A Numerical Integrator for Forward Dynamics Simulations of Folding Process for Protein Molecules Modeled as Hyper-Redundant Robots

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***Abstract*— This paper investigates development of an efficient numerical integrator for forward dynamics simulation of the protein folding process, where protein molecules are modeled as robotic mechanisms consisting of rigid nano-linkages with many degrees-of-freedom. To address the computational burden associated with fixed step-size explicit Euler methods, we develop a fast numerical scheme with an adaptive step-size strategy for computing the folding pathway of protein molecules.**

I. INTRODUCTION

Developing efficient numerical integrators plays a crucial role in forward dynamics simulations of many emerging robot models such as continuum and soft robots (see, e.g., [1]). Protein molecules, according to the kinetostatic compliance method (KCM), can also be modeled as a large number of rigid nano-linkages folding under the effect of interatomic forces [2]–[4]. The KCM framework, which is a computationally promising approach to numerical simulation of folding dynamics, relies on the explicit Euler integration scheme with fixed step-size to integrate the protein dynamics towards a steady-state associated with a folded molecule conformation. However, each integration step requires heavy computations of interatomic force fields. Accordingly, the explicit Euler method with fixed step-size, which requires a larger than needed number of iterations for convergence to steady-state, imposes an unnecessary computational burden.

In this paper, we address the aforementioned shortcoming by utilizing the pseudo-transient continuation (ΨTC) framework [5] and developing a fast numerical integrator with an adaptive step-size control strategy for computing the folding pathway of protein molecules evolving according to the KCM-based dynamics.

II. THE EXPLICIT ΨTC NUMERICAL INTEGRATOR

The flow chart of the explicit ΨTC numerical scheme with step-size adaptation tailored to the underlying KCM-based folding dynamics is depicted in Figure. We first present the explicit ΨTC solution to PFPCP under the assumption of a fixed step-size and discuss its convergence and numerical stability properties 1. The step-size adaptation rule of the numerical integrator is based on the so-called *switched evolution relaxation* (SER) technique that is widely used in the ΨTC literature. Figure 2 depicts the free energy $\mathcal{G}(\boldsymbol{\theta})$ of the protein molecule during the folding process associated with a protein backbone chain with a configuration vector of dimension 32, as well as its transient conformations, and the associated step-size evolution, namely, δ_k.

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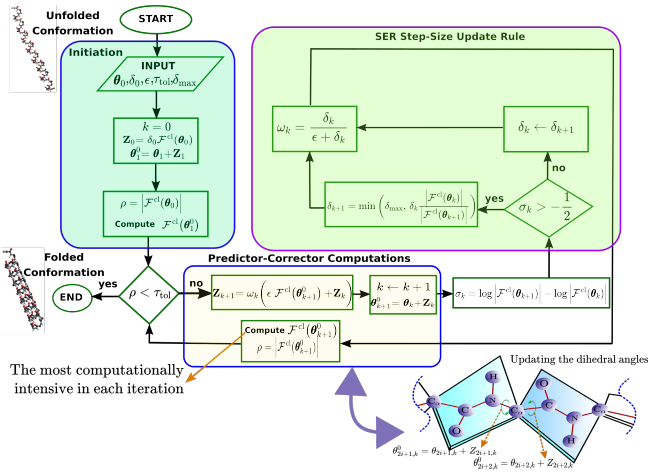

Fig. 1: The flow chart of the proposed explicit ΨTC scheme for integrating the KCM-based forward dynamics of protein molecules modeled as hyper-redundant serial robotic mechanisms.

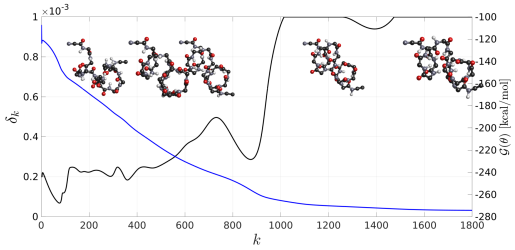

Fig. 2: The free energy of the backbone chain of a protein molecule with a 32-dimensional dihedral angle vector (blue curve; $\mathcal{G}(\boldsymbol{\theta})$ on the right axis), its transient conformations, and the step-size of the explicit ΨTC scheme (black curve; δ_k on the left axis). The five plotted backbone chain conformations from left to right correspond to iterations 100, 300, 500, 1000, and 1400, respectively.

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