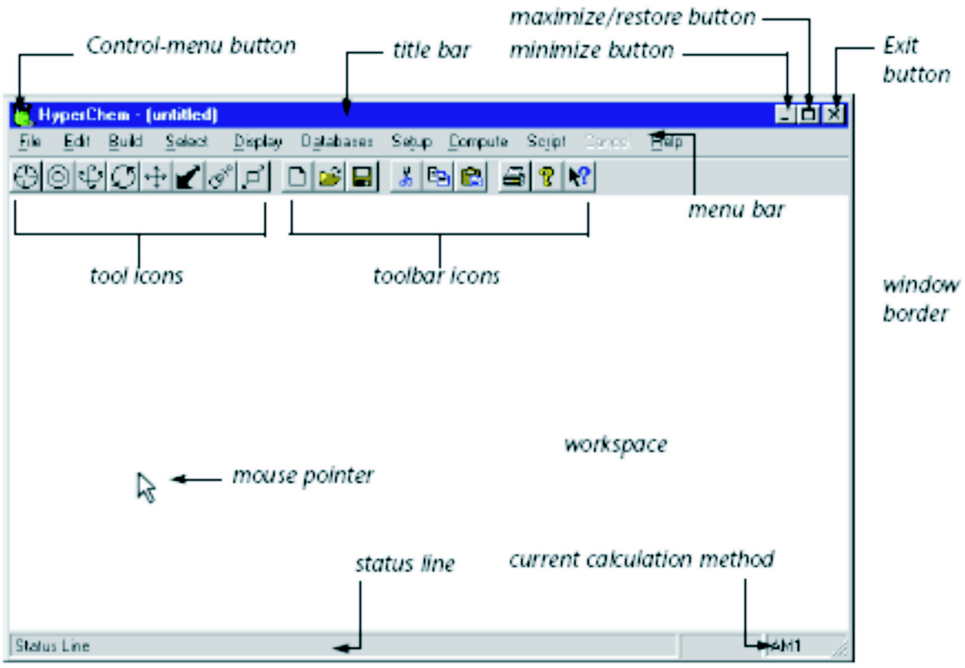
Laboratory 1
HyperChem

Lesson	Information covered	Time to complete
Getting Started	Opening HyperChem; introduction to the user interface; opening and closing a file, and using labels and molecular renderings.	20 minutes
Basic Drawing and Editing Techniques	Drawing, selecting, copying, and deleting atoms and bonds.	10 minutes
Creating Small Molecules in 2D and 3D	Drawing and editing a 2D sketch of a molecule and transforming it into a 3D model.	10 minutes
Translating, Rotating, and Scaling Molecules	Using the tools in the tool bar to move and manipulate molecular structures.	10 minutes
Measuring Structural Properties	Measuring and adjusting the geometry of molecular structures.	35 minutes
Creating a Polypeptide	Creating biopolymers using the amino acid and nucleic acid databases.	15 minutes
Selecting and Displaying Subsets	Using specific selection techniques to select subsets for movement, display, calculation, and analysis.	15 minutes
Working with Macromolecules	Working with molecules from the Brookhaven Protein Data Bank; performing site-specific mutagenesis.	35 minutes

Getting started - starting HyperChem

The HyperChem window opens. Depending upon the version of HyperChem you are using, the window may look slightly different from that below.



Tool Bar

The left side of the Tool bar contains the eight tools icons that you use to draw, select, display, and move atoms and molecules - rotate out of plane, rotate in plane, next one is translate and Z-translate, last two: magnify/shrink. To the right are the four tool icons associated with annotations. To the right of this are the toolbar icons which provide shortcuts for operations such as reading and writing files, copying and pasting structures, and using the on-line help.

Open a file *c60.hin* (in HyperChem directory samples/aromatic)

Using Display Settings

HyperChem automatically uses the display settings from the last session. You choose the display settings by using menu items on the Display menu. To open the Display menu:

- L-click on Display on the menu bar.

The Display menu opens.

Using Labels

If the molecule is displayed with labels, remove them
To remove the labels:
L-click on Labels. The Labels dialog box appears. Even if the currently displayed molecule is labelled, the dialog box opens with the default setting of None for both atom and residue label types.

L-click on OK.
The dialog box closes and the labels are removed.
To use labels:

- L-click on Labels.
- Choose Symbol as the atom label type, and then choose OK.

The dialog box closes and the molecule is labelled by atomic symbol.

Using Different Molecular Renderings

You can use various molecular renderings when you display a molecular system. To change the molecular rendering:

- Choose Rendering on the Display menu.

The Rendering dialog box opens:
Choose Balls in the list, and then click on the "tab" at the top labelled Balls to show the Balls Options property sheet.
After that try different options.

Basic Drawing and Editing Techniques

To draw an atom:

Open the Element Table dialog box. There are two ways to do this:

- Select Default Element on the Build menu, or
- Double-click on the Drawing tool.

The Element Table dialog box appears. Choose element from the periodic table.

You can leave the Default Element dialog box open and move it so you can see the HyperChem workspace. This is useful when you want to draw molecules with many heteroatoms.

Draw several atoms at various locations in the workspace.

To draw a bond:

- Move the cursor above the first atom you drew.
- Press and hold down the left mouse button. This is the location of the first atom of the bond you are drawing.
- Continue to hold down the left mouse button and drag (L-drag) diagonally toward the top of the workspace. Release the mouse button. This is the location of the second atom in the bond. A line representing a bond between two carbon atoms appears.

Now, Starting in an empty area of the workspace, draw six bonds to form a ring of carbons. L-click on the middle of one of the bonds makes the bond double or triple.

To select a group of atoms using rectangular selection:

In this exercise, you learn basic selection techniques by selecting atoms. First, you must set the level of selection (atoms, residues, or molecules) that you want and set multiple selection. To select atoms L-click on the Selection tool (second tool on the left) and move the cursor into the workspace. L-click on one of the atoms you created. L-click on the middle of

one of the bonds you created. The bond is highlighted. The atoms at each end of the bond are selected, highlighting the line that represents the bond. R-click in an empty area of the workspace. All atoms and bonds are deselected.

Selecting Groups of Atoms

Pick a point in an empty part of the workspace toward the topleft corner. LR-drag diagonally, toward the lower-right corner of the workspace. HyperChem displays a rectangle representing the border of the selection area.

To delete a single atom or a bond:

- L-click on the Drawing tool to get into drawing mode (first icon on the left).
- R-click on the atom you want to delete, or on the middle of the bond you want to delete.

The atom or bond disappears.

Creating Small Molecules in 2D and 3D

To draw the 2D sketch:
Double-click on the Drawing tool. The Element Table dialog box opens. Turn Allow Arbitrary Valence on and Explicit Hydrogens off. When you draw with Explicit Hydrogens turned off, hydrogen atoms are not automatically added. Choose Carbon, then close the dialog box. Carbon is set as the default element and the dialog box closes. Draw the following molecules H_2O and NH_3

Saving Your Work in a File !!! - for each case separately as a *hin* file. Ex: water.hin and ammonia.hin

To change bond orders

Point to the middle of the third bond from the left and L-click. The bond order increases from a single to a double. L-click on the bond again causes the double bond increases to a triple bond. R-click reduces the bond order. To make rings aromatic Double-click on any bond of the ring.

Now you can draw benzene molecule and save it as a benzen.hin.

To convert your 2D sketch into a 3D structure, you use the HyperChem Model Builder. Select Add H and Model build on the Build menu. HyperChem produces a 3D representation of the molecule and automatically adds hydrogens. Now save a new structure of benzene after model build. Do the same thing for H_2O and NH_3. Select Labels on the Display menu. Set bond length. Now you can see bond length of selected molecule(if whole molecule was selected).

Translating, Rotating, and Scaling Molecules

Reopen one of a *hin* file. Use XY Translation tool, Z-Translate, rotate tool and zoom tool to find out what happened.

Measuring Structural Properties

To get information on atom characteristics:

Reopen water molecule (water.hin) On the Select menu, make sure that Atoms is chosen and that Multiple Selections is not. L-click on the Selection tool (second tool on the left). L-click on the oxygen atom. The selected atom is highlighted and the atom characteristics appear in the status line!!!!

To measure a bond distance and bond angles:

L-click on the hydrogen-oxygen bond. The bond is highlighted and the bond distance appears in the status line.

To measure a bond angle, L-drag between the two terminal atoms that are bonded to the common third atom.

You measure a torsion angle by dragging the select cursor between the two terminal atoms of a four-atom torsion.

Measure some selected bond and angle foe water, ammonium and benzen. Prepare a table with data.

Creating a Polypeptide

Clear the workspace, either by restarting HyperChem or by selecting New from the File menu. To open the Amino Acids dialog box select Amino Acids on the Databases menu. The Amino Acids dialog box will appear. The first step in building the polypeptide is to determine the secondary conformation. In this exercise, you set the options to build a beta sheet structure. L-click sequentially on **Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg**. When you choose Pro, HyperChem „beeps". This means that it cannot use the desired conformation. In this exercise, you convert the ends of the peptide to zwitterionic form by modifying the N- and C- terminal residues. Choose Make Zwitterion on the Databases menu. Select Labels on the Display menu and L-click on Name+Seq as the option for labeling residues, and then choose OK. Choose Residues on the Select menu. L-click on the Selection tool. R-click in an empty area of the workspace to make sure nothing is selected. L-click on PHE 5. Select Mutate on the Databases menu. In the Mutate dialog box, scroll down the list of residues and choose Thr, then choose OK. The selected phenylalanine is replaced by threonine.

Selecting and Displaying Subsets

Create the alpha helix of six Phe. Remove labels. On the Select menu, make sure Atoms and Multiple Selections are on. L-click on the Selection tool. L-click on the N-terminal nitrogen atom on the left side of the polypeptide to select the N-terminal end. L-click on the C-terminal carbon atom on the right side of the polypeptide to select the C-terminal end. Select Labels on the Display menu and Select symbol as the atom label type.

To investigate the alpha-helical nature of this polypeptide, it helps to visualize the backbone. Use Select Backbone on the Select menu.

Select Color on the Display menu. The Selection Color dialog box appears. Select Red. R-click on an empty area. HyperChem displays the backbone in red.

Select backbone once again. To display only the backbone choose Show Selection Only on the Display menu. Only the backbone and the labels are displayed. Choose Labels on the Display menu. The Labels dialog box appears. Select None for the residues label type, then choose OK.

To display the side chains choose Show All on the Display menu.

Sometimes, it might be helpful to select or display only the parts of a molecular system not currently selected. You can do this using Complement Selection on the Select menu.

Once again select backbone. To select and display the complement of a selected subset: Choose Complement Selection on the Select menu. This selects all parts of the polypeptide except the backbone. Choose Show Selection only on the Display menu and R-click the Selection tool on an empty area of the workspace. This displays all parts of the polypeptide except the backbone.

Working with Macromolecules

Open from /samples/pdb/pdb5pti.ent file. To simplify this exercise, remove the water molecules surrounding.

Set the select level to Molecules. L-click on the Selection tool to get into selection mode. L-click on the BPTI molecule. This selects the BPTI molecule. Choose Complement Selection on the Select menu. This selects only the water molecules. Choose Clear on the Edit menu. Save the file to a different filename.

Choose Select Backbone and press the space bar. Choose Show Selection Only on the Display menu. R-click in an empty area.

To calculate and display hydrogen bonds, get into selection mode and R-click in an empty area to deselect the ring. On the Display menu, choose Show All, and then Scale to Fit. The entire molecule is displayed and centered in the workspace. Remove labels from the display. Turn Show Hydrogens and Show Hydrogen Bonds on. Show Hydrogen Bonds displays possible hydrogen bonds between selected atoms, or, with no selection, displays hydrogen bonds for all molecules in the system. Choose Recompute H Bonds on the Display menu. HyperChem displays the hydrogen bonds as broken lines. Press [PgDn] to zoom in until the hydrogen bonds are clearly visible. Press the space bar to return to a scale-to-fit view.