A central partition of molecular conformational space. II. Embedding 3D structures.

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Abstract—A combinatorial model of molecular conformational space that was previously developed [1], had the drawback that structures could not be properly embedded because it lacked explicit rotational symmetry. The problem can be circumvented by sorting the elementary 3D components of a molecular system into a finite set of classes that can be separately embedded. This also opens up the possibility of encoding the dynamical states into a graph structure.

Keywords—Molecular conformational space, hyperplane arrangement, face lattice, molecular dynamics

I. Introduction

In a previous paper [1] it was presented a combinatorial model of molecular conformational space (thereafter referred as CS), it was shown that it could be described with a fair degree of accuracy by a central arrangement of hyperplanes\footnote{the term central means that all the hyperplanes pass through the origin.} that partitions the space into a set of cells. The arrangement was defined such that, for a molecule of $N$ atoms, the 3-dimensional (3D) conformations in a cell all have the same dominance sign vector: for a given vector $p \in \mathbb{R}^N$ there is an associated dominance sign vector $D(p) = (d_{12}, \ldots, d_{p-1,p}, d_{p-2,p}, \ldots, d_{11})$ whose components are defined as follows

\[ d_{ij} = \begin{cases} + & p_i < p_j \\ 0 & p_i = p_j \\ - & p_i > p_j \end{cases} \quad 1 \leq i < j \leq N \quad (1) \]

There is a set of three dominance sign vectors per 3D conformation one for each coordinate: the partition is actually a product of three partitions [1].

A central concept for the combinatorial study of an hyperplane arrangement is the face lattice poset [2]: the cells in the induced decomposition of $\mathbb{R}^{3N-3}$ ordered by inclusion. It is this hierarchical structure that enables us to manage the sheer complexity of CS since with the simple codes (1) we can encompass from broad regions down to single cells.

The model takes into account two basic symmetries of CS:

1) The translation symmetry: for a molecule with $N$ atoms the model is build in a $(3N-3)$-dimensional subspace, since for each $x$, $y$ or $z$ coordinates the dimension parallel to the vector $(1,1,1,\ldots)$ contains conformations that are obtained by translation along the axis.

2) The scaling symmetry: the points lying on a half-line starting at the origin result from multiplying the coordinates of a given 3D conformation by an arbitrary positive factor. It reflects the fact that the unit length in our system can be arbitrarily defined.

The model however fails to incorporate the all important rotation symmetry, this is due to the fact that combinatorial approaches like ours apply mostly to linear systems. This greatly complicates the embedding of 3D conformations.

To circumvent this problem, the approach we explore in the present communication is how conformations can be embedded in CS starting from its elementary building blocks, and the most elementary component 3D structure is a simplex\footnote{A three-dimensional polytope with four vertices.}. Many structural patterns in molecular systems can be decomposed into simplexes [3].

As we shall see below embedding in CS just a simplex is not simple, but this approach leads us to study a set of combinatorial structures that offer, beyond the embedding problem, the interesting possibility of encoding the dynamical states of a molecular system.

II. Embedding a simplex

![Graph of a simplex](image)

Fig. 1. Graph of a simplex, with the vectors along the edges oriented as to make the graph acyclic. If we assume that $v_1$ lies above the plane of the figure, it corresponds to a right-handed simplex.

From the simplex of Fig. 1 we define the following
set of vectors and their associated central planes:

\[ e_{ij} = v_i - v_j, \quad E_{ij}(x) = \{ x \in \mathbb{R}^3 : e_{ij}.x = 0 \} \quad (2) \]

for \(1 \leq i < j \leq 4\). These six planes generate a partition of 3D space into 24 cells [4] (see Fig. 2): each plane divides the space into positive and negative hemispaces and a zero space in between

\[ E_{ij}^+(x) = \{ x \in \mathbb{R}^3 : e_{ij}.x > 0 \} \quad \text{and} \quad E_{ij}^-(x) = \{ x \in \mathbb{R}^3 : e_{ij}.x < 0 \} \quad (3) \]

a 3D cell results from the intersection of six hemispaces, thus it can be unambiguously characterized by the signs of these six hemispaces (Fig. 2).

It is easy to see that the dominance sign vectors for an arbitrary 3D-reference system centered at the origin can be obtained from this partition: consider for instance the \(z\)-axis and suppose that \(z.e_{12} > 0\), this means that \(z\) is in a cell where the \(e_{12}\) component of the sign vector is +, which in turn implies that \(v_{1z} > v_{2z}\).

Thus the dominance sign vector for each coordinate will be the sign vector of the cell that contains its positive semi-axis.

![Diagram showing the partition of 3D space into 24 cells](https://via.placeholder.com/150)

Fig. 2. Topo graph of the partition (2), each node corresponds to a 3D cell and the edges represent the planes separating the cells. For each node the corresponding sign vector is annotated on the right.

Lower dimensional cells occur for vectors that lie in one or more of the planes \(E_{ij}\), in that case the corresponding components of the sign vector are zero.

The 1-dimensional (1D) cells are rays starting at the origin and running parallel to the vectors

\[ f_{123} = e_{12} \wedge e_{23}, \quad f_{124} = e_{12} \wedge e_{24}, \quad f_{134} = e_{13} \wedge e_{34}, \]
\[ f_{234} = e_{23} \wedge e_{34}, \quad f_{12,34} = e_{12} \wedge e_{34}, \quad f_{13,24} = e_{13} \wedge e_{24}, \]
\[ f_{14,23} = e_{14} \wedge e_{23} \quad (4) \]

the first four are the vectors perpendicular to the faces of the simplex, the last three are perpendicular to pairs of non-adjacent edges. As in (2) they have a set of associated central planes

\[ F_{123}^0, F_{124}^0, F_{134}^0, F_{234}^0, F_{12,34}^0, F_{13,24}^0, F_{14,23}^0 \quad (5) \]

The corresponding sign vectors are the rows in the matrix below

\[
\begin{array}{cccccc}
& e_{12} & e_{13} & e_{14} & e_{23} & e_{24} & e_{34} \\
\hline
f_{123} & 0 & 0 & + & 0 & + & + \\
f_{124} & 0 & - & 0 & - & 0 & + \\
f_{134} & + & 0 & 0 & - & - & 0 \\
f_{234} & + & + & 0 & 0 & 0 & + \\
f_{12,34} & 0 & - & - & - & 0 & + \\
f_{13,24} & + & 0 & + & - & 0 & + \\
f_{14,23} & - & - & 0 & 0 & + & + \\
\end{array}
\]

The zeros in the matrix correspond to the planes that intersect the corresponding 1D cell, this means that the cells encoded by \(f_{123}\) and \(f_{12,34}\), for instance, are surrounded by six and four 3D cells respectively.

The zeros in the sign vector of lower dimensional cells can be seen as a sort of wildcard: they match the sign vectors of all the adjacent cells. The converse is also true: a sign vector from a 3D cell can be obtained by adding up the sign vectors from the adjacent lower dimensional cells [4]. As an example, for the lower left cell of Fig. 2 we have \((- - + + +) = (-00+00)+(-00+0)+(-000) = -SIGN(f_{134}) + SIGN(f_{14,23}) - SIGN(f_{234})\).

III. Embedding a Simplex

There is still another set of sign vectors that will be most useful in characterizing the geometric properties of simplexes: these are the signs of the scalar products of the vectors (2) and (4) between them.

Let us assume that we have a particular right-handed simplex whose set of signs is

\[
\begin{array}{cccccc}
& e_{13} & e_{14} & e_{21} & e_{24} & e_{34} \\
\hline
f_{12} & - & - & - & - & - \\
f_{13} & + & + & + & - & - \\
f_{14} & + & + & + & + & - \\
e_{23} & + & - & + & + & + \\
e_{24} & + & - & + & - & + \\
\end{array}
\]

\[
\begin{array}{cccccccc}
& f_{124} & f_{134} & f_{234} & f_{12,34} & f_{13,24} & f_{14,23} \\
\hline
f_{123} & + & + & + & - & + & + \\
f_{124} & + & + & + & + & + & + \\
f_{134} & + & - & + & + & + & + \\
f_{234} & + & - & + & + & + & + \\
f_{12,34} & + & - & + & + & + & + \\
f_{13,24} & + & - & + & + & + & + \\
f_{14,23} & + & - & + & + & + & + \\
\end{array}
\]

\[
\begin{array}{cccccccc}
& f_{124} & f_{134} & f_{234} & f_{12,34} & f_{13,24} & f_{14,23} \\
\hline
f_{123} & + & + & + & - & + & + \\
f_{124} & + & + & + & + & + & + \\
f_{134} & + & - & + & + & + & + \\
f_{234} & + & - & + & + & + & + \\
f_{12,34} & + & - & + & + & + & + \\
f_{13,24} & + & - & + & + & + & + \\
f_{14,23} & + & - & + & + & + & + \\
\end{array}
\]
The set of sign vectors (7a) refers mostly to the angles between adjacent edges while (7b) are mostly related to dihedral angles between contiguous faces: +, 0 and − are for acute, right and obtuse angles respectively. Thus (7) gives us a rough outline of the geometry of a simplex, and allows a classification of simplexes.

Next we are going to proceed to embed our simplex in CS for the particular case where the z-axis runs parallel to f_{123}. The reason for this special choice will be explained below.

![Diagram of a simplex with sign vectors](image)

**Fig. 3.** View from above of $f_{123}^0$, the plane appears divided in a number of sectors, separating sectors are rays running along vectors whose denomination appears at the outer extreme, vector names bearing a ′ are projections: $x' = x - f_{123}(x,f_{123})/||f_{123}||$. Rays orthogonal to vectors $e'_i$ always correspond to intersections with the planes $E_i^0$. In the inner layer each sector harbors its corresponding sign vector, in the outer layer are the sign vectors corresponding to the 1D cells. Sign vectors should be read in the outward direction. The x and y axis are depicted in a random position.

From Fig. 3 we can see that $F_{123}^0$ has been partitioned into 24 cells, which are delimited by lines along the projections of vectors $e_{ij}$ and from the intersections with planes $E_{ij}^0$ (2); thus each projected $e'_{ij}$ vector is perpendicular to the intersection of the corresponding $E_{ij}^0$ and it divides the plane into two signed moities as in (2) and (3), so the sign vector associated with each cell in Fig. 3 becomes obvious, by construction they are the dominance sign vectors associated to a coordinate axis that is in the cell. Also by construction, the sixth cell after/before the one under consideration is orthogonal to it. Thus by rotating the x and y axis around z in Fig. 3 we can scan the complete set of dominance sign vectors that arise for this particular situation. Before proceeding further let us explain how Fig. 3 can be obtained from (6) and (7).

By construction, see Fig. 1 and (4), $e_{12}$, $e_{13}$ and $e_{23}$ are in circular counter-clockwise order, with the last two vectors in the negative hemispaces of $e_{12}$ (7a) and $f_{124}$ (6). For the remaining projections:

- $e'_{14}$ lies above $F_{123}^0$, by (7b) the same is true of $f_{134}$ and $f_{14,23}$, as $e_{14}$ is contained in the plane perpendicular to these vectors $e'_{14}$ will be located inside the sector determined by $e_{13}$ and $e_{23}$.
- $e'_{24}$ is above $F_{123}^0$ as well as $f_{124}$ and $f_{34}$ (7b), using the same argument as above $e_{14}$ will be located inside the sector determined by $-e_{12}$ and $e_{23}$.
- $e'_{34}$ lies in the −−++ sector relative to $e_{12}$, $e_{13}$, $e_{23}$ and $e_{24}$ (7a), this squeezes $e'_{34}$ between $E_{12}$ and $E_{24}$.

**IV. The Circular Order of the Projected Vectors**

![Diagram of the circular order of the projected vectors](image)

**Fig. 4.** Tope graph of the partition (4) showing the sign vectors of 1D cells. As in Fig. 2 the graph is planar, sign vectors of 3D cells can be obtained by adding the sign vectors around each node. Notice that the columns in (6), or their centrally symmetric sign vectors, all correspond to sign vectors above.

The circular order of the projected vectors in Fig. 3 can be obtained from the signs of the first row in (7b): one can see from Fig. 3 that the shortest path between $e_{12}$ and $e'_{34}$ runs clockwise, while the shortest path from $e_{23}$ to $e'_{24}$ and $e'_{34}$ runs counterclockwise. This is simply due to the fact that $e_{23}$, $e_{24}$ and $e_{34}$, for instance, are contained in $F_{234}^0$ and the angle between $e_{23}$ and $e_{34}$ can not exceed $2\pi$, thus their circular order in the projection depends on whether $f_{234}$ lies above or below $F_{123}^0$.

To obtain the sign vector encoding the circular order in the plane perpendicular to a vector in general position, it suffices to look whether the given vector is in the
positive or negative hemispace relative to the planes (5). Thus the central arrangement generated by (4) partitions the space in 32 cells that are represented by the tope graph of Fig.4.

This settles the problem of the circular ordering of the projected vectors which is completely determined by (6).

Last but not least, it is indispensable for the correct simultaneous allocation of the x and y dominance sign vectors, to determine the relative positions in the circular ordering between the $e'_i$ and the intersections of the $E^0_{ij}$.

As this is not a linear problem in some cases it can only be partially resolved by (7). Ambiguities can arise when building a projection, for instance: if in the example of Fig. 3 $e'_{24}$ and the intersection of $E^0_{34}$ both fell in the same sector. In that case we would have to split the diagram into two alternative ones.

V. THE ENUMERATION OF MINIMAL VECTORS

In the diagram from Fig. 3 the dominance sign vector associated with the \{x, y, z\} reference frame is 

$$((+, +, +, +), (00 + 0 + +)),$$

one can notice that it is squeezed between 

$$((+, +, +, +), (00 + 0 + +)) and (++, 0, +, 0 + +), 00 + 0 + +).$$

The importance of this diagram is that it enumerates all the lower dimensional 2D cells associated with the sign vector \((00 + 0 + +), and since the rows of (6) are all the 1D cells in the partition constructing a diagram like the one in Fig. 3 for every row in (6) allows us to enumerate all the minimal vectors in our system (those bearing a maximum number of zeros), all other sign vectors being combinations of them.

VI. THE GENERAL EMBEDDING PROBLEM

In molecular dynamics simulations atoms are represented by pointlike structures surrounded by a force field, thus any four atoms in a molecular structure can form a simplex. If an order relation has been defined between the atoms of the system, then vectors (2) and (5) can be defined too for every simplex with the node numbers of Fig. 1 representing the order of the atoms.

Some of the vectors (2) and (5) are shared between simplexes through common edges and faces, as a consequence orienting a simplex restricts the range of available orientations in the other simplexes. Embedding a 3D conformation in CS can be done with this simple algorithm:

1) take a set of connected simplexes\(^3\) such that every pair of atoms in the structure is at least in one simplex,

2) choose a simplex with a non empty set of available sign vectors, otherwise terminate the procedure,

3) select one orientation and restrict the available orientations in the other simplexes to the ones compatible with this choice. Repeat step 2.

VII. CONCLUSION

The two main results of this communication are

1) simplexes can be put into a number of discrete classes, not taking into account handedness we have: 258 and 816 sets for (7a) and (7b) respectively, with both combined we have a total of 3936 classes.

2) these classes are related to cells in CS, thus relating the binary sets (7) in a molecular conformation to 3D coordinates.

Embedding just one 3D conformation is not an interesting issue, what really matters is embedding the volume occupied by a molecular system.

Beyond the embedding problem the results above offer the possibility of building a structure encoding the dynamical states of a molecule. This can be seen by analyzing the dynamical activity of all simplexes in a typical molecular dynamics simulation like the one studied in [5], we find that

1) 90% of the simplexes evolve within less than 20 classes,

2) 0.4% remain in a single class for the duration of the simulation, form a connected set and comprise 95% of the dominance relations (1),

3) the most dynamically active simplex spans a range of 171 classes, slightly less than 2% of the total.

A connected set of simplexes can obviously be represented by a graph, where each node can be split into a number of classes (7): its dynamical states. The connectivity between the sets (7) is an issue than has not been explored in this paper, but its determination will allow the connexion between dynamical states in adjacent nodes thus generating the derived graph of the molecular system dynamical states.

This graph is a subject for further research.

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\(^3\) $S_a$ and $S_b$ are connected if there exists a sequence of simplexes $\{S_i\}$ $1 \leq i \leq N$, with $S_1 = S_a$ and $S_N = S_b$, such that for $1 \leq i < N$ $S_i$ and $S_{i+1}$ are adjacent.
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