



A fast algorithm for kinematic chain isomorphism identification based on dividing and matching vertices

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ABSTRACT

Kinematic chain isomorphism identification is a crucial issue in mechanism topology and an important application of Graph Isomorphism to mechanisms. In this paper, a kinematic chain is uniquely represented by a graph, and a fast deterministic algorithm called the Dividing and Matching Algorithm (DMA) is proposed. First, the vertices of each graph are divided by the degree. Then, vertex connection properties in a sub-graph and between sub-graphs are explored. Accordingly the expanded square degree and the correlation degree are proposed, based on which, the Dividing Vertex Algorithm (DVA) is developed to divide vertices into sets. Moreover, it is proved that only the vertices from the corresponding sets between two graphs are possible to be bijective or matched, which avoids exhaustive search. Eventually, a backtracking procedure is employed to match the vertices between corresponding sets by calling up DVA repeatedly. DMA detects whether the adjacency matrices of two graphs can be adjusted to be equivalent by changing the orders of vertices. Justifications for the reliability of each part of DMA are provided. The experiments and comparisons with existing algorithms show the effectiveness and efficiency of DMA.

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1. Introduction

Graph Isomorphism is widely applied to the areas ranging from pattern recognition and computer vision [1,2] to data mining [3], data security [4], bioinformatics [5], and mechanisms [6–43]. In the field of mechanism topology, isomorphism identification is one of the essential and indispensable steps in systematic synthesis of kinematic chains [6,7] and needs computer-aided tool to accomplish computation. Detecting possible structural isomorphism between two given chains is one of the major problems encountered in intelligent computer aided design (CAD) for the design of kinematic chains [8].

Along with the development of computer industry and the trend of more sophisticated mechanism design, computer-aided mechanism design (CAMD) software is developed to be more integrated. The two major aspects of structural studies of kinematic mechanisms, structural synthesis and structural analysis are widely considered as important functions to be integrated into CAMD software. The structural synthesis of kinematic chains involves enumerating and classifying all possible

Abbreviations: DVA, dividing vertex algorithm; DMA, dividing and matching algorithm.

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kinematic chains having a specified number of links and degrees of freedom [9]. Thus, the redundant isomorphic kinematic chains should be eliminated. Otherwise, if isomorphic kinematic chains are classified into valid categories, CAMD software will mislead an engineering design task. In structural analysis, the mechanisms are analyzed based on functional requirements. This mainly includes determining the type of freedom or mobility of the kinematic chain, the structurally distinct mechanisms and the structurally distinct driving mechanisms that can be obtained from the chain [9]. Usually, a number of possibly redundant kinematic chains are generated, and then isomorphism detection and elimination follow.

As demonstrated in [10], the most time-consuming process in structural synthesis and analysis is testing and eliminating isomorphisms (isomorphism test accounts for 99% of the computation time in enumeration of the 230 10-bar chains in [10]). Although new methods for isomorphism testing have been developed, this procedure still requires the majority of the total computing time because of the fact that some type of unique code for each new kinematic chain must be compared with those of all previously found kinematic chains to test for isomorphisms [6]. Thus, isomorphism detection is a critical bottleneck in CAD for the design of kinematic chains.

In the past decades, a considerable number of approaches were proposed to address this problem. T. S. Mruthyunjaya [11] grouped them into characteristic polynomial based approaches, code based approaches, Hamming number based approaches and distance based approach. Uicker and Raicu [12] used the characteristic polynomial of the link–link adjacency matrix of the graph of the chain as an index of isomorphism. However, in general, invariance of the characteristic polynomial constituted a necessary but not sufficient condition for two graphs to be isomorphism [11], which means that this kind of approach is not valid in most cases. Although Yan an Hall [13,14], Mruthyunjaya [15–17], Mruthyunjaya and Balasubramanian [18], and Sohn and Freudenstein [19] improved this approach much to fit it for more isomorphism cases, counter-examples had been found [18] against them. In the code based approach, the adjacency matrices of kinematic chains are brought to a canonical form and the code is defined as a decodable function of the corresponding matrix [11]. The isomorphism test is the comparison between the codes of the chains. Ambekar and Agrawal [20,21] proposed max (min) code; C. Tang and T. Liu [22] proposed degree code; and, J.K. Shin and S. Krishnamurty [23,24] proposed standard code. The code based methods possess the advantages of uniqueness and decodability, and further, can be helpful in classification of the chains. However, such methods are inadequate in efficiency [11]. Rao [25–27] introduced the concept of Hamming distances from information theory to the study of kinematic structure. The Hamming number based approach is far from being considered as a candidate for incorporating in computerized synthesis [11]. One reason is that when the primary Hamming string fails, the cumbersome computation of the secondary Hamming string is involved [28]. Yan and Hwang [29] defined the linkage path code of a kinematic chain. Yadav et al. presented a sequential three-step test for isomorphism and proposed a link–link distance matrix approach [30,31]. The distance based approaches are considered to be not suitable for computerized structural synthesis by Mruthyunjaya [11].

In 2002, Z. Chang et al. [32] proposed an approach based on eigenvalues and eigenvectors of adjacency matrices. J. P. Cubillo and J. Wan [33] discovered the errors of the original theory, and proposed the necessary and sufficient conditions of eigenvalues and eigenvectors of adjacency matrices for isomorphic kinematic chains. P. S. Rajesh and C. S. Linda [34] proved that this approach is able to identify all non-isomorphic chains, with up to 14 links and one, two, and three degrees of freedom, and pointed out that the time complexity would be exponential in the worst case.

H. Ding and Z. Huang proposed the Canonical Perimeter Topological Graph and the Characteristic Adjacency Matrix approach to test isomorphism for both simple joint chains [28,35–37] and multiple joint chains [38]. The time complexity of their algorithm is $O(2^L)$, where L is the number of basic loops of a graph. In general, finding basic loops of a graph costs time with complexity of $O(n)$ or $O(n^2)$, or higher exponential order, depending on concrete algorithm, where n is the number of vertices. However, usually there are not many basic loops in a graph representing a mechanism kinematic chain, which makes this approach run very fast in the automatic synthesis of kinematic chains [39,40].

Evolutionary computation [41–45] and artificial neural networks [46,47] were used to detect kinematic chain isomorphism as approximate solutions. The novel evolutionary approaches proposed by R. Xiao, et al. [41] spent more than 1 s in detecting isomorphism for isomorphic chains with 50 links. The improved HNN approach [47] proposed by M. Zhang et al. spent more than 2 s in detecting isomorphism when the scale of kinematic chains is more than 20 links. The key limitation of these approximate algorithms is the uncertainty of convergence in the fixed number of iterations, which makes the computation time unstable and unpredictable.

In this paper, kinematic chains are represented by graphs and a novel fast algorithm named the Dividing and Matching Algorithm (DMA) is proposed. Our main contribution is to find two connection properties among vertices, named the expanded square degree and the correlation degree respectively, which are used to divide vertices of a graph into sets. In addition, it is proved that for vertices from two isomorphic graphs, only ones having the same connection properties are possible to be bijective. Accordingly, the vertices having the same connection properties compose a set. This avoids exhaustive search for matching vertices because more sets of vertices, less match. In the case that each vertex is a set, no search is needed for a match, which is our goal of developing a timesaving algorithm. The DMA algorithm is a deterministic algorithm and holds the high reliability and fast speed simultaneously. The time complexity of DMA is $O(Mn^2)$, where n is the number of vertices of a graph and M has no reasonable bound. DMA is faster than H. Ding and Z. Huang's approach and heuristic algorithms for some kinematic chain isomorphism tests.

The rest of this paper is organized as follows. Section 2 introduces the basic knowledge of graph method for kinematic chain isomorphism identification. Section 3 presents the DMA algorithm in detail. Section 4 then reports the experiments and comparisons with existing algorithms. Section 5 discusses the time complexity and reliability as well as effectiveness for large scale problems. Finally, Section 6 concludes the paper.

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