Geometry Global Optimization of Large Biological Molecules

Abdel Kenoufi

Scientific COnsulting for Research & Engineering (SCORE) Strasbourg, France, kenoufi@s-core.fr

Keywords: DFT, Order N Algorithms, SIESTA, Symbolic Regression, Genetic Programming, Minima Hopping Method.

One presents a methodology to find the global minimum of a material system (molecule, cluster, bulk) on the potential energy surface (PES) which is its fundamental geometrical configuration (native state for proteins for example). The idea is to compute data at quantum level and to use them to determine a classical inter-atomic potential, which will be used to optimize the geometry of the system. One introduces first the mathematical background of the so-called order N or linear-scaling algorithms[1] which permit *ab initio* calculations within Density Functional Theory framework (Kohn-Sham), of large material systems such as biological molecules for instance. In a second step, the symbolic regression method is introduced in order to determine the inter-atomic potential with mean of genetic programming which is a generalization of genetic algorithm[2]. This permits in third step to use it for the Minima Hopping method[3, 4], which performs global optimization on the PES. The presentation ends with some examples of numerical applications.

References

- A. Kenoufi, J. Polonyi, Projection method for rapid ab initio calculations of metals, Phys. Rev. B 70, ID: 205105, 2004.
- [2] A. Kenoufi, J. F. Osselin, B. Durand, System adjustments for targeted performances comining symbolic regression and set inversion, In "Inverse Problems for Science and Engineering", 2012.
- [3] S. Goedecker, Minima hopping: An efficient search method for the global minimum of the potential energy surface of complex molecular systems, J. Chem. Phys. **120** ID: 9911, 2004.
- [4] A. Kenoufi, Finding low-energy configurations of Bulk Metallic Glasses with Minima Hopping global optimization, University Press, 2009.