32nd URSI GASS, Montreal, 19-26 August 2017

Magnetic molecular dynamics simulations with Velocity Verlet algorithm

E. della Valle(1)*, P. Marracino(1), S. Setti(2), R. Cadossi(2), M. Liberti(1), F. Apollonio(1)
(1) Sapienza University of Rome: Department of Information Engineering, Electronics and Telecommunications (DIET), Via Eudossiana 18, 00184, Rome Italy
(2) IGEA SpA, Via Parmenide 10/A, Carpi, Italy

Abstract

In this paper, we present the implementation of an external static magnetic field with the Velocity Verlet algorithm for performing Molecular Dynamics simulations. Molecular Dynamics simulations allow to understand at molecular level the interaction mechanisms between atoms under specific conditions. We performed our simulation with the Gromacs package, usually used to simulate the action of an external electric field acting on a molecular target. Here, the integration of Newton equation is presented by introducing the Lorentz force for the magnetic field action. The implementation and preliminary trials are reported.

1. Introduction

The problem of magnetic field effects on living objects has a long history. Unfortunately, no consolidated physical foundation of low–level magnetic field action on biosystems has been developed yet [1]. Several models have been advanced to explain the possible mechanisms; almost all have been essentially based on classical or quantistic description of an ion in a binding site, and have studied the problem through the precession of ion thermal motion in magnetic fields [2]. The basic premise of such models is that the effect of the magnetic field can energetically overcome the perturbing influences of thermal noise, moreover in almost all, a rigorous interaction between the ion and its binding site is lacking due to the inability to describe the target at molecular level. This last issue seems an unavoidable requirement to produce affordable results, therefore simulations based on Molecular Dynamics (MD) to study molecules behavior under different physical conditions of magnetic or electric fields seem to become a strategic challenge.
The introduction of an external electromagnetic field into a MD simulation requires a time-dependent forcing function in Newton's second law, to describe the forces exerted on the charge sites by the field. For the constituent electrical and magnetic fields E and B, the forces acting on each charge site are incorporated, through Lorentz force, as follows:

$$m_i \ddot{\boldsymbol{r}}_i = \boldsymbol{f_i} + q_i \boldsymbol{E}(t) + q_i \boldsymbol{v_i} \times \boldsymbol{B}(t) \qquad (1).$$

where q_i is the charge and f_i is the force on the site i. The electric and magnetic fields are taken to be uniform and plane-polarized.
Actually, several works have considered only the electric field component in the Lorentz force [3, 4, 5, 6]. The motivation was that the magnetic field, being normal to the velocity of the particle, "does not work", hence it cannot heat the charged particles, giving them energy. It follows that the magnitude of the velocity of a charged particle is not affected by the presence of a magnetic field. However, the magnitudes of the velocity components perpendicular to B can vary, as can be shown for the cyclotron motion.
In this paper, for the first time, we implemented into the Gromacs package [7], one of the most used tools for MD simulations, a static homogeneous magnetic field. The core of the numerical solution solved by Gromacs has been modified to take into account the magnetic force acting on a charged particle and the results have been compared with the analytical expected behavior for the very simple case of an ion in vacuum.

2. Materials and Methods

Gromacs [7] is a versatile software, used in the for MD simulations, to study molecules behavior under different physical conditions.
To implement the magnetic field, we employed the Velocity Verlet (VV) algorithm proposed in [8], in which the Lorentz force acts on the charged particles, which perform Larmor oscillations at the Larmor frequency when an external magnetic field is applied. In [8] three different methods are reported to solve the motion equations when a static homogeneous external magnetic field is applied. Since we used in our simulations a time step sufficiently small, we adopted the inversion algorithm to solve the equations of positions and velocities, in which the strength of the magnetic field is dependent on the value of the time step.
Since Gromacs is not a software designed for the application of a magnetic field, the first part of our work has been to fully control atom velocities and positions update by the Verlet integration and how to introduce the magnetic field component.
Velocity Verlet [9] integration is a numerical method used to integrate Newton's equations of motion. In particular, in

the Gromacs code it has been implemented through the update at each time step of particle positions **r** and velocities **v** (eq. 2 and eq.3):

$$r(t + \Delta t) = r(t) + \Delta t v(t) + \frac{\Delta t^2}{2m} \boldsymbol{F}(t) \quad (2).$$

$$v(t + \Delta t) = v(t) + \frac{\Delta t}{2m} [\boldsymbol{F}(t) + \boldsymbol{F}(t + \Delta t)] \quad (3).$$

where $F=ma$ is the force applied, m the mass of the particles and Δt the time step used to perform the simulations. We applied the magnetic field in the z direction introducing the Lorentz force along the x and y axis for both positions and velocities equations (eq. 4 and eq. 5):

$$r(t + \Delta t) = r(t) + \Delta t v(t) + \frac{\Delta t^2}{2} [a^c(t) - \Omega e_z \times v(t)] \quad (4).$$

$$v(t + \Delta t) = v(t) + \frac{\Delta t}{2} [a^c(t) - \Omega e_z \times v(t) + a^c(t + \Delta t) - \Omega e_z \times v(t + \Delta t)] \quad (5).$$

where $e_z = (0, 0, 1)$ is the unit vector in the z direction, a^c represents the accelerations, which are independent from atom velocities and the Larmor frequency $\Omega = \frac{qB}{m}$, where B is the magnetic field intensity.

We performed MD simulations considering two different charged particles (Na^+ and Cl^-) in vacuum, to verify the cyclotron motion of the ions when an external magnetic field is applied. We used an NVT (number of particles, volume and temperature are constants) ensemble at a temperature of 300 K using the Nose-Hoover thermostat in a box of 15 x15 x 15 nm^3 of dimensions (Fig. 1). Due to the limit of the algorithm related to the time step ($\Omega\Delta t << 2\pi$) and the magnetic field intensity, we applied a magnetic field B = 10^5 T of intensity in order to be able to see the particle motion in the picosecond time scale with a time step ΔT = 0.1 fs, for a 35 ps of simulation. The initial velocity of the particle has been settled to v = 0.37 nm/ps with an angle $\theta = 1°$ with the respect to the magnetic field application.

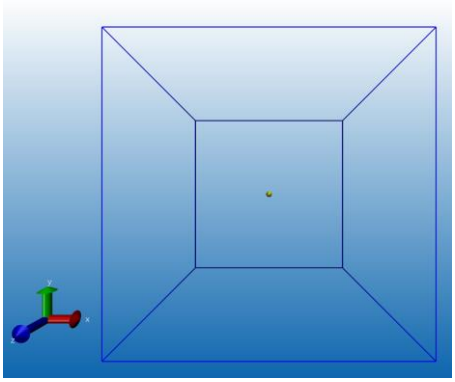

Figure 1. Molecular dynamics model of the Na^+/Cl^- ion in vacuum in a box of 15 x 15 x 15 nm^3.

3. Results and discussion

The first result is presented in terms of the displacement of the Na^+ ion due to the magnetic field. In order to validate our numerical results, an analytical model has been settled implementing the equations 4 and 5 to reproduce the Na^+ particle motion under a B field of 10^5 T of intensity. It is possible to notice in Figure 2a and 2b, how the analytical and numerical model match perfectly. The charged particle exploits a sinusoidal motion in the x and y direction during the MD simulation as predicted by the analytical formula with the same period of 14 ps.

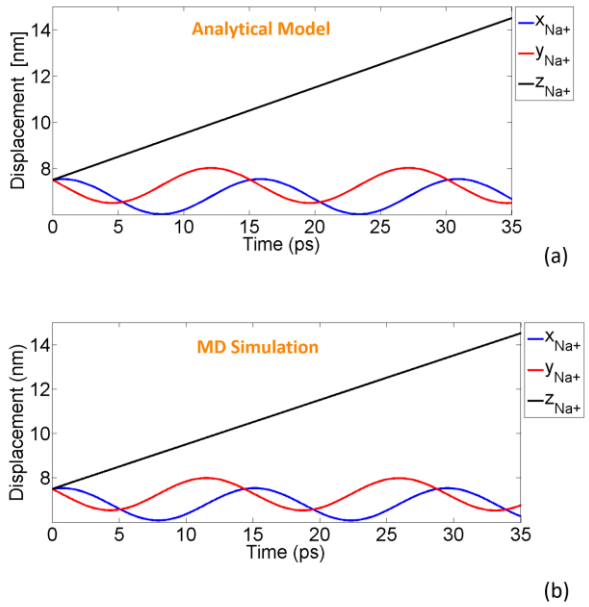

Figure 2. (a) analytical displacement of the Na+ ion in 35 ps; (b) displacement in the box volume of the Na+ charged particle along the three axis x, y and z in the time domain.

During the 35 ps of simulation, the charge particle Na^+ describes an ellipsoid (Fig.3) going in the z direction along the B field application. Due to the positive charge of the Na ion the motion is a clockwise (Fig.3).

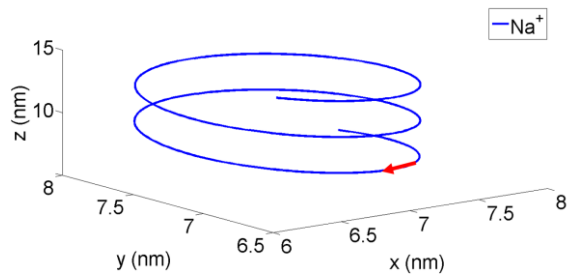

Figure 3. Clockwise motion of the Na^+ particle in the box volume (15 x 15 x 15 nm^3) moving along the z axis.

The period of the sinusoidal motion matches perfectly with the analytical period $T = 2\pi m/qB$ (table 1) considering the

sodium mass $m = 1.67^{-27}$x 23 *kg* and the charge $q = 1.6^{-19}$ C.

Table 1. Period Value T, the Radius of curvature and the pitch of the helix motion of the Na^+ and Cl^- ions.

	T (ps)		R (nm)		h (nm)	
	Na^+	Cl^-	Na^+	Cl^-	Na^+	Cl^-
Analytical	14	22.3	0.72	1	2.8	4.5
Numeric	14.45	22.3	0.73	1.1	2.9	4.5

Moreover, in Figure 4 the projection of the Na^+ motion in the *xy* plane is reported. By calculation the radius of curvature $R = mv/qB$, with the *x* and *y* velocity components ($v_x = 0.1$ *nm/ps and* v_y = - 0.03 nm/ps) results equal to 0.72 nm, perfectly matching with the one in Figure 4 obtained from our MD simulation.

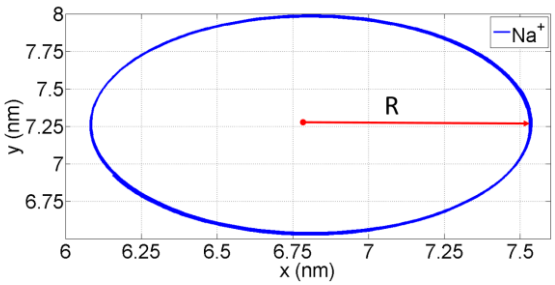

Figure 4. Na^+ motion projected in the *xy* plane perpendicular to the application of the magnetic field, R is the radius of curvature.

Moreover, we analytically calculated the pitch of the sinusoid (table 1), $h = Tv_z$, obtaining a value of 2.8 nm which is in according with the MD simulation as showed in Fig. 5.

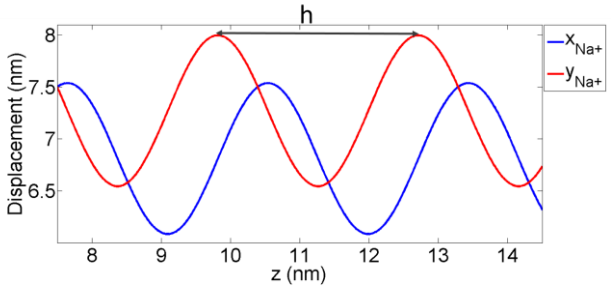

Figure 5. Na^+ motion projected in the *z* plane showing a pitch of the motion *h* equal to 2.9 nm.

The same study has been carried out also for the Cl^- particle with a period of the sinusoid T = 22.3 ps (data not showed) and a radius of curvature R = 1.1 nm in accordance to the analytical formula (table 1) considering the Cl^- mass $m = 1.67^{-27}$x 35.5 *kg*. In Figure 6 the Cl^- motion is reported in the box volume, it is possible to notice how due to the negative charge, the particle moves in a counterclockwise direction along the *z* axis starting from the center of the box.

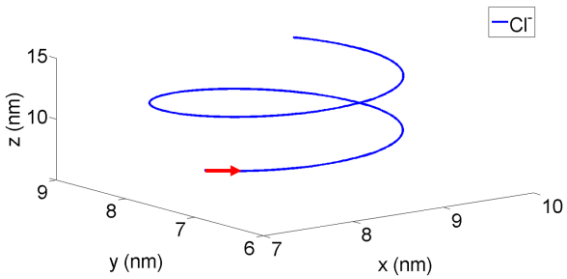

Figure 6. Counterclockwise motion of the Cl^- particle in

The complexity of the target will be increased addressing first the Na^+ ion hydrated with water and then well-known molecular systems as enzymes and relevant biochemical macromolecules. In particular Myoglobin and Superoxide Dismutase (SOD) (Fig.7), which have been already investigated by the authors in presence of electric fields [4, 10] will be investigated.

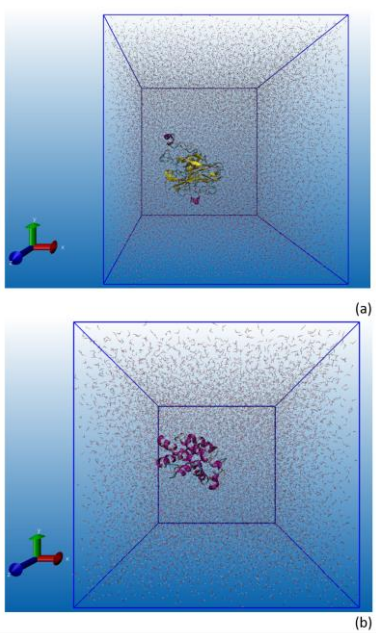

Figure 7. Superoxide dismutase, SOD (a) and myoglobin (b) molecular model, hydrated in a box of 10 x 11 x 9 nm^3 for the SOD and of 8 x 8 x 8 nm^3 for the myoglobin.

4. Conclusions

In this paper, for the first time, the implementation in the Gromacs software of a static external magnetic field by introducing the Lorentz force with the Larmor frequency component into the VV algorithm is presented.

We introduced in the update of velocity and positions the term of the Larmor frequency to insert a magnetic field applied in the *z* direction. The aim has been to give a first validation of our code by preliminary simulations of a charged particle in vacuum. We showed the displacement of a charged particle in a static magnetic field by reproducing the cyclotron motion of a positive or negative ion in vacuum. The results confirmed the expected

behavior of the magnetic field acting on the single particle, giving a first validation of the method implemented.
The future steps will be the study of complex systems as hydrated ion and well known proteins to understand the response of these molecular target to an external magnetic field.

5. References

1. M. Zhadin, F. Barnes, "Frequency and Amplitude Windows in the Combined Action of DC and Low Frequency AC Magnetic Fields on Ion Thermal Motion in a Macromolecule: Theoretical Analysis," *Bioelectromagnetics*, **26,** April 2005, pp. 323-330, doi: 10.1002/bem.20095.

2. D.J. Muehsam, A.A. Pilla, "A Lorentz Model for Weak Magnetic Field Bioeffects: Part I Thermal Noise Is an Essential Component of AC/DC Effects on Bound IonTrajectory," *Bioelectromagnetics*, **30**, September 2009, pp. 462-475, doi:10.1002/bem.20494.

3. M. Casciola, D. Bonhenry, M. Liberti, F. Apollonio, M. Tarek, "A molecular dynamic study of cholesterol rich lipid membranes: Comparison of electroporation protocols," *Bioelectrochemistry*, **100**, December 2014, pp. 11-17, doi:10.1016/j.bioelechem.2014.03.009.

4. P. Marracino, F. Apollonio, M. Liberti, G. D'Inzeo, A. Amadei, "Effect of high exogenous electric pulses on protein conformation: Myoglobin as a case study,"*Journal of Physical Chemistry B*, **117 (8)**,January 2013, pp. 2273-2279, doi: 10.1021/jp309857b

5. F. Apollonio, M. Liberti, A. Amadei, M. Aschi, M. Pellegrino, M. D'Alessandro, M. D'Abramo, A. Di Nola, G. D'Inzeo, "Mixed quantum-classical methods for molecular simulations of biochemical reactions with microwave fields: The case study of myoglobin," *IEEE Transactions on Microwave Theory and Techniques*, **56 (11)**, November 2008, pp. 2511-2519, doi:10.1109/TMTT.2008.2005890.

6. N.J. English, C.J. Waldron, "Perspectives on external electric fields in molecular simulation: Progress, prospects and challenges," *Physical Chemistry Chemical Physics*, **17 (19)**, May 2015, pp. 12407-12440, doi: 10.1039/c5cp00629e.

7. D. Van Der Spoel, E. Lindahl, B. Hess, G. Groenhof, A.E. Mark, H.J. Berendsen, "GROMACS: Fast, Flexible, and Free", *J. Comput. Chem.*, **26,** October 2005, pp. 1701−1718, doi:10.1002/jcc.20291.

8. Q. Spreiter, M. Walter, "Classical Molecular Dynamics Simulation with the Velocity Verlet Algorithm at Strong External Magnetic fields", *J. Comput. Phys.*, **152**, February 1999, pp. 102-119, doi:10.1006/jcph.1999.6237

9. W. C. Swope, H.C. Andersen, P.H. Berens, K.R. Wilson, "A computer-simulation method for the calculation of equilibrium-constants for the formation of physical clusters of molecules: Application to small water clusters", *J.Chem.Phys*, **76**, 1982, pp. 637–649, doi:10.1063/1.442716.

10. P. Marracino, M. Migliorati, A. Paffi, M. Liberti, A. Denzi, G. D'Inzeo, F. Apollonio, "Signal transduction on enzymes: The Effect of electromagnetic field stimuli on superoxide dismutase (SOD)," *Proceedings of the Annual International Conference of the IEEE Engineering in Medicine and Biology Society, EMBS,* art. no**. 6347282**, November 2012, pp. 5674-5677, doi:10.1109/EMBC.2012.6347282