theta_2^6)$  that simultaneously minimizes the position and velocity errors for six precision points along a straight line and their corresponding velocities. Table 2 shows *x-y* coordinates for each precision point and its velocity components  $V_x$ - $V_y$ .

Precision Point	1	2	3	4	5	6
x	20	20	20	20	20	20
У	20	25	30	35	40	45
$V_x$	5.39	1.15	-1.96	-0.54	3.86	-12.52
$V_y$	29.18	29.63	30.00	34.14	53.14	69.63

Table 2. Coordinates and velocities for precision points

BCMOA was implemented with an initial population of 100 bacteria for 2000 iterations.

Due to problem conditions such as six precision points in a straight line with their respective velocities, the synthesis problem is over-constrained (Acharyya and Mandal, 2009), therefore it is possible to expect a very restrictive solution or even may not exist a mechanism that reproduces the desired path under those velocity conditions. The multi-objective optimization problem is relaxed by accepting tolerances between the desired velocities and those reached by the coupler. The BCMOA algorithm can then be implemented by modifying the step sizes as shown in Fig. 3. The optimal fronts A, B, C, D and E represent candidate solutions for which different tolerances in the velocity objective function are accepted.



Figure 3. Optimal Fronts for different step sizes with BCMOA.

Figure 3 shows the specific candidate solutions a1, b1, d1, and e1. These four solutions, which pertain to different optimal fronts, have in common a position error value between 0.053 and 0.055; however the value for the velocity error varies for each coupler position. Figure 4 shows the dimensional and geometrical configurations for candidate solutions a1, b1, d1, and e1, as well as their coupler path (left) and coupler velocity (right). As can be observed, multiple solutions for the mixed synthesis problem were found. Figure 5 shows the Optimal Front found for very low levels of tolerance for both objective functions. Although candidate solutions that pertain to this front represent different values for objective functions, constructively all these solutions can be considered the same, as can be seen in Tab. 3, that shows the variable values for the extreme solutions e2 and e3 in Fig. 5. Figure 6 shows the performance of position and velocity errors for 500 iterations of BCMOA algorithm when front E was found.

Solution	$r_1$	$r_2$	r <sub>3</sub>	r <sub>4</sub>	$\theta_1$	а	b	r <sub>p</sub>
e2	24,462	29,570	59,629	55,947	0,667	-9,395	26,398	7,23
e3	24,463	29,568	59,623	55,952	0,667	-9,396	26,396	7,23
Solution	α <sub>p</sub>	ω <sub>2</sub>	$\theta_{2,1}$	θ <sub>2,2</sub>	θ <sub>2,3</sub>	θ <sub>2,4</sub>	θ <sub>2,5</sub>	θ <sub>2,6</sub>
Solution e2	α <sub>p</sub> 1,236	ω <sub>2</sub> 1,0	θ <sub>2,1</sub> 5,64	θ <sub>2,2</sub> 5,81	θ <sub>2,3</sub> 5,98	θ <sub>2,4</sub> 6,14	θ <sub>2,5</sub> 6,26	θ <sub>2,6</sub> 0,05

Table 3. Variable values for extreme optimal solutions.



Figure 4. Position and velocity errors for different optimal solutions



Figure 5. Optimal Front found by BCMOA algorithm.



Figure 6. Convergence graphics for Front E found by BCMOA algorithm.

## 5. CONCLUSIONS

This paper presents an implementation of the BCMOA bio-inspired algorithm to find the optimal variables values for velocity-position mixed synthesis of a four-bar linkage mechanism. Due to the problem complexity the algorithm tends to converge towards a unique solution, so it was necessary to relax the problem by accepting greater tolerances in the objective functions. Although BCMOA algorithm found an Optimal Front which candidate solutions represent different values for the objective functions, in relation to manufacturing, all these solutions can be considered the same, which is consistent with the restrictive conditions of the problem. The performance of BCMOA algorithm in the solution of this multi-objective optimization problem is highly satisfactory since it allows finding several mechanism configurations that solved the problem for different tolerances in position and velocity errors.

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