Topological Optimization for Continuum Compliant Mechanisms via
Morphological Evolution of Traditional Mechanisms

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Abstract
This paper presents a new topological optimization method, termed the mechanism approach, to synthesize continuum compliant mechanisms for high precision micro/nano-scale manipulation. The proposed approach uses traditional mechanisms as seeds to represent the topology of compliant mechanisms. This representation eliminates disconnected elements and allows alterations of the seed’s “topology” to be possible during the optimization process. The selection procedure for the solid elements is done in a discrete manner, thus there are no ambiguous “gray” elements. Using genetic algorithm as its solver, the proposed approach has higher chances to obtain a global solution compared to gradient-based methods. Convergence capability of the proposed approach is illustrated by the target matching problem where a population of random chromosomes is able to produce a near exact match of the target. Using the proposed approach, a new compliant prismatic joint with better stiffness characteristics than traditional linear spring designs has been developed.

Keywords: Topological optimization, Continuum compliant mechanisms, Mechanism approach, Geometric representation and Genetic algorithm.

I. Introduction
Compliant mechanisms are structures that are able to exhibit high compliance in certain intended directions and high stiffness in other directions. As compliant mechanisms achieve their motions via elastic deformation, they eliminate dry friction, mechanical play, backlash and wear-and-tear (Smith 2000). These characteristics enable compliant mechanisms to achieve highly repetitive motions that are required to carry out micro/nano-scale manipulations (Teo, Chen et al, 2008).

Topological optimization has been applied in the synthesis of compliant mechanisms by determining its best overall material connectivity via finite element analysis (FEA). The design domain of the compliant mechanism is discretized into either a discrete or continuum structure. Discrete/ground structure forms its topology with elements such as truss, beams or frames and its topological optimization is performed by doing size optimization on the elements’ cross-sectional area (Zhan and Zhang, 2010). Elements with zero cross-sectional areas are removed and the optimized size of the remaining elements is determined. This is computationally effective as both
size and topological optimization can be performed simultaneously. Although this optimization process is relatively simpler, its topology is less inclusive compared to their continuum counterpart, resulting in some useful topology to be excluded.

Continuum structure divides the design domain into multiple finite elements which are continuously connected to one another. There are four main approaches. The first two approaches, the homogeneous and Solid Isotropic Materials with Penalisation (SIMP) approaches convert the discrete natured optimization problem into a continuous one. Cavities and artificial densities are assigned to every element in the design domain by the homogeneous (Bendsøe and Kikuchi, 1988) and SIMP (Bendsøe and Sigmund, 2003) techniques respectively. By doing a “size” optimization on the cavities or artificial densities, an optimized topology is obtained via gradient-based methods. Ideally, all the elements in the final optimized topology should either be solid (black) or void (white). However, the homogeneous and SIMP produce ambiguous elements that do not have any physical representation - microscopic voids and “gray” elements with intermediate densities. Designers would have to use their intuition to decide the state of these ambiguous elements and the finalized topology usually does not perform up to expectations.

The third approach, the Evolutionary Structure Optimization (ESO), uses artificial densities as its design variables. By following simple rules, ESO performs the optimization in a discrete manner and thus no ambiguous “gray” elements are produced (Huang and Xie, 2010). Despite this, ESO is largely criticized for its heuristic nature and unguaranteed convergence (Rozvany, 2009). Furthermore, the robustness of ESO is limited as different applications require different sets of rules. The fourth approach, the morphological representation, represents the topology of compliant mechanisms by using the geometrical characteristics of animals as its seed. Skeletons of the animals, represented by Bezier curves, are used to connect the input, output and support points. Flesh is subsequently added to the skeletons to form the corresponding topologies (Tai and Chee, 2000). With this approach, no disconnected elements from the main structure will occur. Note that disconnected elements may happen in other approaches. Furthermore, there are no ambiguous “gray” elements as selection of solid elements is done in a discrete manner. By using genetic algorithm (G.A.), the obtained solution has higher chances to obtain the global minimum compared to the gradient-based approaches. Recent development introduces “passive” Bezier curves and this enhances the search space and flexibility in choosing the number of skeletons (Wang and Tai, 2010). The main drawbacks are that the topology of the compliant mechanism is still restricted by its seed despite the added passive curves and no holes can be introduced within each Bezier curve as all the elements within the flesh components are always solid. This approach also requires more computational time and power to implement.

From the review, the morphological representation is a better approach for the synthesis of compliant mechanism. However, it can be further improved if there is a more flexible way to change the topology of the seed in the optimization process. Noting the resemblance between compliant mechanisms and traditional mechanisms (Wang, 2009), this paper proposes the use of traditional mechanism as the new seeds to perform topological optimization. An appropriate seed can be selected from the list of traditional mechanisms. During the optimization, the link dimensions of the seed will vary, thus even the “topology” of the seed can be evolved. This new approach, term the mechanism approach, has a good convergence rate and is able to produce feasible solutions. Section II will detail the mapping procedure and the effectiveness of this approach will be evaluated in Sections III and IV. Finally, Section V will conclude this paper.
II. Geometrical Mapping for the Mechanism Approach

Based on the degrees of freedom (DOF) requirement of the compliant mechanism, a corresponding traditional mechanism with the same number of DOF will first be selected as the seed. The seed will then be superimposed onto a design domain with all the elements selected as void. The pose of the seed can be varied by the link lengths and their orientations. Each link of the mechanism is represented by one cubic curve, one harmonic curve, and their reflected curves about the link. This is illustrated in Fig. 1 using the four-bar linkage as the seed. The four curves form the boundaries used in the selection of solid elements. Based on the value of \( m \) assigned to each link \( (m \in \mathbb{Z}^+, 1 \leq m \leq 3) \), different combinations of solid elements can be generated. If \( m = 1 \), all the elements bounded between the original curves and the link are solid. When \( m = 2 \), all the elements bounded by the reflected curves and the link are solid. When \( m = 3 \), the solid elements will be the combined elements of the first two cases. In all the cases, the solid elements are selected in a discrete manner and no ambiguous “gray” elements can be formed.

![Figure 1. Curves generated by last link of a traditional four-bar linkage seed](image)

The cubic curves are designed to have one stationary point within the link length so that the harmonic curves can be enclosed. With this configuration, it is possible to create holes within each link. The number of holes for \( m = 3 \) is equal to \((2n - 1)\) where \( n \) is a positive integer that represents the number of troughs and peaks of the harmonic curve. The cubic curves can be described by using three parameters - the link length, \( l \), and another two parameters, \( j \) and \( k \). These three parameters define the coordinates of the stationary point \((x_{1, \text{max}}, y_{1, \text{max}})\) such that \( x_{1, \text{max}} = kl \) and \( y_{1, \text{max}} = jl \). With the boundary conditions \((0, 0)\) and \((l, 0)\) in the \(x_1-y_1\) frame, the cubic curves’ equations are:

\[
y_1 = \pm(ax_1^3 + bx_1^2 + cx_1 + d) \tag{1}
\]

where \( a = \pm j \frac{2k-1}{[k(k-1)]^2} \), \( b = j \frac{3k^2-1}{[k(k-1)]^2l} \), \( c = -(al^2 + bl) \) and \( d = 0 \)

Eq. (1) with the plus sign represents the original cubic curves. Four independent parameters \( s, n, e \) and \( h \) are used to define the harmonic curves. The parameters \( s \) and \( e \) determine the starting and ending point of the curve respectively and \( h \) determines the amplitude of the curve. If \((s+e) \geq 1\) or \( h = 0 \), no harmonic curves are produced and thus no holes are formed. Fig. 2 shows the corresponding parameters for the original curves and \( n = 1 \) for the harmonic curve as there is only one peak. The equations of the harmonic curves for \( sl \leq x_1 \leq l - el \) are:
\[ y_1 = \pm h \sin \left[ \frac{2\pi}{\lambda} (x_1 - sl) \right], \text{where } \lambda = 2l \left( \frac{1-(s+e)}{n} \right) \]  

(2)

Eq. (2) with the plus sign represents the original harmonic curves. A corresponding topology is produced when all the links follow the above-mentioned description and an example is shown in Fig. 3. A vector \( \mathbf{x} \) will be used to represent the design variables (the seed’s links’ length and orientation and the curve parameters) in the subsequent sections.

As the links of the traditional mechanism are physically connected to one another, no elements can be disconnected from the main topology. In addition to creating feasible solutions, topologies created via the mechanism approach are not limited by its seed. During the optimization, if any links’ length approaches zero, even the seed’s “topology” can be changed. As G.A. is used as the solver, the possibility of arriving at the global solution is higher than the gradient-based methods. However, more computational time and power is required to achieve this. The convergence and performance of the mechanism approach will be evaluated by the target matching problem and the design of a compliant prismatic joint respectively.

### III. Target Matching Problem

The target matching problem is a simulated topological optimization problem that evaluates convergence capability (Tai and Akhtar 2005). In this paper, the topology of a random three-bar structure seed is identified as the target. Its topology is described by a design domain with 2500 identical elements where the location of the coupler point and two support points are fixed. The aim of the optimization is to gradually evolve a population of random chromosomes to exactly match the topology of the target. In other words, the target’s topology is the global solution known to the user. To demonstrate the seed’s flexibility, the topologies of the population of chromosomes are represented by four-bar linkages’ seed. If the optimization is successful, this proves that the mechanism approach is able to converge to the global solution and even the “topology” of the seed can be changed. No FEA is involved as the problem deals solely on geometry. The objective is to minimize the number of elements having the wrong state and it is formulated as:

\[
\min \left( f_1 = \sum_{i=1}^{2500} \left| \rho_{i,\text{candidate}} - \rho_{i,\text{target}} \right| \right)
\]

subject to: \( h(\mathbf{x}) < 0 \)  

(3)
The fitness function, $f_1$, represents the number of elements having the wrong state and $\mathbf{x}$ represents the design variables. The variables $p$ represents the state of the element, $p_i = 0$ if element $i$ is void and $p_i = 1$ if element $i$ is solid. The inequality constraints, $h(x)$, ensure that the seeds remain within the design domain. The solution is obtained after a population of 400 chromosomes had undergone 50 generations of evolutions. Fig. 4 shows the seeds for the target and a random initial chromosome’s seed and the convergence plot. Fig. 5 shows some sample topologies during the evolutionary process.

![Figure 4. Seeds for the target, a random initial topology and the convergence plot](image1)

![Figure 5. Sample topologies during the evolutionary process](image2)

The solution has a fitness value of $f_1 = 2$, meaning there are only 2 out of 2500 elements which are in the wrong state and the percentage error $= \frac{2}{2500} \times 100\% = 0.08\%$. In comparison with the results presented in the previous literature (Tai and Akhtar, 2005) which has 3.88% error, the above error is significantly smaller and the solution is a near exact match of the target. The “topology” of the traditional mechanism seed has effectively been changed from a four-bar linkage to a three-bar structure in order to achieve a smooth convergence that arrives near the global solution.

IV. Design of a Compliant Prismatic Joint

The second test problem, the design of a compliant prismatic joint, is used to evaluate the performance of the proposed mechanism approach. The possibility of synthesizing compliant prismatic joint by SIMP was explored in previous literature (Wang, 2009) via optimizing the static condensed stiffness matrix. The obtained result resembles a linear spring prismatic joint as shown in Fig. 6. Despite this interesting finding, optimization of the “rigid” mass was excluded in the previous optimization and some ambiguous “gray” elements are also found in the final solution.

![Figure 6. Sample topologies during the evolutionary process](image3)

In view of this, this paper revisits this problem with the proposed mechanism approach. The design domain is made of stainless steel where the Young’s Modulus, $E$, and the Poisson ratio, $\nu$, are 200GPa and 0.3 respectively. This design domain has two fixed points which are located at the base. The loading point is located at the surface of the centre element in the top row. As this test problem optimizes the stiffness characteristics of the compliant joint, its fitness function is based on the $6 \times 6$
compliant matrix \((C_{6x6})\). The columns of the matrix are formed by the six 6x1 position vectors which describe the position and orientation deformations of the loading point. These six deformation vectors are caused by three unit translational wrenches and three unit rotational wrenches applied in the \(x\), \(y\) and \(z\) axes respectively. In order to evaluate the out-of-plane compliance, the design domain is discretized into 30×25 identical 1 mm cubic 8-node bilinear 3-D finite elements. The selected seed is a simple 4-bar linkage with a coupler point as the compliant prismatic joint is a 1-DOF compliant mechanism. The coupler point of the seed represents the loading point and the two supports represent the fixed points. Fig. 7 shows the seed and the mesh of the design domain.

The stiffness matrix of the whole structure \(K_{\text{structure}}\) and each FE, \(K_e\), are:

\[
K_{\text{structure}} = \sum_{i=1}^{750} (\rho_i K_e) \quad \text{and} \quad K_e = \iiint B^TDB \, dx \, dy \, dz
\]  

(4)

The variable \(\rho\) represents the state of the finite element, if element \(i\) is solid, \(\rho_i = 1\); if it is void, \(\rho_i = 10^{-6}\), to prevent numerical instabilities. The matrices \(B\) and \(D\) are the commonly used deformation matrix and isotropic compliance matrix respectively. Since the six loadings are unit wrenches, their corresponding work functions are simply the deformation of the loading point that is parallel to the unit wrench. The translation and rotational work functions are represented by \(\phi_{T,j}\) and \(\phi_{R,j}\) \((j \in \{x, y, z\})\) respectively. The global nodal deformation vector and rotational displacements are represented by \(u\) and \(\theta_j\) \((j \in \{x, y, z\})\) respectively. Therefore, the six work functions and the rotational displacements are expressed as:

\[
\begin{align*}
\phi_{T,X} &= u_{\text{loading point}} = u^Tf_x \\
\phi_{T,Y} &= v_{\text{loading point}} = u^Tf_y \\
\phi_{T,Z} &= w_{\text{loading point}} = u^Tf_z \\
\phi_{R,X} &= \theta_{X,\text{loading point}} = u^Tm_x \\
\phi_{R,Y} &= \theta_{Y,\text{loading point}} = u^Tm_y \\
\phi_{R,Z} &= \theta_{Z,\text{loading point}} = u^Tm_z,
\end{align*}
\]

(5)

The six global loading vectors are \(f_x, f_y, f_z, m_x, m_y\) and \(m_z\) respectively. The variables \(N_i, u_i, v_i\) and \(w_i\) represent the trial functions and nodal deformations of the loaded finite element in the translational \(x\), \(y\) and \(z\) axes respectively. After applying the boundary conditions, the corresponding six global nodal deformation vectors are obtained by pre-multiplying the six global loading vectors
with the structure’s inverse stiffness matrix. The six 6×1 position vectors which describe the position and orientation deformations at the loading point can be obtained by using \( N_i, u_i, v_i \) and \( w_i \) from the corresponding global nodal deformation vectors. This is represented by pre-multiplying the six global nodal deformations vectors with a constant matrix \( A \).

\[
\therefore C_{6 \times 6} = AK_{\text{structure}}^{-1} [f_x \ f_y \ f_z \ m_x \ m_y \ m_z]
\]

Ideally, the prismatic joint has high compliance in the translational x-direction when it is subjected to a parallel wrench and high stiffness in other directions. Therefore, the ideal design is one with a high intended compliance, \( C_{11} \), and low compliance for other components (parasitic compliance) in the 6×6 compliant matrix. Since the 6×6 compliant matrix is a symmetrical matrix, the fitness function, \( f_2 \), of the test problem is formulated as:

\[
\min \left( f_2 = \left| \frac{\prod_{i=2}^{6} \prod_{j=1}^{i} C_{ij}}{C_{11}^{20}} \right| \right)
\]

subjected to:

\[
g(x) = 0 \text{ and } h(x) < 0
\]

The denominator \( C_{11} \) is raised to the power of 20 because there are a total of 20 parasitic terms. The vector \( x \) represents the design variables. The inequality constraints, \( h(x) \), are used to ensure that the pose of the seed remains in the design domain and the equality constraints, \( g(x) \), represents the FEA governing equations. An optimal topology is obtained after a population of 400 random chromosomes had undergone 100 generations of evolutions. Fig. 8 shows the log-scale convergence plot and the comparison of the optimal topology and a 4-layer linear spring design. Note that a \( n \)-layer linear spring design has \( n \) rows of “rigid” mass (\( n \in \mathbb{Z}^+ \)).

**Table 1. Fitness value comparison of the optimal topology with a series of linear spring design**

<table>
<thead>
<tr>
<th>Design</th>
<th>Fitness Value, ( f_2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Optimal topology</td>
<td>( 3.10 \times 10^{-44} )</td>
</tr>
<tr>
<td>Linear spring topology with different layers of “rigid mass”</td>
<td></td>
</tr>
<tr>
<td>Layers</td>
<td>Fitness Value, ( f_2 )</td>
</tr>
<tr>
<td>1</td>
<td>( 4.75 \times 10^{-31} )</td>
</tr>
<tr>
<td>2</td>
<td>( 9.10 \times 10^{-35} )</td>
</tr>
<tr>
<td>3</td>
<td>( 4.75 \times 10^{-38} )</td>
</tr>
<tr>
<td>4</td>
<td>( 2.17 \times 10^{-39} )</td>
</tr>
<tr>
<td>5</td>
<td>( 5.40 \times 10^{-42} )</td>
</tr>
<tr>
<td>6</td>
<td>( 2.19 \times 10^{-41} )</td>
</tr>
<tr>
<td>7</td>
<td>( 1.24 \times 10^{-42} )</td>
</tr>
<tr>
<td>8</td>
<td>( 2.22 \times 10^{-40} )</td>
</tr>
<tr>
<td>9</td>
<td>( 4.60 \times 10^{-30} )</td>
</tr>
<tr>
<td>10</td>
<td>( 8.98 \times 10^{-38} )</td>
</tr>
</tbody>
</table>

The optimal topology is symmetrical about the y-axis and the "rigid" mass is supported by two thin beams (refer to Fig. 8b). The “rigid” mass has seven layers of elements at the centre and it has four tapered corners. Note that the supports at the base are "L-shaped". As \( C_{11} \) is largely attributed to the deflection of the two thin beams, it can be increased when the length of the beams are increased.
Due to the tapered bottom corners, the supporting thin beams of both the optimized topology and the 4-layer linear spring design have the same effective beam length of 21 mm (refer to Fig. 8). However, despite having more elements, $C_{11}$ of the optimal topology is found to be higher than the 4-layer design. Based on FEA, it was observed that by tapering the top corners of the rigid mass and having an "L-shaped" support, $C_{11}$ of the 4-layer design can be increased. On the other hand, stiffness in the parasitic motions is increased when more layers of mass are added. As the optimal topology has seven layers of mass at its central, it retains most of the high parasitic stiffness characteristics of a 7-layer linear spring design. With these interesting features, the fitness value of the optimal topology ($f_2 = 3.10 \times 10^{-44}$, highlighted in Table 1) outperforms a series of linear spring designs with different layers of mass as shown in Table 1. Note that the 7-layer design has the best performance among the linear spring designs ($f_2 = 1.24 \times 10^{-42}$, highlighted in Table 1) and performance start to decline when there are more than seven layers of “rigid” mass.

![Plot of $\lg(f_2)$ against Generations](image1)

![Convergence plot](image2)

**Figure 8. Convergence plot and comparison of the topologies**

V. Conclusion

In this paper, a new topological optimization method, term mechanism approach, is proposed to synthesize continuum compliant mechanisms by using traditional mechanisms as seeds to represent the topology of compliant mechanisms. One notable advantage is that the proposed approach ensures feasible solutions as it eliminates the possibility of having disconnected elements and ambiguous "gray" elements. As G.A. is used as its solver, the proposed approach has higher chances of obtaining the global solution compared to other gradient-based approaches. The convergence capability of the mechanism approach was demonstrated by the target matching test problem where a population of random chromosomes is evolved to produce a near exact match of the target. It is observed that even the seed’s “topology” is able to evolve during the optimization process. The proposed approach has also exhibited great potential in synthesizing continuum compliant mechanisms as it is shown to be able to develop a new compliant prismatic joint design which has superior stiffness characteristics than existing linear spring designs.

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