FvNano: A Virtual Laboratory to Manipulate Molecular Systems

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ABSTRACT

Ray-casting on Graphics Processing Units (GPUs) opens new possibilities for molecular visualization. We used this technique to develop *HyperBalls*, an improved ball & stick representation replacing tubes linking the atom spheres by hyperboloids that can smoothly connect them. This type of depiction is particularly useful to represent dynamic phenomena and can routinely, accurately and interactively render huge macromolecular assemblies with more than 500,000 particles. Combined with Molecular Dynamics (MD) software and haptic devices, it is possible to manipulate molecular objects to study their properties.

KEYWORDS: Molecular Visualization, GPU acceleration, HyperBalls, Molecular Dynamic.

INDEX TERMS: Molecular Visualization (primary keyword)
Manipulation and Deformation
Haptics for Visualization
Molecular Structure and Function

1 INTRODUCTION

Nowadays, an increasing number of structures of molecular assemblies is available in a variety of databases. With the advances in experimental structure determinations, the size of these assemblies keeps expanding. Besides, it is also possible to recreate models representing molecular constructs that are yet impossible to determine accurately, using symmetry orders or fitting crystal structures into low-resolution maps. Studying such huge structures is part of today's challenges to modern biology.

These limits can now be overcome using new rendering methods exploiting the capabilities of Graphics Processing Units (GPUs). Implementations on this hardware can be used to generate classical representations such as VdW [1] or ball & stick [2-4], but also more complicated molecular surfaces [5-7]. Former visualizations have shown the possibility to render a large number of atoms but were relatively simple, whereas the latter ones are more sophisticated but can only, for the moment, represent peptides [5] or medium size [6, 7] proteins interactively. In the present case, using *HyperBalls* [8], we show how to depict the former representations and create an intermediary surface that can also be considered as a simplified form of the latter renderings.

Combining this visualization with Molecular Dynamics (MD) software such as Gromacs [9] allows us to manipulate molecular assemblies using haptic devices and to guide the simulation.

2 HYPERBALLS AS BASIS FOR THE FVNANO LABORATORY

In this part we will introduce the *HyperBalls* [12] representation, then we will explain how to use the FlowVR software [10] to combine this visualization with an MD program and setup the virtual FvNano laboratory.

2.1 HyperBalls Representation

The *HyperBalls* representation uses the GPU ray-casting method with quadric surface equations to represent a variety of molecular metaphors within a single, unified framework. A general equation is used to describe molecular primitives such as spheres, cylinders and 2-sheeted hyperboloids, depending on a shrink factor *s*. This equation can be written as:

$$(1/s)\,x^2 + (1/s)\,y^2 - 1/(1-s)\,z^2 - R^2 = 0 \qquad (1)$$

Where x, y and z describe the center of the primitive, *s* defines the shrink factor in the interval (0,1) and *R* represents the radius of the primitive (see [8] for detailed discussion). For s = 1 the equation (1) changes to:

A sphere equation: $x^2 + y^2 + z^2 - R_{atom}^{\ 2} = 0$ (for atoms)
A cylinder equation: $x^2 + y^2 - (R_{atom}^{\ 2} - \varepsilon^2) = 0$ (for bonds)

With $|\,\varepsilon^2\,| \leq |\,R^2_{atom1} - R^2_{atom2}\,|$, atom1 and atom2 are the atoms constituting the bond. Equation (1) can be stored in a 4x4 matrix and is used to perform ray-casting on GPUs as presented in [11].

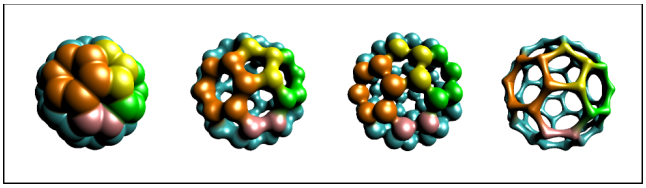

Figure 1. Several representations of a fullerene depicted by varying parameters of the *HyperBalls* method.

The rendering pipeline is divided in three steps. First, OpenGL cube primitives of 1 Å dimension are created at the origin. Parameters such as atom radii, and coordinates are encoded in textures to efficiently transmit this data to the GPU. Using this information, we translate the cubes to the respective atom or link positions and scale them. This step is performed in the GPU vertex shader. We calculate the intersection between ray and surface in the GPU fragment shader using the 4x4 matrix. By combining primitives, different molecular representations such as van der Waals or ball-and-stick can be rendered, and smooth links between atoms are created using hyperboloids (see Fig. 1).

2.2 FvNano Concept

FvNano is a software platform combining interactive physics-based simulations (such as MD) with the *HyperBalls* representation and with interaction devices to virtually manipulate molecular objects. The modular FlowVR core allows an easy integration of features needed by scientists to study molecular systems and to deploy these tools on computer clusters and virtual-reality rooms. It includes *in-situ* visualization, interactive simulation and visual analysis specific to molecular systems.

3 DISCUSSION

3.1 HyperBalls show Dynamic Molecular Phenomena

Visualization of non-covalent bonds in general, and of hydrogen bonds in particular, is a specific point of interest of the *HyperBalls* method. Classically, this particular type of molecular interaction is represented as dashed lines. Another possibility is to visualise interactions in 2D to clarify the scene and focus on a point of interest. A major limitation of these representations is that no clues about the interaction strength are provided: either an interaction exists, or it does not. Using *HyperBalls*, we parameterize the representation in order to observe a change of the hyperboloids as a function of the distance between interacting atoms or molecules. This metaphor is particularly useful to depict the temporal evolution of non-covalent bonds and better understand phenomena such as the formation of hydrogen bonds between water molecules or ion coordination (see Fig. 2). The *HyperBalls* representation is well suited to depict reduced models of big molecular systems such as coarse-grained models or elastic spring networks. Given that the thickness of the bonds can be varied as a function of the distance between atoms, the *HyperBalls* representation provides distinct features for depicting springs or coarse-grained bond behavior (data not shown).

We will present a demo to illustrate these dynamic features. Videos are available at [12].

Futhermore, the use of GPU ray-casting allows us to visualize huge assemblies at real time frame rates. For example, it is possible to visualize virus capsids comprising more than 560,000 atoms with a frame rate of 35 fps. This cannot be achieved with common molecular viewers such as VMD or Pymol, as these tools do not currently use comparable GPU optimizations. A better comparison would be to pure spheres or cylinders. We are working on a comprehensive comparison, but it has not yet been completed. It is also possible to visualize molecular dynamics trajectories of macromolecular assemblies containing more than 300,000 atoms with an interactive frame rate of 17 fps.

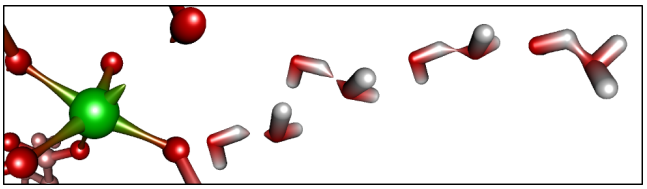

Figure 2. Ion coordination and water bond formation.

3.2 Interacting with Molecular Assemblies

Being able to interact with a molecular simulation allows a scientist to overcome timescale limits and explore reversible or non-reversible events on complex molecular systems during a simulation. One issue is the complexity of the manipulated objects. Visually it is difficult to apprehend the 3D structure of a molecule, especially on a 2D screen. The idea then is to use a pertinent representation and a convenient way for navigation and interaction inside a simulation. By achieving high-performance simulation/visualization and facilitating the use of interactive devices, the FvNano platform offers good conditions for interactive simulation even with large molecular systems. For now, FvNano can be used with 3D navigation devices such as the SpaceBall or the SpaceNavigator. The interaction (selection, atom displacement) is provided *via* the 6DOF Phantom haptic device, which allows force feedback to feel how the system reacts to the interaction. An extension with other devices is straightforward, as FvNano supports the widely used VRPN library. Ongoing work is focused on how to compute and visualize on the fly analysis of simulation properties and explore large dynamic datasets.

CONCLUSION

We have introduced key concepts of the FvNano virtual laboratory intended for interactive visualization and manipulation of large molecular assemblies. All developments of this open source project are available *via* related websites [12,13,14].

FvNano focuses on scalability and interaction with parallel software within high performance computing applications. All visualization, calculation, interaction and analysis modules may be executed in parallel and hybrid environments.

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