Computer Software Reviews

MOBY, Version 1.4. Springer-Verlag New York, Inc.: P.O. Box 2485, Secaucus, NJ 07096-2491. List price $998.00; educational discounted price $498.00. Deep discounts for 10+ copies.

MOBY is a molecular modeling package for the IBM PC or compatibles. It allows for the display and manipulation of molecules, molecular mechanics and quantum chemistry calculations, and molecular dynamics simulations. Besides the IBMPC requirement, the software requires MS-DOS 2.0 or higher, an 8087 math coprocessor, 640K of RAM, and EGA or VGA graphics. Both a hard disk with about 1 MB of free space and a mouse are optional but highly desirable. MOBY is not copy protected.

Installation on an IBM PC-XT with a Paradise graphics card was uneventful. The same was true of an ACMA 386 machine equipped with a Paradise graphics card and operating at 33 MHz. However, the program would not run on a NEC 386 computer with Phoenix graphics controller on the motherboard. The problem appeared to be in the graphics. The documentation that came with the package offered no help, and a (toll) call to the publisher was unproductive.

Molecular data can be input via Cartesian coordinates, or the r, Θ, ϕ protocol, with both allowing a user-defined format or the default format. Both were tested and found to work properly. However, users not familiar with r, Θ, ϕ input will find little help in the instruction manual. Molecule files generated in the MACCS II format by MDL software are also readable, but this was not tested. Finally, the Brookhaven Protein Databank format is allowed, as is input by the screen editor. The Brookhaven format was successfully tested using the demonstration disk provided. However, only five structures are provided in readable form, and apparently no others are available. Users who wish to input other protein data will need to obtain the Brookhaven database on magnetic tape or CD-ROM and transfer to diskette, but the instruction manual offers no advice on how to obtain and convert the data. Screen input was disappointing. There are numerous useful (but poorly documented) screen editing features that make it appear attractive, but there is one serious flaw. After drawing the carbon skeleton on the screen the "relax" operation adjusts the geometry to normal bond angles and distances. Unfortunately the geometry of the molecule at this point is planar, and if a chain carbon is doubly branched, the two substituents will be superimposed. If a molecular mechanics optimization is attempted on this initial structure, the program will crash.

The molecular mechanics calculations use the AMBER force field (Weiner, S. J., et al. *J. Am. Chem. Soc.* **1984**, *106*, 765). This was originally designed for simulation of nucleic acids and proteins, but it has been modified for more general use in MOBY. However, it is clear from the atom list provided that nucleic acids and proteins are still the primary focus. The atom limit is 150; energy terms include bond stretching and bending, torsional, van der Waals, and Coulomb interactions, and hydrogen bonding. To include Coulomb interactions, the partial charges on atom centers must first be determined with the quantum chemistry module. This is discussed below. For atoms not included, e.g., halogens, the user must provide his own input data for the bond lengths, the van der Waals well depth, and the stretching and bending constants. The interaction of these centers with the rest of the up to 2000 centers of the structure can be calculated and substructure minimizations and simulations can be run. The force field was tested with 2,2,4,4-tetramethylpentane, 2,2-dimethylheptane, 1,2-dichloroethane, 1-chloropropane, and ethylene glycol. MM2 parameters were used for chlorine. In all cases, the geometries and energies were about as expected. For example, the two alkanes had bond and torsion angles that were very similar to those found with Allinger's MM2, and the energy difference between the two structures, 7.0 kcal/mol, was reasonably close to the 5.9 kcal/mol found with MM2.

Both MNDO and AM1 methods are available for quantum chemical calculations. Limitations are the following: 60 valence orbitals, 30 atoms, and 72 electrons. Both calculations on specific geometries and geometry optimization are allowed. Methane was used to test both MNDO and AM1. The molecule was built using the screen editor, and the heat of formation was determined without any further geometry optimization. The MNDO calculation gave a heat of formation of −11.5, and AM1 gave −7.92 kcal/mol. Geometry optimization of methane with MNDO required 20 min on a PC-XT. The heat of formation after optimization was −11.9 kcal/mol, the value expected from MNDO.

The molecular dynamics (MD) simulation was not tested. According to the documentation, it can be used in two ways. Dynamic phenomena can be studied in order to describe the macroscopic properties of a system, and the input of additional energy can be used to free a system from a local minimum and thus search the conformational space of the system. Potential users should be advised that the manual provided with MOBY offers no help with MD simulations. One example is provided in the tutorial, but it will be practically meaningless to anyone not already knowledgeable.

It would appear that the display and manipulation of nucleic acids and proteins is considered the major feature of MOBY. As many as 2000 atom centers and 2000 bonds may be displayed. Display options include the following: coloring of atom centers according to atomic number, property, e.g., charge, substructure name, etc.; labeling of atom centers by sequential number, atomic number, element symbol, code symbol, property, etc.; and representation of centers by points, circles, solid spheres, point surfaces, etc. Bonds may be drawn, or left invisible; displays may be resized and rotated, and bond distances, angles, and torsional angles may be displayed as desired. Also, portions of large molecules may be shown and other portions hidden. Finally provision is made for getting hard copies of the graphics display or creating HPGL plot files.

The displays are of high quality, but they are time consuming to produce on slower machines. For example, a Brookhaven protein structure with 208 amino acid residues containing 1692 atom centers was read from the demonstration diskette, and then the bond framework was generated. On a 386 machine operating at 33 MHz the generation of 1746 bonds required about 1 min, but the PC-XT took 20 min. Displaying the van der Waals surface of the two hemoglobin groups with a radius factor of 1 and a point density of 7 took approximately 1 min on the aforementioned 386 computer and 15 min on the PC-XT.

The following points should be considered before buying this package:

(1) It will produce high-quality plots, but a computer at least as fast as a 20 MHz 386 is needed.

(2) The molecular mechanics module in its current form is not suitable for a general audience. However, the documentation suggests that future versions will contain a complete "all atom" parameter list.

(3) The quantum module is slow, particularly if geometry optimization is called for.

(4) It will not run on all IBMPC "compatible" computers. Be certain the vendor will issue a refund in case this happens.

(5) Documentation is poor to nonexistent. If any monetary value is attached to the time required to muddle through the learning process, the cost would more than double.

(6) Not much help is available. For all practical purposes, you are on your own.

In conclusion, MOBY cannot be recommended in its present form. Once the parameter list for molecular mechanics calculations is complete and the manual is re-written, it would be worthy of serious consideration by owners of 386/20, and faster, computers.

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