Using Spartan: A Student's Guide to Molecular Modeling

Due to the relatively recent development of faster computers, molecular modeling has rapidly changed from requiring days of calculation on a mainframe among a few dedicated experts to requiring only seconds for the sophisticated undergraduate. This advancement means that molecular modeling has become an important tool to chemists, and one that allows us to rationalize properties of compounds and their observed reactivity and potentially design molecules with new, better properties for useful materials.

The molecular modeling program that you will be using is called **Spartan** from Wavefunction, Inc.

This document is intended to guide you through Spartan in order to familiarize you with this powerful tool.

Specifically, this course is designed to give you the tools you need in order to accomplish the following:

1. Input or "build" a molecule using the graphical interface.
2. Minimize the energy using molecular mechanics and begin to interpret the implications and limitations associated with this.
3. Set-up and run a higher level calculation; collect and interpret results.
4. Perform, display and interpret results of surface calculations including: density potential surface, HOMO surfaces, and LUMO surfaces.

Here are some tips to help you avoid some of the common problems students have using molecular modeling:

1. Attention to detail – make sure you build (draw) the correct molecule!
2. *Think* about what you are doing and ask yourself: does that answer (output) seem correct?
3. Remember that computers only do what they are asked, so be sure you ask the correct questions (**make sure that your calculations are set-up correctly**).
4. Record the details of your computer modeling experiments in your laboratory notebook like you would a "wet" experiment – this will make it easier to check your work, write reports and find the files you want.
5. Save your work using file names that identify the molecule clearly – this will save you time trying to find the correct file later (a "Spartan" folder with subfolders for specific assignments may also be helpful).
6. Avoid running too many jobs at the same time. While the calculations will usually be queued properly, memory constraints may cause problems.
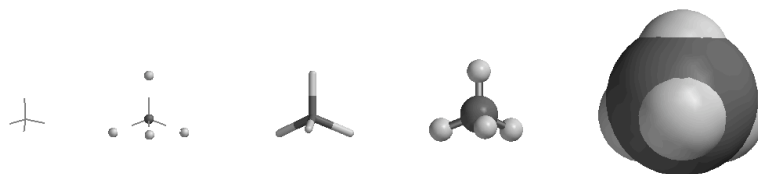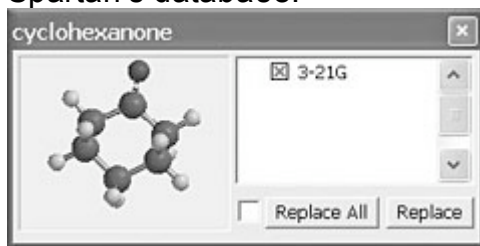
SPARTAN window:
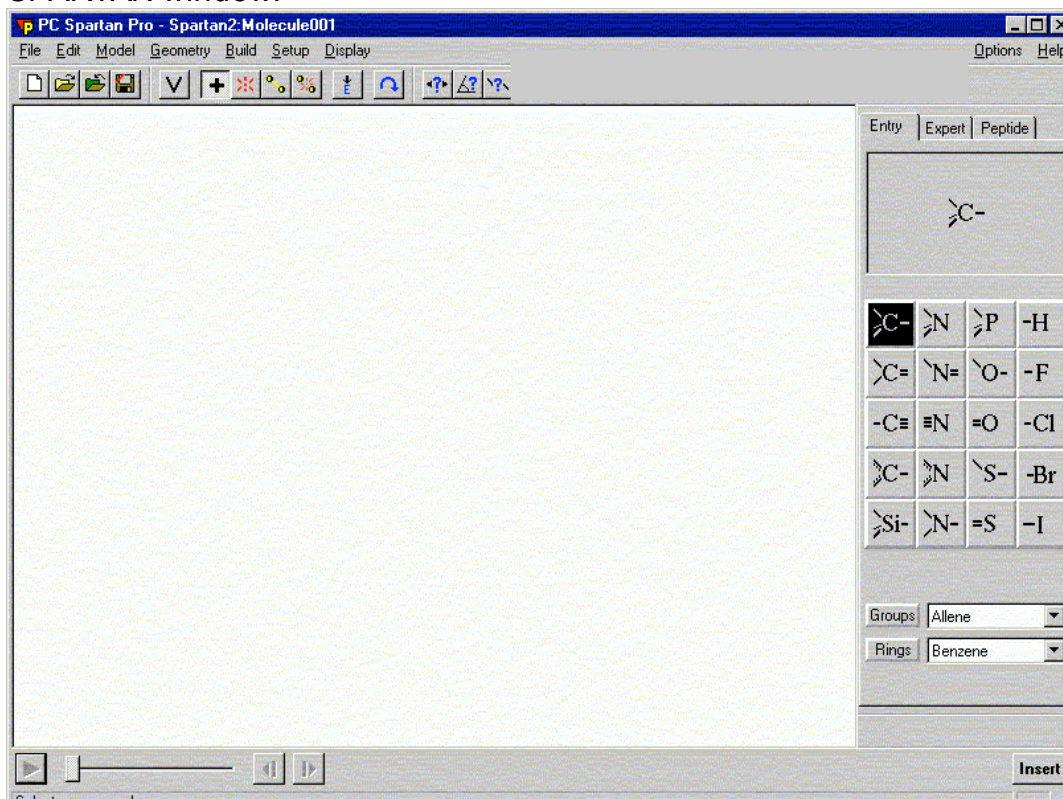
Pull-down menus:
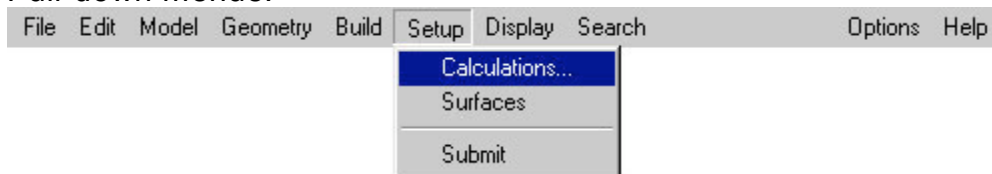
Models:

Spartan's database:

Using the Mouse:

The following functions are associated with the two-button mouse.

keyboard	left button[a]	right button[a]
-	picking, X/Y rotate	X/Y translate
Shift	range picking, Z rotate	scaling[b]
Control	multiple picking, global X/Y rotate[b]	global X/Y translate
Control + Shift	global Z rotate[c]	scaling[b]
Alt	group picking, bond rotation	bond stretching
Control ("Build" mode)	fragment X/Y rotate	fragment X/Y translate
Control + Shift ("Build" mode)	fragment Z rotate	scaling[b]

[a]Left and right buttons together with no modifier keys are used for defining a section box.
[b]Scaling is always applied to all open molecules and fragments.
[c]Global rotations can be either molecule or screen centered. This is controlled by **Global Rotate** in the **Preferences** dialog (**Options** menu).

Mouse/keyboard operations may be broadly separated into two categories: selection (picking) and manipulation (translation/rotation).

Selection:
The left button is used for picking of objects on screen and/or of menu items. Left and right buttons together are used to define a selection box for copying/cutting to the clipboard, as well as for model and color control for designated parts of a molecule. Together with the **Shift** key, the left button allows for picking over a range. Together with the **Ctrl** (**Control**) key, the left button allows for multiple picking. Both range and multiple picking applies not only to text items in lists, but to atoms and bonds in molecules as well. Together with the **Alt** key, the left button allows for selection of an entire group (detached molecular fragment).

Manipulation:
The left button is used for rotation and the right button is used for translation and scaling of objects on screen. With no modifier keys, the left mouse button gives rise to rotation about the X and y (screen) axes; the right mouse button gives rise to translation in the X and Y (screen) directions. Together with the **Shift** key, the left mouse button gives rise to rotation about the Z direction and the right mouse button gives rise to scaling.

The **Ctrl** key in conjunction with the left or right mouse buttons and (optionally)

3

the **Shift** key, signifies a change in focus away from the default for the purpose of rotations and translations. Outside of "build mode", the default is focus on a single molecule (the "selected" molecule). Use of the **Ctrl** key changes focus to the entire set of molecules on screen, meaning that rotations and translations are carried out globally. In "build mode", the default is focus on the full set of fragments which make up the molecule being constructed, and rotations and translations refer to this set of fragments as a whole. Use of the **Ctrl** key changes focus to a single fragment (the "selected" fragment), and rotations and translations now refer only to this fragment.

Use of the **Alt** key in addition to the left mouse button allows for rotation about a "selected" bond and, in addition to the right mouse button, for stretching of the "selected" bond.

Keyboard Functions:

Additional keys control various functions:

3	Shifts into 3D (stereo). Pressing **3** again returns to "normal" mode.
Page Up, Page Down, Home, End	Moves "up" (**Page Up**), "down" (**Page Down**), to the "top" (**Home**) and to the "bottom" (**End**) of the set of open molecules. Also, moves up and down pages in the **Output** dialog.
Insert	In "build mode" only, inserts of a new fragment on screen. This is accomplished by selecting the fragment from the model kit, holding down the **Insert** key and *clicking* on screen.
Delete	In "build mode" only, allows deletion of a an entire fragment or selected portion of a fragment. This is accomplished by holding down the **Delete** key and *clicking* on the fragment. No warnings are provided. **Delete** is also used to delete curves from a plot or entire plots.

Summary of Computational Types/Levels:

Molecular Mechanics**.** The molecular mechanics is the lowest level calculation. The molecular mechanics module provides for the calculation of equilibrium geometries, strain energies and vibrational frequencies, using MMFF94 (Merck Pharmaceuticals) force field. *There are no limits on the size of the molecular mechanics calculations.*

Semi-Empirical. Semi-Empirical is the "medium level" calculation. The semi-empirical module provides for calculation of heats of formation, wavefunctions,

equilibrium and transition-state geometries and vibrational frequencies, using the PM3 model. Elements available are H-Ne, Mg-Ar, Ca, Ti-Br, Zr, Mo-Pd, Cd-I, Hf-Pt and Hg-Bi. *Semi-empirical calculations are limited to 40 atoms.*

Hartree-Fock. Hartree-Fock 6-31G* is the highest level calculation on the student version. *We will typically perform calculations using Hartree-Fock 3-21G.* The Hartree-Fock module provides for calculation of energies and wavefunctions, equilibrium and transition-state geometries, closed-shell and open-shell calculations are supported with split-valence (3-21G) basis sets for H-Xe (except He and Ne) and polarization (6-31G*) basis sets for H-Ar (except He). *Hartree-Fock calculations are limited to 30 atoms.*

> You should realize that: (1) You cannot compare the energies from different types of calculations. (2) You can ONLY compare the energies of isomeric molecules (same number and types of atoms) or systems.

Theoretical Models

Quantum chemical models all ultimately stem from the Schrödinger equation first brought to light in the late 1920's. It treats molecules as collections of nuclei and electrons, without any reference whatsoever to "chemical bonds." The solution to the Schrödinger equation is in terms of the motions of electrons, which in turn leads directly to molecular structure and energy among other observables, as well as to information about bonding. However, the Schrödinger equation cannot actually be solved for any but a one-electron system (the hydrogen atom), and approximations need to be made. Quantum chemical models differ in the nature of these approximations, and span a wide range, both in terms of their capability and reliability and their "cost."

Definitions

3-21G. A Split-Valence Basis Set in which each Core Basis Function is written in terms of three Gaussians, and each Valence Basis Function is split into two parts, written in terms of two and one Gaussians, respectively. 3-21G basis sets have been determined to yield the lowest total Hartree-Fock Energies for atoms.

6-31G*. The 6-31G Basis Set in which non-hydrogen atoms are supplemented by d-type Gaussians. 6-31G* is a Polarization Basis Set.

***Ab Initio* Models**. The general term used to describe methods seeking approximate solutions to the many-electron Schrödinger equation, but which do not involve empirical parameters. *Ab initio* models include Hartree-Fock Models, Møller-Plesset Models and Density Functional Models.

Basis Functions. Functions usually centered on atoms which are linearly combined to make up the set of Molecular Orbitals. Except for Semi-Empirical Models where basis functions are Slater type, basis functions are Gaussian type.

Basis Set. The entire collection of Basis Functions.

Bohr. The Atomic Unit of length. 1 bohr = 0.529167 Å.

Conformation. The arrangement about single bonds and of flexible rings.

CPK Model. A molecular model in which atoms are represented by spheres, the radii of which correspond to van der Waals radii. Intended to portray molecular size and shape. Space-filling model. CPK comes from Corey-Pauling-Koltun, the names of the individuals that made the physical models in 1950-1960s.

Electron Density. The number of electrons per unit volume at a point in space. This is the quantity which is measured in an X-ray diffraction experiment.

Electrostatic Charges. Atomic charges chosen to best match the Electrostatic Potential at points surrounding a molecule, subject to overall charge balance.

Electrostatic Potential. A function describing the energy of interaction of a positive point charge with the nuclei and fixed electron distribution of a molecule.

Electrostatic Potential Map. A graph that shows the value of Electrostatic Potential on an Electron Density Isosurface corresponding to a van der Waals Surface.

Equilibrium Geometry. A Local Minimum on a Potential Energy Surface.

Frontier Molecular Orbitals. The HOMO and LUMO.

Hartree-Fock Approximation. Separation of electron motions in many-electron systems into a product form of the motions of the individual electrons.

Hartree-Fock Energy. The energy resulting from Hartree-Fock Models.

HOMO. Highest Occupied Molecular Orbital.

HOMO Map. A graph of the absolute value of the HOMO on an isodensity surface corresponding to a van der Waals Surface.

Isopotential Surface. An Electrostatic Potential Isosurface. It may be used to elucidate regions in a molecule which are particularly electron rich and subject to electrophilic attack and those which are particularly electron poor, subject to nucleophilic attack.

Isosurface. A three-dimensional surface defined by the set of point in space where the value of the function is constant.

Isotope Effect. Dependence of molecular properties and chemical behavior on atomic masses.

LUMO. Lowest Unoccupied Molecular Orbital.

LUMO Map. A graph of the absolute value of the LUMO on an Isodensity Surface corresponding to a van der Waals Surface.

Molecular Orbital. A one-electron function made of contributions of Basis Functions on individual atoms (atomic orbitals) and delocalized throughout the entire molecule.

Non-Bonded Interactions. Interactions between atoms which are not directly bonded. van der Waals Interactions and Coulombic Interactions are non-bonded interactions.

Quantum Mechanics. Methods based on approximate solution of the Schrödinger equation.

van der Waals Interactions. Interactions which account for short-range repulsion of non-bonded atoms as well as for weak long-range attraction.

van der Waals Radius. The radius of an atom (in a molecule), which is intdended to reflect its overall size.

van der Waals Surface. A surface formed by a set of interpreting spheres (atoms) with specific van der Waals radii, and which is intended to represent overall molecular size and shape.

Vibrational Frequencies. The energies at which molecules vibrate. Vibrational frequencies correspond to the peaks in an infrared and Raman spectrum.

References

1. Hehre, Warren J. *A Guide to Molecular Mechanics and Quantum Chemical Calculations*, Wavefunction, Inc. (2003)
2. *Tutorial and User's Guide: Spartan '06 Windows*, Wavefunction, Inc. (2006)

Summary of Molecular Mechanics: A Guide to using Spartan

	Button	
Keyboard	**Left**	**Right**
-	picking, *X/Y rotate*	*X/Y translate*
Shift	range picking, *Z rotate*	scaling
Ctrl	global *X/Y rotate*	global *X/Y translate*
Ctrl + Shift	multiple picking, global *Z rotate*	scaling
Ctrl (build mode)	fragment *X/Y rotate*	fragment *X/Y translate*
Ctrl + Shift (build mode)	fragment *Z rotate*	scaling
Alt	bond rotation	bond stretching

Molecular Modeling in Ten Steps

1. Draw (either on paper or skip to #2) a proper Lewis Dot Diagram. Using VSEPR, predict the molecular geometry.

2. Build the molecule in Spartan.

3. Select Minimize from the Build Menu

4. Select View from the Build Menu

5. Select Surfaces from the Display Menu and Add a (surface) Density (property) Potential surface; add any other surfaces you wish to calculate

6. Select Calculations from the Setup Menu

7. Select Equilibrium Geometry from the menu and select Hartree-Fock/3-21G (This specifies a Hartree-Fock calculation using the 3-21G basis set. This method generally provides a reliable account of geometries). Select the proper charge and multiplicity of the molecule.

8. Click Submit

9. Save the file in a folder that you will recognize

10. Select Properties from the Display menu and observe