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P01

A Coupled Potential QM/MM Simulation of 2-(2-fury)-3-hydroxychromone

ABDALLAH BRAHIM [1] **, Stève-Jonathan Koyambo-Konzapa**[2]

[1] *Centre National de Recherche pour le Développement (CNRD), BP 1228, N'Djamena, Tchad*

[2] *Laboratoire Matière, Energie et Rayonnement (LAMER), Université de Bangui, P.O. Box 1450 Bangui, République Centrafricaine*

The hybrid simulations quantum mechanics/molecular mechanics (QM/MM) is a method for studying condensed phase chemical reactions. The differents regions of the system where chemical processes occur are treated at an appropriate level of quantum chemical method, while the remainder is described by molecular mechanical. As part of the method, chemical reactivity can be checked, for example using ESIPT. We performed two simulations and make comparaison betwen them of 2-(2-fury)-3-hydroxychromone (FHC) in a periodic box with polar protic solvent. The first simulation, is about classical MD simulations. In the second simulation we will do the same thing, but this time we will use the semi-empirical PM3 Hamiltonian on the FHC molecules.

Keywords : Quantum mechanics, Molecular mechanics, QM/MM, Molecular dynamics, FHC, ESIPT

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P02

In-Silico Analysis of Anti-Viral Activities of Phytochemicals in *Berberis Vulgaris* Against a Receptor of Chickenpox

[1]Omolara O. Adeboye, [2]Saheed A. Agboluaje & [3]Akinlabi J. Adeyemi

[1]Emmanuel Alayande University of Education, Oyo, Nigeria
[2]Atiba University, Oyo, Nigeria
[3]Ekiti State University, Ado-Ekiti, Nigeria

This study investigates the antiviral potential of selected phytochemicals from the leaves of *Berberis vulgaris* through in-silico molecular docking analysis against a chickenpox receptor (PDB ID: 6LG1). A total of thirteen compounds, including Terpinen-4-ol, Viridiflorol, Sabinene, Para-cymene, Globulol, Alpha-terpineol, and others, were analyzed for their binding affinities and inhibition constants, compared with standard antiviral drugs Acyclovir and Tecovirimat. PyRx virtual screening technologies (AutoDock Vina, Open Babel) were used to perform molecular docking, which was visualized using PyMOL and Biovia Discovery Studio. Lipinski's Rule of Five was used to determine drug-likeness. The docking analysis revealed that Globulol exhibited the strongest binding affinity (-8.9 kcal/mol) and the lowest inhibition constant (0.30 µM), surpassing the standard drugs. Alpha-terpinene also showed a promising binding affinity of -7.9 kcal/mol with an inhibition constant of 1.63 µM. In contrast, 1,8-Cineol and Alpha-pinene displayed weaker binding and higher inhibition constants, suggesting reduced inhibitory efficacy. The standard drugs Acyclovir and Tecovirimat demonstrated strong binding affinities (-7.3 and -7.4 kcal/mol, respectively) and low inhibition constants (4.48 µM and 3.78 µM), validating their effectiveness. Based on these findings, Globulol and Alpha-terpinene emerge as promising candidates for further development as potential antiviral agents against chickenpox, showing stronger binding and inhibitory potential than the standard drugs. Further experimental validation is recommended to confirm these in-silico results.

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P03

Modeling Charge Transfer States in Phycobilisomes

Mamaru B. Alem[1], Lorenzo Cupellini[2] and Tjaart P. J. Krüger[1]

[1]Department of Physics, University of Pretoria, Pretoria, South Africa

[2]Department of Chemistry, University of Pisa, Pisa, Italy

Email: mamaru2005@gmail.com, tjaart.kruger@up.ac.za

Abstract

Phycobilisomes are giant (~6 MDa) light-harvesting pigment-protein complexes of cyanobacteria and certain algae, responsible for harvesting sunlight and regulating the flow of absorbed energy to provide the photochemical reaction centres with a constant energy throughput. Single-molecule spectroscopy studies have identified the presence of strongly red-shifted and quenched emission states and they were hypothesised to originate from charge-transfer states residing on phycocyanobilin pigments in the core of phycobilisomes. The quenched states were suggested to be an important, rapidly activated photoprotective mechanism to protect the organism against high solar illumination. An investigation into the molecular origin of these states, the role of the background charge, amino-acid residues around the pigments, and the geometrical configuration of the pigments requires the use of atomistic simulations involving a state-of-the-art QM/MM computational microscope. In this work, the ground-state geometries of the trimeric core units of phycobilisomes retrieved from *Synechocystis* PCC 6803 and *Synechococcus* PCC 7002 were optimized using Density Functional Theory (DFT) employing the CAM-B3LYP exchange-correlation functional together with the 6-31+G* basis set. Linear-response time-dependent DFT (TD-DFT) was used to calculate the excited-state geometries. The results demonstrated that the coupling between the energy states in TD-DFT spectra would serve as a screening tool as a charge transfer states in light-harvesting pigments. Accordingly, care should be taken in considering the natural transition orbitals (NTOs) for CTS analysis. Therefore, a complete analysis of charge transfers energies, hole-electron distance, NTOs, and optimized charge transfer states are needed to confirm the presence of charge transfer states. Amino acids around the D-ring of the bilin have a strong potential to serve as electron acceptor.

P04

Optimization of Post-Processing Tools for Collective Burst Mechanism of Angular Jumps in Water

Edward Ntim Gasu [1,2], Ivan Girotto [1,2], Natalia Manko [1] and Ali Hassanali [1]

[1](Presenting author underlined) The Abdus Salam International Centre for Theoretical Physics

[2] Scuola Internazionale Superiore di Studi Avanzati

This study aimed to optimize the computational efficiency of an automated algorithm for detecting angular jumps in water molecules [1]. The protocol, which analyses dipole moment (DP), hydrogen-hydrogen (HH) vectors, and topological defects in hydrogen bonding across systems of varying sizes, faced performance bottlenecks as system size, trajectory length, and simulation time increased. These challenges led to frequent crashes and prolonged execution times. Initial tests of the DP and HH extraction tool revealed high memory consumption (**117 GB**) and long execution times (**4397 seconds**). To address these challenges, the MDAnalysis package was initially leveraged for input processing and benchmarked against the custom input processing approach. Results showed that converting XYZ trajectory files to binary reduces memory usage and processing time. Among various binary file reading techniques implemented, NumPy's frombuffer function performed best, reducing execution time and memory usage by up to **265-fold** compared to the original method, and **224-fold** relative to MDAnalysis. With optimized input handling, the serial version of the DP and HH extraction protocol ran approximately **3x** faster than the original. Implementing multiprocessing with up to 8 processes further improved performance, achieving a **14x** increase in speed while maintaining low memory usage **(~93 MB**) for all target analysis tasks. Quality checks on the molecular swing evaluation protocol was completed with updated jumps calculation protocol and plotting utilities. Additionally, the speed of the tool for calculating topological defects in hydrogen-bonded water molecules was enhanced using Numba's @njit decorator for functions. While the protocol undergoes further checks to produce a completely optimized automation, we tentatively conclude that binary formatting of custom trajectories coupled with the aforementioned Numpy routines enhanced computational efficiency of post-processing of large molecular dynamics simulations data.

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P05

Impact of drug dispersion on tumor-effector dynamics during combined chemo-immunotherapy with sensitivity analysis

Lazaro R. Mashiku[1,2], **Joseph P. Ndenda**[3], **Reuben Maghembe**[4], **and Sachin Shaw**[1]

[1]*Department of Mathematics and Statistical Sciences, Botswana International University of Science and Technology, Private Bag 16, Palapye, Botswana*

[2]*Department of Graduate Studies, Eastern Africa Statistical Training Centre, P.O. Box 35103, Dar es Salaam, Tanzania*

[3]*School of Mathematics and Statistics, University of Sydney, Camperdown, NSW 2006, Australia*

[4]*Department of Biological Sciences, Faculty of Science, University of Botswana, Private Bag 0704, Gaborone, Botswana*

Solid cancer remains a serious threat to global health despite decades of progress. Traditional chemotherapy treatment has been used to curb the disease despite its inability to reach cancer cells at high enough quantities leading to adverse toxicity on healthy cells, producing severe side effects, and exacerbating patient suffering. Active targeted nano-drugs (ATNDs) acting as transporter systems have become a viable solution to this shortcoming, offering the possibility of more precise cancer targeting. Therefore, in the present study, we develop a numerical model of capturing ATNDs, incorporating movements within and outside the tumor spheroid and the magnetic forces guiding the nanoparticles. By combining a model of ATNDs transport with a tumor-effector dynamic model based on porous media phenomena, we demonstrate how the models may be combined to model drug-loaded nanoparticle transport in an external magnetic field. We analyze the controlled drug delivery against traditional chemotherapy based on the combined effect of immunotherapy and chemotherapy with the dispersion of nano-drugs to lead a solute cloud toward the tumor. We found that the amalgamation of immune and chemotherapy delivered by ATNDs enhances cancer therapy efficacy compared with conventional chemotherapy. Increased drug convection toward the tumor region presented by ascending values of the Peclet number inhibits the growth of tumor cells and prolongs progression-free survival. Increases in source term and vessel permeability also increase the likelihood of tumor suppression, while raising the hematocrit and magnetic number results in reduced tumor cell killing. Sensitivity analysis of the dynamic model parameters has been discussed. This work demonstrates that ATND-delivery systems can improve therapeutic agent delivery to the tumor tissue, and promote tumor cell killing.

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