

Studying the Charge Density of Large Biological Systems Transferring Extremely Localized Molecular Orbitals

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One of the goals of modern theoretical chemistry consists in developing new quantum mechanical strategies to study large molecular systems at a sensitively reduced computational cost. In this context several research groups have developed different linear scaling methods [1] that have been successfully used in important fields, such as molecular material modeling and drug design. A very interesting option to address this challenge is based on the observation that molecules are generally constituted by recurrent functional groups that roughly maintain the same properties in different chemical environments. Therefore, following a sort of LEGO approach [2], one could imagine to define transferable localized Molecular Orbitals (MOs) describing the above mentioned functional units, which would allow to almost instantaneously obtain the wave function (or the electron density) of very large systems.

Unfortunately, the canonical Hartree-Fock MOs and the traditional localized MOs are completely or partially delocalized on the whole systems on which they are calculated and, therefore, they are not suitable for our purpose. Nevertheless, it is possible to resort to the concept of Extremely Localized Molecular Orbitals (ELMOS) [3] that are orbitals strictly localized on small molecular functional units and that can be easily transferred [4, 5] from a molecule to another one.

We have started investigating in detail the transferability of the Extremely Localized Molecular Orbitals to quite large biomolecular systems (e.g., the Leu-enkephalin polypeptide). To accomplish this task, we have compared the resulting electron densities to charge distributions obtained through the transfer of experimental pseudoatoms [6]. In particular, after performing QTAIM analyses, comparisons of some topological properties associated with the obtained electron distributions have been performed.

Our final goal is to construct libraries of ELMOs that cover all the possible functional groups of the twenty natural amino acids, libraries that could be eventually used to develop new ELMO-based techniques for the refinement of macromolecular crystallographic structures, as alternative to already existing strategies that exploit the pseudoatoms transferability.

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