Conformational Transitions of Cyclohexane via Minimal Elastokinematic Models

Michael John Bosco, E. N. Prabhakaran, and G. K. Ananthasuresh

Abstract By modelling cyclohexane as a minimal spatial compliant mechanism, we analyze its well-known conformational transitions using an elastokinematic model that accounts for kinematic and elastic effects while neglecting inertia. Our motivation is to augment 3D-printed compliant ball-and-stick model of cyclohexane using a simple computational model for visualizing the changing energy landscape during transitions. Bending and axial stretch of the bonds are captured using finite element analysis while obeying the intrinsic kinematic constraints. Thus, our computational and physical models are expected to be consistent in terms of motion, force, and energy during the conformational transitions of cyclohexane between boat and chair configurations. Previously underemphasized features of the transition such as in-plane stretching, strain localization, and directional asymmetry in re-laxation are identified and analyzed. These observations provide a mechanical interpretation of the transition pathways and clarify the fundamentally different nature of the boat and chair states. The highlight of our modelling is that we capture the entire transition smoothly from one conformation to another. We argue that our models, both physical and computational, indirectly account for inter-atomic force and steric interactions as equivalent force and moment. Simplicity of our model enables efficient simulation as compared to molecular dynamics and quantum chemistry calculations. Consequently, the energy captured by our models at present is indicative of trends observed in other models, but it is not entirely quantitative. In this paper, we present only the basic spatial flexible hexagon that serves as a building block for later extensions for complex molecules and scenarios.

M. J. Bosco and G. K. Ananthasuresh. Mechanical Engineering, Indian Institute of Science, Bengaluru, India. E-mail: suresh@iisc.ac.in
E. N. Prabhakaran. Organic Chemistry, Indian Institute of Science, Bengaluru, India

1 Introduction

Beginning with one of the early works of Lauwerier [1] and Bottema [2], spatial flexible hexagons such as the one found in cyclohexane (C_6H_{12}) and other cyclic organic molecules have been extensively studied by geometers and kinematicians [3, 4]. The studies of chemists on the same problem are also extensive, both on the experimental and computational aspects after Hermann Sachse's seminal paper in 1890 followed by Barton [5] and Hendrickson [6]. After the observation by Lister [7] that cyclohexane has a stable chair conformation, there have been many investigations on the non-planarity of closed chains in molecules. Experimental observations augmented with analytical and computational approaches led to puckering coordinates put forth by Cremer and Pople [8]. The occurrences of various puckering conformations are still studied using large datasets [9]. Density Functional Theory (DFT) and Molecular Dynamics (MD) simulations are applied to study this problem [10-13]. While all these and many other prior studies are effective in understanding kinematic, energetic, and entropic aspects of closed-chain molecules, there is much to be gained from physical models such as the one shown in Fig. 1. The premise is that coarse-grained physical and elastokinematic models yield energy profiles that resemble those achieved using MD and Quantum Mechanical (QM) calculations but with much less computational effort.

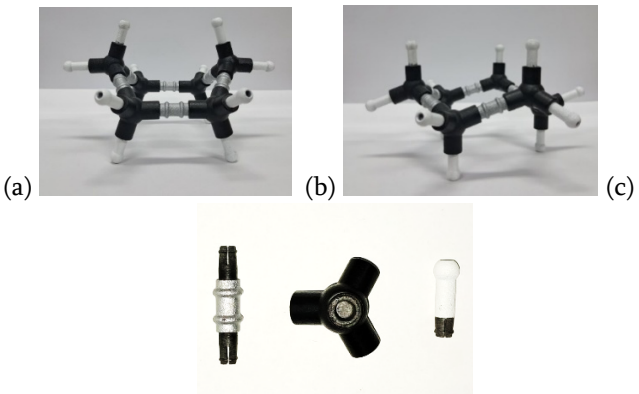

Fig. 1. Physical model of cyclohexane (C_6H_{12}) in (a) boat and (b) chair conformations; (c) Compliant rods (bond) and receiver (sp3 hybridized carbon atom) used to create the model

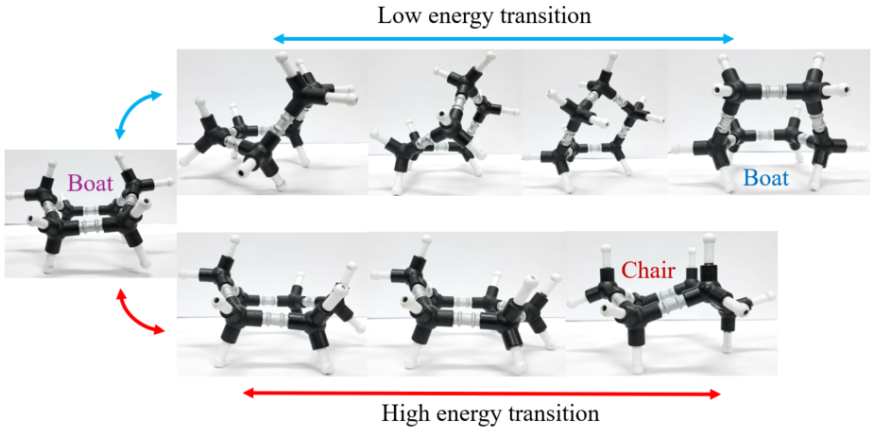

Fig. 2. Transitions between boat and chair confirmations obtained using hand-manipulation

The conformations in Figs. 1 and 2 show the well-known stable states of boat and chair conformations of cyclohexane, and how a physical model can be used to visualize and *feel* the transitions. Friction at the joints allows the model to hold some of the intermediate states without external aids. This physical model is designed and constructed [14] to permit inherent elastic flexibility of the rods representing the bonds. Therefore, they show continuity while the molecule transitions from one conformation to another just as it happens in real molecules. This contrasts with indirectly deriving such information using discrete snapshots of molecular conformations in current QM and crystal structures-based studies. In other words, the current methods need intuition to postulate intermediate and transition state structures of molecules from which minimal energy pathways are predicted. On the other hand, the compliant rods in our models (Figs. 1 and 2) naturally stretch, bend and twist (or simply rotate) to emulate distortions in bond-collinearity and alterations in bond-lengths. Therefore, when a force or moment is applied on a certain segment of the molecule, the rest of the molecule elastically deforms and thus circumvents the need for intuition. Furthermore, the spatiotemporal deformation seen in the models closely mimics the dynamics of the real molecules and aids in gaining intuition and insights. Thus, manipulating hand-held models helps discern structural transitions in a molecule. This is yet to be described or understood from the classical mechanics perspective, which is the objective of this work. With this approach, we aim to complement QM characterization of molecular structures and motions.

The physical models (see Fig. 1) are made using compliant rods of appropriate stiffness (as opposed to rigid sticks or overly flexible rods) connecting the balls representing the tetrahedral, sp3 hybridized carbon atoms. When these models

are manipulated by hand to visualize transitions, one can feel the force and see the motion of the entire molecule. However, the precise drivers for deformation (i.e., axial stretching, transverse bending, twisting or rotating) cannot be easily discerned. And the strain energy distribution within the molecule and strain (and stress) at any point in the molecule at different stages of deformation cannot be felt. More importantly, quantitative information about deformation and energy landscapes, which is crucial to understand, predict, and modify real molecular systems, is also imperceptible. Therefore, we propose a computational simulation of manipulation of physical surrogate models in response to forces and moments applied on them. We use nonlinear finite element analysis (FEA) for simulation and see where the physical surrogates bend, stretch, or twist, and plot energy landscapes. The accuracy of this simulation-based perception needs tuning of the geometric (e.g., cross-section of the rods) and material properties of the model. We explain this in later sections and discuss its potential benefits and underlying challenges.

In Section 2, we describe the design features of physical models and their elastokinematic modelling using FEA. We discuss the results obtained using FEA in Section 3. Conclusions of this work are in Section 4.

2 Elastokinematic Models

The physical model whose 3D-printed prototypes are shown in Fig. 1 is designed to mimic the motion and deformation in real molecules. They retain the bond angles but allow slight (about 2°) bending at the ends of the bonds. And they allow limited extensibility in the bond lengths. There is almost free rotation about the axis of the C-C bonds. The physical models of the three essential building blocks of cyclohexane are shown in Fig. 1c, and the geometric models of the first two are shown in Fig. 3. The rod representing the C-C bond has tapered ends that are also split into four quadrants. These rods are inserted into the appropriately designed blind cylindrical holes in the receiving end that represents the C atom in its sp3 hybridized state. The four cylindrical protrusions form 109.5°. But the compliance of the rods, as stated earlier, allows for slight bending and stretching of the C-C bonds. Consequently, our physical surrogates obey kinematic constraints and provide energetic response by undergoing rigid-body rotations and elastic deformation, as necessary. We use large-displacement and large-rotation (i.e., geometrically nonlinear) finite element analysis to model the elastokinematic behaviour rather than purely kinematic behavior or simplistic elastic network models with rotation springs.

Prior to the simulation, the initial spatial hexagon is rendered in Autodesk's Fusion 360 (https://www.autodesk.com/) through the enforcement of kinematic constraints by prescribing revolute joints at the bonds. On enforcing the last joint, the initial open chain can close to either a boat or chair conformation depending on the orientation of each subcomponent as represented in Fig. 4. This happens because of purely geometric constraints.

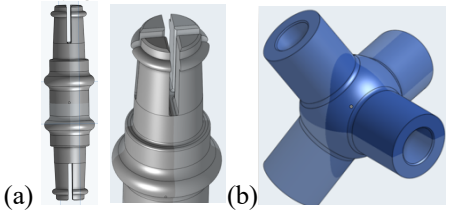

Fig. 3. The essential building blocks of the physical surrogates of cyclohexane

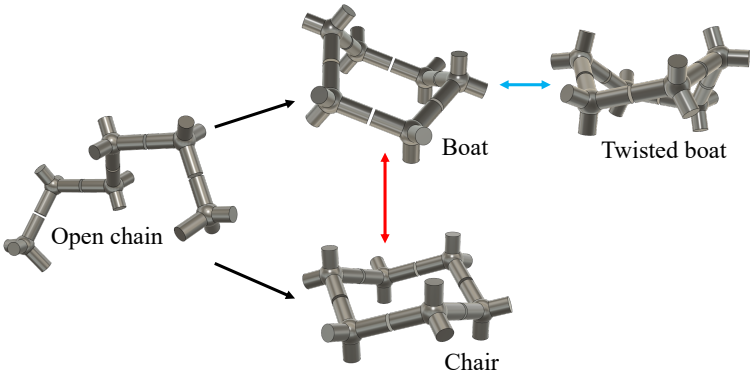

Fig. 4. An open-chain mechanical surrogate of cyclohexane assuming boat or chair conformations even in the CAD software

ABAQUS CAE's (https://discover.3ds.com/) static general study was then used to simulate the transition of boat to chair, and vice versa. To obtain revolute behavior at the bond, we made use of wire features prescribed as hinge connectors. These connectors have one rotational degree of freedom about an axis of a local coordinate system created at every connected bond. The wires have their ends kinematically coupled to the bond-rods in all degrees of freedom. The boundary conditions are applied to the two non-planar atoms of the initial boat geometry. One atom is constrained in all degrees of freedom while the other has a prescribed rotation applied about a local axis passing through its center. The reaction moment and the strain energy developed are computed for the spatial hexagon as it deforms and transitions from boat to chair and vice versa using a two-step definition. Fig. 5a depicts the steps involved in finite element analysis

while Fig. 6 shows the strain energy against the prescribed rotation along with the strained spatial conformations of cyclohexane. We discuss the results and findings next.

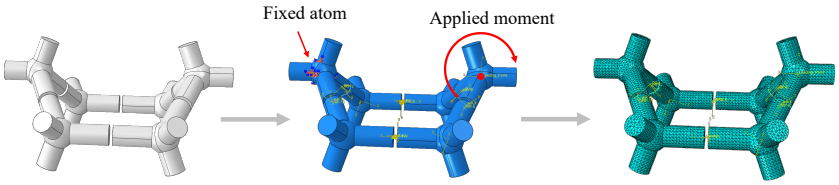

Fig. 5. Finite element meshed model with kinematic constraints and boundary conditions

3 Results and Discussion

In Fig. 6 we observe that both boat and chair are two stable conformations of cyclohexane, and that the strained intermediates contribute to the energy barrier between them. The strain energy plot of Fig. 6 is to be interpreted as a semi-quantitative portrayal of energy between the boat and chair conformations. The trend of the strain energy is important there but not the actual value because we used material properties, forces, and cross-section geometry of the rods to mimic the physical surrogate. We used a circular cross section for the bond-rods. They are elongated wherever a revolute joint is required enabling a clear visualization of strain in the bond during transitions. It may be surprising to see in Fig. 6 that both boat and chair conformations have the same strain energy, but that is not true. The parameter values we have taken are such that the energy of transition is so high that we cannot discern the minute energy in the chair conformation. The von Mises stress overlayed on the FEA meshed model confirms this.

Pure kinematic rotations do not enable boat-to-chair (and vice versa) conformational change in cyclohexane. This is true in our physical model as well as the FE model. The bonds must bend for any transition from chair. As our physical and FE models account for both kinematic and elastic motion and deformation, we can easily capture the continuous strained transition between boat and chair passing through twisted boat conformation. This is not true for other physical models built with connecting rods that lack limited extendibility. So, the rods invariably pull out or cleave from the receivers during boat-chair transition due to mechanical forces. In our models, attention should be paid to the stress (or strain) localization in the rods at their ends. Careful analysis of the deformation data would indicate that the C-C bond stretches ever so slightly.

These observations are consistent with the experimental and computational data reported in the literature.

Fig. 8 presents the boat-to-boat conformations when a prescribed rotation is applied about a connected bond-axis. The strain energy is close to zero in these transitions that pass through twisted-boat intermediates. Manipulation of the physical surrogate confirms that boat-to-boat transition hardly needs any effort. Both these observations from our physical models and elastokinematic finite element analysis corroborate established studies using Hartree-Fock (HF) and QM methods, confirming two strain-free cyclohexane conformations: the rigid chair and the flexible boat/twist-boat [5, 6, 15] with a strained transition energy barrier between the two [16].

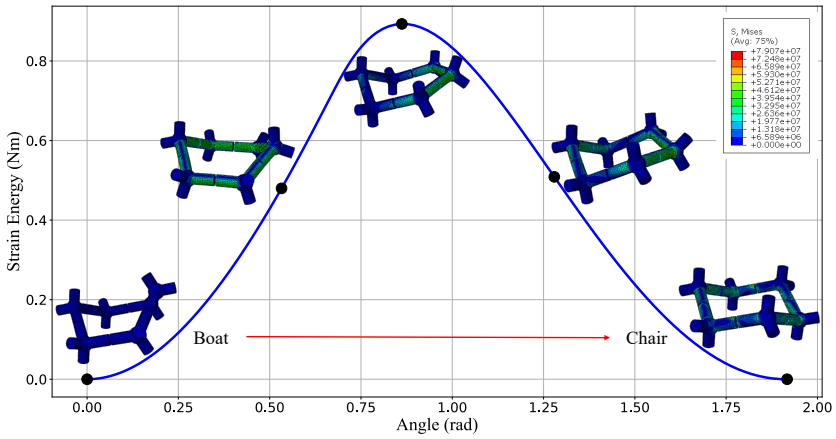

Fig. 6. Strain energy vs. prescribed rotation along with the boat to chair conformations depicted for various conformations

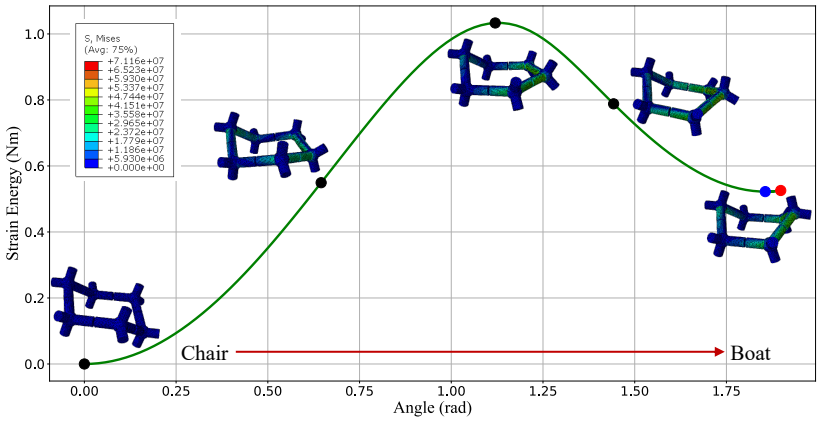

Fig. 7. Strain energy vs. prescribed rotation along with the chair to boat conformations when torsional springs are included at the revolute joints

To capture energy differences as in Fig.7 between stable conformations we add a torsional spring at every revolute joint. In this simulation, we consider the chair to be in the initial zero energy state. A prescribed rotation is applied to one of the two atoms not lying on the plane common to four atoms while the other atom is fixed in all degrees of freedom. The prescribed rotation is deactivated after reaching its prescribed value to allow the strained boat state (red spot) to settle to a stable configuration (blue spot).

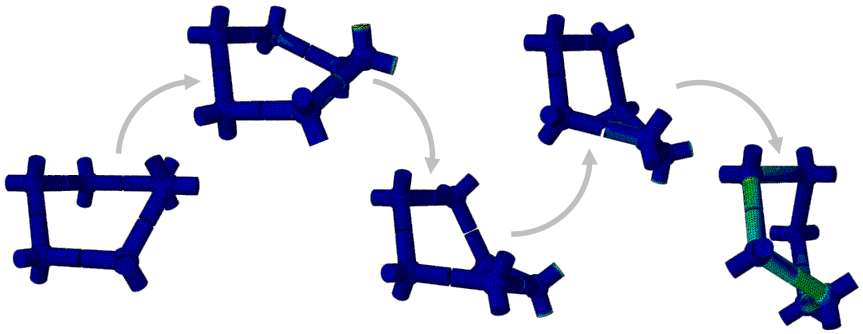

Fig. 8. Boat-to-boat conformations on the application of a prescribed rotation

Based on the physical model and its FEA, we note that elastic features built into the physical model architecture allow molecular dynamics to be physically replicated with high fidelity, in cyclic molecules and constrained molecular segments. In cyclic systems, rotation about a single bond is not expressed in isolation; instead, it naturally propagates as a set of concomitant chemically allowed adjustments across the remaining bonds in the ring. This enables direct visualization and tactile experience of the continuity of molecular motion, closely reflecting the correlated nature of conformational changes in real molecules. Consequently, the effects of substitution patterns, ring double-bonds, their migration, and the introduction of additional substituents, on overall molecular dynamics become immediately apparent, providing users with intuition generated by the structure itself, rather than requiring prior abstract reasoning about conformational outcomes.

4 Conclusions

Ball-and-stick models that permit arbitrary bond angles and unrestricted rotations, allow chemically invalid structures to be assembled, while space-filling

models obscure bond connectivity and do not reveal internal motion. In contrast, our compliant ball-and-stick models encode hybridization, bond order, and rotational constraints directly into its mechanical design, ensuring that only chemically permissible geometries and motions are realized. This enables simultaneous, physically faithful visualization of both molecular structure and selective conformational dynamics—capabilities not available in existing physical model systems. Furthermore, geometrically nonlinear finite element analysis reveals elastokinematic response that is consistent with quantum mechanical and molecular dynamics simulations. Quantitative validation of this will be pursued in future work. Even more importantly, this study on cyclohexane has the potential to be extended to other molecules to gain insights without having to rely on intuition alone in predicting conformational changes.

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