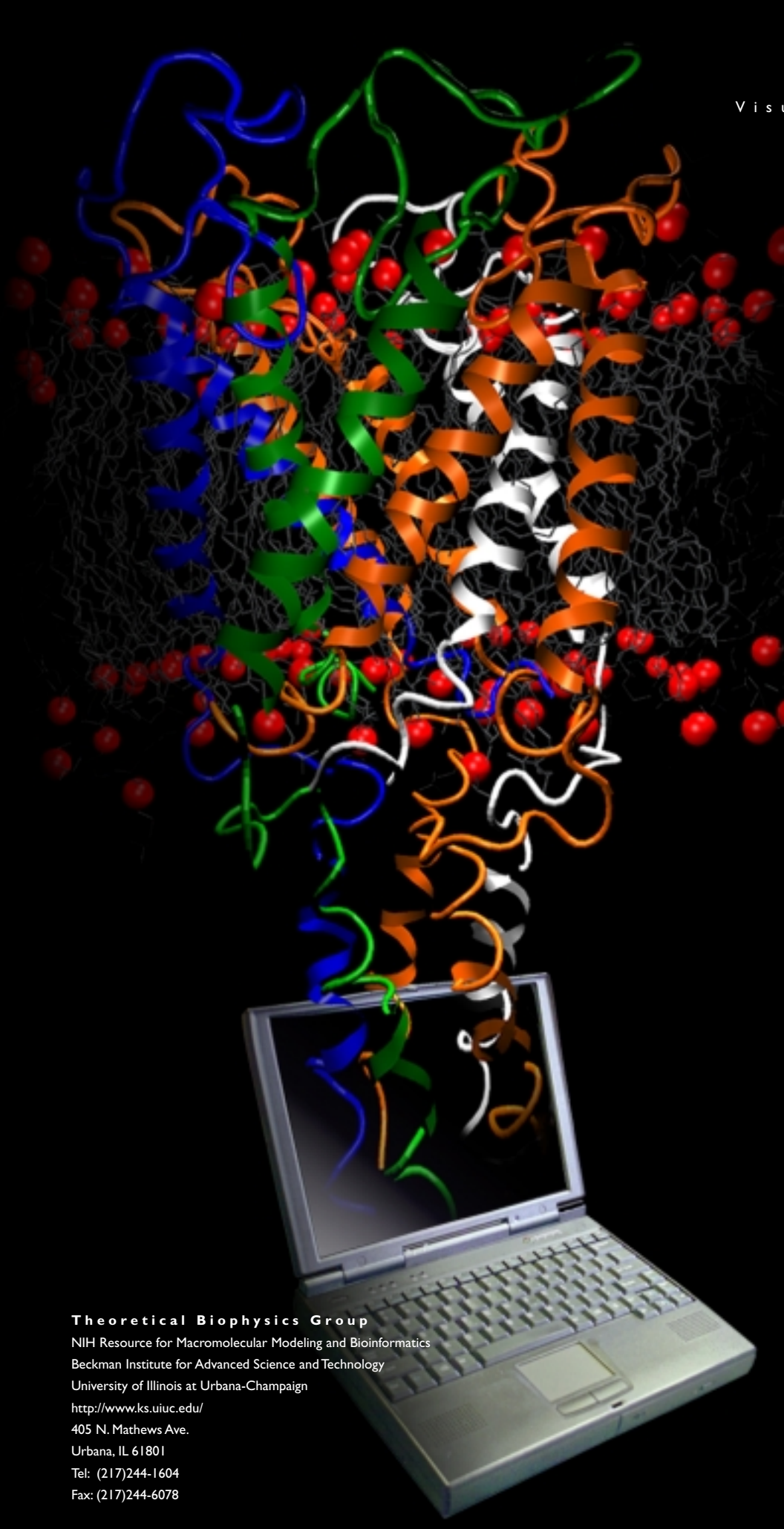
VMD

Visual Molecular Dynamics



VMD is a versatile, modifiable, fully documented molecular visualization program, and is freely distributed.

VMD facilitates the study of macromolecules in an immediate and visual way.

VMD benefits research and training in biology, physics, chemistry, biochemistry, and biophysics.

VMD supports Microsoft Windows 95/98/NT, and a wide variety of UNIX platforms.

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

VMD is the visualization component of MDScope, an interactive computing environment for the simulation and study of biopolymers.

VMD can act as a graphical front-end for external molecular dynamics programs by displaying and animating remotely simulated molecules.

VMD offers numerous methods for rendering and coloring molecules and for animating and analyzing molecular dynamics trajectories.

FEATURES

- Flexible atom selections
- Tcl based command and scripting language
- Static docking and structure alignment
- Display of multiple molecules simultaneously
- PDB, PSF, DCD and CRD file reading support
- Automatic conversion from other file formats
- Accelerated 3D rendering and stereoscopic display
- Scene export to external ray tracers

Theoretical Biophysics Group
NIH Resource for Macromolecular Modeling and Bioinformatics
Beckman Institute for Advanced Science and Technology
University of Illinois at Urbana-Champaign
http://www.ks.uiuc.edu/
405 N. Mathews Ave.
Urbana, IL 61801
Tel: (217)244-1604
Fax: (217)244-6078