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Comparing position and force control for interactive molecular simulators with haptic feedback

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ABSTRACT

This paper presents a novel tool for the analysis of new molecular structures which enables a wide variety of manipulations. It is composed of a molecular simulator and a haptic device. The simulation software deals with systems of hundreds or thousands of degrees of freedom and computes the reconfiguration of the molecules in a few tenths of a second. For the ease of manipulation and to help the operator understand nanoscale phenomena, a haptic device is connected to the simulator. To handle a wide variety of applications, both position and force control are implemented. To our knowledge, this is the first time the applications of force control are detailed for molecular simulation. These two control modes are compared in terms of adequacy with molecular dynamics, transparency and stability sensitivity with respect to environmental conditions. Based on their specificity the operations they can realize are detailed. Experiments highlight the usability of our tool for the different steps of the analysis of molecular structures. It includes the global reconfiguration of a molecular system, the measurement of molecular properties and the comprehension of nanoscale interactions. Compared to most existing systems, the one developed in this paper offers a wide range of possible experiments. The detailed analysis of the properties of the control modes can be easily used to implement haptic feedback on other molecular simulators.

1. Introduction

The conception of new medicines, the synthesis of alloys, the prototyping of bio-nanorobots [1] as well as the transmission of information between two nanomachines [2,3], and the development of bio-microelectromechanical system devices (bio-MEMS) [4,5] are made possible thanks to molecular simulators. Since ease of manipulation is one of the key points of such tools, haptic devices are widely used. They provide a natural manipulation mode of the molecules and force information is easily interpreted by operators. It has been demonstrated that it helps operators to understand nanoscale phenomena. Its use is recommended for educational purposes [6–8], but it is not limited to academic courses. It can also help chemists and biologists to find specific locations in complex molecular systems (for example docking sites) [9], or to characterize the molecular properties [10].

The benefits of haptic feedback depends on the coupling used. In particular, how to reach the entire virtual environment using a haptic device with a limited workspace is a key issue to get an interactive system. Several techniques are proposed, from the concept of *c* lutching (freezing the displacement of the virtual object while enabling the user to modify the position of the haptic handle), to the *Bubble technique* (position control is used for fine positioning, and rate control is used for large displacements) [11]. As an alternative, the concept of *Active Haptic Workspace* is considered [12]. As in the *Bubble technique* position control is used inside the *AHW*, and objects are rotated and translated when the cursor is outside. In all cases, when the user is close to the point of interest, a common position coupling scheme is used to control the object and send the interaction forces to the user. Thus, even if complex techniques are used, the choice of the haptic coupling used remains unchanged when dealing with a precise area of the workspace.

The haptic coupling structure depends on the available inputs and outputs. In almost all the works dealing with molecular systems, position control is used (the user sets the position of the molecule, and feels the interaction forces through the haptic interface). However, stability is difficult to ensure due to long computation times, scaling factors used to link the macro and nano worlds, and the high variation of the forces. In most of the works, the system stability is guaranteed at the expense of the fidelity of the force feedback. Either the accuracy of the molecular interactions computed is decreased by using simpler models [13], or the damping added to the coupling deteriorates the transparency [14]. Scaling factors are also a major issue for stability [15]. Position control

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may also lead to instabilities as the position of the molecule is first set according to the user input, before being corrected during the update step of the simulation using the equation of motion to take into account physical constraints, as it is explained in this paper.

In addition to the haptic coupling specificity described above, the system must fulfill several requirements to be usable for the analysis of molecular structures. It should enable the manipulation of the molecules, the measurement of their inherent properties and should provide a deep understanding of the nanoscale interactions. According to potential users (including bio-physicist researchers and researchers working in pharmacological firms), the system should present:

- R_1: a fast and accurate manipulation and reconfiguration computation,
- R_2: different manipulation choices (both the whole molecule and a single atom), different force feedback (both the internal and external interaction forces),
- R_3: transparent and stable haptic coupling schemes despite the computation time.

The system we propose is composed of a molecular simulator, SAMSON, and two haptic coupling schemes. SAMSON enables a fast computation of the interaction forces and of the reconfiguration of the system thanks to a tree representation. The molecules can be manipulated by setting both a position and a force thanks to the methodology used to compute the solution of the equation of motion. Regarding the haptic coupling, a force control scheme is used in addition to position control to compensate for the lack of stability of the position mode while dealing with large displacements. It will also be seen that this control mode is more suited to molecular simulators. Moreover, new applications are possible thanks to this coupling. The control schemes presented are widely used for macroscale teleoperations. Even if force control has already been mentioned for molecular simulation in particular in [16] and [17], to our knowledge, this is the first time it is detailed and analyzed for molecular simulation. It can be implemented in our system thanks to the molecular dynamics equation solved.

We did a preliminary work where some of the potential applications of our system (conception of new molecules, analysis of molecular properties, etc.) are described [18]. We now present a comparison of position and force control. A detailed description of the molecular simulator and the control schemes, as well as how they are connected, is made to compare the adequacy of the two control modes to molecular dynamics simulators. The stability sensitivity of the coupling schemes is considered for the specific application of molecular interactions. The sensitivity is defined as the variation of the magnitude of the roots of the control schemes' characteristic equation with respect to given parameters. Relevant experiments of all the stages of the analysis of a molecule are performed and highlight the specificity of each control mode. Based on the experimental results, it seems that the system we propose could be used for the analysis of new molecules, thanks to the two complementary control modes, and to its adequacy with the requirements (R_1-R_3).

The rest of the paper is organized as follows. The molecular simulator is presented in Section 2. Based on the available inputs and outputs, the two control modes (position and force control) are detailed and compared in Section 3 in terms of adequacy with the simulator. The transparency and the sensitivity of the coupling schemes' stability is analyzed in Section 4. In Section 5, examples of manipulations that can be handled by our tool are presented. The advantages and drawbacks of each control scheme discussed in previous sections are compared with these experimental data. Section 6 concludes the paper. A table summarizing the notations is provided in Section 7.

2. Molecular simulator

As mentioned in Section 1, the molecular simulator must deal with reconfigurable objects of hundreds or thousands of degrees of freedom. Several approaches have been used, such as simplifying the force fields, or considering only rigid molecules. The resulting loss of accuracy limits the possible applications. The simulator we detail hereafter uses a special representation of the molecules, and a specific algorithm based on a quasi-statics method to simulate the motion of the molecular system. This leads to a fast computation of both the internal and external forces and a fast reconfiguration of the molecule [19,20]. Since the simulator has an open architecture, and most functions are implemented as plug-ins, the haptic coupling can be directly integrated into the equations solved by the simulator. This increases the variety of control modes that can be proposed compared to most of the commercially available software.

2.1. Representation of a molecule

The method relies on a recursive, divide-and-conquer representation of the molecular system, where any non-rigid group of atoms is considered to be the union of *two* groups of atoms. Thus, any molecular system is associated to a *binary assembly tree*, in which the leaf nodes represent the user-defined rigid bodies (atoms, or group of atoms). The internal nodes represent the subassemblies, and the root node represents the complete molecular system (Fig. 1).

Using the spatial notation, the equation of motion of each rigid body is [21]:

$$I \cdot a = F_{ext} + F_{int} - v \times I \cdot v \tag{1}$$

where a (resp. v) is the spatial acceleration (resp. velocity) of the molecule. I is its inertia. F_{ext} is the sum of the forces applied by other molecules and F_{int} is the sum of the internal forces applied to the considered rigid body. These forces depend on the force field being used in the simulation to model interatomic interactions. In our current implementation, the force field is derived from a well known molecular mechanics force field, CHARMM [19], which models interactions through van der Waals, electrostatic and dihedral contributions.

2.2. Computation of the solution of the equation of motion

To solve the equation of motion for each rigid body, the simulator follows traditional approaches: at each time step, the interatomic forces are first computed, then the acceleration of the system is determined and used to update its state and the internal configuration of the molecule. This operation is made easier thanks to the tree representation, which enables to recursively compute the forces and accelerations from the root node to the leaves after having recursively computed the coefficients of the equation in a bottom-up pass. Thanks to the chosen representation of the molecule, and the way of solving the equation of motion, systems of hundreds of degrees of freedom can be simulated in tenths of a second.

2.2.1. Manipulation modes

To enable the user to manipulate the molecule (or one of the rigid bodies), its action must be taken into account while solving the equation of motion. Thanks to the open architecture of the software, two solutions are possible. They are detailed hereafter:

Position mode. One way to control the simulation through the haptic device is to control the position of the manipulated rigid body or molecule. In the algorithm, the instantaneous position