Molecular Visualization and Simulation in VR

John E. Stone
Theoretical and Computational Biophysics Group
Beckman Institute for Advanced Science and Technology
University of Illinois at Urbana-Champaign
http://www.ks.uiuc.edu/Research/vmd/
http://www.ks.uiuc.edu/Research/gpu/

Indiana University, Wednesday March 6th, 2019
# AVL Virtual Reality Workshop Series – Spring 2019

**Wednesdays @ 4:00pm – Franklin Hall Reality Lab (052)**

**Bonus: VR Expeditions select Mondays (FH 052 @4:00pm)**

<table>
<thead>
<tr>
<th>Date</th>
<th>Topic</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jan. 16</td>
<td>The Medium of Virtual Reality</td>
<td>Bill Sherman</td>
</tr>
<tr>
<td>Jan. 23</td>
<td>A Survey of VR Experiences</td>
<td>Chauncey Frend</td>
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<tr>
<td>Jan. 30</td>
<td>(no talk – cancelled for weather)</td>
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<tr>
<td>Feb.  6</td>
<td>VR for Simulation and Training</td>
<td>Chauncey Frend</td>
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<tr>
<td>Feb. 11</td>
<td>VR Expedition: Experiential Gaming</td>
<td>Jeff Rogers</td>
</tr>
<tr>
<td>Feb. 13</td>
<td>VR for Architectural review</td>
<td>Jeff Rogers</td>
</tr>
<tr>
<td>Feb. 18</td>
<td>VR Expedition: Cultural Heritage</td>
<td>Tassie Gniady</td>
</tr>
<tr>
<td>Feb. 20</td>
<td>Developing Mobile VR Experiences</td>
<td>Jeff Rogers</td>
</tr>
<tr>
<td>Feb. 25</td>
<td>VR Expedition: Creative Tools in VR</td>
<td>Chauncey Frend</td>
</tr>
<tr>
<td>Feb. 27</td>
<td>Scientific Visualization with VR</td>
<td>Bill Sherman</td>
</tr>
<tr>
<td>Mar.  6</td>
<td>Molecular Visualization and Simulation with VR</td>
<td>John Stone</td>
</tr>
<tr>
<td>Mar. 13</td>
<td>(no talk – Spring Break)</td>
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</tr>
<tr>
<td>Mar. 20</td>
<td>Virtual Tourism</td>
<td>Tassie Gniady</td>
</tr>
<tr>
<td>Mar. 25</td>
<td>VR Expedition: Science Education</td>
<td>Bill Sherman</td>
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<tr>
<td>Mar. 27</td>
<td>(no talk – IEEE VR Conference)</td>
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<tr>
<td>Apr.  3</td>
<td>Archaeology Training with VR</td>
<td>Laura Shackelford / Cam Merrill / Alan Craig</td>
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<tr>
<td>Apr. 10</td>
<td>VR-Unity Extravaganza</td>
<td>Bill Sherman</td>
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<tr>
<td>Jan. 17</td>
<td>Introduction to Text Analysis</td>
<td>Tassie Gniady and David Kloster</td>
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<tr>
<td>Jan. 24</td>
<td>Introduction to Topic Modeling</td>
<td>Tassie Gniady and David Kloster</td>
</tr>
<tr>
<td>Jan. 31</td>
<td>Introduction to Sentiment Analysis</td>
<td>David Kloster and Tassie Gniady</td>
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<tr>
<td>Feb. 7</td>
<td>Introduction to Document Similarity</td>
<td>David Kloster and Tassie Gniady</td>
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<tr>
<td>Feb. 14</td>
<td>Hands-on Text Extravaganza</td>
<td>Tassie Gniady and David Kloster</td>
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<tr>
<td>Feb. 21</td>
<td>Rome Reborn: Visiting Rome in A.D. 320</td>
<td>Bernie Frischer</td>
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<tr>
<td>Feb. 28</td>
<td>Virtual Reality in the Art History Classroom</td>
<td>Matthew Brennan</td>
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<tr>
<td>Mar. 7</td>
<td>Painting Virtual Art: An Artist’s History through VR</td>
<td>Margaret Dolinsky</td>
</tr>
<tr>
<td>Mar. 13</td>
<td>(no talk – Spring Break)</td>
<td>N/A</td>
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<tr>
<td>Mar. 21</td>
<td>Augmented Reality / Virtual Reality</td>
<td>Chauncey Frend</td>
</tr>
<tr>
<td>Mar. 28</td>
<td>3D Digitization</td>
<td>Jeff Rogers and Tassie Gniady</td>
</tr>
<tr>
<td>Apr. 4</td>
<td>Advanced Media</td>
<td>Chris Eller</td>
</tr>
<tr>
<td>Apr. 11</td>
<td>Create your own VR Tour</td>
<td>Matt Mercer and Tassie Gniady</td>
</tr>
<tr>
<td>Apr. 18</td>
<td>XR Extravaganza</td>
<td>Jeff Rogers</td>
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Impact of Virtual Reality Workshop Series

Molecular Visualization and Simulation in VR

Presented by John E. Stone, Senior Research Programmer, U. Illinois
VMD – “Visual Molecular Dynamics”

• Visualization and analysis of:
  – Molecular dynamics simulations
  – Lattice cell simulations
  – Quantum chemistry calculations
  – Cryo-EM densities, volumetric data
  – Sequence information

• User extensible scripting and plugins

• http://www.ks.uiuc.edu/Research/vmd/

Cell-Scale Modeling

MD Simulation

Structure

Parameterization

Analysis

Preparation with QwikMD

Parallel Analysis

Remote Visualization

X-ray, cryo-EM, cryo-ET, NMR

Refinement with MDFF
Goal: A Computational Microscope
Study the molecular machines in living cells

Ribosome: target for antibiotics

Poliovirus
VMD Visualization Concepts
Biomolecular Visualization Challenges

- Geometrically complex scenes
- Spatial relationships important to see clearly: fog, shadows, AO helpful
- Often show a mix of structural and spatial properties
- Time varying!
Structure Visualization

Molecular representations provide different levels of abstraction, atomic detail vs. higher level organizational information

- Atoms, VdW spheres, bonds, ball-stick, …
- Molecular orbitals (quantum chemistry)
- Molecular surfaces
- Coarse-grained “beads”
- Ribbons, secondary structure, “cartoon” reps, RNA/DNA
Selection, Filtering

- Most viz tools allow interactive visual picking, menu-driven selections of structure components to display or operate on
- VMD also extensively uses a text-based selection language (think google):
  - “water within 10 of protein and z > 0”
  - Allows selection on user-defined fields
  - Promotes synergy between interactive and scripting interfaces
  - Works very well when dealing with huge time-varying structures
Computed Properties

- Smoothing of thermal noise
- Secondary structure
- Hydrogen bonds, salt bridges
- Forces, energies, stress, strain
- Time averaging of electrostatic fields, occupancy maps
- Quality-of-fit cross correlation with cryo-EM density maps
- Normal modes, principal component analysis, essential dynamics
- Cluster simulation trajectory timesteps by structural similarity

Chemoreceptor trimer-of-dimers analysis with Bendix plugin in VMD
Display of Computed Properties on Structures

Per-residue solvent-accessible surface area of Ubiquitin

PME electrostatic potential contour for a helicase on a volumetric slice plane
CheA kinase PCA: first principal component porcupine plot
Visualization of Molecular Dynamics

- Molecular dynamics simulations save trajectories of atomic coordinates as simulated time progresses.
- Researchers study trajectories by analyzing force profiles, energies, structural changes, etc.
- Visualization selections, graphics, structure properties recomputed for each trajectory timestep!
Petascale Computing - A Key Instrument for Life Science
MDFF Solves Structures from X-ray Crystallography and Cryo-EM

Electron microscopy

X-ray crystallography

FEI microscope

APS at Argonne

Electron density of protein in action at low resolution

Ideal protein structure at high resolution

Acetyl – CoA Synthase
Immersive Visualization and VR for Structural Biology
Immersive Viz. w/ VMD

- VMD began as a CAVE app (1993)
- Use of immersive viz by molecular scientists limited due to cost, complexity, lack of local availability, convenience
- Commoditization of HMDs excellent opportunity to overcome cost/availability
- This leaves many challenges still to solve:
  - Incorporate support for remote visualization
  - UIs, multi-user collaboration/interaction
  - Rendering perf for large molecular systems
  - Accomodate limitations idiosyncracies of commercial HMDs

VMD running in a CAVE w/ VR Juggler
Benefits of VR for Structural Biology

• By far the easiest structure exploration and navigation experience

• Well designed VR “tools” easier to use than conventional windowed visualization interfaces
Goal: Intuitive interactive viz. in crowded molecular complexes

Results from 64 M atom, 1 μs sim!

Close-up view of chloride ions permeating capsid hexameric centers
What Sorts of Tasks Do Researchers Need to Perform in VR

- Heavily skewed toward 3-D atomic structure visualization, analysis, dynamics
- Prime Example: Superposition and direct comparison of multiple modalities of structure information arising from different experimental and computational structure determination methods
  - Conventional windowed visualization interactions can be “clunky” until user uses 6DoF input devices and develops dexterity to use them effectively
  - VR HMDs and hand controllers simple to use and understand
  - Key interactions contextual with the structure/data being interacted with and the visualization or analysis task at hand
What General “VR UI Tools” Are Useful in This Area

- Navigation, teleportation, scaling, view-reset
- Selection
- Grabbing, pulling, orientation
- Hand-held lighting
- Clipping of drawn geometry, to allow peeling away of obscuring layers of atomic structures, density isosurfaces, etc.
Tool Examples: Grabbing, Moving
Tool Examples: Clipping Geometry
Tool Examples: Hand-Held Lighting
Interactions That are Difficult to Support Within Conventional VR

• Simultaneous interaction between the 3-D atomic structure visualizations and potentially large numbers of other 2-D plots or projections

• Large tabulated displays of quantitative properties, e.g., amino acid residue sequences, gene sequences, other 1-D properties

• Sometimes a “BIG STEREOSCOPIC TV” wins, although they have become difficult to find now…
Data Size Challenges and The Ultimate Limits on What We Can Visualize Interactively
Next Generation: Simulating a Proto-Cell

- Emulate aspects of the *Mycoplasma mycoides* bacterium
- 200nm diameter
- ~1 billion atoms w/ solvent
- ~1400 proteins in membrane

Cryo-ET image of ultra-small bacteria (scale bar 100nm)  
Next Generation: Simulating a Proto-Cell

- ORNL Summit: NVLink-connected Tesla V100 GPUs enable next-gen visualizations
- 200nm diameter
- ~1 billion atoms w/ solvent
- ~1400 proteins in membrane
Proto-Cell Data Challenges

• 1B-atom proto-cell requires nodes with more than TB RAM to build complete model…
• 1B-atom proto-cell binary structure file: 63GB
• Trajectory frame atomic coordinates: 12GB, 1.2TB/ns of simulation (1 frame per 10ps)
• Routine modeling and visualization tasks are a big challenge at this scale
  – Models contain thousands of atomic-detail components that must work together in harmony
  – Exploit persistent memory technologies to enable “instant on” operation on massive cell-scale models – eliminate several minutes of startup during analysis/visualization of known structure
  – Sparse output of results at multiple timescales will help ameliorate visualization and analysis I/O
  – Data quantization, compression, APIs like ZFP
VMD Petascale Visualization and Analysis

• Analyze/visualize large trajectories too large to transfer off-site:
  – User-defined parallel analysis operations, data types
  – Parallel rendering, movie making

• Supports GPU-accelerated Cray XK7 nodes for both visualization and analysis:
  – GPU accelerated trajectory analysis w/ CUDA
  – OpenGL and GPU ray tracing for visualization and movie rendering

• Parallel I/O rates up to 275 GB/sec on 8192 Cray XE6 nodes – can read in 231 TB in 15 minutes!

  Parallel VMD currently available on:
  
  ORNL Titan, NCSA Blue Waters, Indiana Big Red II, CSCS Piz Daint, and similar systems

NCSA Blue Waters Hybrid Cray XE6 / XK7
22,640 XE6 dual-Opteron CPU nodes
4,224 XK7 nodes w/ Telsa K20X GPUs
VMD supports EGL for in-situ and parallel rendering on clouds, clusters, and supercomputers

• No windowing system dependency
• Easily deploy parallel VMD builds supporting off-screen rendering
• Maintains 100% of VMD OpenGL shaders and rendering features
• Support high-quality vendor-supported commercial OpenGL implementations in HPC systems that were previously limited to Mesa

Poliovirus
VMD EGL Rendering: Supports full VMD GLSL shading features, multisample antialiasing, ray cast spheres, 3-D tex mapping, ...

Swine Flu A/H1N1 neuraminidase bound to Tamiflu
64M atom HIV-1 capsid simulation

High Performance Molecular Visualization: In-Situ and Parallel Rendering with EGL.
Molecular Structure Data and Global VMD State

Scene Graph

Graphical Representations
- DrawMolecule
- Non-Molecular Geometry

User Interface Subsystem
- Tcl/Python Scripting
- Mouse + Windows
- 6DoF Input “Tools”

Display Subsystem
- VMDDisplayList
- DisplayDevice
- OpenGLRenderer
- GLX+X11+Drv
- OpenGL Pbuffer/FBO
- Windowed OpenGL
- EGL+Drv
- OpenGL Pbuffer/FBO

Graphical Representations
- Molecular Structure Data and Global VMD State
- User Interface Subsystem
- Display Subsystem
- Scene Graph
VMD w/ OptiX 5

- Interactive RT on laptops, desktops, and cloud
- Large-scale parallel rendering: in situ or post hoc visualization
- Remote RT on NVIDIA GPU clusters
- Stereoscopic panoramic and full-dome projections
- Omnidirectional VR for YouTube, VR HMDs
- GPU memory sharing via NVLink on Quadro GP100, Tesla P100
- VMD+OptiX 5, NVIDIA NGC container: https://ngc.nvidia.com/registry/
- In-progress:
  - OptiX denoising support: fast turnaround w/ AO, DoF, etc
  - Denoising to enable practical use of path tracing in VMD


Lighting Comparison, STMV Capsid

Two lights, no shadows

Two lights, hard shadows, 1 shadow ray per light

Ambient occlusion + two lights, 144 AO rays/hit
Interactive Remote Visualization and Analysis

- Enabled by hardware H.264/H.265 video encode/decode
- Enable visualization and analyses not possible with conventional workstations
- Access data located anywhere in the world
  - Same VMD session available to any device
- Linux prototype in-development using NVIDIA Video Codec SDK, easy-to-use NvPipe wrapper library
Using Omnidirectional Stereoscopic Projections to Permit Remote Ray Tracing for VR HMDs
HMD Ray Tracing Challenges

• HMDs require high frame rates (90Hz or more) and minimum latency between IMU sensor reads and presentation on the display.
• Multi-GPU workstations fast enough to direct-drive HMDs at required frame rates for simple scenes with direct lighting, hard shadows.
• Advanced RT effects such as AO lighting, depth of field require much larger sample counts, impractical for direct-driving HMDs.
• Remote viz. required for many HPC problems due to large data.
• Remote viz. latencies too high for direct-drive of HMD.
• Our two-phase approach: moderate-FPS remote RT combined with local high-FPS view-dependent HMD reprojection w/ OpenGL.
VMD Molecular Structure Data and Global State

Scene Graph

Graphical Representations
- DrawMolecule
- Non-Molecular Geometry

User Interface Subsystem
- Tcl/Python Scripting
- Mouse + Windows
- VR Input “Tools”

Display Subsystem
- VMDDisplayList
- DisplayDevice
- OpenGLDisplayDevice
- FileRenderer
- Windowed OpenGL GPU
- OpenGL Pbuffer GPU
- Tachyon CPU RT
- TachyonL-OptiX GPU RT
- Batch + Interactive

Scene Graph

Graphical Representations

User Interface Subsystem

Display Subsystem
VMD TachyonLOptiX: Multi-GPU on NVIDIA VCA Cluster

Scene Data Replicated, Image Space + Sample Space Parallel Decomposition onto GPUs

VCA 0: 8 K6000 GPUs

VCA N: 8 K6000 GPUs
Progressive Ray Tracing Engine
Ray tracing loop runs continuously in new thread
Decodes H.264 video stream from remote VCA GPU cluster

Camera + Scene

Omnistereo Image Stream

HMD Display Loop
HMD loop runs in main VMD application thread at max OpenGL draw rate
View-dependent stereo reprojection for current HMD head pose
HMD distortion correction

15Mbps Internet Link

Remote VCA GPU Cluster
Ray tracing runs continuously, streams H.264 video to VMD client
Stereoscopic Panorama Ray Tracing w/ OptiX

- Render 360° images and movies for VR headsets such as Oculus Rift, Google Cardboard
- Ray trace panoramic stereo spheremaps or cubemaps for very high-frame-rate display via OpenGL texturing onto simple geometry
- Stereo requires spherical camera projections poorly suited to rasterization
- Benefits from OptiX multi-GPU rendering and load balancing, remote visualization
A) Monoscopic circular projection. Eye at center of projection (COP).

B) Left eye stereo circular projection. Eye offset from COP by half of interocular distance.

C) Stereo eye separation smoothly decreased to zero at zenith and nadir points on the polar axis to prevent incorrect stereo when HMD sees the poles.
Remote Omnidirectional Stereoscopic RT Performance @ 3072x1536 w/ 2-subframes

<table>
<thead>
<tr>
<th>Scene</th>
<th>Per-subframe samples AA : AO (AO per-hit)</th>
<th>RT update rate (FPS)</th>
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<tbody>
<tr>
<td>STMV shadows</td>
<td>1:0</td>
<td>22.2 18.1 10.3</td>
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<td></td>
<td>2:0</td>
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<tr>
<td></td>
<td>4:0</td>
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<tr>
<td>STMV Shadows+AO</td>
<td>1:1</td>
<td>18.2 16.1 12.4</td>
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<td>1:2</td>
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<td></td>
<td>1:4</td>
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<tr>
<td>STMV Shadows+AO+DoF</td>
<td>1:1</td>
<td>16.1 11.1 8.5</td>
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<td>2:1</td>
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<td>2:2</td>
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<tr>
<td>HIV-1 Shadows</td>
<td>1:0</td>
<td>20.1 18.1 10.2</td>
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<td>2:0</td>
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**HMD View-Dependent Reprojection with OpenGL**

- Texture map panoramic image onto reprojection geometry that matches the original RT image formation surface (sphere for equirectangular, cube for cube map)
- HMD sees standard perspective frustum view of the textured surface
- Commodity HMD optics require **software lens distortion and chromatic aberration correction** prior to display, implemented with multi-pass FBO rendering
- **Enables low-latency, high-frame-rate redraw** as HMD head pose changes (150Hz or more)
Ongoing VR Work

- OpenXR – cross platform multi-vendor HMD support
- Ray tracing engine supports NVIDIA RTX Ray Tracing HW Acceleration
- Future:
  - AI denoising for better average quality
  - Interactive RT stochastic sampling strategies to improve interactivity
  - Improved omnidirectional cubemap/spheremap sampling approaches
  - AI multi-view warping to allow rapid in-between view generation amid multiple HMD head locations
  - H.265 for high-res omnidirectional video streaming
  - Multi-node parallel RT and remote viz. on general clusters and supercomputers, e.g. NCSA Blue Waters, ORNL Titan
- Tons of work to do on VR user interfaces, multi-user collaborative visualization, …
Acknowledgements

• Theoretical and Computational Biophysics Group, University of Illinois at Urbana-Champaign
• NVIDIA CUDA and OptiX teams
• Funding:
  – NIH support: P41GM104601
  – DOE INCITE, ORNL Titan: DE-AC05-00OR22725
  – NSF Blue Waters:
    NSF OCI 07-25070, PRAC “The Computational Microscope”, ACI-1238993, ACI-1440026
“When I was a young man, my goal was to look with mathematical and computational means at the inside of cells, one atom at a time, to decipher how living systems work. That is what I strived for and I never deflected from this goal.” – Klaus Schulten
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- **Adapting a message-driven parallel application to GPU-accelerated clusters.**

- **GPU acceleration of cutoff pair potentials for molecular modeling applications.**

