

New hybrid materials: multiscale modeling of the organic-inorganic interaction

Abstract

A new frontier in Materials Science is represented by the design of new materials which exhibits user-selected physical and chemical properties. New materials for micro and opto electronics, for instance, are mostly derived by complex biological molecules (DNA portions, polymers, peptides etc). Aside to the problem of selecting the biomolecular region with given properties and functions, a major technological problem is represented by the adhesion of these molecules onto inorganic supports (needed for the engineering of solid-state devices). Modeling this new class of organic-inorganic systems is a challenging task for theoretical analysis. However, there is still a lack of basic knowledges of the interaction at the atomic level between inorganic and biological objects. At this respect, the availability of high performance computing platforms, coupled with sophisticated numerical approaches, can play a key role in providing a detailed description of what happens at the atomic level when these materials interact. Multi-scale Molecular Dynamics simulations coupled with optimization methods can provide a preliminar qualitative description of these new materials in terms of atomic configuration, total energy and electronic structures.

Introduction

The pioneering work of Brown [1] and Belcher and co-workers [2], showed that it is experimentally possible to identify, out of billions of possibilities, peptides sequences that could specifically bind to one inorganic material. These studies, on the one hand, opened the way to use peptide sequence for recognizing inorganic materials, on the other hand to use biomolecules as building blocks in nanotechnology with applications in photonics, electronics, catalysis, sensing and energy storage. In order to interpret experimental data and to model possible binding of peptides onto inorganic surfaces, theoretical tools are needed. While simulations with model potentials give the possibility to select a small number of stable binding configurations, only ab-initio electronic structure calculations and molecular dynamics can give qualitative and, in some cases, quantitative information on the physical and chemical properties of these materials. We have set up the following workflow:

a peptide with an all β -strand conformation and with the desired amino acid sequence is built by using the ArgusLab package. The β -strand secondary structure corresponds to that of a completely unfolded peptide with side chains in a fully extended conformation; the folding of such polypeptide chain is performed by classical Molecular Dynamics to attain the putative conformation of the molecule in water;

the resulting equilibrium configuration of the folded peptide is then docked to both a graphene sheet and a single wall nanotube (SWNT); the system composed by the peptide AND the inorganic substrate are then relaxed, at finite temperatures, by using the CPMD (Car-Parrinello Molecular Dynamics) package. This method allows to find the ground state configuration by finding the total energy by expanding the hamiltonian and the electron wavefunctions of the system in a plane wave basis and then by solving the quantum equations of motion. CPMD and all the code run in the ENEA Grid environment.

Fig. 1: The peptide in a fully extended conformation was constructed through the ArgusLab program by consecutive addition of the amino acids in a β -strand conformation. The peptide was prepared for the folding simulation solvating the molecule in a cubic periodic box of 7.0 nm of side with @ 11336 water molecules and adding 1 Cl⁻ counter-ion to neutralize the total box charge. The system was initially energy-minimized by 1500 steps of steepest descent with a tolerance of 15 kJ mol⁻¹ nm⁻¹ and then equilibrated by 100 ps of MD at the temperature of 300 K with position restraints on the peptide heavy atoms. This simulation was performed 10 ns with a time-step of 0.002 ps. All bond lengths were constrained with the LINCS algorithm. Starting atomic velocities were derived from a Maxwellian distribution at the selected initial temperature. The MD simulation was performed with the GROMACS software package. The trajectory was analysed with GROMACS tools. This part of the simulation has required about 1 month on a last generation processor.

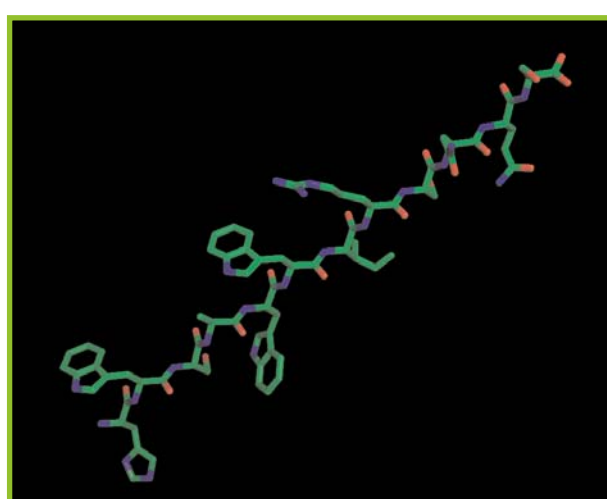


Fig. 2: The peptide converged after 5 ns of simulation in water and maintained the same structure during the remaining 5 ns. The folded conformation was stabilized by several hydrogen bonds between the His-1 at N-terminal and the last 4 residues at the C-terminal.

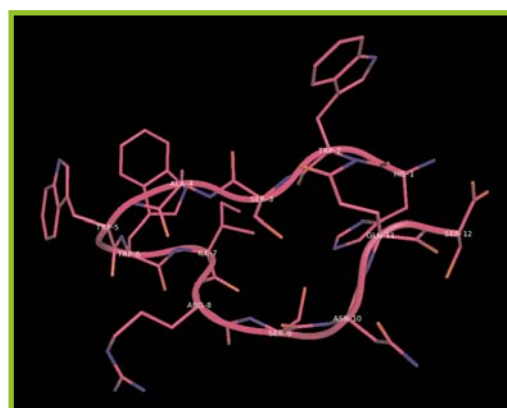


Fig. 3:

The MD derived peptide was docked to a graphene sheet by using the program AutoDock which implements a Genetic Algorithm (GA). Both the molecule and the graphene sheet were considered as rigid bodies. The peptide was centred in a cubic box of about 4.8 nm of side and a grid spacing of 0.803 Å. The ligand, i.e. the graphene sheet, was placed outside the box at a random distance as starting position for the docking to the peptide. A total of 50 GA runs were performed, with a gene mutation rate of 0.02 and a maximum number of generations and energy evaluations of, respectively, 2.7×10⁴ and 2.5×10⁷. The number of individuals in a population was set to 150 and the number of top individuals to survive to each next generation was 1. The whole runs required a total time of about 24 h. The majority of the results are distributed in only two clusters (with 16 and 19 elements), whereas the resting ones are dispersed in seven clusters scarcely populated. However, the two best clusters exclusively differ for a rotation of about 30° of the graphene sheet around the axis orthogonal to the sheet plane. The lowest binding energy is the same in both the cases (-10.9 Kcal/mol).

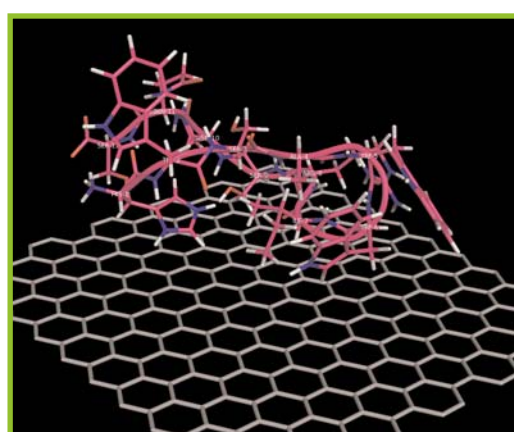


Fig. 4: The docking of the peptide on a single-wall nanotube. Docking has been performed by using the same procedure as for the graphene sheet. Results are distributed only in two clusters. The most populated cluster displays 29 elements and the lowest binding energy (-10.0 Kcal/mol).

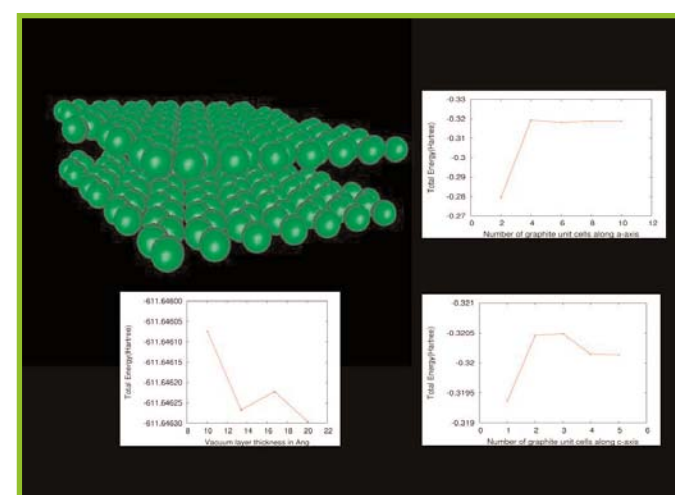
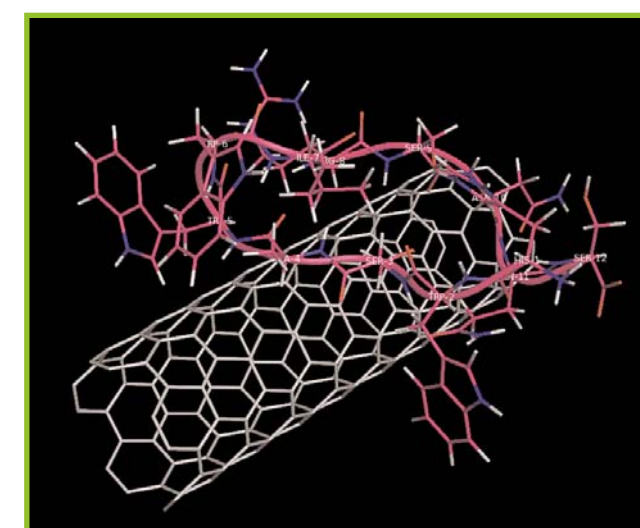


Fig. 5: A deeper understanding of the nature of the interaction between organic and inorganic materials requires an electronic structure ab-initio method. We used CPMD (Car Parrinello Molecular Dynamics) which is a code that performs MD, geometry optimization and calculates many other electronic structure related properties within the framework of the plane-wave/pseudopotential-density functional method. In the following calculations we used

Perdew-Burke-Ernzerhof exchange-correlation functional and norm-conserving Trouiller Martins type pseudopotentials. We checked, performing a total energy convergence study, that at least an energy cutoff of 60 Hartree was needed. The first step was the optimize the physical description of both the inorganic and the organic part of the whole system. The (0001) graphite surface was modeled as a supercell made of $m \times n$ elementary cells of graphite and a vacuum layer on top. In order to determine the minimum number of cells necessary to get a sufficient numerical accuracy, we have calculated the total energy of the system varying m with n fixed (fig. 5b), varying n with m fixed (fig. 5c) and increasing the thickness of the vacuum layer (fig. 5d). To get a precision of the order of 10⁻⁴ Hartree a supercell made of 8x8x4 graphite cells and a vacuum layer of at least 10 Å are needed. In the following calculations, due to the limited amount of computational resources, we used a slab of only 1 graphite elementary cell along the c axis and the graphite atoms were kept fixed in the geometry relaxation of the whole system.

Fig. 6: Due to the high computational resources required by an ab-initio method, we could only perform simulations between a graphite monolayer and a single unit of the peptide previously described. Since from experimental studies it seems that the tryptophan is the amino acid of the peptide that plays a major role in the interaction with graphite structures, we limited ourselves to study the interaction of the (0001) graphite with a single tryptophan molecule.

After a full ionic relaxation by using CPMD of the tryptophan molecule, we have obtained an optimized atomic configuration with a mean variation of the bonds equal to 0.025 Å (root mean square) with a maximum variation of 0.06 Å between atoms C4 e C6 (Fig. 6a), respect to the starting configuration. Fig. 6b shows the total electronic charge plotted using a charge isosurface while Fig. 6c reports the spectrum of the Kohn-Sham occupied electronic states.

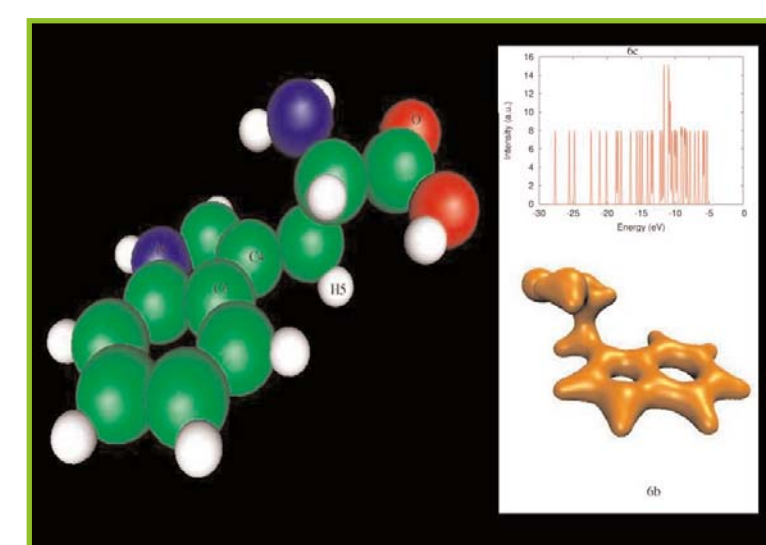
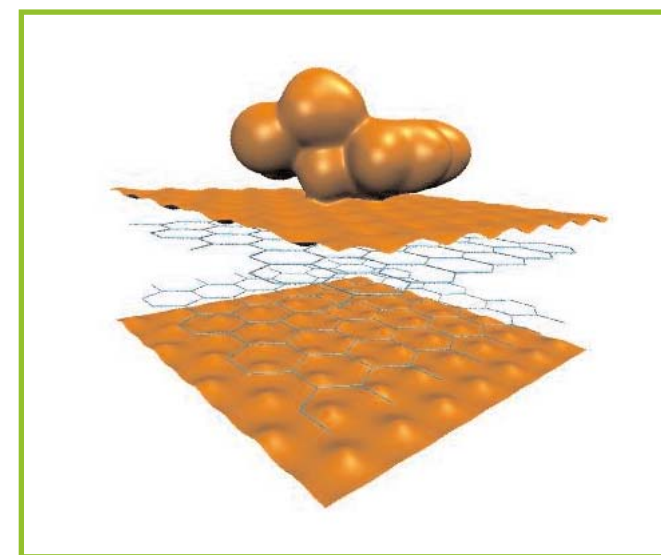


Fig. 7: We have relaxed the structure formed by a graphite monolayer and a tryptophan molecule on top of it starting from an initial configuration obtained from simulations performed with classical force fields. At the end of the relaxation the tryptophan stays with the aromatic ring nearly parallel to the graphite surface at a distance of about 4 Å, while the closest atoms are the hydrogen atoms H4 and H5 (see Fig. 6) at a distance of about 3 Å. The cohesion energy of the graphite-tryptophan system is very low (0.03eV) showing that van der Waals forces are very important in this kind of interactions and needs to be modeled properly. Van der Waals forces can be modeled as suggested in ref. [3] and tests are now running to



optimize the involved parameters. Note that the simulation of the graphite-tryptophan system with CPMD required about 30 cores with 1GB RAM/core and a simulation time of many days in order to get a full relaxed structure. So that in order to simulate the interaction of the peptide with a graphite structure, much more processors and RAM memory are needed.