

Texture mapping parametric molecular surfaces

Bruce S. Duncan and Arthur J. Olson

The Scripps Research Institute, La Jolla, California 92037

Texture mapping is an increasingly popular technique in molecular modeling. It is particularly effective in representing high-resolution surface detail using a low-resolution polygonal model. We describe how texture mapping can be used with parametric molecular surfaces represented as expansions of spherical harmonic functions. We define analytically the texture image and its transformation to a parametric surface. Unlike most methods of texture mapping, this transformation defines a one-to-one correspondence between the surface and the texture; texture coordinates are derived from the location of the surface point and not from physical properties at the surface point. This has advantages for the interactive visualization of surface data. We control the interactive response time by lowering the resolution of the polygon mesh while retaining the highresolution detail of the texture, or we can lower the resolution of the texture image with the same polygonal model. By using a well-defined convention for texture coordinates, we can use the same image for the original surface or its parametric representation, and we can rapidly switch between images that represent different surface properties without recomputing the texture coordinates. Parametric surfaces allow new flexibility for the visualization of molecular surface data.

Keywords: Texture mapping, molecular surface, spherical harmonics

INTRODUCTION

Texture mapping is a procedure to represent high-resolution surface detail using a low-resolution geometric model. ^{1,2} It is available in many advanced renderers and is increasingly popular in molecular graphics to show properties on molecular surfaces. These surfaces are frequently isodensity contours of a three-dimensional scalar function

Color plates for this article are on p. 237.

Address reprint requests to Dr. Olson at The Scripps Research Institute, 10666 North Torrey Pines Road, La Jolla, California 92037. Received 3 February 1995; revised 15 May 1995; accepted 18 May 1995.

or surfaces derived from Richards's definition of the molecular surface.³ The article by Teschner et al. presents an overview of texture mapping in molecular modeling as well as many striking images.⁴

Some molecular surfaces have an analytic representation, but this analytic description is usually defined implicitly or covers only a limited region of the surface. For example, algorithms that compute analytic molecular surfaces^{5–8} represent the spherical and toroidal patches of the surface, but the complete surface is the union of these small patches. Consequently, molecular surfaces are usually represented as a collection of polygons for computation or rendering.

For some applications, however, a single parametric description that represents the entire molecular surface is desirable. One such method is to approximate the surface as an expansion of spherical harmonic functions. With this method there is a single parameterization that describes the entire surface; it is not composed of the union of discrete segments. This technique has several advantages for computation and interactive graphics. For example, we control the resolution of the surface by changing the number of terms in the expansion, and control the resolution of the triangle mesh independently of the surface resolution. We have applied this technique in a program to predict protein-protein interactions and for the real-time display of spherical harmonic surfaces during normal mode vibrations.

An important step in texture mapping is to define the correspondence between the polygonal model and the texture image. One method is to use texture coordinates derived from the physical properties (electrostatic potential, hydrophobicity, etc.) at the surface points. This procedure has the advantage that it is easy to do texture mapping using these property-based texture coordinates. This method, however, has limitations. Texture mapping a different set of surface data requires changing the texture coordinates in the geometric model; an expensive procedure in some renderers. Also, it is not possible to use a high-resolution texture with a coarsely triangulated geometric model because the texture image defines the color coding of the surface data only at individual points and is not a planar representation of the surface topography.

In contrast, the methods described here rely on the computation of a one-to-one correspondence between the tex-

ture image and the molecular surface. Thus, the texture image is analogous to a cartographic representation (world map) of the surface. These texture coordinates define the spatial location of the surface points and not physical properties of the surface points. We call this type of representation *location-based texture coordinates*. An important feature is that this representation is independent of the spatial resolution (number of terms in the expansion) and the triangulation (number of surface triangles) of a spherical harmonic surface. To display a new set of surface data, only the texture image must be changed; the geometric model is constant. In this article we describe the advantages of location-based texture coordinates and spherical harmonic surfaces for texture mapping and show applications of these techniques to our modeling tasks.

SPHERICAL HARMONIC REPRESENTATIONS

Spherical harmonic representations approximate the large-scale features of protein surfaces. 9,12,13 The most important feature is the surface geometry, that is, the Cartesian coordinates of the surface points. Any surface function, however, can be represented by this method. Important surface functions include shape measures, electrostatic potential, and hydrophobicity. Spherical harmonic functions are appropriate for representing surface data down to a scale of about 1 Å. This is suitable for many applications because the scale of most surface properties is greater than the size of individual atoms. It is more difficult to represent detailed surface geometry than most surface properties. A fundamental limitation of spherical harmonic basis functions is that they can represent only surfaces that are topologically equivalent to a sphere, but we believe that parametric surfaces using other basis functions will have similar rendering and computation advantages.

In the following descriptions we refer to geometric objects of various dimensions. It is important to distinguish between the dimension of the parameterization of an object and the dimension in which the object is embedded. For example, a plane is a two-dimensional object that can be embedded in three-dimensional space. The molecular surfaces that we use are two-dimensional and are topologically equivalent to the two-dimensional surface of a sphere. An important concern is the parameterization of the surface. The parameterization gives the dependent variables that define the three-dimensional surface position as functions of independent variables called parameters. For example, the spherical harmonic technique uses the θ and ϕ spherical angles as independent variables (two-dimensional surface coordinates). This two-dimensional coordinate represents a specific point on the surface at which the dependent variables (three-dimensional Cartesian coordinates) are deter-

We generate spherical harmonic representations with the following procedure. The input data represent a triangulated molecular surface computed by available programs. An important step is the topological mapping of the original molecular surface into a sphere. This is necessary because the spherical harmonic functions are defined on a unit sphere, and the mapping procedure defines a one-

to-one relation between the molecular surface and a unit sphere. After this mapping, expansion coefficients are computed by integrating the product of each Cartesian coordinate of the molecular surface (X, Y, Z), with the spherical harmonic functions. This produces three sets of expansion coefficients, one for each Cartesian coordinate. Surface integrals are evaluated using a uniform grid in spherical coordinates. A grid element is computed by extending a ray from the origin of the unit sphere and finding the triangle that the ray intersects. This triangle has a corresponding triangle on the molecular surface. We obtain the value in the integration grid by interpolating the Cartesian coordinates of the vertices of the molecular surface triangle. To complete the grid, we repeat this procedure for each (θ, ϕ) spherical coordinate, using constant angle increments. After integration, spherical harmonic surfaces are generated by summing the product of the expansion coefficients and the spherical harmonic functions. Evaluation is also done using constant angle increments in spherical coordinates, and the Cartesian coordinate at an arbitrary spherical point is computed from the four nearest grid points using bilinear interpolation.

An important feature of this method is that we can define arbitrarily the spherical coordinates used to generate the Cartesian surface coordinates. We choose these spherical coordinates so that the polygon mesh of the surface has a well-defined hierarchical structure. We subdivide the faces of a regular solid to create a set of spherical coordinates used to generate Cartesian surface points. We frequently use the spherical coordinates obtained by subdividing the faces of a regular icosahedron to produce a triangular mesh. Our visualization techniques use this hierarchy to give the user interactive control of the resolution of the mesh. Details of this mesh structure are in Ref. 10.

Our spherical harmonic programs perform a wide variety of computation and modeling tasks, including representation of surface geometry and surface properties, interactive computation of the interfacial surface between two interacting proteins, and real-time visualization of spherical harmonic surfaces during normal mode vibrations. Each of these applications can benefit from increased surface detail and efficient rendering using texture mapping.

TEXTURE MAPPING

A typical application of texture mapping is to apply a two-dimensional image to a surface. For molecular modeling applications, the two-dimensional image usually represents a physical property such as electrostatic potential, hydrophobicity, or atom type. Polygonal regions within a texture image are specified using the texture coordinates (u, v), which are floating point numbers between 0 and 1. Each vertex of a polygon in the geometric model also has a (u, v) texture coordinate, and a corresponding polygon can be located in the texture image. During rendering, the subimage contained within this region in the texture image is applied to the polygon of the geometric model.

Texture mapping can also be done in one or three dimensions. In one-dimensional texture mapping, the u and v texture coordinates are set to the same value; this produces a surface indexed by a single scalar quantity. Three-

dimensional texture mapping uses the three texture coordinates, (u, v, w), which are usually derived from the Cartesian coordinates of the surface point.

We distinguish between two methods of defining texture coordinates. Most procedures to texture map molecular surfaces use what we call property-based texture coordinates. In this method, the texture coordinate of each vertex is defined using a physical property at the surface point. For example, it is straightforward to use texture mapping to display simultaneously the electrostatic potential and the hydrophobicity of a surface if the u texture coordinate is set proportional to the potential and the v coordinate proportional to the hydrophobicity. These surfaces can be rendered using a texture image with the u coordinate color coded by potential and the v coordinate color coded by hydrophobicity. An advantage of this method is that it is easy to apply and does not have distortion artifacts. This method has the limitation that we cannot lower the triangulation of the polygonal model while retaining the high-resolution information in the texture image.

Texture coordinates can also be defined so that they specify a location on the surface (location-based texture coordinates) instead of a physical property. A limitation of this type of texture coordinate is that the texture image may be stretched or compressed when applied to a polygon. For example, an image can be applied to a plane or cylinder without distortion but not to a sphere or irregularly shaped surface. This distortion can limit the applicability of twodimensional texture mapping. Location-based texture coordinates are frequently used in other computer graphics applications because the geometric models are usually simpler than molecular surfaces. In spite of these limitations, location-based texture coordinates have advantages for interactive graphics. One advantage is that there is a one-to-one correspondence between the surface and the texture image. This allows the same texture image to be used on surfaces with different triangulations or spatial resolutions. The main difficulty in using location-based texture coordinates is to overcome the problem of the distortion of the texture when applied to an irregular surface. Because our molecular surfaces have a well-defined parametric representation, we can use this information to define a series of coordinate transformations that eliminate this problem.

COORDINATE TRANSFORMATIONS

The explicit mapping of the entire molecular surface to the texture image is an important concern in applying two-dimensional texture mapping with location-based texture coordinates. A fundamental problem is that a molecular surface cannot be mapped into a plane without distortion. To quantify this distortion, we define a series of transformations from the molecular surface to the texture image. An advantage of parametric surfaces is that the transformation from a plane to a surface can be defined precisely. By creating texture images using these transformations, we can apply the resulting image to the surface without distortion. This is analogous to creating a planar map of the Earth using the knowledge of how the map will be stretched and compressed when applied to a sphere to form a globe.

The coordinate transformations used by our procedures

are summarized below. The function arguments denote the independent variables of the parameterization.

$$S \xrightarrow{T \text{map}} S(\theta, \phi) \tag{1}$$

S is the original molecular surface in Cartesian coordinates; it has no parameterization and is represented as a set of discrete points. $S(\theta, \phi)$ is the mapping of this surface to a unit sphere. $T_{\rm map}$ is the topological mapping procedure by which each surface point is assigned a unique (θ, ϕ) spherical coordinate. Conversely, a Cartesian surface point can be defined for each point on the unit sphere by interpolating the values in the discrete set S.

After mapping the surface to a sphere, the spherical representation is projected to a planar one as follows:

$$S(\theta, \phi) \xrightarrow{Projection} S(u, v)$$
 (2)

S(u,v) is the projection of the unit sphere to a unit square. Coordinates inside the square are referenced by the texture coordinates (u, v) which are derived from the spherical coordinates (θ, ϕ) as follows: $u = \theta/\pi$ and $v = \phi/2\pi$. The Projection procedure is a simple spherical mapping, although more complex cartographic projections could be used. Note that this projection is not strictly one to one because the poles $(\theta = 0 \text{ and } \theta = \pi)$ are singular points. These relations describe transformations of the original molecular surface to a plane. With these transformations, each point of the molecular surface (excluding the poles) is assigned a unique texture coordinate. Also, a Cartesian surface point can be defined for each point in the unit square using interpolation.

There are also relations between the Cartesian molecular surface and its spherical harmonic approximation. These relations are summarized as follows:

$$S(\theta, \phi) \xrightarrow{Integration} Coefs[l,m]$$
 (3)

Coefs[
$$l,m$$
] $\xrightarrow{Evaluation} H(\theta,\phi)$ (4)

Coefs[l,m] are the expansion coefficients indexed by the parameters l and m, which denote specific spherical harmonic functions. $H(\theta, \phi)$ denotes the spherical harmonic representation of the surface. Recall that the Integration procedure evaluates the inner product of the Cartesian coordinates with the spherical harmonic functions to obtain the expansion coefficients, and the Evaluation procedure sums the product of the expansion coefficients and the spherical harmonic functions to obtain the spherical harmonic surface. Evaluation occurs at selected points on the unit sphere defined by their (θ, ϕ) coordinates. These spherical harmonic surfaces are defined on a unit sphere and can be projected to a unit square as described above.

$$H(\theta, \phi) \xrightarrow{Projection} H(u, v)$$
 (5)

Note that the projection transformation alters only the parameterization; the coordinates of the vertices and the topological relations between them (the polygon definitions) do not change. The triangle mesh of the molecular surface and its unit sphere representation are identical. For spherical harmonic surfaces, the triangle mesh on the unit sphere is

topologically equivalent to the triangle mesh of the spherical harmonic surface in Cartesian coordinates. By composing these transformations we form a link between the original molecular surface points and the points of the unit square.

One limitation of this projection is that the poles ($\theta = 0$ and $\theta = \pi$) are singular points and there is a possibility of an inconsistency where the $\phi = 0$ line wraps around to meet the $\phi = 2\pi$ line. If a triangle crosses this boundary, the texture image can be applied incorrectly. Some hardware renderers remove this inconsistency by using a periodic texture, that is, truncating the integer part of the texture coordinate when it is greater than 1. One limitation, however, is that not all hardware renderers allow arbitrary dimensions for periodic textures and restrict the dimensions to be an integral power of 2. We find this limitation unacceptable. Consequently, we developed a procedure that adds vertices and polygons to the surface to ensure that no polygons cross this boundary. With this method, we can use texture images of arbitrary dimensions without an inconsistency at the boundary of the texture. Property-based texture coordinates do not have this wrapping problem because the texture image does not have a one-to-one correspondence with the surface points. As described previously, propertybased texture coordinates have limitations because it is difficult to render a high-resolution texture on a low-resolution polygonal model, and the texture coordinates must be changed when displaying a new set of surface data. Because our texturing procedures use an explicit relation between the texture image and the molecular surface, they do not have these limitations. Our procedures are, however, more complex than those used for property-based texturing.

VISUALIZING SURFACE DATA

Many of our rendering procedures are implemented using the Application Visualization System (AVS), a data-flow system for scientific visualization. 14,15 Visualization methods are carried out by connecting supplied or custom AVS modules to form a network. Within an AVS network, polygons, vertices, and texture images are passed between modules and the AVS renderer. Rendering is done on a DEC 3000 AXP model 500 workstation with a Denali graphics accelerator from Kubota Pacific. The Denali has hardwareassisted texture mapping, and on platforms that do not have this feature, AVS does texture mapping in software, although this is considerably slower. AVS imposes data-type constraints between modules, but the user defines the data semantics. Our AVS data structures for molecular applications are described in Ref. 16. The modular structure of AVS, however, results in additional overhead when creating geometries. Texture mapping reduces this overhead as discussed below.

We now describe how to visualize surface information on molecular or parametric surfaces. We use two procedures to create the texture image. If the surface property does not have a parametric description, the texture image is created by sampling and interpolating the original data. If the surface property has a spherical harmonic or other parametric representation, the texture image is created analytically. The analytic representation has the advantage that calcula-

tions often have higher precision, especially in cases in which first or second derivatives are required.

An advantage of this procedure is that texture coordinates have a one-to-one correspondence with the molecular surface; no texture coordinates are duplicated. Because of this convention, the same texture image can be used on the original molecular surface or its spherical harmonic representation. Each of these surfaces is transformed to a unit square through its unit sphere representation. Examples of these procedures are given below.

Rendering numeric surface data

We use our spherical mapping procedure to create a texture image for the original molecular surface or its spherical harmonic representation. The following procedure creates a texture image for an atomic property that does not have a parametric representation but is defined at each surface vertex. Recall that each point on the molecular surface has a unique (θ, ϕ) spherical coordinate. These coordinates are normalized to form the texture coordinates (u, v). A texture image that covers this texture space is created using a modified version of the ray intersection procedure described above. For each spherical coordinate, we determine the triangle (in the unit sphere representation of the molecular surface) that the ray intersects. Each vertex of this surface is assigned to a specific atom of the original structure. Recall that we create an integration map for the spherical harmonics by interpolating the vertex data from this intersection triangle. To create texture data, we simply use the datum value of the closest vertex. This creates sharp boundary between data elements instead of a smooth transition that would be obtained by interpolation. By repeating this procedure over the entire unit sphere using a constant angle increment, we create a two-dimensional array of the atomic property to be used as the texture data. This array is color coded to create the texture image. One advantage of AVS is that it has interactive tools to specify the color coding of the data array.

One limitation of this method is the computational cost of sampling the unit sphere representation to create data on a unit square. This procedure creates a high-resolution representation of the surface data but the number of pixels in the texture image is much greater than the number of vertices in the polygonal model. A limitation is that each surface property (Cartesian coordinate, shape measures, hydrophobicity, etc.) would require resampling the sphere. To improve the efficiency we precompute the intersection triangle and the triangle interpolation constants for each spherical coordinate so that interpolation of new surface data can be done more rapidly. We do not need to recompute the intersection triangles for each new surface property. This table, however, must be sampled or recomputed for different angle increments.

Rendering parametric surface data

Because spherical harmonic expansions can represent surface properties in addition to surface geometry, we can analytically define the surface data used in the texture image instead of numerically interpolating the data values on the

unit sphere. With spherical harmonics we can define texture images of surface data at different spatial resolutions. For example, to represent the surface hydrophobicity we first create its spherical harmonic representation from the numerical surface data. After computing the expansion coefficients, we reconstruct the hydrophobicity at the desired level of detail. To use texture mapping we compute a two-dimensional data array of the hydrophobicity in spherical coordinates using a constant angle increment. This creates a two-dimensional array of hydrophobicity values indexed by the θ and φ coordinates. By color coding these data we produce the texture image.

Color Plate 1 shows the molecular surface of bovine pancreatic trypsin inhibitor (BPTI; from 1tpa.pdb [Ref. 17]) and an order 30 spherical harmonic representation. The surfaces are color coded by the order 20 residue-based hydrophobicity, and the same texture image is used for both surfaces. Because there is a single mapping from a surface to the unit sphere, the (θ, ϕ) spherical coordinates for the original molecular surface, the spherical harmonic surface, and the hydrophobicity are the same.

With this method we can create different combinations of surfaces and properties: molecular surfaces with a sampled texture, molecular surfaces with a parametric texture, parametric surfaces with a sampled texture, and parametric surfaces with a parametric texture.

Texture mapping intermolecular interfaces

Our parametric surface representations were developed for a program to analyze and predict protein—protein interactions. Parametric methods are well suited to this problem because most intermolecular interfaces have significant complementarity of geometric and physical properties even at low spatial resolution.

One method to analyze these interactions is to create an interfacial surface between two interacting molecular surfaces. This highlights the geometry of the interface and creates a surface where the physical properties of each subunit can be displayed to assess the complementarity of shape, hydrophobicity, charge, and so on. Similar methods have been used by others. An advantage of parametric representations is that the interfacial surface can be computed and displayed with the same interactive control techniques as the surfaces themselves.

The interface is defined as the locus of points "halfway" between two molecular surfaces. For each point of the first surface, we find the point of the second surface that is closest to it. The interface point is the midpoint between these two points. We use a binary spatial subdivision tree to generate the pairs of close points. 19 This procedure is repeated for each point of the first surface. The surface defined by the interface points is created using the polygon definitions (vertex connectivity) of the first surface; the connectivity of the interface points does not have to be recomputed. The interface denotes a potentially significant interaction if the distance between the points is less than about 2.0 Å. A polytriangle clipping procedure culls triangles if the pairwise distance is greater than a user-specified threshold. An interesting feature is that this procedure works for molecular surfaces, spherical harmonic surfaces, or even combinations of the two.

Interfaces defined by the closest point criterion have the advantage that they can be computed interactively but are only an approximation. One limitation is that the interface definition is asymmetrical; interchanging the two surfaces yields a slightly different interface. Also, the correspondence between the two surfaces using the closest point criterion is not always continuous in regions where there are gaps between the surfaces. These effects are shown in Figure 1.

To assess the complementarity at the interface, we can display it using vertices color coded by the surface properties of the interacting subunits. This procedure has the disadvantage that displaying a new surface property on the interface (e.g., shape, electrostatic potential, hydrophobicity) requires that we execute the module that generates the interface geometry from the closest point information. This operation is expensive in AVS because of the overhead of the data-flow model. In contrast, switching between texture maps is rapid when the geometry is constant. We define the texture coordinates of the interface using one of the interacting subunits, and can use different texture images for this subunit and the interface. (One limitation of AVS 5.02, however, is that the Geometry Viewer module can have only one dynamic texture, that is, a texture that is generated from other AVS modules.)

Another application of these procedures is to show properties of one subunit displayed on the surface of the other subunit. The interface generation procedure determines a correspondence between the surface points of one subunit and the other. Using this relation, we set the texture coordinate of a vertex of one subunit to the value of its corresponding vertex on the other subunit. Triangles outside the interface region are assigned texture coordinates of (-1, -1) so that they will not be texture mapped. Color Plate 2 shows an example of texture mapping of an intermolecular interface.

TEXTURE DATA PROCESSING

Our procedure for generating texture coordinates allows us to create a planar topographic representation of surface properties. One advantage of this representation is that a wide variety of image processing tools can be brought to

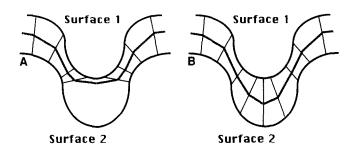


Figure 1. Limitations of the closest point criterion for defining intermolecular interfaces. (A) The interface from surface 1 to surface 2. (B) The interface from surface 2 to surface 1. Note that in interface A, not all points of surface 2 inside the pocket are mapped by the closest point criterion.

bear for analyzing and processing surface data. These include contouring, interpolation, compositing, and filtering.

AVS has interactive tools for computing isovalue contours of two-dimensional image data. One limitation of contouring is that contour lines show aliasing (pixelation) with small (500 by 250 pixel) texture images. For some applications this aliasing is unacceptable. One method to reduce aliasing is to interpolate the data to create a larger texture image before contouring. Color Plate 3 shows a BPTI molecular surface and its order 10 spherical harmonic surface texture mapped with hydrophobicity data. The spherical harmonic texture image was reconstructed to order 20 and interpolated to a size of 1 000 by 500 pixels so that the contour lines appear smooth.

Many image-processing operations such as convolution or Fourier transforms can be used with the texture data. Care must be exercised, however, to ensure the proper symmetry of the image operations. Recall that in our representation, data at the left edge of the texture image are continuous with the right edge. Operations that do not observe this symmetry will introduce an artifact at the edge of the texture. Also, we must be aware that an area element in the texture image is not the same when applied to the molecular surface.

Although these methods must be applied carefully when analyzing surface data, many applications in animation do not have such stringent requirements. We believe that these tools can be used effectively in animation of molecular interactions to produce more illustrative and computationally efficient renderings of proteins and other cellular components.

In most of our applications, we display surface properties by color coding the data, and use hardware-assisted texture mapping to do this efficiently. Another method is to code the data using different texture elements (dots, crosshatch, etc.) instead of color. In addition, we can select regions within different texture elements and composite them into a single image for application onto a surface. Selection can be done interactively or based on surface data. By this method, we can represent several surface regions or surface properties using different texture elements. For example, Figure 2 shows an order 10 surface of BPTI texture mapped using three texture elements. The regions for each element were selected interactively. Because these texture elements are not created by the spherical mapping procedure, there is distortion at the poles. This method can be improved by modulating the texture elements using the surface area information so that they tile the surface more uniformly.

INTERACTIVE VISUALIZATION

The need for photorealistic rendering in numerous graphics applications will increase the development of hardware-assisted texture mapping, and the computational cost of texture mapping relative to triangle rendering is likely to decrease in the future. With AVS, it is more expensive to recreate a geometry with new texture coordinates than it is to apply a new texture map. We believe that many of the new graphics environments will have this characteristic. Instead of doing expensive polygon manipulation, we try to do operations using the texture data. For example, by pre-

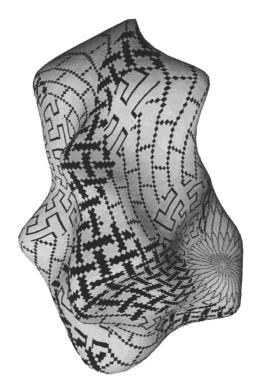


Figure 2. An order 10 spherical harmonic surface of BPTI texture mapped using three texture elements whose positions were selected interactively.

computing several texture images we can rapidly switch between them or do animations by altering the colormap.

One advantage of AVS is that the texture image can be sampled interactively to reduce its size and improve interactive response time. With the Denali renderer, texturing a 90 by 180 pixel image (2° increments) is about twice as fast as texturing a 360 by 720 pixel image (0.5° increments). For some surface properties there is little degradation of the surface detail after sampling the texture image to 2° increments.

One feature of the Denali renderer is that surfaces can be rendered in a mode called "Outline Gouraud," in which a wireframe mesh showing the polygon outline is rendered with the Gouraud shaded polygon. During texture mapping, the wireframe mesh is colored using vertex colors. With this rendering option, we can simultaneously display high-resolution surface detail as a texture map and lower resolution information using the vertex colors. The AVS renderers on other platforms may blend the texture image with the Gouraud shaded triangles using the vertex colors.

One advantage of the parametric surface representation is the hierarchical structure of the subdivision mesh. As described in Refs. 10 and 16, we interactively control the resolution of the triangle mesh independent of the resolution of the spherical harmonic surface. An important observation is that the low-resolution triangle mesh indexes the correct texture coordinates. Thus we can change the surface triangulation using the same texture image. This is an important feature for interactive applications; by altering the complexity of the scene we can change the interactive response time. We can rapidly switch between different triangulation meshes, surface coordinates, or texture images. These con-

trols are interactive and independent. Color Plate 4 shows four images of BPTI rendered with the same texture image but different surface triangulations.

We have used these methods to represent and display spherical harmonic surfaces during normal mode vibrations, ¹⁰ and texture mapping can also be applied to these surfaces.

One application that we are investigating is the use of these procedures in molecular animation. For some applications, the low-resolution description of molecular structure is more instructive than a detailed atomic model; cartoon diagrams of molecular information are common. The tools described here are ideal for this application. Even in cases in which atomic detail is required, the spherical harmonic methods can be applied to define quickly the motion of the surfaces using low-resolution representations before rendering the detailed model.

CONCLUSION

Texture mapping is a powerful tool for adding surface detail to geometric models and improvements in graphics hardware will increase its applicability to molecular graphics. Texture mapping molecular surfaces and isodensity contours is well established, but parametric surfaces allow many rendering and geometry attributes (resolution, triangulation, texture coordinates) to be controlled interactively and independently. A key element in implementing our procedures is the use of location-based instead of property-based texture coordinates. The spherical harmonic representation is flexible; many computations can be done using the original molecular surface or its spherical harmonic approximation. We can also apply image processing tools to the texture data.

We believe that it is important to give the user control of the rendering parameters that affect the interactive response time. With our framework, we can develop techniques that run on a wide variety of hardware platforms without sacrificing functionality. These methods increase the flexibility and applicability of texture mapping for molecular applications.

Additional images rendered with these techniques are available on the World Wide Web at: http://www.scripps.edu/pub/olson-web/doc/harmony/harmony.html.

ACKNOWLEDGMENT

This work was funded by NIH Grant GM38794 (to A.J.O.).

REFERENCES

1 Catmull, E.E. A Subdivision Algorithm for Computer Display of Curved Surfaces. Ph.D. Dissertation, University of Utah, Salt Lake City, 1974

- 2 Blinn, J.F. and Newell, M.E. Texture and reflection in computer generated images. *CACM* 1976, **19**(10), 542–547
- 3 Richards, F.M. Areas, volumes, packing and protein structure. *Annu. Rev. Biophys. Bioeng.* 1977, **6**, 151–176
- 4 Teschner, M., Henn, C., Vollhardt, H., Reiling, S., and Brinkmann, J. Texture mapping: A new tool for molecular graphics. *J. Mol. Graphics* 1994, **12**, 98–105
- 5 Connolly, M.L. The molecular surface package. J. Mol. Graphics 1993, 11(2), 139-143
- 6 Connolly, M.L. Analytical molecular surface calculation. *J. Appl. Crystallogr.* 1983, **16**, 548–558
- 7 Sanner, M.F. Modeling and Applications of Molecular Surfaces. Ph.D. Dissertation, Université de Haute-Alsace, France, 1992
- 8. Sanner, M.F., Olson, A.J., and Sphener, J.-C. Reduced surface: An efficient way to compute molecular surfaces. *Biopolymers* (in press)
- 9 Duncan, B.S. and Olson, A.J. Approximation and characterization of molecular surfaces. *Biopolymers* 1993, 33, 219–229
- 10 Duncan, B.S. and Olson, A.J. Approximation and visualization of large-scale motion of protein surfaces. *J. Mol. Graphics* 1995, this issue
- 11. Duncan, B.S. and Olson, A.J. Predicting proteinprotein interactions using parametric surfaces. In: *Pro*ceedings of the 13th Molecular Graphics Society Meeting, 1994
- 12 Max, N.L. and Getzoff, E.D. Spherical harmonic molecular surfaces. *IEEE Comput. Graphics Appl.* 1988, **8**(4), 42–50
- 13. Leicester, S.E., Finney, J.L., and Bywater, R.P. Description of molecular surface shape using Fourier descriptors. *J. Mol. Graphics* 1988, **6**(2), 104–108
- Upson, C., Faulhaber, T.J., Kamins, D., Laidlaw, D., Schlegel, D., Vroom, J., Gurwitz, R., and van Dam, A. The Application Visualization System: A computational environment for scientific visualization. *IEEE* Comput. Graphics Appl. 1989, 9(4), 30-42
- 15 Bowie, J.E., Olson, A.J. (eds.). Data Visualization in Molecular Science. Addison-Wesley, New York, 1995
- 16 Duncan, B.S., Pique, M., and Olson, A.J. AVS for molecular modeling. In: *Proc. AVS '93 Conf.*, Int. AVS Center, Research Triangle Park, North Carolina, 1993
- 17 Bernstein, F.C., Koetzle, T.F., Williams, G.J.B., Meyer, E.F.J., Brice, M.D., Rodgers, J.R., Kennard, O., Shimanouchi, T., and Tasumi, M. The Protein Data Bank: A computer-based archival file for macromolecular structures. J. Mol. Biol. 1977, 112, 535-542
- 18 Goodsell, D. Personal communication.
- 19 Barnes, J. and Hut, P. A hierarchical O(N log N) force-calculation algorithm. Nature (London) 1986, **324**(4), 446–449