Mathematical problems of nuclear configuration averaging

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The concept of the average of a family of related nuclear configurations, for example, the average of those configurations which are slightly distorted versions of a given stable conformer of a molecule, has a role as both interpretative tool and also as a reference configuration in practical, computational use. However, depending on the actual coordinates used along which the average is defined, the average of nuclear configurations is not necessarily a physically viable arrangement, a fact that has to be taken into account when generating the corresponding electron density averages. Some of the associated mathematical and computational problems are described and the validity of a macroscopically motivated approach to conformation averaging is discussed.

KEY WORDS: conformational deformations, small amplitude vibrations, shape similarity, shape complementarity, active conformation, conformation averaging, union surfaces, electron density averaging

1. Introduction

The concept of nuclear configuration is quantum-mechanical, implying that models involving precise nuclear positions are necessarily approximate and are only convenient, classically motivated tools for the description of nuclear arrangements. Nevertheless, nuclei have much greater masses than electrons, hence exhibit stronger particle-like properties than electrons in a molecule, consequently, it is often useful to model molecules with a formal geometrical nuclear arrangement in mind [1]. However, these nuclear arrangements are subject to a quantum mechanical uncertainty, consequently, topological techniques are more suitable for their description than classical, geometrical tools. A differential topological and algebraic topological approach has served as the basis of a detailed description of nuclear configuration spaces of polyatomic molecules and the associated potential energy hypersurfaces [2–85]. One important constraint that is not universally appreciated is the fact that even within a semiclassical, geometrical model, the nuclear configuration space restricted to the 3N - 6 internal coordinates of a poly-

atomic molecule (in fact, of the entire stoichiometric family of molecules to which the actual polyatomic molecule belongs) is not a vector space, and cannot even be converted into one without loss of information [50]. Hence, geometrical tools are somewhat restricted even without invoking quantum mechanical uncertainty and the realization for the need of topology.

Of course, it is also well recognized that even within a semiclassical model, the nuclei of a polyatomic molecule are in continuous motion, and in fact, the zero point vibrational motion implies that we are dealing with a distribution of nuclear arrangements and not with any fixed nuclear configuration. In this context, some form of average nuclear configuration appears as a useful concept.

In this contribution some of the quantum mechanical and mathematical problems associated with nuclear configuration averaging are discussed, placing earlier studies [82,85] on the subject in a broader and more general perspective. In particular, with the introduction of combinatorial quantum chemistry approaches [86], involving electron density fragment data libraries or fragment density matrix libraries, containing many variants corresponding to slightly distorted nuclear configurations and slightly distorted fragment surroundings, the need for nuclear configuration averaging has acquired additional significance.

2. Averaging according to Cartesian or internal coordinates

Consider first two slightly distorted conformers of a nonlinear molecule A, where in the two conformers the internal coordinates are nearly the same, allowing a formal superposition of the two structures where the largest deviation in any of the corresponding Cartesian coordinates is less then 0.1 Å. By carrying out a direct averaging of all pairs of Cartesian nuclear coordinates, the resulting conformation will be rather reasonable, showing a deviation of any nuclear coordinate from that in either of the two molecules less than 0.05 Å.

Rotate now either of the two conformations by 180° according to any axis. An averaging of the corresponding pairs of Cartesian coordinates will lead to a chemically impossible arrangement for all but some nearly linear molecules, where all nuclei are crowded into a tube along the rotation axis, having a square base with edge length of 0.1 Å.

Clearly, the mutual arrangements of the two conformers is of major importance for averaging, and if the deviations in the molecular shapes are small, then it is reasonable to carry out averaging of the optimally superimposed arrangements. Such optimum superpositions can be obtained by least square fitting, or by other, more efficient methods in special cases.

Let us consider now a pair of L and D amino acids. In any mutual arrangement of the two molecules, even in the case of an optimum superposition, a direct averaging of the Cartesian coordinates of the nuclei of these two nuclear configurations would lead to chemically impossible results.

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Instead of Cartesian coordinates, an averaging procedure can be associated with internal coordinates. If a chemically reasonable conformational change interconnects the two conformers for which an average internal configuration is required, then it is reasonable to consider those internal coordinates along which the dominant components of the configuration change occurs. For example, if the two configurations are two rotamers derived from one another by a 60° rotation of a methyl group, then a direct Cartesian coordinate averaging would produce the correct dihedral angles but much too short C–H distances. However, an averaging along the rotational internal coordinate would lead to a reasonable structure that belongs to a 30° internal rotation of the methyl group (relative to either of the two conformers), with chemically reasonable C–H distances.

In such instances, averaging along internal coordinates is advantageous.

3. Energy considerations

The involvement of chemically unreasonable nuclear arrangements appears as a fundamental problem associated with some approaches to nuclear configuration averaging. One possibility to overcome these difficulties is based on energy considerations. In general, low energy conformations are likely to occur, whereas many high energy conformations are unlikely; high energy appears as a practical criterion for excluding highly unreasonable nuclear arrangements. Energy in most instances determines the degree of accessibility of a given nuclear arrangement, hence it is reasonable to apply energy conditions to facilitate the choice of rearrangement paths in the nuclear configuration space, along which the averaging is to be performed.

3.1. Single catchment region

In the simplest case, we shall make the assumption that the two configurations A and B to be averaged are similar enough that they belong to the same catchment region of a minimum of the potential energy hypersurface [50]. In such case it is reasonable to consider the internal coordinates defined by the quadratic form of the Hessian matrix at the energy minimum, that is, the eigenvectors of the Hessian which are the actual normal coordinates for the vibrations of the minimum energy conformation. Within this local coordinate system of the manifold describing the complete nuclear configuration space, the distance between the two configurations A and B is well defined, furthermore, there is a unique shortest line interconnecting A and B. An interpolation between A and B along this line can then be used for averaging. A simple internal coordinate averaging with reference to the given minimum energy conformation K of the catchment region can be obtained by

$$C_{\rm av,K} = 0.5A_K + 0.5B_K,\tag{1}$$

where vectors $C_{av,K}$, A_K , and B_K , are representing the two original and the new average nuclear configurations expressed in terms of the normal coordinates of energy minimum K.

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If a weighted average is required, for example, by emphasizing energy, a weighting different from the value 0.5 can be used. In the case of energy weighting, emphasizing the greater importance of lower energies,

$$C_{\text{av},K,E} = \frac{E_B}{E_A + E_B} A_K + \frac{E_A}{E_A + E_B} B_K \tag{2}$$

can be used, where E_A and E_B are the respective energies for nuclear configurations A and B, and the $C_{av,K,E}$ notation refers to averaging using energy weighting with reference to the internal coordinates corresponding to the normal coordinates of the local energy minimum K.

Usually, in both the unweighted and energy weighted cases, such an averaging procedure results in an averaged nuclear arrangement that belongs to the same catchment region of energy minimum K. However, if the shortest path between the two configurations, A and B, taken within the nuclear configuration space M using the local metric defined by the local coordinate system of the given catchment region leads to configurations not falling within the catchment region, than it is possible that average configuration so obtained also falls within a different catchment region, with a different local coordinate system. Whereas the average is a valid concept even in such unusual cases, nevertheless, such a case may be taken as an indication that the actual average configuration has lesser physical significance with respect to the configurations A and B.

3.2. Two neighbor catchment regions

In a somewhat more complicated case that may often arise, the two nuclear configurations A and B to be averaged belong to two neighbor catchment regions of the potential energy hypersurface [50].

In such a case, the manifold model of the potential energy hypersurface specifies two, usually rather different internal coordinate systems, one for each of the two critical points (usually energy minima) of the two catchment regions. The differentiable manifold model assumes some overlap between the local coordinate systems, but this overlap is not required to extent over the entire neighbor catchment region. Consequently, if coordinates are required for averaging, then either one of the two local coordinate system can be taken as dominant, or one may rely on the underlying metric d of the reduced nuclear configuration space M, a metric space, but not a vector space, and a space usually without a global coordinate system.

If extension of one local coordinate system, say that of nuclear configuration A, to be applied to the nuclear configuration B in the other catchment region is practical (for example, if the configuration B does not lie too far from the boundary of the catchment region of configuration A), then the methods applied for the single catchment region problem, discussed in the previous section, are applicable.

If, however, this is not feasible, then one may rely on the global metric d(A, B) of the reduced nuclear configuration space M. Since the two catchment regions are neighbors, there must exist a transition structure nuclear configuration T that lies on the

common boundary of the two catchment regions. Note that in special cases there might exist more than one such transition structure nuclear arrangement; in such a case that T_i transition structure is selected for which the sum of its distances from the structure A and structure B is minimum, where these distances are measured by the global metric of the reduced nuclear configuration space M:

$$d(T_i, A) + d(T_i, B) = \text{minimum.}$$
(3)

Whereas for the selection of appropriate transition structure T_i the global metric dof the nuclear configuration space M is the natural tool, nevertheless, this metric is cumbersome for the actual averaging process, since it is independent from any local internal coordinate choice. Consequently, the actual interpolation will rely on a path from conformation A, through the transition structure T_i , to the conformation B. This path p(A, B) has two segments, a segment $p(A, T_i)$ from A to T_i that is linear in the local metric of the catchment region of conformer A, and a second segment $p(T_i, B)$ from T_i to the conformation B, that is linear in the local metric of the catchment region of conformer B. Using the terminology of homotopy theory of algebraic topology, the complete path p(A, B) is the product of the two segment paths, $p(A, T_i)$ and $p(T_i, B)$,

$$p(A, B) = p(A, T_i)p(T_i, B),$$
(4)

where the parametrizations of $p(A, T_i)$ and $p(T_i, B)$ are given by the arc length as measured by the local metrics in each of the two catchment regions, respectively, and the parametrization for p(A, B) preserves proportionality of the locally measured arc lengths.

With these constraints, the parameter u of path p(A, B) = p(A, B, u) can be chosen so that

$$0 \leqslant u \leqslant 1,\tag{5}$$

where u = 0 corresponds to the beginning, and u = 1 corresponds to the endpoint of the path:

$$p(A, B, 0) = A \tag{6}$$

and

$$p(A, B, 1) = B.$$
 (7)

Note that nonlinear relations between overlapping local coordinate systems within a differentiable manifold may occur, hence the two segments may appear nonlinear when described in terms of the coordinate system of the other catchment region.

The fully parametrized path from A to B fulfills the natural expectation for energy that the involvement of the transition structure is likely to ensure that the path does not visit very high energy, hence unreasonably distorted conformations. In the possession of this path, in complete analogy with the single catchment region case, the direct, un-

weighted average of the two nuclear configurations A and B is taken as the point along the path with parameter value

$$u = 0.5, \tag{8}$$

that is,

$$C_{\text{av},A,B} = p(A, B, 0.5).$$
 (9)

If, on the other hand, an energy-dependent weighting is required, then

$$C_{\text{av},A,B,E} = p\left(A, B, \frac{E_A}{E_A + E_B}\right),\tag{10}$$

where the

$$u = \frac{E_A}{E_A + E_B} \tag{11}$$

parameter choice provides the required energy weighting, placing greater emphasis on the structure that is of lower energy.

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