Conformational Analysis Using Chem3D

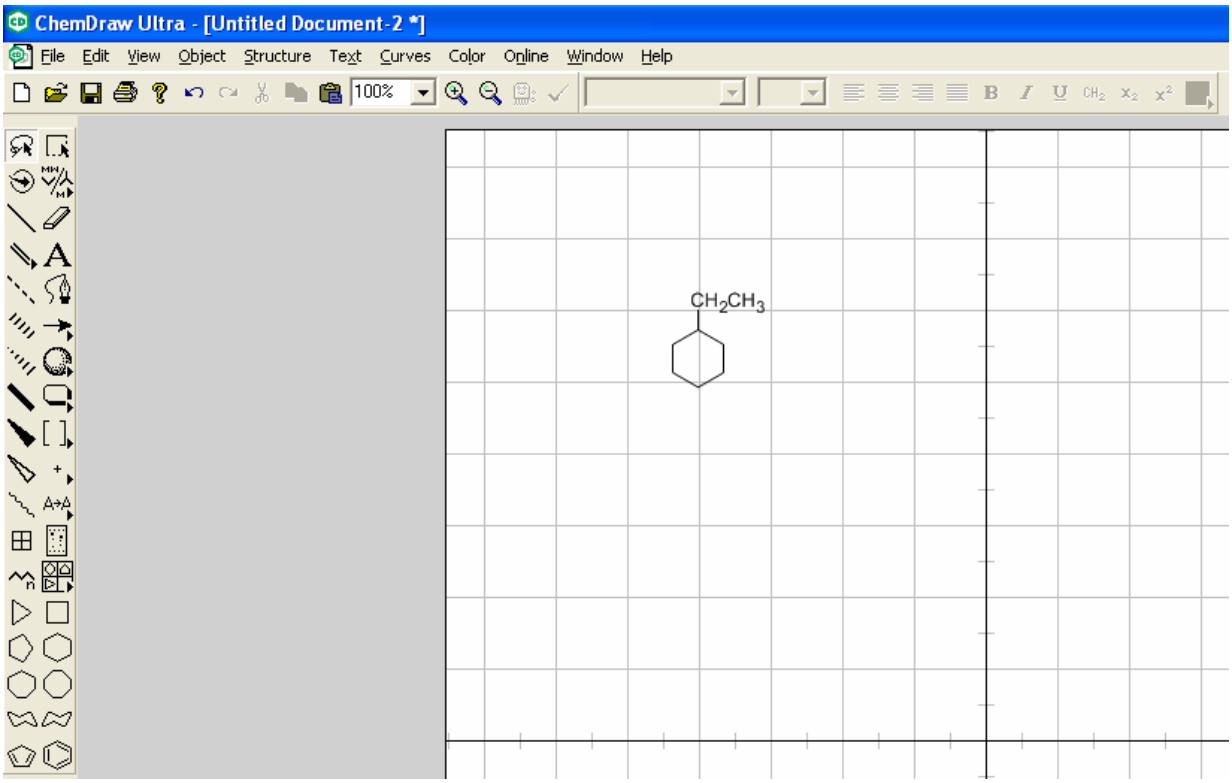
Honors 3719 Fall 2007

Introduction

In Chapter 3 of the Carey text we discuss the relative energies of the different ***conformations*** that are possible within simple acyclic and cyclic molecules. In the first lab exercise of 3719 you became familiar with the Spartan program that comes with the textbook and used it to build and analyze a number of molecules in order to introduce you to the software and how it may be used as you study. For the Honors component of Chemistry 3719 we will take this modeling idea further and use the ChemDraw package to build and analyze more complex molecules.

ChemDraw

Using your YSU email address you should download the ChemDraw package from the following address. http://scistore.cambridgesoft.com/sitelicense.cfm?sid=469
You may download at home or, if you are unable/reluctant do that, the complete suite of programs is available on the computers in both labs on the 5th floor of Ward Beecher. You'll be able to save your work to the desktop or, better, to a Zip disk or memory stick.
ChemDraw is the program we use to construct molecules for the slides in class and the exams we give in Organic chemistry. It takes a little getting used to but is pretty intuitive. The exercises below will give you practice at drawing structures and getting used to the different menus.

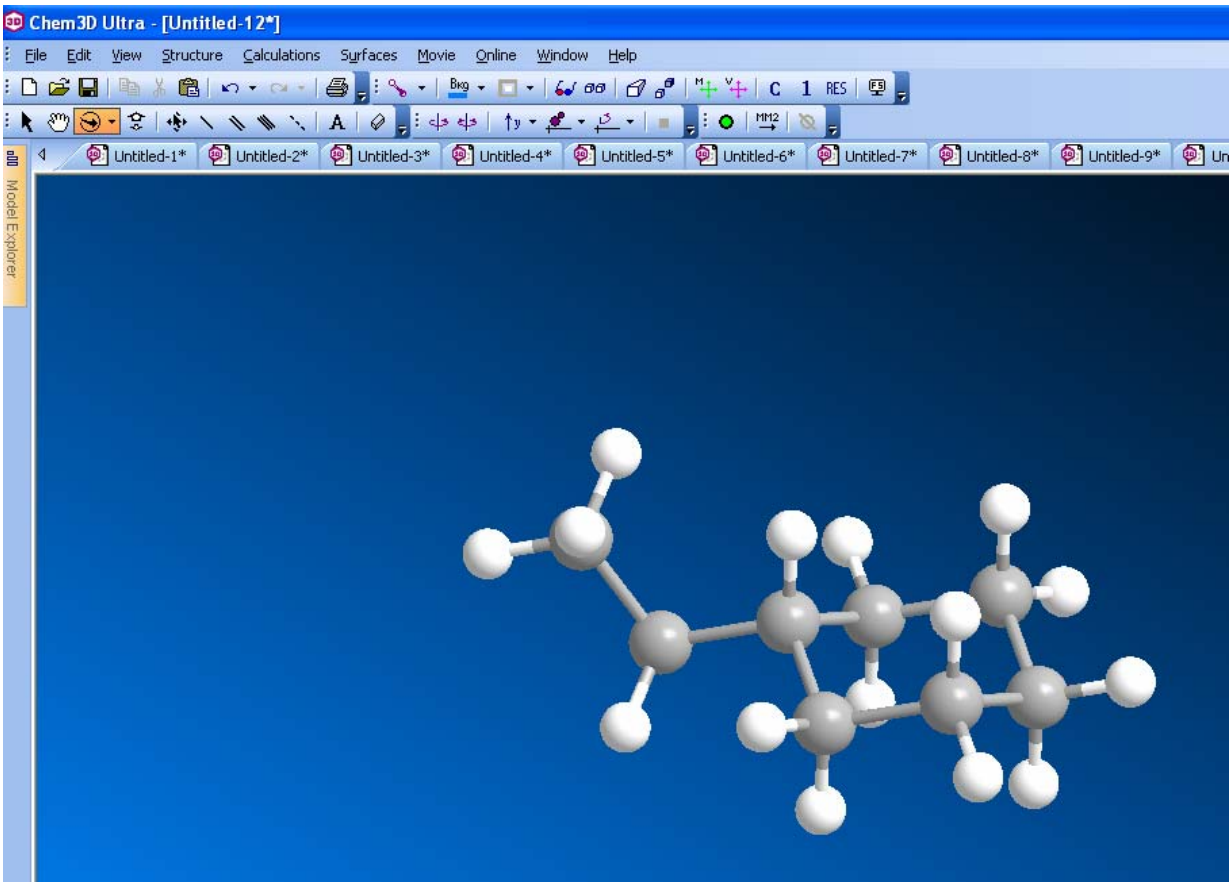


The basic layout is shown above and the first thing you need to do is define the settings by clicking "File → Apply document settings from → ACS document 1996" (this gives us a standard set of bond lengths, font sizes, etc.). Once that's done the Tool palette on the left of the

screen is used to construct the actual molecules (if you don't see this click on "View → Show main tools"). To draw ethylcyclohexane you would click on the six-membered ring tool and then click on the blank page. To add the ethyl group you would click on the "single bond" tool and then click on one of the corners of the six-membered ring and drag the mouse so that the bond shows coming off the cyclohexane ring. As in class this is a CH_3 group by default (i.e. the H's aren't shown) so if you wanted an ethyl group you would use the "text tool" "**A**" and click on the end of the bond and type "CH_2CH_3" in the text box. This works for any other groups you want to add (e.g. Br, OH, etc.). The first exercises in Honors 3719 can be done using these basic instructions; to save your work is the same as any other Windows software ("File → Save as").

Chem3D

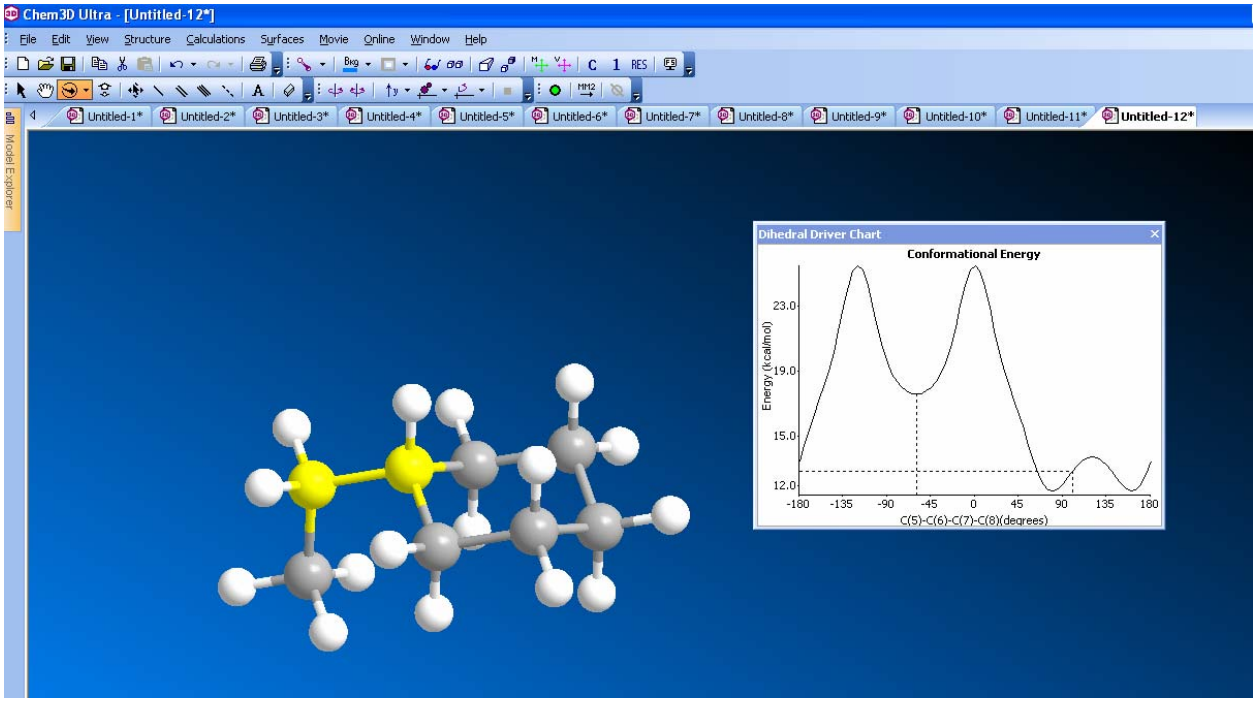
Opening Chem3D gives a blank page onto which you are able to paste the molecules you create and copy from ChemDraw. Ethylcyclohexane is shown below in the typical "ball and stick" representation. Using the "View → model display → display mode" sequence allows you to change the view, for example to simpler "wire frame" or "sticks" views or the (more realistic) "space filling" view. For calculation purposes the "ball and stick" representation is usually the most convenient to use.



To change the position of the model on the screen you use the "hand" tool on the second row of the tool bar; the orientation of the model on the screen is altered by using the "rotate" tool, which is highlighted in orange on the above picture. Once you have the view and orientation you need you're ready to start doing energy calculations.

The Dihedral Driver

The first type of calculation to run is using the "dihedral driver" to get the most stable orientation of the substituent relative to the ring. Click on the "arrow" (to the left of the "hand") and then click on the bond between the cyclohexane ring and the ethyl substituent; this bond should now be highlighted in yellow. Click "Calculations → dihedral driver → single angle plot" and the substituent will rotate through 360° resulting in a graph showing the relative energies of each conformation (see below). Clicking on a point on the curve will show the model that corresponds to that particular energy. For some of the beginning exercises you'll be using this tool to look at simple acylic molecules such as alkanes and creating graphs similar to those seen in Chapter 3. For the more complicated molecules you need to run the dihedral driver to find a good starting point for the calculations to ensure you're not starting at the wrong point.



Energy Minimization

Many of the questions posed through the term as part of Honors 3719 will require you to find the "minimum energy conformation" of two closely related molecules, and then see which of the two is more stable, and discuss the underlying reasons for the results (based on concepts from 3719). In the ethylcyclohexane example, having found the lowest energy conformation of the ethyl group relative to the ring (by using the dihedral driver), the molecule may be "minimized" to get an idea of the overall energy of the lowest energy conformation. We'll be doing two sets of calculations for each molecule you make. Firstly MM2 energy minimization; having found the lowest energy conformer from the dihedral driver, close the graph to be left with a model of that low energy conformer, then click "Calculations → MM2 → minimize energy" and "Run" on the dialog box that appears. The result of the calculation appears in the "Output" box at the bottom of the screen and you should make a note of the "Total" number that is displayed. The second type of calculation is using the AM1 protocol, which is run by clicking "Calculations → GAMESS interface → Minimize (Energy/Geometry)" and then selecting "AM1" from the

"method" menu in the dialog box and pressing "Run" to do the calculation. The result again shows in the "Output" box and you should record the "Heat of Formation" in Kcal/mol.

Answering Questions

For the pairs of molecules you're given during the semester you will carry out the above sequences to calculate the relative energies of each molecule within the pair and then answer set questions for each system. To begin, draw structures of 1,2-dibromoethane, hexane, and 2-methylbutane in ChemDraw and then take each model (one at a time) into Chem3D and get used to manipulating the picture on the screen. Change each model to the different views possible ("wire frame," "sticks," or "space filling") and then use the dihedral driver on each to generate graphs of rotations around different bonds. Once you are comfortable with each menu and how things work, go ahead and answer the following questions about these molecules. All of the information needed here is somewhere in Chapter 3 of the text.

For butane – when you use the dihedral driver on the C-2 – C-3 bond how many maxima appear on the conformational energy plot? Do each of these maxima correspond to different conformations or are some of them the same? Explain, using terms from class such as "eclipsed," "staggered," "gauche," and "anti" why the least stable conformation on the graph is so high in energy and why the most stable is so low. Why is considering the C-2 – C-3 bond here more useful than looking at C-1 – C-2? Make the model and run the dihedral driver to compare with what you found for the C-2 – C-3 bond.

For 1-chloro-2-iodoethane – Use the dihedral driver on the Chlorine – C-1 bond and make a note of how many minima and maxima you get after the 360° rotation. Do the same for the C-3 – C-4 bond and then discuss why the graph is different now. Draw Newman projections of the most stable and least stable conformers. From the values on the conformational energy plot, what is the barrier (in kcal/mol) for going between the two gauche conformations?

For 2-methylbutane – Use the dihedral driver on the C-2 – C-3 bond then rotate the molecule so that you are looking at it from the end like a Newman projection. Draw Newman projections of all of the low energy conformers and all the high energy conformers. Even though the graph is not symmetrical why are the two lowest energy conformers equivalent in energy?