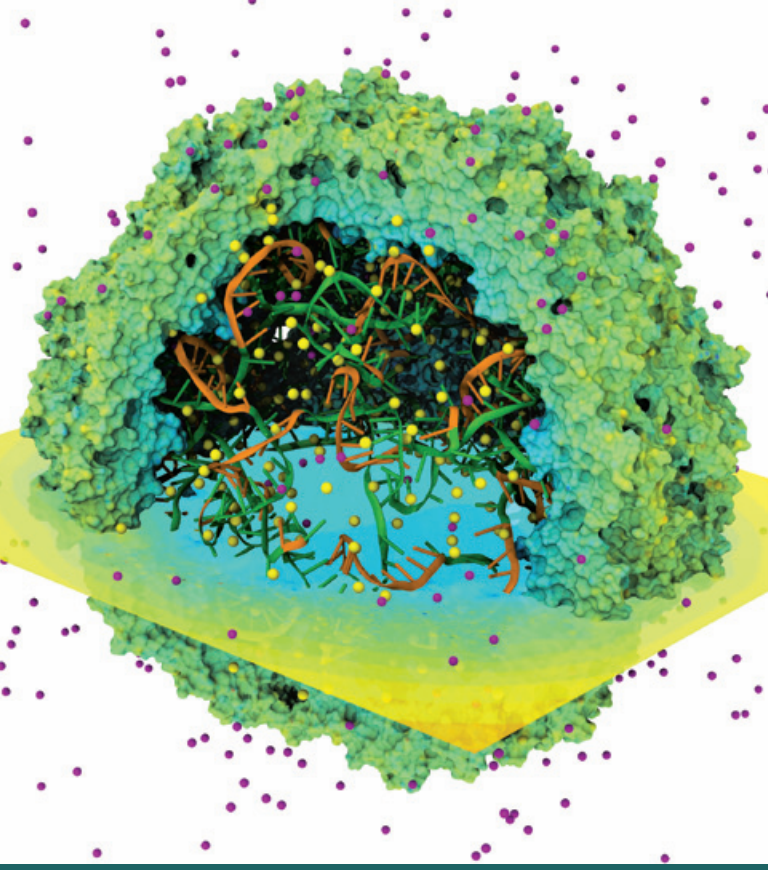


VMD

Visual Molecular Dynamics

www.ks.uiuc.edu/Research/vmd

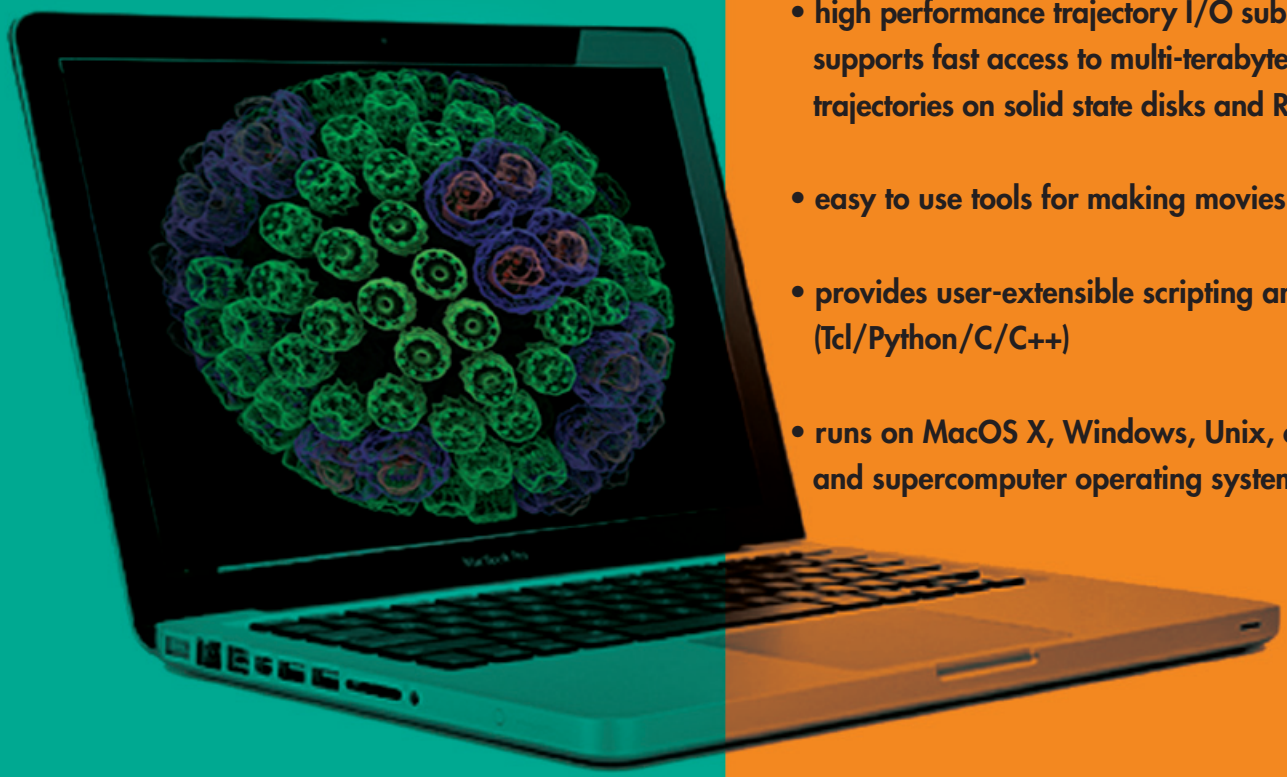
VMD is freely available for download.

ILLINOIS

VMD

Visual Molecular Dynamics

- interactively displays sequences, density maps, molecular structures, and molecular dynamics simulation trajectories
- facilitates structure building, simulation preparation, and analysis
- drives interactive molecular dynamics simulations
- permits shared visualization sessions
- built-in photorealistic ray tracing, with ambient occlusion lighting
- takes advantage of multi-core CPUs, GPU-accelerated computing with CUDA and OpenCL, and allows parallel analysis and rendering on clusters and supercomputers using MPI
- supports hundreds of the most commonly used molecular data file formats



- high performance trajectory I/O subsystem supports fast access to multi-terabyte trajectories on solid state disks and RAID arrays
- easy to use tools for making movies
- provides user-extensible scripting and plugins (Tcl/Python/C/C++)
- runs on MacOS X, Windows, Unix, clusters, and supercomputer operating systems

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The Theoretical and Computational Biophysics Group (TCBG) brings molecular graphics, molecular modeling, and bioinformatics software to bear on questions of biomedical relevance. Research and development of activities center on the structure and function of supramolecular systems in the living cell, and on the development of efficient computing tools for the life sciences. Directed by Professor Klaus Schulten, the multidisciplinary TCBG operates the National Institutes of Health Center for Macromolecular Modeling and Bioinformatics.