On the other hand, living organisms arguably employ radically different computing concepts that leverage the physics of biological materials. For example, self-organization, self-repair, and self-reproduction are commonly found in biological systems but are difficult to achieve with conventional computing systems. New computing paradigms, such as cellular automata, neural networks, and evolutionary computing, may provide clues to utilize the complexity of molecular dynamics for information processing.

Molecular computing devices are not likely to compete with and replace conventional computing technology. Rather, they are complementary approaches to silicon-based systems, and a hybrid system which incorporates molecular devices into artificial systems would find potential application domains in, for example, medical and environmental applications. It is, thus, expected that molecular computing will be one of the important technologies, together with other technologies such as synthetic biology, in the age of biomolecular nanotechnology.

Cross-References

- ▶ Computational Systems Bioinformatics for RNAi
- ▶ Nanotechnology Applications in Polymerase Chain Reaction (PCR)
- ▶ Self-Assembly
- ▶ Synthetic Biology

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Molecular Dynamics Method

▶ Computational Study of Nanomaterials: From Large-Scale Atomistic Simulations to Mesoscopic Modeling

Molecular Dynamics Simulations of Interactions Between Biological Molecules and Nanomaterials

▶ Molecular Dynamics Simulations of Nano-Bio Materials

Molecular Dynamics Simulations of Nano-Bio Materials

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Synonyms

Molecular dynamics simulations of interactions between biological molecules and nanomaterials

Definitions

Nano-bio materials are materials that are composed of biomolecules (protein, DNA, RNA, lipids) and nanoscale materials (nanoparticles, nanotubes, nanocrystals).

Molecular dynamics simulation is a computer simulation technique that is based on integration of Newton's equations of motion and reflects physical movements of atoms and molecules.

Overview

Introduction

Nanotechnology has received increasing public attention as more and more practical applications of nanoparticles and nanomaterials are emerging, especially in the biomedical field. For example, inorganic nanoparticles (NPs) functionalized with synthetic or biological molecules have been used in a broad range of biomedical applications, including imaging, diagnostics, and drug delivery. The advantage of using NPs in biomedical applications is that a single nanoparticle can simultaneously carry imaging probes, drug molecules, receptor-binding molecules, and antibodies on the surface, which promise the most efficient drug delivery platform and detection scheme. However, interactions of NPs with biological molecules may lead to structural and functional changes, which in turn may result in unexpected biological reactions and toxicity. For example, it has been shown that metallic NPs, quantum dots, and carbon nanotubes can translocate to the brain from different entry points, such as skin, blood, and respiratory pathways.

Moreover, the properties of NPs, such as size, shape, hydrophobicity, charge density, and chemical composition, can directly influence the ability of NPs to enter the cellular environment, bind to proteins, activate receptors, and translocate and accumulate in target tissues, as depicted in Fig. 1. Biological molecules can also be used as scaffolds for precise deposition of NPs for electronic and optical devices. However, the effect of nanomaterials on the biomolecular structure and function is not yet elucidated, which limits advancements within the potential applications and the development of new ones. A better understanding of the biological effects of NPs requires knowledge of the mechanisms of interactions between NPs and biomolecules.

Computer simulations can yield a wealth of insights on interfacial dynamics, structures of ligands, electrostatics, and binding of biomolecules. One of the most promising and rigorous methods for simulating complex and large-scale processes in various materials and biosystems is molecular dynamics (MD) simulations. MD simulations have been used for gaining comprehensive information on "nano-bio" systems, including ligand dynamics on NPs, conformational transitions of biomolecules, protein and ligand binding, enzymatic catalysis, and the dynamic, thermodynamic, and mechanical properties at different spatial and temporal resolutions [20]. Thus, MD simulations are a natural complement to experimental techniques at the nanoscale to yield insight on molecular interactions involved in nanoparticle–biomolecule binding and mechanisms of molecular recognition.

Overview of Molecular Dynamics Simulations

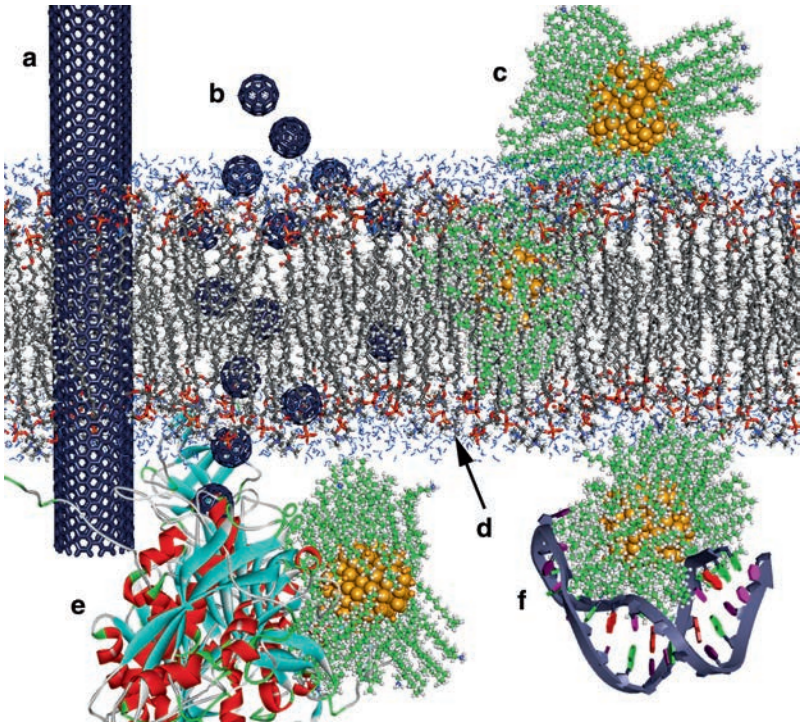
The steps of an MD simulation are given in Fig. 2. First, the initial system is built; coordinates of some specific biological molecules can be obtained from databases such as the Protein Data Bank [1], while others must be developed using in-house scripts. The initial velocities are assigned from a Boltzmann distribution at the desired temperature. The force field parameters for all of the components are assigned. The system is then evolved with Newton's equations of motion for each Δt, which provides new positions and velocities for each atom.

The potential energy of the system is calculated from force field parameters, which are comprised of both the bonded and nonbonded interactions. The bonded interactions include bond lengths, angles, and dihedrals, whereas the nonbonded terms are mainly electrostatics and van der Waals. The total potential energy can then be defined by the following equation:

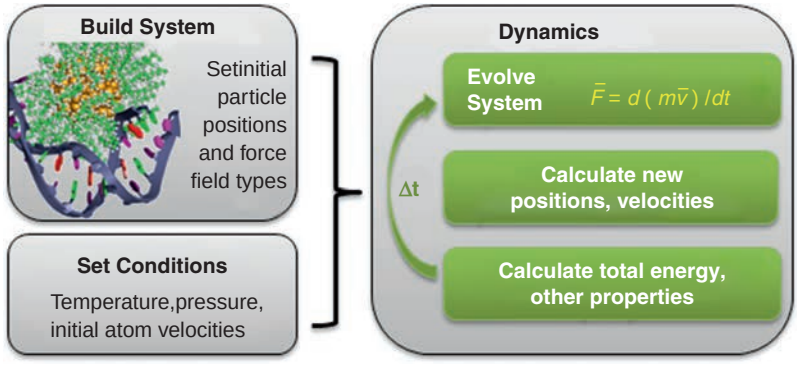
$$U = \sum_{\text{bonds}} k1(r - r_{eq})^2 + \sum_{\text{angles}} k2(\phi - \phi_{eq})^2 + \sum_{\text{dihedrals}} \frac{Vn}{2}(1 + \cos(n\varphi - \gamma)) + \sum_{\text{nonbonded}} \left[4\epsilon_{ij} \left(\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} + \left(\frac{\sigma_{ij}}{r_{ij}} \right)^{6} \right) + \frac{q_i\, q_j}{\epsilon r_{ij}} \right],$$

where r_{eq} and ϕ_{eq} are equilibration structural parameters, $k1$, $k2$, and Vn are force constants, n is dihedral multiplicity, and γ is phase angle for torsional angle parameters.

The choice of a force field is dependent on the chemical composition of the system and the molecules



Molecular Dynamics Simulations of Nano-Bio Materials, Fig. 1 Atomistic view of the interactions of different types of nanoparticles, (**a**) carbon nanotubes, (**b**) buckyballs (fullerenes), and (**c**) gold nanoparticles, with biological molecules, (**d**) a lipid membrane, (**e**) a protein, and (**f**) nucleic acids



Molecular Dynamics Simulations of Nano-Bio Materials, Fig. 2 The main components of an MD simulation

under study, and thus dictate the reliability of the results. A recent review outlines the comparison between most widely used protein force fields [2]. For example, the CHARMM27 [3] force field can be used to simulate DNA, RNA, and lipids, while for CHARMM22 [4] force field is parameterized to simulate proteins. The AMBER program contains force field parameters for DNA, RNA, and proteins (Cornell force field [5]); small molecular ligands (GAFF force field [6]); and carbohydrates (GLYCAM force field [7]). Other all-atom force fields include OPLS [8], which contains parameters for proteins, carbohydrates, and nucleic acids. United atom models such as GROMOS [9] are also available that treat nonpolar hydrogens implicitly, which is commonly done for lipid membranes. The challenge, however, for bio-nano systems is that there is no generalized force field for metallic, carbon, and complex NPs and coarse-grained representations of the molecules, and thus the parameters are calculated on a case-by-case basis. In addition, all-atom MD simulations are not possible for some systems of interest and thus some level of coarse-graining is required, which necessitates a whole new set of force field parameters. An example of a commonly used coarse-grained force field for bio-nano systems is MARTINI [10].

Solvent molecules are often included in the simulation. The most complex solvent is water, and a variety of water models have been developed; the most commonly used models are SPC, TIP3P, and TIP4P. Explicit solvent simulations are the most accurate and can provide information on specific solvent–nanoparticle or solvent–biomolecule interactions; however, they are more computationally extensive since significantly more atoms are being included in the simulations. MD simulations can be significantly accelerated by treating the solvent with continuum dielectric methods. In this case, only the intrasolute electrostatics need to be evaluated. Even though implicit MD simulations are less accurate than simulations with explicit solvent, they permit not only much longer simulations and larger molecules but also provide a variety of sampled conformations.

The time length of simulations is typically based on the type of processes under study and must ensure that a sufficient amount of phase space is sampled. Typically, to observe any significant conformational change of biological molecules, the simulations time needs to be on the order of hundreds of nanoseconds. A useful measure of the accuracy of a simulation is the total energy of the system, which means that typically throughout the simulations, the total energy should not increase. The size of deviations of the total energy gives the measure of precision of the integration. The accuracy of the integration procedure depends on the value of the time step. For the simulations to be as long as possible, the time step needs to be chosen as large as possible. However, the maximum time step is limited by the highest frequency motions in the system, which is typically on the order of a femtosecond.

Advantages and Limitations

The challenges in using an MD description of complex nano-biosystems are the severe limitations of time and length scales, limited to several hundreds of nanoseconds, and moderately sized biomolecules and NPs. However, as computer speed and memory increase, so do the simulation time and size limits. For example, for all-atom simulations the reasonable simulation time 10 years ago was on the order of 1 ns, but now about100 ns time length can be obtained for the same size of a system. The main advantage of an MD simulation is that only details of the microscopic interactions need to be specified and no assumptions are made about the character of the processes under investigation. Moreover, the MD simulation method is capable of providing a complete microscopic description of the dynamical processes involved.

Most importantly, the reliability of MD simulations depends on accurate force fields for all system components. The classical MD simulation method also prevents study of processes like proton transfer, tunneling effects, zero-point motions, behavior of electrons and atomic nuclei, and making/breaking chemical bonds. Problems like these require modeling that applies the laws of quantum mechanics, the fundamental physics equations that describe electrons. However, because of the complex nature of the equations, these models can handle only a few atoms at a time. Some efforts are underway to create force fields that overcome these barriers. Considerable improvements in force fields have also been achieved, making simulations more reliable and accurate.

Application of MD Simulations to Study Nano-Biosystems

In the subsequent sections, an overview of utilizing MD simulations for investigations of a variety of properties of nano-biosystems is provided. Figure 1 summarizes the types of systems that are included in this entry and specific simulation conditions for five simulations highlighted here are summarized in Table 1. The overview begins with carbon nanoparticles, which are the most actively and successfully used systems for simulations of nanomaterials. Then, the application of MD technique to other nano-biosystems, such as functionalized gold nanoparticles, will be addressed. The focus is on the interactions of these nanoparticles with lipids, proteins, and nucleic acids that have been investigated with MD simulations are then summarized.

Interactions of Carbon NPs with Biological Molecules

The most common type of carbon NPs are fullerenes or buckyballs (Fig. 1b) and carbon nanotubes (Fig. 1a). Both of these carbon NPs are important in many technologically relevant areas due to their unique properties. Buckyballs have potential as drug delivery mechanisms and medical diagnostic devices because of their size, spherical shape, stability, and the ability to be functionalized with other atoms; however, their hydrophobic character is a drawback to some medical applications.

Molecular Dynamics Simulations of Nano-Bio Materials, Table 1 Summary of the simulations highlighted in this work

	CNT-protein nanobiosensor [11]	C60-potassium channel [12]	NP-membrane [13]	NP-protein [14]	NP-DNA [15]
Level of MD	All-atom	All-atom for C60, proteins; united atoms for lipids	Coarse-grained	Coarse-grained NP; all-atom protein	All-atom
Software	Gromacs	NAMD	Gromacs	CHARMM	NAMD
Force field	Amber99	CHARMM27	Martini	Param22	CHARMM
Electrostatics	Particle mesh Ewald	Particle mesh Ewald	Particle mesh Ewald	Generalized Born and explicit solvent	Particle mesh Ewald
Ensemble	NPT (1 atm., 300 K)	NPT (1 atm., 300 K)	NPT (1 bar, 305 K)	Constant T (300 K, 450 K)	NVT (300 K)
Solvent	TIP3P water + 0.1 M NaCl	TIP3P water	water	TIP3P water	TIP3P + 0.5 M NaCl
Time step (fs)	1.5	2	20	2	2
Simulation time (ns)	10.14–11.25	10–213	60	8	8
Number of atoms	8,200–40,338	90,300–173,000	~65,000	~7,000	~32,000

Carbon nanotubes (CNTs) have unique mechanical and electrical properties, as well as strong chemical reactivity due to their high surface area. Their large diameter-to-length ratio provides unique applications, such as microcatheter reinforcements for tissue engineering scaffolds. CNTs can have an impact on biomolecules by enhancing their electrochemical reactivity and promoting protein electron transfer. They are very attractive materials for the design of electrochemical biosensors ranging from an amperometric enzyme electrode to DNA hybridization biosensors. For example, a CNT-based sensor has been developed for detection of hepatitis B virus (HBV), which enables a diagnostic application for nontreated human blood.

A significant amount of MD simulations at various levels of detail have been employed to explore the interactions of CNTs and buckyballs with lipids, proteins, and nucleic acids [16–18]. These simulations have revealed the physicochemical details for a variety of applications. Such focus areas include potential mechanisms for toxicity of carbon nanoparticles and the design of engineering devices such as sensors, drug delivery vehicles, and actuators. Factors for the carbon NPs that were studied include diameter size, structural alignments, aromaticity, nanoparticle curvature, degree of hydrophobicity, and the local environment. Two recent exemplary articles are summarized next.

MD Simulations of a Carbon NP Nanobiosensor

A nanobiosensor has been shown experimentally to be a feasible device for detecting adenovirus proteins, particularly the Knob proteins. This nanodevice is comprised of a single-walled CNT that is functionalized with the coxsackie-adenovirus receptor (CAR) protein. However, many questions remain about the system, including how structural rearrangements and dynamics may impact its efficiency, as well as the specificity of CAR when bound to the CNT outside its native environment. Johnson and coworkers [11] recently performed MD simulations on this nanobiosensor system to provide some molecular insights into these questions. They investigated three different types of systems in its physiological aqueous conditions CAR with a bound Knob protein, and then both systems attached to a CNT. The physiological conditions were created by adding a 100 mM concentration of Na^+ and Cl^- ions to the aqueous system comprised of TIP3P water molecules; an additional three Na^+ ions were added to also neutralize the slightly negative charge on CAR. The CNT was covalently attached to residue Asn98 on CAR through a carboxylic acid defect on the CNT surface, which replicates the experimental conditions that are done via diimide-activated amidation.

The systems were built from a crystal structure of the CAR-Knob complex from the Protein Data Bank. Since CAR is known to only undergo minor structural

rearrangements upon binding Knob, this crystal structure was claimed by the authors to be sufficient for both the bound and unbound configurations, after the structural properties were equilibrated from an MD run; structural equilibrium was defined as when the root-mean-square-deviation of the C_α atoms no longer varied with time. The CNT was built the same length as the MD box, connecting terminal atoms across that box boundary, thus creating an infinite tube with the use of periodic boundary conditions. In addition, the positions of the CNT atoms were constrained with a harmonic potential, which reduces the computational cost of the simulations with minimal effect on the results. The atomistic MD simulations were run with a 1.5 fs time step, for around 11 ns, and with the NPT ensemble at 1 atm and constant temperature of 300 K.

The use of the Amber99 force field was first validated by comparing the simulations on the systems without the CNT in the physiological aqueous environment to known experimental information, such as NMR observations of the structural and dynamical properties of CAR. For the MD simulations of the systems with the CNT present, some interesting observations were made. First, for the systems with the CNT, physisorption of the proteins onto the CNT surface was observed, which still preserved most of the structural features of the unbound CAR and unbound CAR-Knob; the most significant changes occurred in the loop regions and C-terminus since the CNT can restrict the configurational space of the bound proteins. In addition, for the CAR-Knob-CNT complex, a salt bridge and some hydrogen bonds were lost between the proteins, but not enough to impact its overall stability. Therefore, it was concluded that the CNT does not significantly perturb CAR, except for reducing the available configurational space due to confinement. These results indicate that comprised of protein receptors that rely on large conformational changes as part of their mechanisms could be significant.

MD Simulations of C60 Embedded in Potassium Channels

Potassium (K^+) channels are ion channels that span the cell membrane and are selective for K^+. They control a wide variety of cell functions that are involved in biological processes such as nerve impulses, or smooth muscle contraction. The selectivity is due to the so-called selectivity filter, which is a highly conserved sequence. K^+ channels are also targets for a variety of pore-blocking toxins that (1) bind to the extracellular pore entrance and prevent ion conduction; or (2) permeate the pore channel and disrupt binding sites within the pore. Since studies have indicated that fullerenes can cross the lipid membranes of cells, it is expected that they could also impact K^+ channels.

Kraszewski and coworkers [12] recently performed extensive MD simulations to investigate molecular aspects of how K^+ channels are impacted by the presence of the C60 buckyball. They investigated three different types of channels, specifically those comprised of the proteins KcsA, MthK, and Kv1.2 embedded into a fully hydrated DOPC lipid bilayer, which included water molecules and counter ions to neutralize the overall system charge. The total system sizes ranged from 90,300 (KcsA) to about 173,000 atoms (Kv1.2). Up to six C60 molecules were put near the pore region. As a comparison, systems were built of the C60 molecules in a water box and with a fully hydrated DOPC layer without the proteins. The atomistic MD simulations were run with the NAMD software program, using the CHARMM27 force field, where united atoms were used to represent the lipid molecules and chemical bonds between hydrogen and heavy atoms were constrained to their equilibrium values elsewhere.

The C_{60} molecules were first put near the pore on the extracellular region. The MD simulations revealed that no C_{60} molecules anchor or block the selectivity filter of the K^+ channels. In addition, for the voltage-gated K^+ channel, Kv1.2, the C_{60} molecules bound to residues within the voltage sensor domain, which triggered a large conformational movement. When the C_{60} molecules were put near the pore on the intracellular region, a different behavior was observed. Quick binding of the C_{60} molecules was observed, which resulted in conformational changes that plugged the ionic conduction pathway. Finally, when the C_{60} molecules were placed within the membrane core, the C_{60} molecules were observed to migrate laterally toward the membrane proteins, and eventually bind to interhelical domains, which can alter their function. Therefore, these simulations revealed a variety of potential molecular mechanisms for binding of C_{60} nanoparticles, depending on the structure and properties of the channel as well as the initial locations of the nanoparticles.

Interactions of Functionalized Nanoparticles with Biological Molecules

Ligand-protected nanoparticles (Fig. 1c) consists of metallic nanocrystals coated by a monolayer of thiolated molecules. The ligands control the specific properties of the nanoparticle, such as solubility, electro-optical and catalytic behavior. Such nanoparticles can be dispersed in various solvents without irreversible aggregation. Functionalized NPs are a much more challenging case for simulations and modeling than carbon NPs due to their complexity, overall size, and features at multiple length and time-scales. In addition, not only are functionalized NPs composed of various organic and inorganic components, but the nanoparticle corona of functionalized ligands is also a dynamic entity by itself. However, MD simulations have been performed to elucidate details about the structure and dynamics of these complex NPs. Recent atomistic MD simulations of NPs functionalized with alkanethiol ligands provided atomistic data on the ligand shell organization and indicated that the ligand's tilt angle is affected by solvent, temperature, nanoparticle size, and the ligand tail length [19, 20].

The complexity of ligand behavior, recognition, dynamic interactions, and assembly between ligand functionalized NPs and biomolecules is not trivial to simulate and challenges the current limits of the MD simulation techniques. To date, most of the simulations that address the interactions between functionalized NP and biological molecules (proteins, ligands, and nucleic acids) have a simplified representation of the nanoparticle and a few simulations have explicit ligands represented via a united-atom approximation, which have provided insights into their biorecognition properties.

A few such studies are summarized next.

Functionalized NPs with Lipids

Properties of functionalized NPs, such as size and type of ligands, can directly control the ability of a NP to enter the cell. The properties that control the NP uptake in cells can cause cellular response and undesirable toxic effects and can also control the performance of NPs in imaging, biosensing, and drug delivery. An understanding of the processes controlling the uptake and accumulations of the NPs by the cell is important for NP design, assessment of nanoparticle toxicity, and improvement of the NP properties for use in imaging and drug delivery applications. However, the rules of uptake kinetics have not yet been determined. In order to gain a deep understanding of NP translocation through a membrane, a complete picture of the processes at the molecular level is needed, which can be delivered through MD simulations. To the best of our knowledge, only coarse-grained MD simulations of NP interactions with the membrane have been used. The advantage of the coarse-grained representation of lipids and NPs is the ability to use larger time and size scales at the expense of observing the intricate behavior of H-bonding network formation and the atomic interactions.

Lin and coworkers [13] recently performed coarse-grained MD simulations of penetration of lipid membrane by gold nanoparticles. They investigated two kinds of lipids, DPPC and DPPG, and NPs with alkyl thiol chains that can contain two different functional group, ammonium and carboxylate, using GROMACS 3.3.2 package [9]. The coarse-grained representation of NPs and lipids was compatible with the MARTINI force field [10]. The gold NP was 2.2 nm in diameter functionalized with 104 alkyl thiol ligands. The NPs were charged with 70% cationic or anionic coverage represented by the charge on the end functional ligand group and both electronegative and electroneutral bilayers were examined. The coarse-grained force field for the NP was parameterized to represent experimental values of the radius of gyration, the diffusion coefficient, and the average carbon distance. The membrane bilayer was composed of 1,152 coarse-grained lipids in a periodic box filled with explicit water and ions. The initial placement of NPs was chosen to be 7 nm above the bilayer center. The system was carefully equilibrated for a cumulative time of 20 ns before the production run of 40 ns was performed with a 20 fs time step.

The simulations revealed that NP charge and surface change density (electrostatic interactions) control the ability of the NP to penetrate, adhere, or repel from the lipid bilayer. Interestingly, NP penetration into the lipid bilayer causes lipid disarrangement and formation of a hydrophilic pore that can transport water molecules. The extent of membrane disruption was determined to depend on the NP charge density. Thus, the simulations indicate that control over the NP cellular uptake can be achieved through charge density of the functional groups.

Functionalized NPs with Proteins

The effect of protein interactions with various NPs and nanomaterials can shed light on their possible toxicity and aggregation behavior linked to some neurological disorders. The interface, which is composed of covalent or secondary bonding interactions between NPs and proteins, is highly complex. The properties of this interface may largely affect the protein structure and function. Only a few MD studies were devoted to study protein–NP interactions.

Simulations by Aubin-Tam and coworkers [14] were performed on nanoparticle–protein conjugates comprised of Cyt c from *Saccharomyces cerevisiae* to understand the effect of the NP ligand on protein structure. The NP was modeled as a dummy atom that is 1.5 nm in diameter with Lennard Jones parameters. A total of 21 bathophenanthroline disulfonate (BPS) ligands were uniformly distributed on its surface. The coordinates for the Cyt c protein structure was obtained from the PDB databank (PDB id 2BCN), mutated and covalently linked to the NP surface. MD simulations were performed for 8 ns at 300 and 450 K using CHARMM and param22 all-atom force-fields and the generalized Born implicit solvent. Simulations were also performed in explicit solvent to verify the results in implicit solvent.

MD simulations of Au nanoparticle/Cyt C conjugates indicated that NP labeling induces site-specific, local-to-global structural perturbations to the protein [14]. Protein conformations obtained at 300 and 450 K showed that side chains of positively charged residues interact with BPS ligands, and that perturbation of the secondary structures depends on the NP attachment site, which agrees well with the experimental observations. MD simulations of the semi-rigid, coarse-grained protein/nanoparticle model revealed the importance of lysine and arginine amino acids on the interactions of Cyt C and nanostructured surfaces, which suggest the design rules for peptides with enhanced surface adsorption [21, 22]. Thus, MD simulations can be successfully employed for identifying mechanisms responsible for fine tuning of the biorecognition properties of the nanocomplex, and more detailed investigations are needed in this area.

Functionalized NPs with Nucleic Acids

MD studies have been successful at corroborating and elucidating experimental findings, or exploring fundamental aspects of DNA dynamics and structure [23]. For example, MD simulations were applied to a 12-base-pair DNA duplex tethered on a neutral silica surface to assess its structural and orientation changes [24]. MD simulations were used to study the conformation of seven DNA strands attached to the (111) gold surface via a six-carbon alkylthiolate linker [25]. These simulations indicated that while the overall structure is disordered, both base stacking and non-Watson-Crick base pairing can be formed between short single-stranded regions of adjacent DNAs. Moreover, the separation distance between DNAs is similar to one calculated by theory and estimated from experiments.

MD simulations of a 2-nm gold nanoparticle functionalized with four single-stranded DNA molecules were used to determine the structure and dynamics of DNA thiolates on a gold surface [15]. The 10-mer of ssDNA polythymines and poly adenines were symmetrically distributed on four (111) gold surfaces of an NP. The interactions between gold atoms were represented by Lennard Jones parameters, and the CHARMM force field was used for the ssDNAs. The resultant DNA-functionalized NP structure was placed in a box with water and 0.5 M NaCl. After equilibration, the NVT Langevin production simulations were carried out using NAMD at 300 K for 8 ns. The results indicated that base–base stacking is better for poly adenines than for poly thymines and the effective radius of DNA-NPs agrees well with experiment. Thus, the MD simulations provided an insight onto the dynamics of DNA strands on the gold NP surface.

In addition, atomistic MD was used to study the behavior of the DNA strands during the assembly of layer-by-layer DNA capsules, which produced a prediction of the optimal length for the NP assembly [26]. Thus, MD simulations were able to provide important information on the behavior of DNA strands on the surface of the NPs; however, the DNA-driven assembly is outside of the reach for atomistic MD simulations. A recent coarse-grained model [27] of DNA-driven NP assembly indicated the possibility to explain the DNA-induced crystallization of NPs and established a general phase diagram.

Summary and Future Directions

The future development of many biomedical devices and the optimization of current systems are dependent on the fundamental knowledge of properties of the interface between NPs and biomolecules. MD simulations are capable of producing such fundamental

knowledge, but on limited time and length scales. While the interactions of carbon-nanostructures are significantly explored by MD simulation techniques, the use of MD simulations for other systems such as colloidal gold and magnetic and inorganic nanoparticles is not covered as much. With the increase in computational power and improvements of algorithms, as well as the development of new hardware systems such as GPU systems, it is expected that more MD simulations will be used for detailed studies of interactions between biomolecules and NPs.

Further work is needed on the understanding of interactions between nanomaterials and biomolecules, such as on the surface of inorganic and organic nanoparticles and nanofilms. The investigations at the atomistic and molecular levels will provide information on collective biomolecular behavior and change in properties and will ultimately enable access to new and valuable future applications.

Cross-References

- ▶ Ab Initio DFT Simulations of Nanostructures
- ▶ Computational Study of Nanomaterials: from Large-Scale Atomistic Simulations to Mesoscopic Modeling

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Molecular Encapsulation

► Nanoencapsulation

Molecular Layer Deposition (MLD)

► Atomic Layer Deposition

Molecular Modeling on Artificial Molecular Motors

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Synonyms

Catalytic bimetallic nanorods; Catalytic Janus particle; Nanomotors

Definition

Molecular motors are nanoscale objects capable of converting a certain energy source (chemical energy, photons, etc.) to mechanical work.

Background

One universal driving force for nanotechnology is miniaturization. The realization of nanometer scaled machineries needs nanometer scaled motors to provide mechanical power for nanofluidic and nanorobotic devices. Another underlying theme for nanotechnology is biomimetic. The fascinating biological world, as optimized by billions of years of evolution, provides answers of science and engineering challenges. In this regard, biomolecular motors play important roles in almost all important physiological processes in a cell, including transportation, actuation, nanostructure assembly, and disassembly. All the aforementioned functionalities are performed at the nanometer scale, thus molecular motors are important enablers in nanotechnologies inspired by biology.

Molecular motors can be classified as active nanostructures (capable of energy conversion or structural transformation upon a local stimuli), as opposed to passive nanostructures (usually operate within a bulk and are not designed to function upon local stimuli). According to Roco's classification, molecular motors belong to the second generation of nanotechnology applications and will play an important role in the third generation (nanosystems) [1].

Survey of Experiments

Artificial molecular motors have been fabricated with supramolecules [2], metal nanocrystal, [3] or magnetic colloidal chains [4]. The operation of these motors is mostly powered by an external agitation such as light, an electric/magnetic field, or oscillating chemical concentration. Therefore, unlike biomolecular motors, the motions of the above artificial motors are not strictly autonomous. Recently, it has been shown that catalytic bimetallic nanorods (illustrated in Fig. 1) exhibit interesting self-propelled motion in hydrogen peroxide solutions [5, 6]. Interestingly, these nanorods have comparable size, speed, and energy source (catalytic chemical reactions) to bacteria.