Learning from Molecular Models II – Cycloalkanes

Textbook Reference – Chapter 4.9-4.14

Overview

Cyclic structures present conformational complexities not present in acyclic molecules. In this lab you will use molecular models to explore the conformations of some cyclic alkanes, especially cyclohexane and its mono- and di-substituted derivatives.

As in the previous molecular modeling exercise, you will build both physical models as well as geometry-optimized virtual models on Avogadro. Always record the energy and other key data (e.g. torsion angles and interatomic distances) next to the drawings you make of each model.

Definitions

Strain - Any factor that increases the potential energy of a molecule.

Torsional Strain - Strain associated with an eclipsed single bond.

Steric Strain - Strain due to two atoms being too close to each other in space. If the distance between the atoms is less than the sum of the Van der Waal's radii of the atoms then there is steric strain.

Angle Strain - Strain due to bond angles in a molecule not being able to attain ideal values (i.e., the values predicted by VSEPR theory). The strain results from a combination of extra electron pair repulsion (bonding electron pairs too close) and/or poor orbital overlap resulting in weak, bent bonds.

Ring Strain – The total strain associated with a cyclic structure. This could be due to one or more of the three fundamental types of strain, torsional, steric, and angle.

PROCEDURES

General Guidelines for Examining Models. We are particularly interested in detecting the types of and total amount of strain present in a particular structure. Since there are only three types of strain, we check for each, one at a time:
- **Torsional Strain.** Sight directly down each C-C bond in the molecule to see if any of them are eclipsed or partially eclipsed. (By partially eclipsed we mean not perfectly staggered.) Or use Avogadro to measure torsion angles throughout the molecule. The presence of torsion angles significantly off from 60° or 180° indicates the presence of eclipsed (or partially eclipsed) bonds.
- **Steric Strain.** Use a space-filling model and check to see if there are any atoms not bonded to each other that are "bumping" into each other. Or use Avogadro to check for hydrogens that are closer to each other than 2.4 Å. (Twice the Van Der Waals radius of hydrogen.)

- **Angle Strain.** Ball and stick model kits use balls (atoms) with predefined "ideal" bond angles. Therefore, when a molecular structure requires non-ideal bond angles the sticks (bonds) are forced to bend. Inspect your models for the presence of bent bonds as an indication of angle strain. In Avogadro, you can measure the bond angles between carbons in your rings and check for how close they agree with the ideal tetrahedral bond angle of 109.5°.
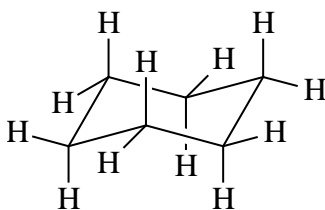
Part 1. Conformations of Cyclohexane

Flat Cyclohexane
Construct a model of cyclohexane by joining six carbons in a ring and then adding two hydrogens to each carbon. First force the six carbons all lie in one plane. What types of strain would be present in this hypothetical planar form of cyclohexane? Draw a structural diagram and label it to show the types of strain present.

Because of the large amount of strain present, it is difficult to build a model of planar cyclohexane in any molecular modeling program. Therefore, use the provided Avogadro structure file, "flat.cml", to examine the molecule on your computer. Determine the energy by clicking "Extensions", "Molecular Mechanics", "Calculate Energy". Measure both the C-C-C bond angles and the HCCH torsion angles as a way to provide more evidence for the conclusions you reached above. Also measure the distance between Hs on adjacent carbons.

Chair Cyclohexane
By rotating some of the bonds you should be able to make your cyclohexane model look like the figure below. The model should sit firmly on the desktop with three hydrogens serving as legs. This model represents the **chair conformation** of cyclohexane.

Examine the cyclohexane chair conformation carefully and draw it in the manner shown above. Look for strain in the chair conformation using the General Guidelines on page 1. What types of strain if any does cyclohexane possess? Explain.

Use the "Optimization" tool in Avogadro and watch what happens to the flat cyclohexane molecule. Check the resulting model to make sure it looks like the chair conformation above. If it doesn't use the Manipulation tool to drag one of the carbons out of plane with the others and retry the optimization. Once you have a chair in Avogadro (check with the instructor if uncertain), record the mimimized energy value and go ahead and measure the HCCH torsion angles, C-C-C bond angles, and distances between Hs on different carbons.

Note that the cyclohexane chair is highly symmetrical. Examine your model for the presence of planes of symmetry. How many of these does it possess? The chair conformation possesses other symmetry elements as well, including a 3-fold rotational axis of symmetry through the center of the ring, and three 2-fold rotational axes of

symmetry. (Ask the instructor to show you these.) It is important to recognize this symmetry when looking at perspective drawings of the cyclohexane chair, which can disguise the fact that all six carbons are exactly equivalent in terms of their chemical environments and their relationships to other carbons in the ring.

Note that three of the hydrogens point straight up and three point straight down. These hydrogens are said to be in **axial** positions. (Imagine the ring as a wheel. These hydrogens point out in the same direction as the axis of the wheel would.) The other six hydrogens radiate outward along the perimeter of the ring. These hydrogens are in **equatorial** positions.

Go back to your first drawing of chair form cyclohexane and this time label all of the hydrogens as equatorial (eq) or axial (ax).
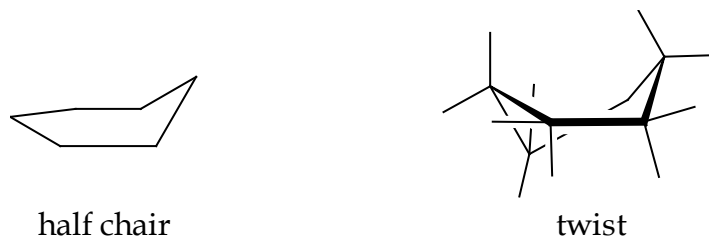
Boat Cyclohexane
By grasping one of the carbons with an axial hydrogen pointing down and forcing it to point up (bond rotations are required), you should be able to get your model to look like a boat. (See figure below.) This conformation of cyclohexane is referred to as the **boat**.
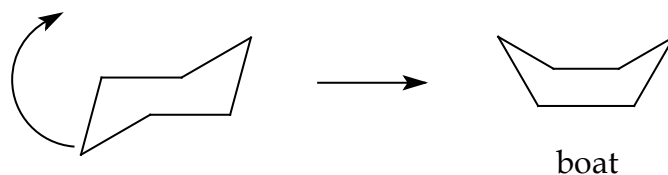
boat

Look for strain in the boat conformation using the methods outlined previously. Depict any strain you find with a structural drawing, e.g., a Newman projection for torsional strain.

Use the provided Avogadro structure file "boat.cml" to calculate the strain in the boat and try to pinpoint its origins by measuring bond angles, torsion angles, and distances between Hs. Like with the flat cyclohexane you will need to determine the energy by clicking "Extensions", "Molecular Mechanics", "Calculate Energy".

Other conformations of cyclohexane include the **half chair** and the **twist** conformations:

half chair   twist

Twist Cyclohexane
The **twist** (also called the "twist boat") can be arrived at by starting with the boat, grasping the carbons that would represent the bow and stern of the boat, and pulling them slightly away from each other and in opposite directions with respect to the plane of symmetry which they lie in. (See figure below).
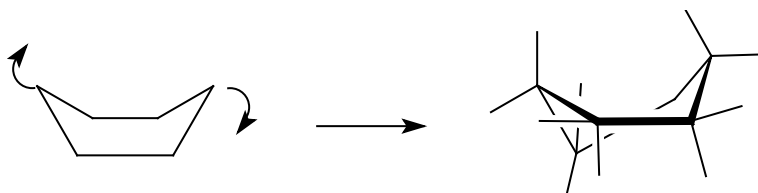
Look for strain in the twist conformation using the same process as before. Depict any strain you find with a structural drawing, e.g., a Newman projection for torsional strain. Compare to the boat, does the twist have more or less strain?

Run an energy minimization on your boat molecule and what conformation results? Record the energy and calculate the strain. Check torsion angles and distances between Hs and compare to those found in the boat.

Half Chair Cyclohexane
The **half chair** can be arrived at by stopping halfway on the way from the chair to the boat. At this point, five of the carbons lie in the same plane. Make a model of the half-chair and look for strain using the same process as before. Depict any strain you find with a structural drawing, e.g., a Newman projection for torsional strain.

Use the provided Avogadro structure file "halfchair.cml" to calculate the strain in this conformation as well as measure some bond angles, torsion angles, and distances between Hs that may be causing strain.

Post-lab question #1. Rank the various conformations of cyclohexane from lowest potential energy (least strain) to highest energy (most strain). Make an energy diagram for bond rotations in cyclohexane. Which conformations are conformers?

Part 2. Conformers of Methylcyclohexane

For the remainder of the lab consider chair conformers only.

Also, continue to make the models both with your model kit and in Avogadro, using the latter to calculate energies and look for strain by measuring angles and HH distances.

Methylcyclohexane with equatorial Me
Remove an equatorial hydrogen from the cyclohexane model and add a CH_3 group in its place to form methylcyclohexane. Draw this structure using a perspective drawing to those used for chair cyclohexane above. Look for strain interactions and diagram any that clearly are present.

Methylcyclohexane with axial Me
Now grasp and invert any carbon (C-1) to form a boat conformation. Then take C-4 and invert it to remake a chair conformer. This process inverts the chair conformer and is called ***chair flipping*** (See figure below).
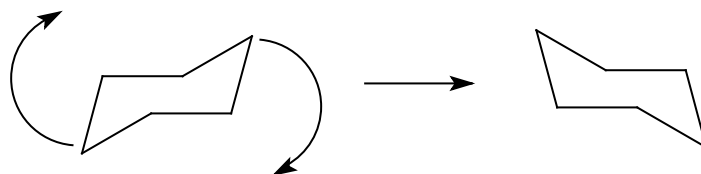
Draw this other chair conformer of methylcyclohexane and inspect it for potential strain interactions. How much strain in present in this conformation and what type of strain is it? Diagram this strain in the structure you drew.

Notice that chair flipping switches all equatorial groups to axial and vice versa. One must also realize that chair flipping comes about solely by single bond rotations and therefore happens very rapidly at room temperature. In other words, all cyclohexane compounds exist as a pair of chair conformers, in which the only difference is the equatorial/axial status of the attached groups.

Part 3. Conformers of *tert*-Butylcyclohexane

***tert*-Butylcyclohexane with equatorial t-Bu**
As before, make a model and check it for strain and draw it. Determine the minimized energy using Avogadro.

***tert*-Butylcyclohexane with axial t-Bu**
Use this opportunity to practice flipping a chair model and make this molecule. How strained is it and what is the strain due to?

Part 4. Conformers of Dimethylcyclohexanes

***trans*-1,2-Dimethylcyclohexane**
Make a model of 1,2-dimethylcyclohexane with both methyl groups in equatorial positions. Draw this structure. Force the ring to be planar for a moment and verify for yourself that the methyl groups are indeed *trans* to each other. With it back in a diequatorial chair, look strain interactions in this model and label them on your structure drawing.

Flip the ring to its other chair conformation. Observe the positions of the methyl groups now. Did the methyl groups' stereochemical relationship (i.e., *cis* or t*rans*) change? Look for strain interactions in this flipped chair and note your observations diagraming specific interactions on your structure drawing. Which chair conformer of *trans*-1,2-dimethylcyclohexane is more stable?

***cis*-1,2-Dimethylcyclohexane**
Make a model of 1,2-dimethylcyclohexane with one of the methyl groups in an equatorial position and the other in an axial position. (You may wish to force the ring to be planar for a moment in order to prove that the methyl groups are indeed *cis*.) Look for strain in this structure and diagram the strain interactions.

Flip the ring of your model to its other chair conformer. Did the methyl groups'

stereochemical relationship (i.e., *cis* or *trans*) change? Did the situation regarding strain change? Which chair conformer of *cis*-1,2-dimethylcyclohexane is more stable?

trans-1,3-Dimethylcyclohexane
Make a model of *trans*-1,3-dimethylcyclohexane. Examine ring flipping and draw both chair conformers. Observe each conformer for strain interactions. Which chair is more stable? Why?

cis-1,3-Dimethylcyclohexane
Make a model of *cis*-1,3-dimethylcyclohexane. Examine ring flipping and draw both chair conformers. Observe each conformer for strain interactions. Which chair is more stable? Why?

trans-1,4-Dimethylcyclohexane
Make a model, examine ring flipping, draw both conformers and look for strain as before. Which chair is more stable? Why?

cis-1,4-Dimethylcyclohexane
Make a model, examine ring flipping, draw both conformers and look for strain as before. Which chair is more stable? Why?

1,1-Dimethylcyclohexane
Make a model, examine ring flipping, draw both conformers and look for strain as before. Which chair is more stable? Why?


Post-lab question #2
Part 1. Realize that because each isomer exists primarily as its more stable chair conformer, it is the stability of the more stable chair that determines the stability of the isomer. Given this, what is the order of stability of the seven isomers of dimethylcyclohexane?

Using the idea that gauche dimethyl interactions and 1,3-CH_3-H diaxial interactions both cause about 0.9 kcal/mol of steric strain allows good predictions of the amount of strain in any particular dimethylcyclohexane conformer. Simply count up the number of these interactions present in any given conformer and multiply by 0.9 kcal/mol.

Compare the predicted strain values for the dimethylcyclohexane conformers to the results of your Avogadro molecular mechanics calculations. (Make a table and explain any discrepancies between predicted and computed values.)

Part 5. Conformers of 1,3,5-Trimethylcyclohexanes

There are two stereoisomers of 1,3,5-trimethylcyclohexane, *cis-trans-trans* and all-*cis*. Which isomer is more stable? (Make models to make sure!). Draw each stereoisomer in its most stable conformer.

all-*cis*   *cis-trans-trans*
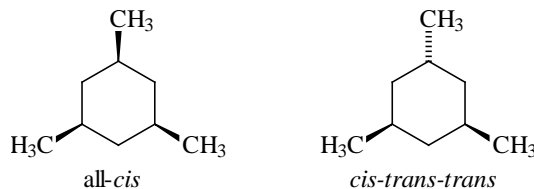
Part 6. Conformers of *tert*-Butylmethylcyclohexanes

Consulting models if necessary, determine and draw the most stable conformer of each of the following compounds.

trans-1-*tert*-butyl-4-methylcyclohexane
cis-1-*tert*-butyl-4-methylcyclohexane
trans-1-*tert*-butyl-3-methylcyclohexane
cis-1-*tert*-butyl-3-methylcyclohexane
trans-1-*tert*-butyl-2-methylcyclohexane
cis-1-*tert*-butyl-2-methylcyclohexane
1-*tert*-butyl-1-methylcyclohexane

Remember that the difference in stability between alternative chair conformers when a t-Bu group is involved is quite large (part 3). Therefore, when t-Bu is present it is always the case that effectively 100% of the molecules are in the conformation that has the t-Bu group equatorial. Hence, the presence of a t-Bu group can be used to lock the chair into a single chair conformation.

Part 7. Other cycloalkanes

Make models of **cyclopropane**, **cyclobutane**, **cyclopentane**, and **cycloheptane**. Make a conformational drawing of each and identify strain interactions in each.

Post-lab question #3. For the unsubstituted cycloalkanes of C3-C7 make a table that lists the calculated energies from molecular mechanics, the strain energies, and the strain per CH_2 group. Also include strain energies as calculated from heats of formation of these compounds. The table should also indicate the types of strain (torsional, steric, and/or angle) present. Discuss the table both in terms of the accuracy of the MM calculations and in terms of the reasons for the varying strain values seen in these different size rings.