Pre-Submission Letter: Molecular Dynamics: From Basics to Application

An outline of the scope of the proposed contribution

The training/tutorial hybrid article "Molecular Dynamics: From Basics to Application" is designed as a university-level course for first-year master users. Its goal is to teach users how to leverage molecular dynamics (MD) to solve scientific problems independently through a series of nine exercises. The first five exercises serve as a solid foundation for understanding the basics of MD. They start with energy conservation and time steps and then progress by introducing thermostats, barostats, and long-range electrostatics treatment. Users get to experiment with various algorithms, gaining a practical understanding of their benefits and drawbacks. With the following two exercises, the course continues beyond core concepts. These cover more advanced MD features and their practical applications. Users get to bridge theory and practice by calculating the solvation free energy and binding free energy of natural systems, understanding the theoretical foundations of these calculations and their real-world implications. The final two exercises encourage users to apply their new-found knowledge in computational biophysics more self-reliantly. The eighth exercise requires users to set up a protein simulation autonomously. The task is to assess convergence and the sampling space of the simulation, highlighting issues of ergodicity and time correlation. The final exercise involves a molecular docking project, introducing users to various computational tools commonly used by computational scientists. The goal is to follow a step-by-step tutorial to propose one or two compounds likely to stabilize the protein-protein complex of interest. The tutorial guides the decision-making process, but ultimately, the users must select promising stabilizers.

By the end of the course, users will have gained firsthand experience with various algorithms used in MD simulations. They will know how to tackle scientific questions independently using GROMACS and other computational tools.

An explanation of how the proposed manuscript differs from existing published work

Several attributes of this training/tutorial hybrid article contribute to its uniqueness. However, several components are partly covered in other articles in the 'Journal of Living Molecular Science.' Firstly, the accessibility of this tutorial is distinctive. Unlike most other articles that assume a certain familiarity with MD simulations, this tutorial is designed to be embarked on even by users with no prior experience in computational science. Secondly, this hybrid article can be smoothly incorporated into an academic course, with online materials divided into 'student' and 'teacher' repositories. The student repositories provide the necessary materials for the exercises, while the teacher repositories contain the results and bash scripts for automatically generating the solutions. What truly sets this hybrid article apart is its autodidactic approach. Users are encouraged to arrive at their own conclusions for best practices in MD simulations, empowering them to write a report that can be compared to the model reports in the git repository. Also, there is an emphasis on vivid, descriptive figures, facilitating a better understanding.

The availability of model reports is particularly valuable when the material is used in an academic course to clarify the learning goals. There is some overlap with the article 'A Live CoMS Best Practices Guide Best Practices for Quantification of Uncertainty and Sampling Quality in Molecular Simulations' by Grossfield et al. This publication describes the sampling convergence itemized in the eighth exercise in much greater detail. However, while their article is a best-practice guide, this work offers an interactive tutorial, which adds significant value. There is also a considerable overlap with the article 'From Proteins to Perturbed Hamiltonians: A Suite of Tutorials for the GROMACS-2018 Molecular Simulation Package' by Justin Lemkul and the sixth and seventh exercises. The systems and the goals are identical, but the didactic approach differs. Herein, the theory is laid out in more detail, and instead of only giving the user instructions, the algorithms are explained mathematically and physically, making the tutorial more engaging and active for the audience.

Whether the manuscript is adapted from a previous article

No

A summary of the expertise that the proposed authors have on the subject

Martin Zacharias - professor of theoretical biophysics at the Technical University of Munich since 2009 - has been using and developing MD tools for more than 30 years, teaching courses on MD simulations for 15 years, and designing student tutorials for molecular modeling and MD simulations.

Maria Reif - PhD in Physics - developed methods and has more than ten years of experience with MD simulation techniques. She was involved in training and teaching MD methods for ten years and designed practical student tools for MD and free energy simulations.

Shu-Yu Chen - PhD in Physics - has experience with MD simulations for more than six years.

Luis Vollmers - M.Sc. Chemistry - has experience in performing MD simulations and developing MD tools and MD teaching material for more than four years.
Tristan Alexander Mauck - B.Sc. Physics - participates in designing tutorials on MD simulations for students.

A description of the plan for how the article will be updated, including the plan for transferring authorship if the original authors are unable to update it.

The materials are stored at a GitHub repository owned by Luis Vollmers, where they will be maintained. If the primary author cannot maintain the materials anymore, this task will fall to Dr. Maria Reif.

The proposed license enabling the article to be released freely to the public

The Authors recommend CC-BY-NC as a license.

System and/or software requirements the researcher will need to complete the tutorial:

GROMACS 2018 or newer
VMD 1.9.x
Linux (tested for 22.04)