

PORTING LEGACY APPLICATIONS TO IMMERSIVE VIRTUAL ENVIRONMENTS

A Case Study

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Abstract: Immersive virtual environments are becoming increasingly common, driving the need to develop new software or adapt existing software to these environments. We discuss some of the issues and limitations of porting an existing molecular graphics system, PyMOL, into an immersive virtual environment. Presenting macromolecules inside an interactive immersive virtual environment may provide unique insights into molecular structure and improve the rational design of drugs that target a specific molecule. PyMOL was successfully extended to render molecular structures immersively; however, elements of the legacy interactive design did not scale well into three-dimensions. Achieving an interactive frame rate for large macromolecules was also an issue. The immersive system was developed and evaluated on both a shared-memory parallel machine and a commodity cluster.

1 INTRODUCTION

As immersive environments become more ubiquitous, so does the desire to adapt legacy three-dimensional applications to operate within these environments. However, tightly integrating the functionality, particularly interactive functionality, of a legacy three-dimensional application within an immersive virtual environment (IVE) may not be possible without major redesign of the application's architecture. This paper addresses design issues, implementation issues, and the overall effectiveness of extending PyMOL (DeLano 2002), an existing open-source molecular graphics software system, to support the visualization and manipulation of virtual macromolecules within an IVE.

PyMOL was successfully extended using CAVELibTM to render its molecule representations inside a CAVE-like IVE. This allows crystallographers to physically walk around the macromolecule representations and view them from multiple perspectives. Extending the rendering capabilities was straight-forward; however,

integrating the interactive molecular editing features of PyMOL was less successful. The initial intent was to provide a true three-dimensional interface for all the molecular editing capabilities of PyMOL. Providing this interface was hindered by two underlying design principles of PyMOL. First, virtual objects are selected in PyMOL using an off-screen buffer color-coding scheme, which is inappropriate for immersive environments. Secondly, all PyMOL editing is done directly to the chemical data structures and not to their graphic representations. For large molecular structures this introduces an inefficiency that makes interactive editing impossible. Therefore, our port is currently incomplete: it only allows the manipulation (translation and rotation) of complete molecular structures but not individual atoms and bonds. However, this is still a useful result, allowing crystallographers to investigate the fitting between two or more molecules.

This work is motivated by a larger pilot study to determine if there is added value in using immersive visualization as a molecular research tool. The shape

of a molecule provides the basis for its function. This is the principle behind *rational drug design*, which uses structural information to design drugs that bind with high affinity and specificity to a therapeutic target. The effective visualization of three-dimensional molecular structure can play a critical role in understanding molecular function, leading to better drug design. However, understanding the complex irregular geometry of multiple macromolecules is a daunting task. Even more complicated is interacting with and manipulating these complex three-dimensional structures. Therefore, immersive visualization of molecule structures has long been proposed to cope with the complex three-dimensional nature of molecule biology (Ihlenfeldt 1997).

There exists a common intuition that an immersive virtual environment can provide an improved interface to view and interact with complex three-dimensional datasets compared to the more traditional graphics workstation (van Dam 2000). This intuition is based on the fact that an IVE provides the user with an egocentric three-dimensional point-of-view, allowing the user to view and interact with the data space using “natural skills.” There have been recent studies that have shown that some three-dimensional tasks can be improved when the data is presented and manipulated in an IVE (Pausch 1997, Arns et al. 1999, Swan et al. 2003, Gruchalla 2004). However, the results are mixed. Several of these and other studies have also shown reduced performance in accomplishing various tasks in an IVE (Pausch 1997, Arns et al 1999). The suggestion is that the applicability of an IVE is highly task dependent. Therefore, the principle thesis of our larger effort is to determine if an immersive interface can improve the rational design of drugs that target a specific molecule.

2 PYMOL

PyMOL is a powerful and versatile open-source, cross-platform molecular graphics system with an embedded Python interpreter. It is capable of real-time visualization using OpenGL[®] and the generation of high-quality, ray-traced images. PyMOL supports most of the common representations for molecular structures: wire bonds, cylinders, spheres, ball-and-stick, dot surfaces, solid surfaces, wire meshes, backbone ribbons, and cartoon ribbons. Proteins and electron densities can

be imported from many file types (e.g., PDB, SDF, and MOL) (DeLano 2002).

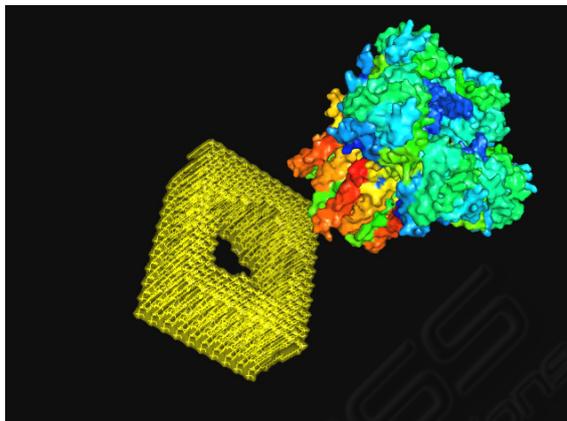


Figure 1: A PyMOL rendered visualization of a membrane-bound protein docking to a membrane (yellow).

PyMOL is written in C, but its primary interface is an embedded Python interpreter. The basis for its sophistication is the PyMOL scripting language, a superset of Python. All of the features of PyMOL are accessible through a command-line interface. PyMOL also provides an external Tcl/Tk GUI and a simple internal OpenGL menu system. Both are merely wrappers around PyMOL scripting commands: button presses in the GUI generate PyMOL script that is then evaluated by the embedded interpreter (DeLano 2002).

There are several immersive molecular visualization tools that have already been developed. VRMol is an immersive application that allows for the interactive investigation of multiple complex molecules (Hasse et al. 1996). RealMOL is another more recent example of an interactive immersive molecular research tool (Ai and Fröhlich 1998). However, in the context of our larger research goals, extending PyMOL provided several advantages over existing immersive molecular applications. The driving motivation behind this work is to design an empirical experiment to study the benefits of using immersive visualization in rational drug design. A team of crystallographers, from which we will draw our test subject population, recommended PyMOL for its sophistication, quality of visualizations, and user-adjustable parameters. PyMOL is currently being used within this target population as a desktop molecular research tool. Drawing from an experienced user-base will allow us to conduct a comparative study of a real-world application on real-world problems. A secondary factor in the selection of PyMOL was that it has been released

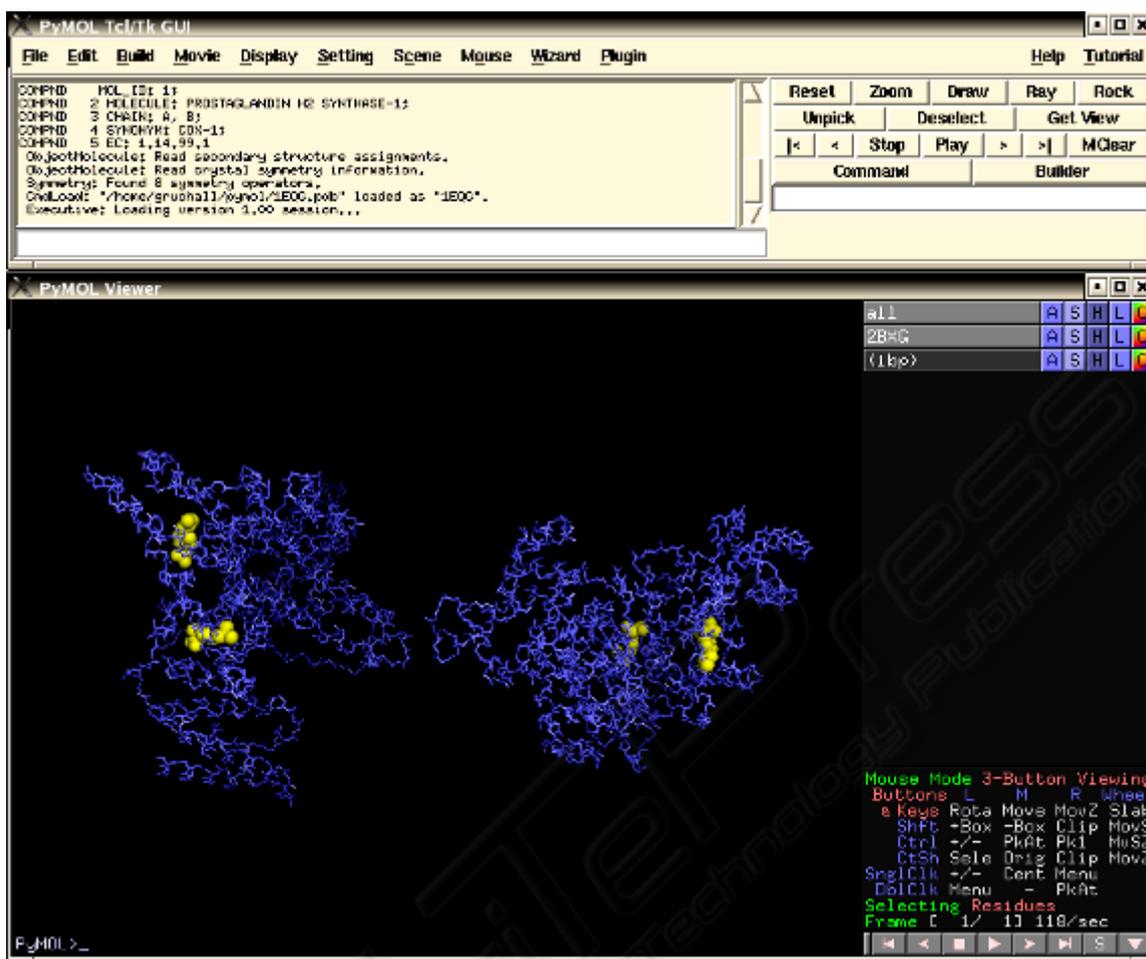


Figure 2: Desktop version of PyMOL (DeLano 2002). PyMOL provides a Python-based scripting language, which can be used directly at the command prompt or indirectly through the Tcl/Tk GUI or the simple OpenGL menu system.

under an open-source software license. This provides us the opportunity to contribute to both the immersive visualization and molecular research communities.

3 IMMERSIVE PORT

The intent of the project was to extend PyMOL's three-dimensional rendering and manipulation capabilities into an IVE, allowing crystallographers an egocentric view of molecular structures. Furthermore, the scientist would be able to manipulate the macromolecule at a component level: selecting and manipulating atoms, bonds, and structures directly using a six-degree of freedom input device. The goal of the port was not to replace the desktop version of PyMOL, but rather to augment and enhance the desktop version with an

immersive counter-part. Three architectural areas of PyMOL had to be addressed to provide this functionality: the rendering architecture, thread control architecture, and interaction architecture.

PyMOL provides two mechanisms to render molecular structures: the standard OpenGL pipeline for interactive visualizations, and a built-in ray-tracer for generating static, high-quality images for publication. For the purposes of this port, we were only interested in interfacing with PyMOL's interactive visualization capabilities. We used CAVELib™ to handle the hardware-specific details of the IVE display system. An immersive display callback function was added to PyMOL that is called from the CAVELib™ display loop for each rendered view. CAVELib™ handles the necessary projections for each view and synchronization among views in the IVE. The immersive display function is almost identical to the PyMOL display function, with two exceptions: it allows CAVELib™ to handle

stereoscopic rendering, and it bypasses the additional back-buffer render used in the picking scheme discussed below.

PyMOL is a multi-threaded application with separate threads for the rendering and interaction, the embedded Python interpreter, and the Tcl/Tk GUI. This architecture was easily extended to handle the multiple threads used to render each immersive view. This involved simply adding an additional mutex to prevent resource competition between the immersive displays and the windowed display, and between the immersive interactions and the command driven interactions. Although the development required to extend the thread architecture was minimal, the difficulty of understanding the PyMOL thread control should not be understated. Thorough understanding of the PyMOL and CAVElibTM threads was critical in the success of the port.

PyMOL provides limited but functional molecular editing capabilities. From the command-line, entire molecular structures can be manipulated (e.g., rotated, translated). PyMOL also provides limited mouse-driven editing capabilities. These capabilities allow the individual atoms and bonds of a protein to be selected and transformed. Extending these capabilities to a true three-dimensional interface was hindered by two underlying design principles of PyMOL. First, virtual objects are selected in PyMOL using a back-buffer color-coding scheme. When the user clicks a mouse button, a function renders each pickable object into the back-buffer using a distinct color. The color at the mouse position is read back, and is used to index an array of visible objects. Unfortunately, this process does not scale to a three-dimensional pointing device. The position of the three-dimensional pointing device cannot be projected into the two-dimensions of a single back-buffer since there may be multiple views in an immersive environment. This is further complicated by stereographic projection, since there may be multiple back-buffers per view. Extending PyMOL's architecture to support data structures that can be efficiently selected in three-dimensions will require a sizable effort. As a temporary work-around, we have provided the ability to select objects from the command-line that can then be manipulated within the IVE.

The second problem in adapting interactions into three dimensions was the design of the data structures used to model the molecular structures. PyMOL editing is done directly to the chemical data structures and not to their graphic representations: transformations are applied to each individual atom,

then, the graphical representation of the molecule is reconstructed from the transformed atoms. For large molecules, the construction or reconstruction of certain types of graphics representations (e.g., solid surfaces) can cause a delay of several seconds. Since most PyMOL interaction originates from the command-line, this inefficiency was tolerable. However, for manipulation of objects inside an IVE the potential multiple-second lag between the user's movements and the visualization response was clearly unacceptable as operational feedback. Indeed, if the internal structure of a molecule is modified, the graphics representation may need to be reconstructed. However, if the internal structure of a molecule is not edited and only the molecule's relative position or orientation has been changed, the graphics representation does not have to be reconstructed -- it can simply be transformed with a transformation matrix.



Figure 3: User interactively docking a protein to a membrane (yellow) inside an immersive virtual environment.

To allow rapid independent manipulation of complete molecular structures, we added transformation matrices to encapsulate the position and orientation of the graphics representations during editing. This provides a crystallographer means to investigate the fitting between two or more molecules inside the IVE interactively (see Figure 3). Once the relative positions and orientations of the graphical representations are decided upon, a scripting command has been added to transform and synchronize the chemical data structures with the graphics representations. Currently, there are no means to interactively modify internal molecular structures from within the IVE.

4 RESULTS

System performance is critical, as our pilot users are interested in visualizing and interacting with macromolecules on the order of tens of thousands of atoms. For example, the macromolecule 1GRU has over 58,000 atoms (Ranson et al. 2001). Even a medium-resolution surface representation of this macromolecule has close to one million triangles. To maintain satisfactory spatiotemporal correlation between a user's actions and system responses, an update rate of at least ten frames per second must be achieved (Bowman et al. 2005). Furthermore, the application is stereoscopic, requiring two views to be rendered per frame. Therefore, we would require a throughput of twenty million Gouraud-shaded polygons with specular highlighting per second. This throughput figure is of course for one molecule only, yet for the application to be of value to users, they must be able to interactively manipulate multiple molecules.

Our initial development efforts were carried out on a 20-processor SGI Onyx 3800 with four InfiniteReality3 graphics pipes. The appeal of developing on such a machine is the simplicity of software development: a single application is executed on a single machine, with multiple rendering threads running in parallel. The distinct disadvantage of such a hardware environment is that its graphics performance trails that of recent hardware.

To deliver the performance necessary to maintain interactivity, we ported our immersive version of PyMOL to a four-PC cluster equipped with QuadroFX 3000G graphics cards from NVidia. The clear advantage of such a system is its high-performance graphics capabilities and cost-effective upgrade path, but this system incurs its own costs. With four applications running simultaneously on separate machines, synchronization becomes an issue. CAVELib™ does provide synchronized tracker and controller data to the application; therefore, if the application responds deterministically to these inputs, the cluster nodes will behave identically. Unfortunately, there is no mechanism that automatically synchronizes application-specific events and data.

To avoid requiring that the user replicate commands manually across the four PCs, we have implemented a command distribution mechanism using CAVELib™'s synchronized communication functions. As described earlier, most of PyMOL's functionality is exposed through extensions to the embedded Python interpreter, which accepts

commands as character strings. To achieve command synchronization, we intercept the strings before they are sent to the interpreter, and distribute them to the remote cluster nodes. The only limitation of this approach is that commands must be entered on the master node, since CAVELib™ only exposes a synchronized scatter operation from master to non-master nodes. A major benefit of this approach is that most user-initiated events, even from PyMOL GUIs, are handled as command strings, so these are automatically distributed and synchronized across the cluster.

We performed a small pilot study to assess the usability of the immersive port. Three University of Colorado biochemistry groups were invited to study a molecule of their choice using the immersive version of PyMOL. The biochemistry groups conducted actual research on how the structure of their molecule related to its function. Typically, three or four members of the team would work collaboratively inside the IVE, while one team member would control the visualization from a desktop computer using the PyMOL command-line and desktop interfaces.

Despite the limitations of the immersive port, our pilot users indicate that the immersive version of PyMOL is indeed useful as a research tool. In fact, the immersive examination of the selected molecules led all three research groups to a new understanding of their molecule's functional structure. All three groups reported the discovery of a large spatial feature, such as an empty space or ridge that had not been previously recognized during extensive previous work with the molecule using the PyMOL on the desktop.

5 CONCLUSIONS

In this paper, we discussed some of the issues and limitations of porting PyMOL into an immersive virtual environment. We successfully extended PyMOL to render its molecule representations inside an IVE. However, the interactive molecular editing features of PyMOL have not been completely nor effectively integrated into our immersive version. As a consequence of how three-dimensional objects are represented and how they are selected in PyMOL, full immersive integration of the interactive features will not be realized without a significant amount of work. This port serves as an example that legacy three-dimensional applications designed for a desktop may have made underlying assumptions that will complicate an immersive port. In fact, to fully

integrate the interactive features of a legacy application may require major architectural changes. The following observations can be made from the effort to port PyMOL:

- PyMOL's use of the OpenGL rendering pipeline provided a direct means to extend the molecular visualizations to an immersive platform using CAVElib™.
- Thread-safety was a key issue. Without PyMOL's existing thread-safe architecture the immersive extension would have been vastly more complicated.
- Being based on an embedded Python interpreter, commands strings were easily distributed across a cluster.
- Some object selection schemes designed for two-dimensional pointing devices do not scale well for three dimensional pointing devices.
- Although PyMOL provided molecular editing capabilities, these were not designed to support the interactivity necessary in an IVE.

Much work remains before the immersive PyMOL will be fully capable of supporting rational drug design. The ability to select molecules, bonds, and atoms using a three-dimensional pointing device will be critical to the success of the project. New data structures will need to be added to PyMOL to support this ability. Additionally, the performance of PyMOL must be improved to reach the frame rates necessary for interaction with large macromolecules. Since PyMOL was not architected for rendering to multiple windows, all OpenGL rendering must be done in immediate mode. We are currently investigating options for improving performance, such as allowing display lists to be used in the presence of multiple rendering contexts. Finally, since PyMOL's internal GUIs are rendered using OpenGL, we have begun investigating the possibility of directly rendering them in the immersive environment. Although we do not aim to replicate all of PyMOL's functionality within the IVE, this should improve the overall usability of the immersive port.

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