Self-Consistent Field Convergence for Proteins: A Comparison of Full and Localized-Molecular-Orbital Schemes

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The computational description of systems with tens of thousands of atoms such as proteins is still a molecular mechanics' domain. However, method and hardware developments are gradually leading to a paradigm change. Nowadays, semiempirical wavefunction based MNDO-like [1] NDDO (Neglect of Diatomic Differential Overlap) self-consistent field (SCF) calculations are also applied routinely to larger systems. Besides linear-scaling methods such as divide and conquer (D&C) [2] or localized-molecular-orbital (LMO) [3] techniques, conventional full SCF calculations based on a massively parallel code (EMPIRE [4]) now allow very large systems to be treated without local approximations.

During the development of the massively parallel EMPIRE code, [4] it became evident that SCF convergence is very slow for gas-phase calculations on zwitterionic (i.e. almost all) proteins using a full SCF routine, whereas such calculations converge very effectively using the LMO-SCF technique implemented in MOPAC (MOZYME) [5]. Comparative calculations with both techniques showed that the very slow inductive charge-transfer process that made the conventional SCF calculations so slow to converge is prevented in the LMO-SCF scheme. [6] Therefore, the LMO procedure can lead to artificially over-polarized wavefunctions in gas-phase calculations. For a better understanding of this phenomenon, example molecules have been constructed to demonstrate this behavior.



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