

Voro3D: 3D Voronoi tessellations applied to protein structures

Franck Dupuis^{1,*}, Jean-François Sadoc², Rémi Jullien³, Borislav Angelov^{2,†} and Jean-Paul Mornon¹¹Laboratoire de Minéralogie Cristallographie Paris, CNRS UMR 7590 Universités Paris 6 et 7, case 115, 4 Place Jussieu, 75252 Paris, France, ²Laboratoire de Physique des Solides, CNRS UMR 8502, Université Paris 11, Orsay, France and ³Laboratoire des Verres, CNRS UMR 5587, Université Montpellier 2, Montpellier, France

Received on May 7, 2004; revised on June 3, 2004; accepted on June 9, 2004

Advance Access publication June 24, 2004

ABSTRACT

Summary: Voro3D is an original easy-to-use tool, which provides a brand new point of view on protein structures through the three-dimensional (3D) Voronoi tessellations. To construct the Voronoi cells associated with each amino acid by a number of different tessellation methods, Voro3D uses a protein structure file in the PDB format as an input. After calculation, different structural properties of interest like secondary structures assignment, environment accessibility and exact contact matrices can be derived without any geometrical cut-off. Voro3D provides also a visualization of these tessellations superimposed on the associated protein structure, from which it is possible to model a polygonal protein surface using a model solvent or to quantify, for instance, the contact areas between a protein and a ligand.

Availability: The software executable file for PC using Windows 98, 2000, NT, XP can be freely downloaded at <http://www.lmcp.jussieu.fr/~mornon/voronoi.html>

Contact: franck.dupuis@sanofi-aventis.com; jean-paul-mornon@lmcp.jussieu.fr

The efficiency and the relevance of the Voronoi tessellations to describe protein structures were proven almost 30 years ago with the work of Richards (1974). Ever since, the success of this method has never ceased. To study different aspects of protein structures and folding, numerous research teams have been using this mathematical tool in different ways (for a review see Poupon, 2004). A tessellation is a way of subdividing space into regions associated with each element of a set of discrete points in order to characterize their topological relations. For each of these elements, the Voronoi process associate with a polyhedron, called Voronoi cell, defined by the intersection of contact planes build midway between points. For a given set of points, the Voronoi decomposition is unique and absolute since there is no empty space between cells. The cell faces therefore define unambiguously the contacts between the associated point and its nearest neighbours which can also be called as Voronoi neighbours. As far as we know, most of the teams involved in this approach use home-made algorithms and curiously enough, it seems that no tool devoted to visualization and especially dedicated to Voronoi tessellations applied to protein structures exists, or is available on the Web. As already shown by us (Soyer *et al.*, 2000; Dupuis *et al.*,

2004), the mere observation of the Voronoi polyhedra associated with a protein structure provide a precious information on the local fold properties. Thus, it is not difficult to imagine the helpfulness of a tool that would allow the visualization of these three-dimensional (3D) geometrical decompositions superimposed on the protein structures on a computer screen.

Voro3D provides such a tool and focuses on the amino acid packing, since each residue can be represented by one point. It uses any file containing atomic coordinates deposited in the Protein Data Bank (PDB) format. Difficulties appear when considering amino acids close to the protein surface because the associated cells appear as elongated or even as open ones. To overcome this problem, Voro3D proposes to embed the molecule in a model environment that was described in another work (Angelov *et al.*, 2002). This environment is a relaxed random packing of spheres spread around the studied structure. It was designed in order to play the role of a solvent with packing properties close to those of proteins. The volume of these spheres is taken close to the mean volume occupied by amino acids, leading to a default diameter of 6.5 Å.

Nevertheless, the user can select other values for the sphere diameter, the number of the layers of the sphere and the number of relaxations (nine relaxations are sufficient to reach convergence). A small 3D viewer (Fig. 1) displays a glimpse of the protein buried in its environment. To perform the tessellation, Voro3D prompts the user to choose between a simple tessellation or a weighted one. This latter case was described previously (Sadoc *et al.*, 2003) and the best weight values were calculated. These values are used as default ones but can be easily changed through a dedicated dialog box.

When the calculation procedure is over, the protein structure and its associated tessellation appears in a second 3D viewer where it can be translated, rotated and enlarged. Under this viewer on the left-hand side, a table displays values concerning the Voronoi cells, such as volume, area, environment accessibility or secondary structure assignment as defined by the VoTAP (Dupuis *et al.*, 2004). For each cell, the face characteristics can be displayed in another table appearing on the right-hand side. Some visualizing parameters can also be modified in the table, such as the number of represented cells, colour, transparency, label, etc. For instance, if all the cells are selected with no transparency, a polyhedral protein surface appears. The data concerning cells and their faces are gathered in two different files and the 3D views appear in a VRML file which can be exported on the Web or in any MS office software. Finally, a contact matrix can be established according to those described previously (Dupuis *et al.*, 2004).

*To whom correspondence should be addressed.

†Present address: Institute of Biophysics, Bulgarian Academy of Sciences, Acad. G. Bonchev Strasse, Block 21, Sofia 1113, Bulgaria

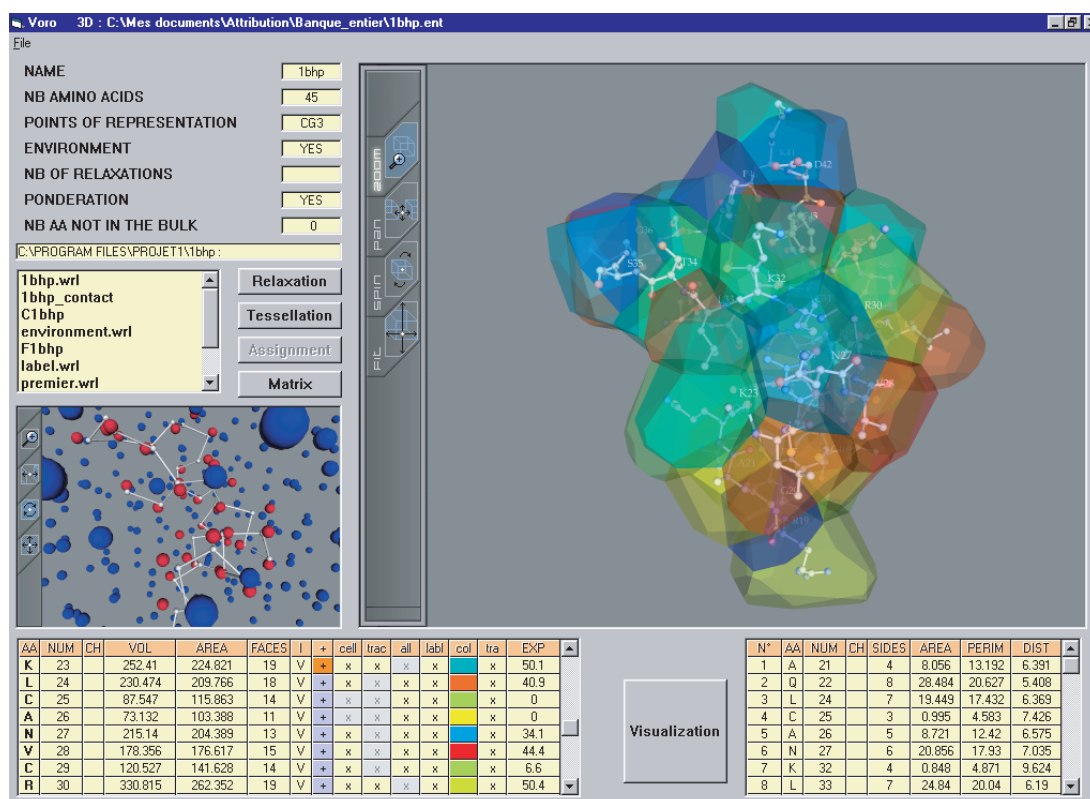


Fig. 1. An example of a typical Voro3D user interface. The main 3D viewer presents the weighted tessellation of the beta-purothionin structure (PDB code 1bhp). The tables list cell properties and graphics parameters.

Work is in progress to add to this tool for the visualization of information such as colour by environment accessibility, secondary structures and Van Der Waals spheres.

REFERENCES

Angelov,B., Sadoc,J.F., Jullien,R., Soyer,A., Mornon,J.P. and Chomilier,J. (2002) Nona-tomic solvent-driven Voronoi tessellation of proteins: an open tool to analyze protein folds. *Proteins*, **49**, 446–456.

Dupuis,F., Sadoc,J.F. and Mornon,J.P. (2004) Protein secondary structure assignment through Voronoi tessellation. *Proteins*, **55**, 519–528.

Poupon,A. (2004) Voronoi and Voronoi-related tessellations in studies of protein structure and interaction. *Curr. Opin. Struct. Biol.*, **14**, 233–241.

Richards,F.M. (1974) The interpretation of protein structures: total volume, group volume distributions and packing density. *J. Mol. Biol.*, **82**, 1–14.

Sadoc,J.F., Jullien,R. and Rivier,N. (2003) The Laguerre polyhedral decomposition: application to protein folds. *Eur. Phys. J. B*, **33**, 355–363.

Soyer,A., Chomilier,J., Mornon,J.P., Jullien,R. and Sadoc,J.F. (2000) Voronoi tessellation reveals the condensed matter character of folded proteins. *Phys. Rev. Lett.*, **85**, 3532–3535.