Stereoscopic viewing system for proteins using OpenRasmol: a tool for displaying a filament of proteins

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We have made a stereoscopic viewing system for a large assembly of proteins using OpenRasmol. The stable version 2.7.1 of OpenRasmol is modified for the system, which uses an eye-ware instead of trained bare-eyes. Software rendering and other benefits in OpenRasmol are reserved. A 3-D graphic board is used just for the active stereo method, not for the acceleration of rendering. Our modification is simple one. In the results, an actin filament of 16-mers, where one actin monomer has about 400 residues, in space filling model can be rendered in stereoscopic viewing mode and can be made one turn within 10 seconds as quick as non-stereoscopic mode. Other 3-D molecular graphics programs with 3-D accelerator boards cannot render such a large assembly of molecules in stereoscopic usage mode as quickly as the modified OpenRasmol. An attractive application of our system is stereoscopic viewing with a large 200 inch screen in passive stereo method. Simultaneous usage is available for more than 100 persons with inexpensive eyewares. The large screen allows us to investigate an interior of a groove in an actin filament in detail. Our modified OpenRasmol is distributed following the license, RASLIC, as an open source code at our web site (www.irisa-lab.bio.kyutech.ac.jp/openrasmol), where video files showing rendering speeds of our modified OpenRasmol are also available.

Key words: Molecular graphics, Space filling model, Virtual reality system, protein assembly, F-actin

Increasing number of protein 3-D structures in the protein data bank lead to progress in visualization software and hardware for viewing 3-D structures of proteins. Space filling model of protein is widely used in spite of its high demand of computer resources. Main reason is surely that we cannot distinguish repulsive contact between atoms in wire frame representation of covalent bonds. Interactive representation, translation, rotation and zooming, in the space filling mode produces intuitive understanding of a 3-D structure of a protein molecule by realizing an envelope of the protein. These circumstances require real-time representation in space filling mode. But 3-D structures of a large protein or a protein assemble are cannot be understood despite of the slow response of rendering. On the other hand, hard ware graphics board provides simple usage of input/output devises, especially stereographic rendering. This situation leads us to the hybrid of software rendering and hardware graphics board. But, stereographic calculation is not so easy, especially instantaneous usage with 3-D pointing devices. For example, Java3D does not provide such a plat home.

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Molecular graphics software, OpenRasmol\textsuperscript{3,4} (http://www.openrasmol.org), has been widely used in the world, which has following features. First, OpenRasmol displays molecules in various models including space filling model based on a three dimensional structure of a molecule from a file with a standard format, for example Protein Data Bank format\textsuperscript{1}. Second, an image of a molecule is rendered in a unique algorithm\textsuperscript{3} without using a particular 3-D graphics board. OpenRasmol can quickly render any large molecule so that it can have potential of interactive translation and rotation of a molecule. Many functions for analyzing molecular structure exist in OpenRasmol. For example, hydrogen bond and covalent bond capability between two atoms can be examined. Bare-eyes stereo viewing\textsuperscript{2} was also supported in OpenRasmol, but it is a little inconvenient for users. Hence, adding a new feature for stereoscopic viewing with eye-wares\textsuperscript{2} has been requested by OpenRasmol users. Source codes of OpenRasmol are open. Anyone can use and modify the program. Licenses on OpenRasmol are documented in the OpenRasmol web site. OpenRasmol is portable to UNIX (SUN\textsuperscript{™}, SGI\textsuperscript{™}, HP\textsuperscript{™}, etc.), Linux\textsuperscript{™}, MS-Windows\textsuperscript{™}, and Macintosh\textsuperscript{™} platform. In this study, we have added a new function to utilize virtual reality techniques\textsuperscript{2}, especially, stereo-graphic display using a large screen with a three dimensional pointer.

We have planned to construct stereoscopic viewing system keeping all benefits of OpenRasmol advantages. To achieve the purpose, we carefully gave modifications to OpenRasmol caused by addition of new 3-D devices that are appropriate input and output devices for virtual reality system. We changed two parts; one is already built in stereoscopic view function for bare-eyes, which is modified to use active stereo function\textsuperscript{2}, the other is a three dimensional pointer in order to show structural information by clicking an atom. Our modified OpenRasmol is based on version 2.7.1 released in 1999, which is a stable version for a long time\textsuperscript{4}.

**Method**

Our modifications have three new features. First, both software and hardware rendering is used (Figure 1). Mole-

![Figure 1](image-url)  
**Figure 1** Schematic illustration of data flow of our modified OpenRasmol: hardware and software parts are connected to enable both quick rendering and usages of 3-D devices in time. The instantaneous geometry is calculated in the software to find the corresponding 3-D object that 3-D pointer is pointing. Because the geometry data contained in 3-D graphics board cannot be extracted from the board. The shaded part is added to OpenRasmol for modifications in this work.
molecules are rendered in software rendering. Software Z-buffer in Rasmol has been used for this purpose. Second, 3-D pointer has been made with 3-D input devices. Third, finding function of matched position of 3-D pointer position with an atom in virtual reality space utilizes Rasmol Z-buffer, which reduces computational cost of geometrical calculation of interactive operation, e.g. rotation. Hardware rendering usually does not allow direct usage of calculated geometrical positions of 3-D objects in the graphics memory on-board. To identify the 3-D object that a 3-D pointer points, programmers are forced to make the function that search the painted 3-D object from geometry calculated in the application in spite of the existence of the same calculated geometry contained in the graphics board.

OpenRasmol can quickly display any larger molecule in space filling model. It renders faster than other software even if which works with 3-D hardware rendering accelerator. Other software which uses a hardware rendering accelerator can display images of a small molecule very quickly. But, even now, size of memory on the hardware accelerator is limited to less than few hundred of mega bytes. A large molecule or assembled molecules whose total 3-D object size is over a few mega bytes cannot utilize hardware acceleration and is displayed slowly. For this problem especially for space filling model, most of molecular graphics viewers have a rough rendering mode during rotation and translation of molecules where spheres corresponding to atoms are displayed low polygons. OpenRasmol does not have such limitation and has a software rendering module optimized for molecular graphics. For example, assembled proteins having about 4000 residues consisting of about 40000 atoms in total can be displayed interactively during rotation as quickly as a small molecule even in space filling model of all atoms.

OpenRasmol can render a molecule with complicated shape composed of many spheres in space filling model. Accelerating the speed of rendering a lot of fused spheres was a difficult task. First release version of Rasmol preceding OpenRasmol has succeeded in it by using raster rendering for spheres. OpenRasmol renders dot by dot following raster rendering using Z-buffer technique inside the application. Surface of a regularized sphere is divided into discrete cells in the preparation without using vector rendering, e.g. triangulation of a sphere, and hidden-surface culling is performed with the prepared cells at final rendering of fused spheres. Some hardware specific optimizations in the compilation of the program are used in the codes of OpenRasmol, e.g. “resister” instructions in C language codes. Hence, the amount of calculations does not depend on the number of spheres, but depends on the resolution of the final image. Consequently, a large molecule consisting of many atoms can be rendered quickly by using OpenRasmol.

On the other hand, stereoscopic viewing using eye-wares requires some special hardware. There are two types of eye-wares, which are active stereo and passive stereo. Active stereo eye-wares are known as crystal eye-wares and are used for a variety of research and other fields. Active stereo requires a hardware which outputs serial signals of time divided for both left and right images. 3-D graphics boards with quad buffer stereo are widely used. Most of these boards adopt OpenGL™ 6.7. OpenGL™ is well known and implemented in a wide variety of platforms, e.g. SGI™, SUN™, Apple Macintosh™, PC (MS-Windows™ or Linux™).

To achieve our purpose, both active stereo function in a 3-D graphics board and software rendering inside OpenRasmol are required. We utilized left and right images in OpenRasmol and transferred them into left and right buffers inside the 3-D graphics board for active stereo function by using gDrawpixels™ that is one of functions of OpenGL. We have ported the modified OpenRasmol to Linux™, SUN™, and SGI™ machines. In the case of 3-D stereo, a usual pointer, e.g. a mouse, cannot move depth direction. We have also made 3-D pointer that uses real-time 3-D position sensors™ (Isotrack™). A 3-D arrow object is displayed and clickable to show what atom in the molecule is clicked in 3-D space. Therefore, 3-D interactive pointer has depth coordinate and the arrow is invisible inside the molecule as a result of hidden surface removal.

Applications

We checked our system for assembled proteins. An actin filament™ is used as an example which is a double helix consisted of arranged actin monomers of about 400 residues in each monomer (Figure 2). The term “polymerization” is used in the formation of an actin filament. But in physicochemical sense, actin monomers are associated into an actin filament. There is no covalent bond between actin molecules in the actin filament. Many studies on actin molecules have been reported because actin has wide variety of biological functions in a cell as a motor protein. It is important to investigate the structure of actin filament where ATP, phalloidin and other small molecules are attached depending on biological conditions. Experiments with X-ray diffraction or electron microscope require detailed stereoscopic visualization of molecules in a large filament structure. In the application of computer graphics, size of an actin molecule is large to render in space filling model because a sphere representing an atom needs a lot of polygons to be displayed with a smooth surface. An actin filament consisting of 16 molecules is used as a sample to check modified OpenRasmol for stereoscopic viewing. Speed of stereoscopic rendering using the modified OpenRasmol is enough for large proteins and assembled proteins like actin filaments.

Speed performance is enough to display all atoms in the actin filament in space filling model. Further, real time rendering in stereoscopic view is achieved during rotation operation by a user. We have tried modified OpenRasmol on Linux™ (pentium™ 4, 1.8 GHz), SUN™ (Blade 200), and SGI™ (Octane R1000) machines, with graphics boards,
ATI™ RADEON 9200 128 MB/RADEON 8500 128 MB, SUN™ XVR-500, and SGI™ SI, respectively. We measured the time for one rotation operation on the Linux™ machine which has 1024×768@100 Hz display mode. It takes less than 10 seconds for one rotation operation about the axis of the actin filament composed of 16 molecules, even in the case of stereoscopic viewing mode. On the other hand, a molecular graphics application, VMD5, which uses hardware rendering with a graphics board, cannot achieve one rotation for the actin filament because of slow responses. In this case, required graphical memory is larger than that in the graphics board. Readers can check the speed of the modified OpenRasmol by accessing video files showing the speed of rotation of an actin filament at the web site (http://www.irisa-lab.bio.kyutech.ac.jp/rasmol). Other machines listed above have almost the same potential of rendering in modified OpenRasmol as the Linux™ machine.

It is useful to watch these proteins on a large screen because both a global structure of associated proteins and detailed structures in proteins are simultaneously recognized. In the next step, we applied this modified OpenRasmol to a large screen of 200 inches to cover all range of vision of a user to the best advantage of virtual reality system. Passive stereo method2 is used for a large screen. Unfortunately, bright liquid crystal projectors for a large screen cannot be used for active stereo method. Response speed of liquid crystal is not enough to 100 Hz refresh rate, which is slowest speed of flicker free in active stereo method. Then passive stereo method is adopted with polarized light system consisting of special screen and inexpensive eye-ware of polarizers. To keep convenience of usage of the modified OpenRasmol, we used an active-passive converter of commercial product, CYVIZ™ xpo.2.

Large size of the screen changes degree of intuitive understanding of detailed structure of an actin filament. For example, we can easily recognize a groove along a spiral path of the filament8 where interior and exterior of the filament is connected through space. The groove is known as an outgoing channel for phosphate (Pi) molecules dephosphorylated from ATP attached interior of the filament. Stereoscopic viewing enables us to take a good look at complicated interior of the filament from the exterior, e.g. locations of ATP, Ca, and phalloidin. On a large screen, the filament is looked like the thick trunk. An actin molecule at just front of our eyes is looked as if it were protruded from the trunk.

Discussion

In these days, entries of large proteins and protein assemblies are increasing. Our approach is suitable for these progresses in protein data bank1 of three dimensional structures. Many works relating to molecular graphics displaying large molecules especially proteins use high performance 3-D graphics board which can render many polygons using specialized processors in the board. Nowadays high performance graphics board is getting more inexpensive. But the targets of biology, bioinformatics, or biophysics are sometimes huge assemblies of large proteins with many functions by cooperation of protein assemblies.

Our work is relating to an application of VR system to molecular model for especially biomolecules. Large molecules which are represented as seventy thousands spheres

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**Figure 2** Images of an actin filament using space filling model in modified OpenRasmol. A) whole image of the filament, More than 70000 spheres are rendered in this figure. Each heavy atom is colored gray (carbon), red (oxygen), blue (nitrogen), or yellow (sulfur), respectively. B) Image zoomed about 5 times from the previous one. The filament consists of 16 monomers each of which has about 400 residues. Each molecule is colored in gradation from blue to red along the main chain of the protein. Display resolution is XVGA. For convenience, figures are monocular mode, but stereoscopic viewing mode is enabled in the system of modified OpenRasmol.
can be displayed quickly in responding for user manipulations, translation, rotation, and resizing. Stereoscopic viewing enables us to get intuitive recognition for interior of the molecular assemblies for example actin fibers for filaments made of 16 monomers. Many proteins are known to bind an actin filament and have biological functions with actin filaments. Concave regions in the surface of the actin filaments and narrow grooves connecting the interior and exterior of actin filaments can be visualized stereoscopically in our system.

Observation using VR system is an appropriate application for protein assemblies having functions as a skeleton of the cell in molecular details. Dynamic operation for visualized protein assemblies requires very high computer resources in cooperation of software and hardware rendering. Software rendering enable quick drawing of many spheres as atoms belong to each protein. Hardware function of 3-D graphics board enables us to use stereoscopic display outputs together with 3-D devices for manipulating molecules. Our work shows the system for displaying biomolecules by using both software and hardware techniques. Our work is unique because the size of protein does not affect display speed for rendering in spite of the many objects of spheres.

Our stereoscopic viewing system with modified OpenRasmol is satisfactory for a structured assembly of proteins. Remarkable success is application to interactive rotation of an actin filament on a large screen. Some researchers in molecular science are trained to view two images put side by side that are taken from left and right angles into one stereoscopic view with bare-eyes. But only half of the screen is the maximum size of stereoscopic viewing with bare eyes. Especially in the case of a large screen with bare-eyes method, a user cannot see as one stereoscopic view because of too wide field of vision. Furthermore, some people cannot get a stereoscopic view by nature only with bare-eyes. A passive stereo system, with a polarized light and a large screen, is suitable for simultaneous usage for many users. Stereoscopic eye-wares for passive stereo viewing are very inexpensive than for active stereo ones. This work has been pushed forward by quick progress in basement of computer graphics. We are not going to explain details in this article on how to configure stereoscopic systems using XIG™ Accelerated X with one inexpensive “monaural” graphics card (e.g. ATI™ RADEON 8500) on an inexpensive but powerful Linux™ machine.

In actual application, our system has been used for educational or research seminars on molecular science for multiple users. For a single user, this system can be used as a high resolution 3-D display system. If you have already had an active stereo system, you can compare your 3-D molecular graphics program with our modified OpenRasmol. Then you can check how fast the response of modified OpenRasmol in rendering molecules even when a lot of molecules are displayed at the same time. Our modified OpenRasmol is distributed following the license, RASLIC, as an open source code at our web site (www.irisa-lab.bio.kyutech.ac.jp/openrasmol), where video files showing rendering speed of our modified OpenRasmol also exist.

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