Divide-and-Conquer-Based Method for the Reaction Uniqueness Analysis in Overconstrained Multibody Systems

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EXTENDED ABSTRACT

1 Introduction

In the modeling and simulation of complex mechanical or robotic systems, the method of multibody systems (MBSs) is very useful since it enables full automation of calculations. In the basic approach, a mechanism is modeled as a system of rigid bodies forming kinematic pairs. The system is subjected to kinematic or force inputs. A special but often encountered class of MBSs are mechanisms with redundant constraints. The introduction of redundant constraints into the system is usually the result of a conscious decision of the designer, made after considering the advantages (e.g., greater system strength) and disadvantages (e.g., the requirement for greater accuracy of system parts and the introduction of assembly stresses). Modeling such mechanisms is difficult, and one of the main problems is the nonuniqueness of some reaction forces.

The essence of the problem is that the results of numerical simulations may, in some cases, differ from reality. The physical (in the sense of real) reactions of the system are always defined (although they are not always easy to measure or calculate). Therefore, the described problem of nonuniqueness is related only to mathematical models of MBSs. In the case of overconstrained systems, it is impossible to determine all generalized reaction forces [1], and thus also physical reactions in kinematic pairs.

In some cases, the problem of reaction nonuniqueness does not affect the correctness of the obtained simulation results, so it can be ignored, but in other cases, it cannot be omitted. Examples of tasks where specific reaction forces need to be known are contact force testing, strength analysis, or design tasks [2], e.g., selection of bearings or dimensional synthesis of bodies. In such cases, ignoring the nonuniqueness of the calculated reaction forces of redundant systems results in incorrect outcomes of numerical simulations [1].

Nonuniqueness is a feature of overconstrained MBSs, which does not depend on the type of coordinates adopted for its description but is related only to the structure of the studied system [1]. In some cases, detection of the global indeterminacy of the reactions is satisfactory, but for some tasks, the issue may be investigated in more depth. Despite the global indeterminacy of all reactions, some reaction forces (e.g., total reactions in some kinematic pairs or their components) can be unique [1].

There are methods to determine which of the reaction forces of a system with redundant constraints will be unique and which will not. Two of them are worth mentioning here. The first method is the constraint-matrix-based approach [1] that can be used to study MBSs described by selected types of coordinates, for which all kinematic pairs are treated in the same way—a set of constraints is formulated for each of them. Such coordinates are, for example, absolute coordinates. For this method, the obtained constraint matrix contains components corresponding directly to all kinematic pairs of the system, which allows studying the relationship between them—their uniqueness or nonuniqueness. Another method that allows for testing the uniqueness of reaction forces is the free-body-diagram approach [3]. This method can be used for systems described by any type of coordinates.

A specific class of mechanical systems contains systems described by joint coordinates. Kinematic and dynamic analysis of such systems can be carried out using recursive algorithms. So far, no uniqueness analysis method has been adapted to such algorithms. This contribution aims to present a method of testing the uniqueness of reaction forces for systems described by joint coordinates, which is included in the divide and conquer algorithm (DCA) [4, 5] being known as one of the most effective recursive algorithms.

2 Method

The divide and conquer algorithm reveals its exceptional effectiveness in analyzing the dynamics of complex MBSs when parallel processing techniques are used for computation. It uses a method of recursive binary assembly (an exemplary assembly is presented in Fig. 1). The DCA constitutes a building block of various methods developed for generalized multibody dynamics. Some of those introduced changes to deal with closed kinematic loops [5] and pointed out the problem of redundant constraints and reaction uniqueness. The classic version of the DCA algorithm has four stages [4]. The first two are *the First Preliminary Pass* and *the Second Preliminary Pass*. Cartesian positions, orientations, and velocities of the bodies are determined in these two, knowing the joint coordinates in kinematic pairs of the system. In addition, transformation matrices, needed in further calculations, are defined. The next step is *the Main Pass*, where the equations of motion of the analyzed system are formulated. This stage is run in order from the leaves toward the root of the assembly tree. The last computational step is *the Back-Substitution*

Pass. In this phase, the forces and the accelerations of the bodies of the system are determined. This step goes from the root toward the leaves of the assembly tree.

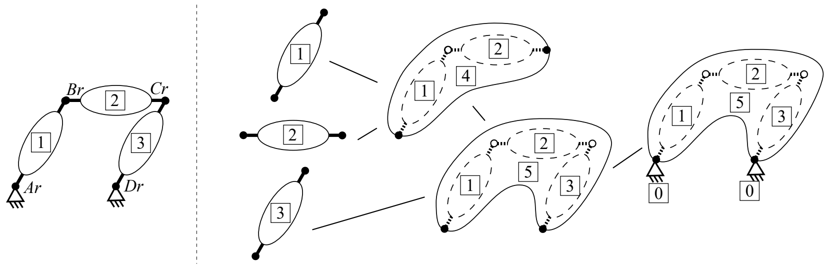

Figure 1: Four-bar mechanism (on the left) and its recursive binary assembly (on the right)

The novel approach for the uniqueness analysis takes into account the recursive nature of the DCA method. The process of accumulation of bodies into subassemblies, through the successive elimination of reaction forces occurring in kinematic pairs, proceeds in accordance with the assembly tree, which is associated with the structure of the MBS. This computational step ends when the recursions reach the root of the graph. At this point, the entire MBS is represented as a single articulated body containing all the bodies of the MBS. Next, connections of this object with the fixed base are considered. After completing this step (*the Main Pass*), the uniqueness analysis of the reaction forces may be performed by using the following algorithm: (1) the uniqueness of the reactions between the single articulated body and the fixed base is checked, and the obtained results are propagated in the binary assembly, (2) it is taken into account that the reactions of individual bodies with one kinematic pair are unique and the second propagation is done, (3) if there are individual bodies with two kinematic pairs, in which the uniqueness of reactions in only one of the kinematic pairs is not known, then the uniqueness of the second joint reaction may be determined, and the new uniqueness data may be propagated again, (4) step (3) is repeated until the uniqueness of all reactions is verified.

3 Conclusions

The uniqueness analysis of the reactions can be carried out using the method derived for systems described by joint coordinates. Previously, it was possible to analyze the uniqueness of reaction forces by modeling MBSs, e.g., in absolute coordinates for the constraint-matrix-based analysis method (i.e., a new mathematical model had to be created) or using the FBD approach, which requires the virtual cutting of kinematic pairs and balancing of forces and torques. As is easy to see, both approaches increase the workload. Such concepts of the uniqueness analysis are unsuitable to be implemented in software that uses the DCA in its calculations.

This paper presents a new recursive method for the uniqueness analysis of the systems described by joint coordinates. It is formulated for one of the most effective algorithms for MBSs—DCA, which can be used for parallel calculations. It should be added that so far, the DCA methods have lacked a component that would allow for the analysis of the reaction forces' uniqueness. The discussed method does not destroy the structure of the DCA, so it can be added to the existing parallel algorithms of this method. At the present stage, the discussed method can be used to test the uniqueness of reaction forces in kinematic pairs, but only for a particular class of systems. Generalizing the recursive methods for testing the uniqueness of reaction forces to other cases of MBSs is a potential direction for further research on the proposed method.

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