

# Jaguar 7.9

## Quick Start Guide

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# Document Conventions

In addition to the use of italics for names of documents, the font conventions that are used in this document are summarized in the table below.

Font	Example	Use
Sans serif	Project Table	Names of GUI features, such as panels, menus, menu items, buttons, and labels
Monospace	<code>\$SCHRODINGER/maestro</code>	File names, directory names, commands, environment variables, command input and output
Italic	<i>filename</i>	Text that the user must replace with a value
Sans serif uppercase	CTRL+H	Keyboard keys

Links to other locations in the current document or to other PDF documents are colored like this: [Document Conventions](#).

In descriptions of command syntax, the following UNIX conventions are used: braces { } enclose a choice of required items, square brackets [ ] enclose optional items, and the bar symbol | separates items in a list from which one item must be chosen. Lines of command syntax that wrap should be interpreted as a single command.

File name, path, and environment variable syntax is generally given with the UNIX conventions. To obtain the Windows conventions, replace the forward slash / with the backslash \ in path or directory names, and replace the \$ at the beginning of an environment variable with a % at each end. For example, `$SCHRODINGER/maestro` becomes `%SCHRODINGER%\maestro`.

Keyboard references are given in the Windows convention by default, with Mac equivalents in parentheses, for example CTRL+H (⌘H). Where Mac equivalents are not given, COMMAND should be read in place of CTRL. The convention CTRL-H is not used.

In this document, to *type* text means to type the required text in the specified location, and to *enter* text means to type the required text, then press the ENTER key.

References to literature sources are given in square brackets, like this: [10].



# Getting Started

This manual contains exercises designed to help you learn the basic tasks you will need to prepare and initiate Jaguar calculations from Maestro. For more information about Jaguar features, see the *Jaguar User Manual*.

This chapter contains instructions for setting up the tutorial.

**Chapter 2** contains exercises on running various basic Jaguar calculations: single-point energies with both DFT and LMP2 theory, geometry optimizations, and orbital plotting.

**Chapter 3** contains exercises that show you how to predict and display properties, covering  $pK_a$  prediction, potential energy surfaces from coordinate scans, mapping a 3D property (ESP) onto a surface, and noncovalent interactions. Some of the exercises include building molecules in Maestro.

**Chapter 4** contains exercises on using MacroModel and Jaguar together for conformational searches.

**Chapter 5** contains a set of exercises for transition state searches, intrinsic reaction coordinate calculations, frequency calculations.

**Chapter 6** contains exercises for generating and plotting a VCD spectrum that includes averaging over conformers.

Help for each of the Jaguar tasks is available in the Maestro online help.

To do the exercises, you must have access to an installed version of Maestro 9.3 and Jaguar 7.9, and for the conformational searches, MacroModel 9.9. For installation instructions, see the *Installation Guide*. The directory in which the software is installed will be referred to as the installation directory.

The preparations that must be made for the exercises are to create a working directory to keep all your input and output files, start Maestro, ensure that this directory is Maestro's current working directory, and create a project. These tasks are described in the following sections.

## 1.1 Preparing for the Exercises

To run the exercises, you need a working directory in which to store the input and output, and you need to copy the input files from the installation into your working directory. This is done automatically in the Tutorials panel, as described below. To copy the input files manually, just unzip the jaguar zip file from the tutorials directory of your installation into your working directory.

On Linux, you should first set the SCHRODINGER environment variable to the Schrödinger software installation directory, if it is not already set:

**csh/tcsh:**            `setenv SCHRODINGER installation-path`

**sh/bash/ksh:**        `export SCHRODINGER=installation-path`

If Maestro is not running, start it as follows:

- **Linux:** Enter the following command:

```
$SCHRODINGER/maestro -profile Maestro &
```

- **Windows:** Double-click the Maestro icon on the desktop.

You can also use Start → All Programs → Schrodinger-2012 → Maestro.

- **Mac:** Click the Maestro icon on the dock.

If it is not on the dock, drag it there from the SchrodingerSuite2012 folder in your Applications folder, or start Maestro from that folder.

Now that Maestro is running, you can start the setup.

1. Choose Help → Tutorials.

The Tutorials panel opens.

2. Ensure that the Show tutorials by option menu is set to Product, and the option menu below is labeled Product and set to All.
3. Select Jaguar Quick Start Guide in the table.
4. Enter the directory that you want to use for the tutorial in the Copy to text box, or click Browse and navigate to the directory.

If the directory does not exist, it will be created for you, on confirmation. The default is your current working directory.



5. Click Copy.

The tutorial files are copied to the specified directory, and a progress dialog box is displayed briefly.

If you used the default directory, the files are now in your current working directory, and you can skip the next two steps. Otherwise, you should set the working directory to the place that your tutorial files were copied to.

6. Choose Project → Change Directory.

7. Navigate to the directory you specified for the tutorial files, and click OK.

You can close the Tutorials panel now, and proceed with the exercises.

## **1.2 Creating a Maestro Project**

You should create a new named Maestro project to save your work, in case you want to complete the exercises at a later time. If you are using an existing Maestro session, it is advisable to create a new project to keep the tutorial separate from your other work. When you start Maestro, a scratch project is created, which must be named in order to keep it for later use.

1. Choose Project → New.

The New Project dialog box is displayed. The Look in option menu should contain the current Maestro working directory.

2. In the File name text box, type `JaguarTutorial`.

3. Click Save.

This procedure creates a project named `JaguarTutorial`. The work that you do during the exercises that follow is automatically saved in this project for later use.

## **1.3 Setting Preferences**

By default, only the primary Jaguar properties are shown in the Project Table. In these exercises you will be using other properties, so the preference to show these properties by default must be set.

1. Choose Maestro → Preferences.

2. Under Project Table in the tree on the left, click Properties.

3. Under When new entries are added, select Show all properties.



# Running Basic Jaguar Calculations

This chapter is designed to introduce you to the basic capabilities of Jaguar 7.9 and its interface with Maestro 9.3. The first two exercises provide instructions on drawing and symmetrizing a benzene molecule, which is used for calculations in the following exercises. If you want to skip the structure-building exercises, you can start with the calculations at [Section 2.3 on page 7](#). The remaining exercises should be done in sequence.

## 2.1 Drawing a Benzene Molecule

In this exercise, you will draw a benzene molecule in the Workspace. Although drawing benzene is not necessary because there is a benzene fragment in the organic fragment library, drawing structures can be useful when it is difficult to build them from fragments, such as structures with multiple fused rings.

1. Clear the Workspace.
2. Click the Draw button on the Build toolbar.



The button is indented to indicate that Draw mode is active. The default atom selected for drawing is carbon. If you want to choose a different atom, click and hold on the button and select an element from the menu that is displayed.

3. Click once in the Workspace.

An asterisk appears enclosed in a purple cube. This cube marks the active drawing atom. When there is an active drawing atom, clicking again in the Workspace while in Draw mode places another atom and bonds it to the original atom. Clicking a second time on the active drawing atom makes it inactive.

4. Draw a six-membered ring by clicking in the Workspace five more times in the proper configuration, then clicking on the first atom.

As you move the mouse, a yellow line connects the pointer to the active atom. The atoms are all placed in the same plane.

Next, you will adjust the C–C bond orders and add hydrogens.

5. Click the next atom in the ring.

The bond changes to a double bond.

6. Click this atom a second time.

The purple square disappears to indicate that active drawing has finished. You can now click another atom to start drawing in a different location.

7. Click the next atom in the ring once.

The purple square reappears, indicating that drawing is active again.

8. Click the next atom in the ring twice.

A double bond is drawn, and the purple square disappears.

9. Click the next atom in the ring once, and the following atom twice.

A third double bond is drawn, and the carbon skeleton with its bonding is complete.

10. Double-click the Add hydrogens button (on the Edit toolbar).



The double-click adds hydrogens to all atoms. You can add hydrogen atoms to selected atoms in the structure by clicking once, and then picking the atoms.

## 2.2 Symmetrizing the Structure

The molecule you drew is planar, but is likely to have no other symmetry. In this exercise you will symmetrize the structure so that it has full  $D_{6h}$  symmetry, then clean up the structure.

1. Choose Edit → Symmetrize Workspace.

The Symmetrize Workspace panel is displayed. The point group is likely to be  $C_s$ .

2. If the point group is not  $D_{6h}$ , adjust the tolerance and click Find Point Group until the correct point group is located.

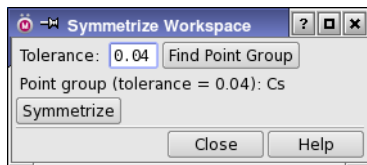


Figure 2.1. The Symmetrize Workspace panel.

If you can't find the correct point group, use a lower point group, such as  $D_{2h}$ . You will then have to repeat the process to get the full point group.

3. Click Symmetrize.

The structure takes on the specified point group. If the point group is not  $D_{6h}$ , repeat [Step 2](#) and [Step 3](#). You might have to decrease the tolerance to find the right point group.

4. Close the Symmetrize Workspace panel.

5. Clean up the structure (use the Clean up toolbar button).

6. Open the Symmetrize Workspace panel and check that the point group symmetry is still  $D_{6h}$ . If not, click Symmetrize.

This second symmetrization may be necessary because the geometry cleanup perturbs the structure away from its symmetry to ensure that a minimum is found.

7. Close the Symmetrize Workspace panel.

8. Click the Create Entry button on the Workspace toolbar.



The Create Project Entry dialog box is displayed.

9. Type benzene in the Title text field and click Create.

A project entry titled benzene is created.

## 2.3 Single Point Calculation

The default single-point energy calculation set up in Maestro is a density-functional calculation with the B3LYP functional and a 6-31G\*\* basis set. The molecule is assumed to be singlet and uncharged. To run a default calculation, you can build or include a molecule in the Workspace and submit the job with no special options.

If you are starting with this exercise without running the previous exercises, complete the following steps before continuing.

a. Clear the Workspace.

b. Click the Phenyl fragment on the Fragments toolbar, then click in the Workspace.

A benzene molecule is placed in the Workspace.

c. Click the Create Entry button and create a Project Table entry titled benzene.

Now you are ready to run the calculations.

1. Choose Applications → Jaguar → Single Point Energy.

The Jaguar panel opens. For this calculation you can use the defaults. The default structure is the Workspace structure, as you can see from the Use structures from option menu.

2. Click the Start button.

The Jaguar - Start dialog box opens. This dialog box provides controls for the running of the job and the incorporation of the results into Maestro. By default, the job name is the entry name and the job is run on the local host (the host on which you are running Maestro).

3. In the Output section, choose Incorporate → Replace existing entries.

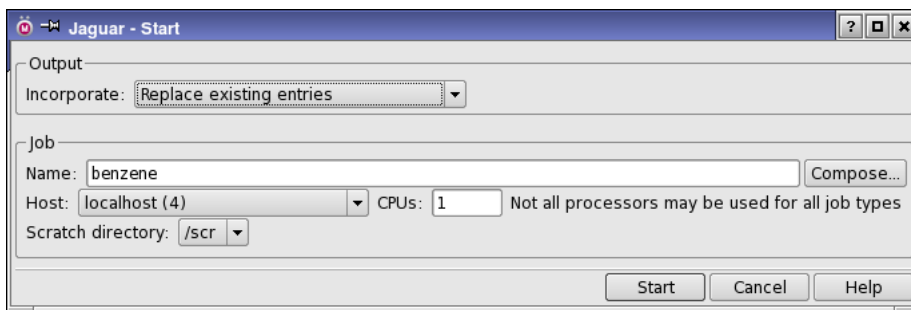
The incorporation mode is persistent, so the next time you run a job, the mode selected is the last mode that you used.

4. (optional) In the Job section, choose a host from the Host option menu.

5. Click Start.

This job should take only a few seconds. The job status is indicated by the Jobs button on the status bar in the Workspace. You can click this button to open the Monitor panel for details of the job's progress. If you want the Monitor panel to open when you start a job, you can set a preference in the Preferences panel (Jobs → Monitoring).

When the job finishes, the original entry in the Project Table is replaced with the new entry, and the properties of the previous entry are overwritten. Hereafter, the Monitor panel will not be mentioned, but you can close it or leave it open as you wish.



**Figure 2.2.** The Jaguar - Start dialog box.

## 2.4 Geometry Optimization With DFT

In this exercise, you will optimize the geometry of the output structure from the previous exercise, at the BLYP/6-31G\*\* level.

1. Ensure that the entry from the previous exercise ([Section 2.3](#)) is displayed in the Workspace.
2. Choose Applications → Jaguar → Optimization in the main window.  
The Jaguar panel is displayed, set up for a geometry optimization.
3. Ensure that Workspace is selected from the Use structures from option menu.
4. In the Theory tab, choose Gradient-corrected from the Show option menu below the list of functionals, then choose BLYP from the list (the default).

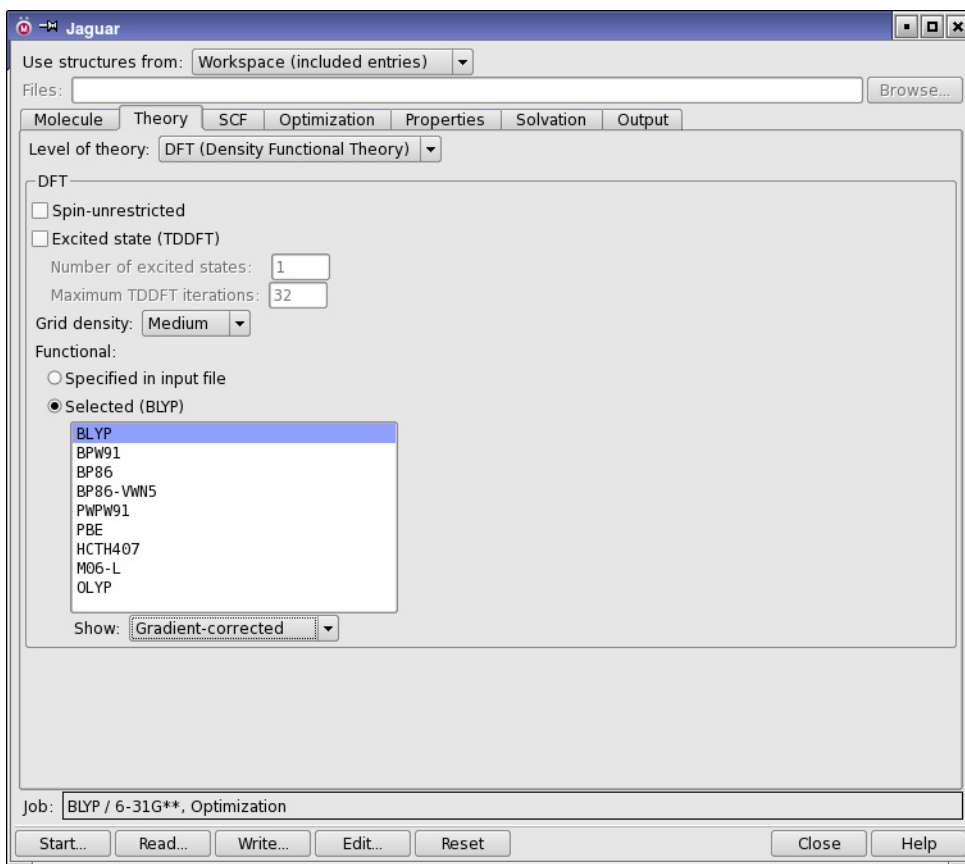


Figure 2.3. The Theory tab of the Jaguar panel.

You can view the input file contents by clicking the Edit button. Notice the addition of keywords in the **gen** section. A BLYP calculation is specified by `dftname=blyp` and a geometry optimization is specified by `igeopt=1`. Close the panel by clicking Cancel.

5. Click Start.

The Start dialog box opens.

6. In the Output section, choose Incorporate → Append new entries individually.
7. (optional) In the Job section, choose a host from the Host option menu.
8. Type `benzene_dft` in the Name text box, and click Start.

This job takes a few minutes to finish. When it has finished, a new entry is added to the Project Table. The job name is listed in the Job Name column.

## 2.5 Localized MP2 Energy Calculation

In this exercise, you will determine the MP2 energy of benzene at the DFT geometry.

1. Ensure that the entry from the previous exercise is displayed in the Workspace.
2. Choose Applications → Jaguar → Single Point Energy in the main window.
3. Ensure that Workspace is selected from the Use structures from option menu.
4. In the Theory tab, choose LMP2 (local MP2) from the Level of theory option menu.

Since benzene is aromatic, you should use a special form of LMP2, which allows all the electron pairs of the ring to be excited into an expanded virtual space (a semi-delocalized LMP2). This can be achieved automatically by adding keywords directly to the input file.

5. Click Edit.

The Edit Job panel is displayed.

6. In the &gen section, add `idelocv=1` and `ireson=1`.

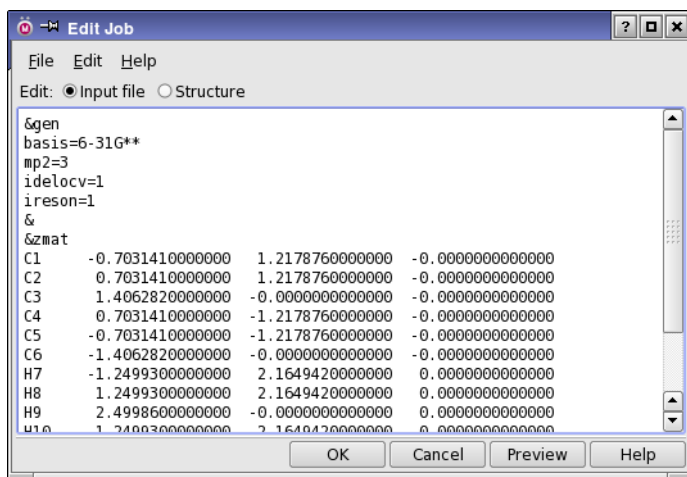
You can set `ireson=1` by choosing Partial Delocalization from the Resonance option menu. Here, the keyword is added directly because the `idelocv=1` setting cannot be made in the GUI.

7. Click OK.
8. In the Jaguar panel, click Start.

The Start dialog box opens.

9. (optional) In the Job section, choose a host from the Host option menu.





**Figure 2.4.** The Edit Job panel showing the new gen section contents.

10. Type benzene\_mp2 in the Name text box, and click Start.

This LMP2 job takes several minutes.

11. Examine the output file, benzene\_mp2.out, using a text editor.

## 2.6 Displaying Orbitals in Maestro

Maestro can display surfaces, including orbital and density plots generated by Jaguar. In this exercise, you will see how to produce and display orbital plots. A later exercise displays the electrostatic potential mapped to an isosurface of the density ([Section 3.3 on page 23](#)). You will use the output from the DFT calculation you ran earlier to generate and display a surface plot of the HOMO and LUMO of benzene.

The generation of surfaces require a wave function. For this exercise the wave function is obtained from the restart file, but surfaces can be generated at the end of any job. However, no SCF iterations are needed, so an initial guess calculation is sufficient to generate the surfaces.

1. In the Jaguar panel, click Read (at the bottom of the panel).

The Jaguar Read file selector is displayed. If you do not have the Jaguar panel open, choose Applications → Jaguar → Single Point Energy in the main window.

2. Navigate to and select the Jaguar restart file, benzene\_dft.01.in.

The restart file contains the geometry and wave function for the geometry optimization performed in [Section 2.4](#).

3. Ensure that Read As is set to Geometry and settings.

Reading the settings is useful if you want to make use of the converged wave function, the Hessian, or other information that is stored in the file. In this exercise, the calculation will make use of the wave function.

4. Click Open.

A new project entry is created and included in the Workspace.

You can view the input file information by clicking the Edit button in the Jaguar panel. Do not change any of the settings, but notice that in the **guess** section there is a converged wave function. Close the panel by clicking Cancel.

5. Choose Applications → Jaguar → Initial Guess Only.

By default, when you read a restart file, the task is set to the task in the job that generated the restart file. To change the task, you must go back to the Applications menu and choose a different task. In this case, the restart file was for a geometry optimization.

6. In the Theory tab, check that the level of theory is DFT.

7. In the Properties tab, select the check box in the Surfaces row.

Controls for the selection of surfaces are displayed in the lower part of the tab. If you have a wave function, these controls include a list of orbitals with their occupation number and eigenvalue. If you do not have a wave function, the controls allow you to specify the range of orbitals to plot relative to the HOMO and the LUMO.

8. Select Molecular Orbitals.

9. From the Alpha list, select orbitals 20 through 23 (click 20, shift-click 23).

10. Click Start.

The Start dialog box opens.

11. (optional) In the Job section, choose a host from the Host option menu.

12. Type `benzene_mo` in the Name text box, choose Replace existing entries from the Incorporate option menu, then click Start.

The job takes about one minute. The results are automatically incorporated and the first surface (the HOMO) is displayed in the Workspace. Since both the HOMO and the LUMO are degenerate orbitals, the orbital displayed could be either of the degenerate pair.

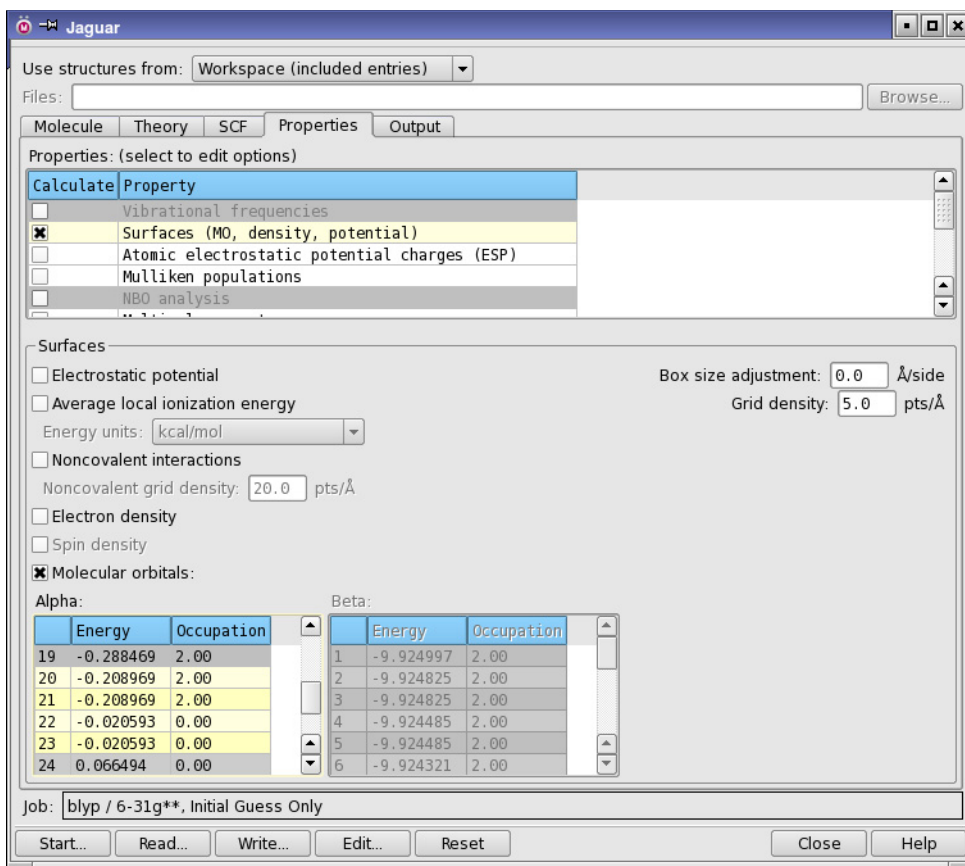


Figure 2.5. The Properties tab.

13. If the Project Table panel is not open, click the Table button on the Project toolbar.



14. In the Project Table, click the S button in the Title column for the benzene entry.

The Manage Surfaces panel opens. The table shows the surfaces generated by the job.

15. Click the V column for orbital 21.

Orbital 21 replaces orbital 20 in the Workspace.

16. Move the Isovalue slider.

The volume occupied by the orbital changes with the isovalue.

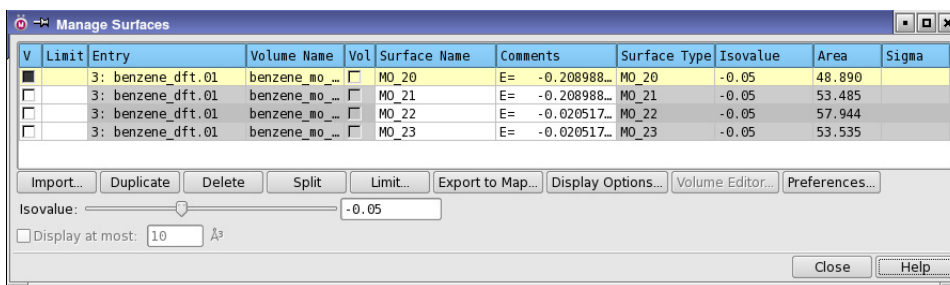


Figure 2.6. The Manage Surfaces panel.

17. Reset the isovalue to -0.05.

18. Click Display Options.

The Surface Display Options dialog box opens. This dialog box has controls for the style, transparency, and color scheme.

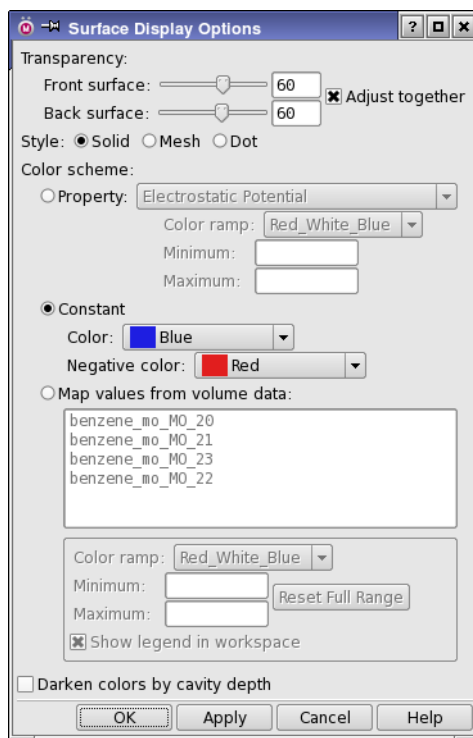
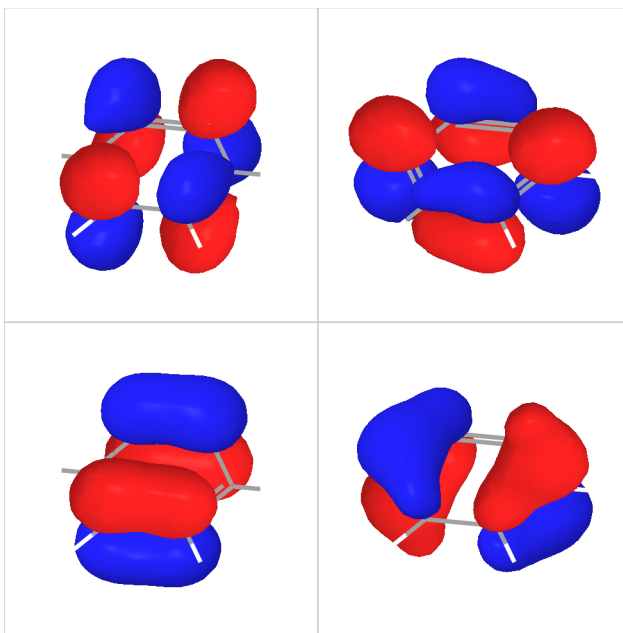


Figure 2.7. The Surface Display Options dialog box.



**Figure 2.8.** The benzene HOMO and LUMO orbitals, tiled.

19. Experiment with changing the transparency, the style, and the colors of the positive and negative lobes.
20. Close the Surface Display Options dialog box.
21. Click the V column for orbital 20, and shift-click the V column for orbital 23.  
All four HOMO and LUMO orbitals are displayed in the Workspace, but they are superimposed.
22. From the Tile entries toolbar button menu, choose Tile by Surface.



The orbitals are displayed in separate areas of the Workspace. Each is in its own mini-Workspace, which can be manipulated as usual. By default all tiles are transformed by an action (rotate, translate), but you can deselect Transform All Tiles on the Tile entries button menu to perform actions on a single tile.

23. Click the Tile entries toolbar button to exit Tile mode.

The orbitals are again superimposed.

To save images of the Workspace like those shown in [Figure 2.8](#), set up the color of the Workspace contents and background, choose Workspace → Save Image, then make settings and supply a filename in the Save Image panel.

# Calculating and Displaying Properties

The set of exercises in this chapter covers the calculation of various properties of molecules, including numeric values, functions of coordinates, and 3D functions of the electron distribution. Each of these properties is visualized in Maestro in some way.

## 3.1 Prediction of $pK_a$ Values

In this exercise, you will calculate the  $pK_a$  of methylamine (or rather, of its conjugate acid, the methylammonium cation). In the first part of the exercise, you will build the structure, and in the second part you will run the  $pK_a$  calculation.

1. Click the Clear button on the Workspace toolbar.

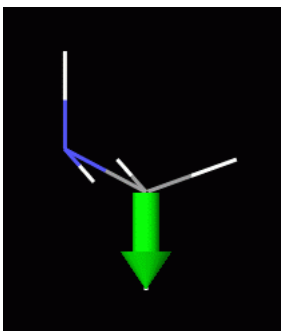


2. Choose Edit → Build → Fragments.

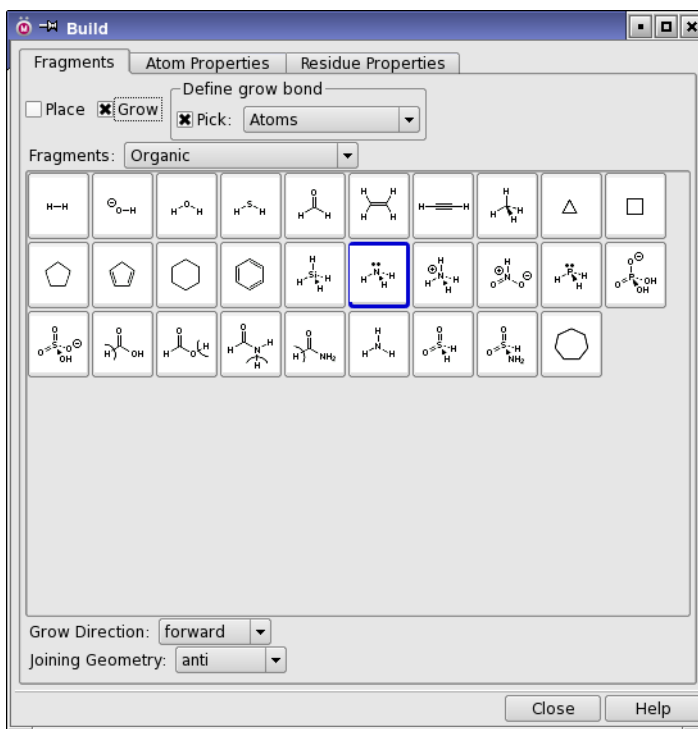
The Build panel is displayed, with the Fragments tab on top and the organic fragments library displayed (see [Figure 3.2](#)).

3. Select Grow.
4. In the Organic library, click the Amine fragment.

An amine group is placed in the Workspace. The green arrow marks the grow bond.



**Figure 3.1.** The methylamine molecule showing the grow bond.



**Figure 3.2. The Build panel, showing the Fragments tab.**

- Click the Methyl fragment.

A methyl group is attached to the amine group.

- Click the Create Entry toolbar button to create a project entry named methylamine.
- Close the Build panel.

Now you are ready to run the calculation.

- Choose Applications → Jaguar → pKa.

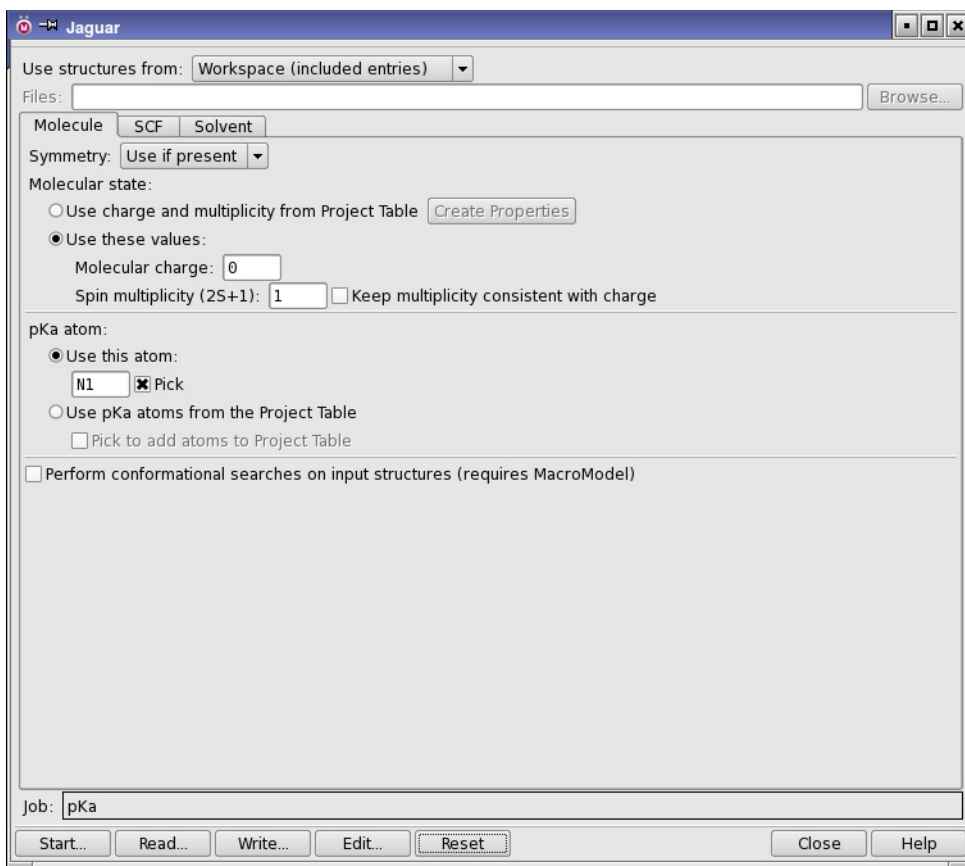
The Jaguar panel opens with the Molecule tab displayed, set up for pK<sub>a</sub> calculations. In the lower section, you can specify the pK<sub>a</sub> atom. Use this atom is selected by default.

- Click Reset.

This clears any data from the previous calculation.

- In the pKa atom section, select Pick.





**Figure 3.3. The Molecule tab for  $pK_a$  calculations.**

11. Click on the nitrogen atom in the Workspace.

The nitrogen atom is marked and its label is displayed in the text box.

12. Select Workspace from the Use structures from option menu.

13. Click Start.

The Start dialog box opens.

14. Choose Replace existing entries from the Incorporate option menu.

15. Set the job name to methylamine and click Start.

The calculation of  $pK_a$  values involves several steps and can be time-consuming. This job takes a few minutes to finish. The output  $pK_a$  is the only data written to the file `methylanine.out`. When the job finishes, the  $pK_a$  value is added to the methylanine entry as a property.

Next, display the  $pK_a$  value as an atom label on the  $pK_a$  atom in the Workspace, with the following instructions.

16. Choose **Workspace** → **Atom Labels**.

The Atom Labels panel opens.

17. Click **Remove All**.

18. Click **Add**.

The Add Label Fields dialog box opens.

19. Select **pKa water** from the list, and click **OK**.

20. Pick the nitrogen atom in the Workspace.

The  $pK_a$  value is displayed next to the nitrogen atom.

## 3.2 Coordinate Scans

Jaguar can run calculations at regular intervals along one or more (up to 5) coordinates. These coordinate scans can help you to map out the potential energy surface for changes of interest. In this exercise, you will perform a scan over two coordinates, and plot the results as a contour map. The molecule is chloromethyl fluoromethyl ether, which you will build in Maestro.

1. If the Fragments toolbar is *not* displayed, click **Fragments** on the Manager toolbar, or choose **Window** → **Toolbars** → **Fragments**.
2. Click the **Clear** button on the Workspace toolbar.



3. Select the hydroxyl fragment.



The fragments are shown as full molecules, with H atoms added to the fragment to complete the molecule. The H atoms are replaced when you join fragments. The hydroxyl fragment therefore appears as a water molecule. If you pause the pointer over the fragment, the fragment name is displayed in the tooltip (Balloon Help).

- Click in the Workspace.

A water molecule is placed in the Workspace.

- Select the methyl fragment.



- Click on each of the hydrogen atoms of the water molecule in the Workspace, in turn.

Each hydrogen atom is replaced with a methyl fragment, so that you now have dimethyl ether.

Next you will change two of the hydrogen atoms into halogen atoms.

- If the Build toolbar is *not* displayed, click Build on the Manager toolbar, or choose Window → Toolbars → Build.
- From the Set element button on the Build toolbar, choose F.



- Click the methyl hydrogen furthest to the right.

The hydrogen atom is changed into a fluorine atom.

- From the Set element button on the Build toolbar, choose Cl.

- Click the methyl hydrogen furthest to the left.

The hydrogen atom is changed into a chlorine atom.

If the element you want is not on this button menu, you can set the element by choosing Edit → Build → Atom Properties, then choosing Element from the Property menu, and picking the element from the periodic table that is displayed. You can also right-click on an atom and choose Set Element, then choose the element.

Now that the molecule is built, you are ready to do the calculation.

- Choose Applications → Jaguar → Relaxed Coordinate Scan.

The relaxed scan optimizes the geometry for all the coordinates other than the scan coordinates. You can also do rigid scans in which the geometry is not relaxed. These are faster, but do not give as good a picture of the minimum energy surface.

- In the Scan tab, choose Dihedral from the Type option menu of the Add new coordinate section.

14. Pick the Cl atom, then the C, the O and the C of the ether linkage.

When you have finished picking, the dihedral is added to the Defined coordinates table.

15. In the Selected coordinate section, enter -180 in the Starting value text box, 180 in the Final value text box, and 60 in the Increment text box.

When you press Enter, the Number of steps text field is updated, and the value is entered into the table.

16. Now pick the F atom, then the C, the O and the C of the ether linkage (in order from the F atom).

A new coordinate is added, and the values in the Selected coordinate section are set to the same values as for the previous coordinate. If for some reason this does not happen, enter -180 in the Starting value text box, 180 in the Final value text box, and 60 in the Increment text box.

17. Click Start.

The Start dialog box opens.

18. Ensure that Append new entries as a new group is selected from the Incorporate option menu.

19. Set the job name to ether\_scan.

20. (Optional) If you have multiple processors available, you can distribute the job by entering the number of processors in the CPUs text box.

As the number of points for each coordinate is 7, a suitable number of processors for even load balancing would be 7, but you can choose any number you like. Each point in the scan takes about 3 minutes.

21. When the job is incorporated, choose Tools → Plot Coordinate Scan → Two Coordinates in the main window.

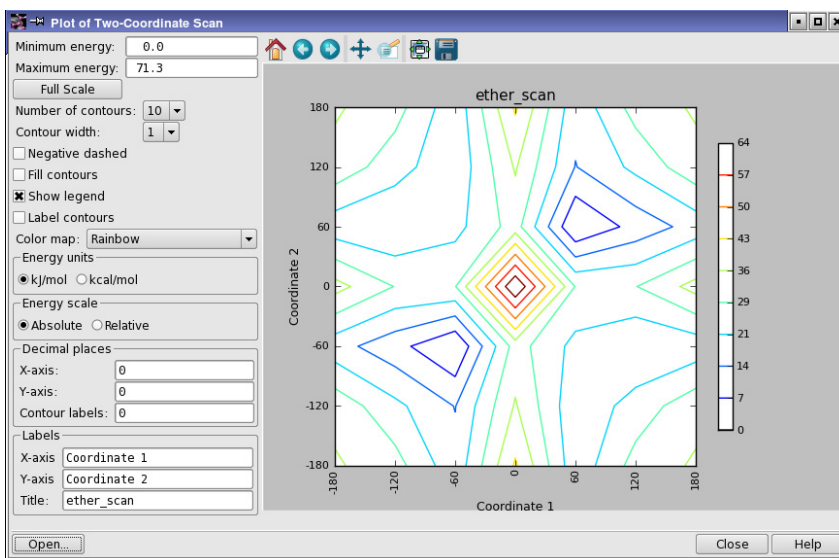
The Plot of Two-Coordinate Scan panel opens.

22. Click Open.

A file selector opens.

23. Navigate to and select ether\_scan.grd, and click OK.

A contour plot of the scan is displayed. You can experiment with the settings.



**Figure 3.4. Contour plot of the coordinate scan.**

Note the symmetry in the plot. The large peak at 0 degrees in both coordinates is where the halogens are the closest. The minimum is at 60° in both coordinates, not at 180° where the halogens are furthest apart. This is because there is a noncovalent interaction between the halogen on each of the carbons and a hydrogen atom on the other carbon.

### 3.3 Property Maps

In this exercise you will create a map of the electrostatic potential (ESP) of vinyl alcohol, label atoms in the Workspace with atomic properties derived from the ESP, and examine the electrostatic potential (ESP) on the molecular surface.

First, the molecule must be built.

1. Click the Clear button on the Workspace toolbar.



2. Select the methyl fragment on the Fragments toolbar, and click in the Workspace.



A methane molecule is added to the Workspace.

3. Click on one of the hydrogen atoms of the methane molecule.

A methyl group is added to the molecule, to produce ethane.

4. Select the hydroxyl fragment.



5. Click on one of the hydrogen atoms.

A hydroxyl group is added to the molecule, to produce ethanol.

6. Click the + bond order button on the Build toolbar.



7. In the Workspace, click on the C–C bond.

The bond should now be represented by a double line, indicating that the bond order has changed to double. Two hydrogens have been removed. The hydrogen on the hydroxyl group is not in the plane, but you can fix it by cleaning up the geometry.

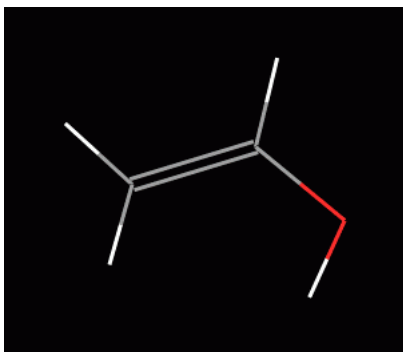
8. Click the Clean up button on the Build toolbar.



The hydrogen moves to an in-plane position.

It is a good idea to clean up structures before optimizing them, and, if the molecule has symmetry, to symmetrize it before cleaning it up (Edit → Symmetrize Workspace).

9. Create a project entry for this structure with the title `vinyl alcohol`.



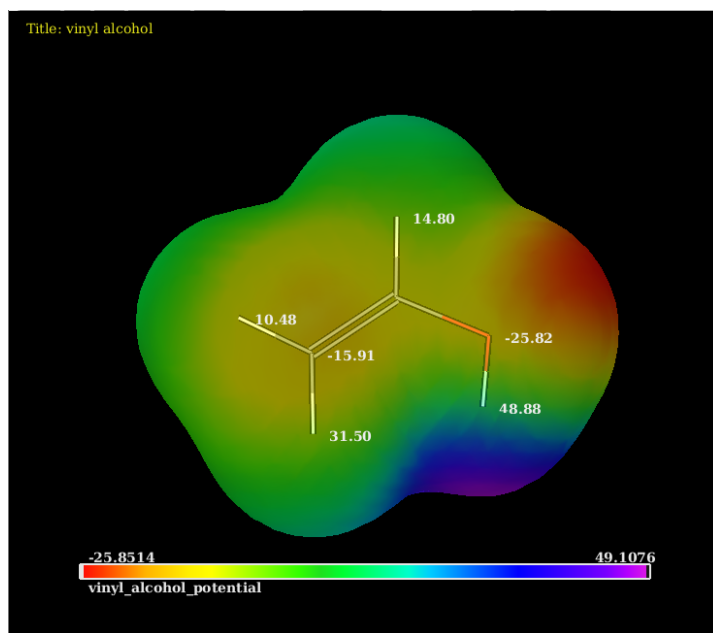
**Figure 3.5.** The completed vinyl alcohol structure.

Next, set up and run the calculation:

10. Choose Applications → Jaguar → Single Point Energy.
11. Click Reset to restore the default settings, and confirm the action.
12. In the Properties tab, click the check box for Surfaces.  
The Surfaces controls are displayed.
13. In the Surfaces section, select Electrostatic potential and Electron density, and ensure that no other surface types are selected.
14. Click the check box for Atomic electrostatic potential charges in the Properties table.
15. Click Start.
16. Name the job `vinyl_alcohol`.
17. Choose Replace existing entries from the Incorporate jobs by option menu.
18. Click Start.  
When the job finishes (after a minute or so), the structure is replaced, and the electron density surface is displayed.
19. Click the S button in the Title column of the Project Table for the vinyl alcohol entry.  
The Manage Surfaces panel opens.
20. Click Display Options.  
The Surface Display Options panel opens.
21. Under Color scheme, select Map values from volume data.
22. Select `vinyl_alcohol_potential` from the volume data list.
23. From the Color ramp option menu, choose Rainbow.
24. Click OK.

The density surface is colored by the values of the electrostatic potential at the surface. Note the negative (red) region near the oxygen, and the blue-purple (positive) region near the hydroxyl hydrogen.

The ESP analysis is performed automatically whenever an ESP plot is requested. The results of this analysis are added as entry properties. In addition, the minimum and maximum ESP values on the molecular surface for each atom are included as atom properties. You can use these to label the atoms with the ESP.



**Figure 3.6. The ESP for vinyl alcohol mapped to the density isosurface.**

25. Choose Workspace → Atom Labels.
26. In the Composition section, click Remove All, then click Add.  
The Add Label Fields dialog box opens at the Atom Properties tab.
27. Select Min surface ESP, and click OK.
28. Ensure that Add labels (replace) is selected from the Pick to option menu.
29. Ensure that Pick is selected in the Label atoms section.
30. Pick the oxygen atom and the carbon atom furthest from it in the Workspace.

These atoms are labeled with their minimum ESP value on the surface, which is negative.

31. Click Remove, then click Add.
32. Select Max surface ESP and click OK.
33. Pick the four hydrogens.

These atoms are labeled with their maximum ESP on the surface. The value for the hydroxyl hydrogen is positive and fairly large, and the hydrogen cis to it also has a fairly large value. The other two hydrogens, on the other side of the double bond, have smaller ESP values.



### 3.4 Displaying Noncovalent Interactions

This exercise illustrates the use of the reduced gradient and the Laplacian of the density to view noncovalent interactions and sites for nucleophilic attack.

Noncovalent interactions can be considered as weak bonds. They are characterized by critical points of the density, where the gradient of the density is zero. A “bond critical point”, which indicates a bonding interaction, is a point at which the density is a minimum along the bond but a maximum perpendicular to the bond. It is connected to the two atoms that are bonded by a “bond path”.

In this exercise, you will look at a hydrogen bond as an example of a noncovalent interaction. The molecule is 3-hydroxypropanal, which you will build first.

1. Click the Clear Workspace button.



2. Select the methyl fragment on the Fragments toolbar, and click in the Workspace.



A methane molecule is added to the Workspace.

3. Click on one of the hydrogen atoms of the methane molecule.

A methyl group is added to the molecule, to produce ethane.

4. Select the carbonyl fragment.



5. Click on one of the hydrogen atoms.

A carbonyl group replaces the hydrogen atom, to form propanal.

6. Select the hydroxyl fragment.



7. Click on the hydrogen atom on the terminal methyl group that is parallel to the C=O bond of the carbonyl.

A hydroxyl group is added, with the hydrogen pointing towards the carbonyl oxygen. There should be a hydrogen bond between the hydrogen and the oxygen, as you will see.

8. On the Labels toolbar, select Intra H-Bonds from the HBonds button menu.



9. Click on any of the atoms in the Workspace.

A yellow dotted line is placed in the Workspace between the hydrogen and the oxygen, indicating the presence of a hydrogen bond.

10. Create a project entry named 3-hydroxypropanal.

Now that the molecule is built, you can run the calculation to generate the required surfaces.

11. Choose Applications → Jaguar → Optimization.
12. Click Reset to reset the options, and confirm the reset.
13. Ensure that Workspace is selected from the Use structures from option menu.
14. In the Properties tab, select the check box for Surfaces.

The Surfaces options are displayed below the Properties table.

15. Select Noncovalent interactions, and clear the options for all other surface types.
16. Click Start.
17. From the Incorporate option menu, choose Replace existing entries.
18. Name the job 3-hydroxypropanal, and click Start.

The job takes a few minutes. When it finishes, three surfaces are incorporated: the reduced gradient, the strength, and the Laplacian. By default the reduced gradient isosurface is displayed.

In addition to the surfaces, the bond critical point of the noncovalent interaction is displayed as a dummy atom (not visible in wire frame representation) with the bond paths represented by zero-order bonds (blue lines). You can see that the critical point is in the middle of one of the surfaces.

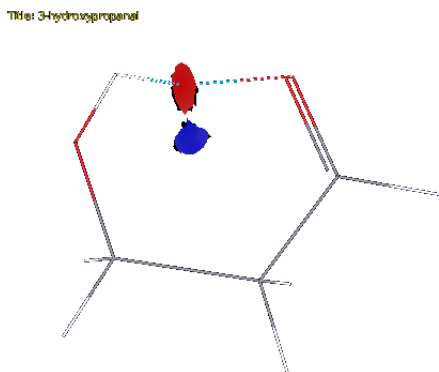
19. Click the S button in the Title column for the 3-hydroxypropanal entry.

The Manage Surfaces panel opens.

20. Click Display Options.

The Surface Display Options panel opens.

21. Under Color scheme, select Map values from volume data.



**Figure 3.7. The reduced gradient surfaces and bond paths for 3-hydroxypropanal.**

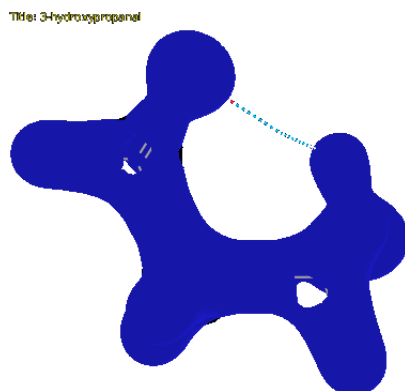
22. Select 3\_hydroxypropanal\_strength from the volume data list.
23. From the Color ramp option menu, choose Red-White-Blue.
24. Click OK.

The hydrogen bond is indicated by a red region, which encloses the bond critical point. The blue region encloses a “ring critical point”. A ring critical point should be present inside any ring. The existence of such a point indicates that the hydrogen bond is truly bonding in nature, because the presence of that bond closes the 6-membered ring. The strength of the weakest bond in the ring is related to the distance between the ring critical point and the bond critical point.

Next, you will look at the Laplacian surface to identify sites for nucleophilic attack.

25. In the Manage Surfaces panel, click the In column for the Laplacian surface.
26. Rotate the molecule and its surface to identify the holes in the surface.

The Laplacian surface can be used to identify places of electron excess and deficiency, and in turn, sites of reactivity. In this example we see that there are holes (places of electron deficiency) in the isosurface on the carbon atoms, and no holes on the hydrogens or oxygens. The holes identify potential sites for nucleophilic attack, as well as the preferred angle of attack. You can see that a nucleophile would attack the carbonyl carbon from above or below the plane, and that the hydroxy-substituted carbon has its largest hole in the Laplacian isosurface on the side opposite to the hydroxyl group, as expected.



**Figure 3.8.** The Laplacian surface showing the holes at the carbonyl and the methoxy carbons.

# Conformational Search, Refinement, and Analysis

This set of exercises covers the use of Jaguar to refine the results of a MacroModel conformational search, and the analysis of the resulting conformations. The analysis involves several tasks: calculating relative QM energies, creating a sequential index for the optimized structures, coloring, superimposing, and labeling the structures, plotting the energies, and calculating RMSD and maximum deviation.

You must have a MacroModel license as well as a Jaguar license to run these exercises.

## 4.1 MacroModel Conformational Search

In this exercise you will import the target molecule and perform a conformational search with MacroModel.

1. Import 2-pentafluorobutadienylphenol from the file `c4f5c6h4oh.mae`.

This structure is in a planar conformation that is highly strained.

2. Choose Applications → MacroModel → Conformational Search.
3. In the Potential tab, choose None from the Solvent option menu.

Both the MM and the QM calculations will be run in the gas phase.

4. In the CSearch tab, deselect Retain mirror-image conformations.

The remaining options can be left at their defaults.

5. Click Start.

The Start dialog box opens.

6. For the Incorporate option, choose Append new entries as a new group.
7. Name the job `mm_conf8`, and click Start.

The job should take only a minute or so, and produce 7 conformers, ranked according to their MM energies.

## 4.2 Setting Up Properties to Facilitate Comparisons

The conformers all have the same title, so to distinguish them in the Jaguar calculations, you will modify the titles, by appending an index, which you will generate. This index will also be used for plotting the results.

1. Select all 7 conformers in the Project Table.

They should be selected by default following the job incorporation.

2. Choose Property → Calculate.

The Calculate Properties panel opens.

3. From the Property list, select Sequential index.

4. For Calculate for entries, select Selected.

5. Click Calculate.

A new property, Sequential index, is added to the Project Table. You can close the Calculate Properties panel.

6. Choose Property → Merge.

The Merge Properties panel opens.

7. From the Available properties list, select Sequential index.

8. Click the right arrow button to add this property to the Properties to merge list.

9. From the Destination property list, select Title.

10. In the Separator text box, enter an underscore character (\_).

11. By Merge values for, click Selected Rows.

The Sequential index property is appended to the title, separated from the original title by an underscore.

## 4.3 Optimization of Conformers with Jaguar

With the conformers given distinguishing titles, you can now proceed to optimize them with Jaguar. If you do not want to run these calculations, you can skip to the next exercise.

1. Choose Applications → Jaguar → Optimization.

The Jaguar panel opens, set up for an optimization job.

2. Click Reset to clear any settings from previous exercises.

3. From the Use structures from option menu, choose Project Table (selected entries).

The MacroModel conformers should still be selected from the last set of operations. If they are not, make sure that they are selected before proceeding.

4. In the Molecule tab, choose 6-31G from the Basis set option menu, \*\* from the Polarization option menu, and ++ from the Diffuse option menu (i.e. choose 6-31G\*\*++ for the basis set).
5. In the Theory tab, choose M06-2X from the Hybrid option menu.
6. In the SCF tab, choose Ultrafine from the Accuracy level option menu.
7. Click Start.
8. Name the job `qm_confs`.

You can distribute the job across multiple processors if they are available. Each conformer takes about 1.5 hours to optimize.

9. Click Start.

When the job finishes, the optimized conformers are incorporated into the Project Table.

## 4.4 Calculating QM Relative Energies

In this exercise you will convert the set of absolute energies produced by Jaguar into a set of relative energies for comparison with the MacroModel energies. If you skipped the last exercise, import the file `qm_confs_out.mae` into the project, and use these conformers.

1. Ensure that the optimized conformers are selected.

If they are not, click the group title row to select them. If you imported them from `qm_confs_out.mae` they should already be selected.

2. Choose Scripts → Project Table → Jaguar Energy Converter in the main window.

A new property, Jaguar Relative Energy, is added to the Project Table. This property contains the energies of the selected structures relative to the lowest, in kcal/mol. The MacroModel results are in kJ/mol, so the next step is to convert the QM energies.

3. Choose Table → Calculator in the Project Table panel.

The Project Table Calculator panel opens.

4. In the Create text box, enter QM Relative Energy.
5. Click Properties, select Jaguar Relative Energy, and click OK.

6. Click \*.
7. In the Constant text box, enter 4.184.
8. Ensure that Selected rows only is selected.
9. Click Execute, then click Close.

A new property, QM Relative Energy, is added to the Project Table, with the relative energies in kJ/mol.

## 4.5 Superimposing the Structures

In this exercise, the structures will be superimposed so that the benzene rings are on top of each other. In this way, you can compare how the butadienyl side chain is placed relative to the ring in each of the conformers.

1. Ensure that only one of the conformers is displayed in the Workspace.
2. Select all the MacroModel conformers and the Jaguar-optimized conformers (click one group, shift-click the other).
3. Choose Tools → Superposition.

The Superposition panel opens.

4. Under Entries to superimpose, select Selected entries.
5. Ensure that neither Calculate 'in place' nor Create RMSD property is selected.
6. Click the Select atoms toolbar button, and pick the atoms of the benzene ring, the oxygen atom, and the carbon of the butadienyl group that is attached to the ring.
7. In the SMARTS tab, click Get from Selection.

When you click the button, the molecules are superimposed.

8. Close the Superposition panel.
9. Select only the optimized conformers.
10. Press CTRL+N.

The entries are included in the Workspace.

From the superimposed structures it is clear that there are three pairs of conformers, in which the butadienyl group is in approximately the same position but the hydroxyl has the opposite orientation. In the next exercise, the structures will be colored and labeled so it is easy to tell which is which.



## 4.6 Coloring and Labeling the Structures

In this exercise, the entries will be colored and labeled to distinguish them from each other. Coloring by entry allows you to distinguish them easily, but the color does not indicate which entry is which. Adding a label identifies the entries. The label used here is the sequential index, which was created in [Section 4.2](#). This index will also be used for plotting.

1. Ensure that the optimized conformers are included in the Workspace.
2. In the main window, choose Entry from the Color Scheme button menu on the Representation toolbar.



Each entry is colored with its own color.

3. Choose Workspace → Atom Labels.
4. Clear any selection in the Atom properties list of the Composition tab.
5. Select Sequential index in the Entry properties list.
6. In the Label atoms section, click Select.

The Atom Selection dialog box opens.

7. In the Atom tab, choose Atom name from the list on the left.

A list of atom names is displayed in the center.

8. Choose F19 from the Atom name list.
9. Click Add, then click OK.

The atom named F19 (a fluorine at the end of the side chain) is labeled with the sequential index.

10. Close the Atom Labels panel.

The structures are now clearly distinguished, and it can be seen that the three pairs are structures 1 and 4, 3 and 6, and 5 and 7. Conformer 2 does not have a matching structure with the opposite orientation of the hydroxyl, but this may have been filtered out in the conformational search.

## 4.7 Plotting the Conformer Energies

Which of the structures is the lowest can be seen by looking at the Project Table, but comparing the MM and QM energies is much easier in a plot. In this exercise, you will create a plot that contains both the MM and the QM relative energies.

1. Ensure that the optimized conformers are selected.
2. In the Project Table panel, click the Plot toolbar button.



The Manage Plots panel opens.

3. Click New Scatter Plot.

The Scatter Plot panel opens, with a blank plot.

4. From the X-Axis option menu, choose Sequential index.
5. From the Y-Axis option menu, choose QM Relative Energy.

The relative conformer energies from Jaguar are plotted.

6. For the Color, choose Red.
7. In the Project Table, select the entry group that contains the MacroModel conformers.
8. In the Scatter Plot panel, click New Data Set.

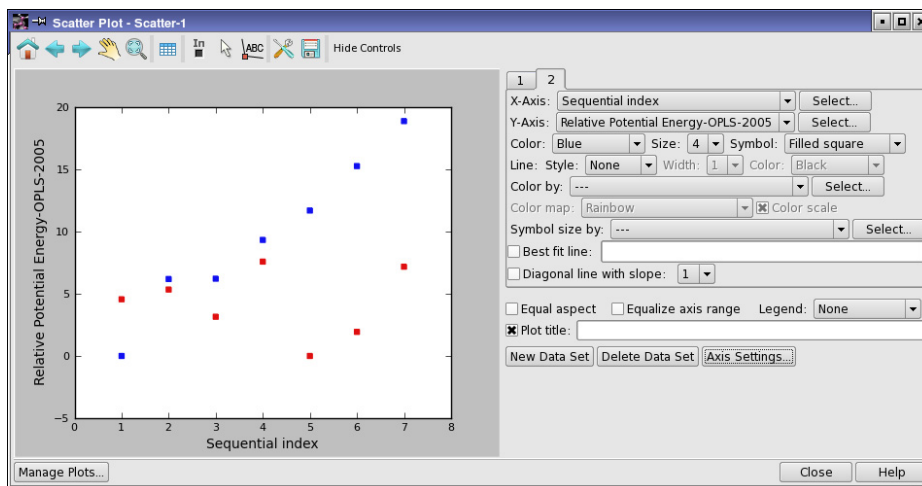


Figure 4.1. Plot of conformer energies.

9. From the X-Axis option menu, choose Sequential index.
10. From the Y-Axis option menu, choose Relative Potential Energy-OPLS-2005.

The relative conformer energies from MacroModel are plotted on the same chart.

11. For the Color, choose Blue.

The QM calculations predict much lower energies for conformers 5–7 than the MM calculations, and as a result the energetic ordering of the conformers is different. Of the conformer pairs, the lower energy structure is the one that has the phenolic hydrogen pointing towards the butadienyl group. The range of energies is smaller in the QM calculations than in the MM calculations. The differences between QM and MM probably indicate that the force fields do not do as good a job on the energetics of these strained structures as QM, because they are not parametrized for such structures. However, the geometries are quite similar for conformers 5–7. These will be compared in the next exercise.

## 4.8 Examining Geometry Differences

In this exercise, you will use the scatter plot to display the MacroModel and Jaguar conformers in the Workspace, and also calculate the RMSD and maximum difference between the MM and QM optimized structures for each conformer.

1. Click the Pick to include entries button on the scatter plot toolbar.



2. Select the two points for conformer 7 (drag over them, or use shift-click or control-click).

The structures are displayed in the Workspace, and are quite well superimposed.

3. Select the two points for conformer 6, then for conformer 5.

These structures are also quite well superimposed.

4. Select the two points for conformer 4, then for conformer 1.

These structures are not so well superimposed.

To supplement the visual inspection, you will now calculate the deviation of the atom positions between the pairs of structures with a Python script.

5. **Windows:** open a Schrodinger Command Prompt window (from the Start menu), type `sh`, and change to the working directory with `cd` commands.

6. In your working directory, run the following command:

```
$SCHRODINGER/run rmsd.py -b -m qm_confs.mae qm_confs_out.mae
```

This script prints the maximum deviation and RMSD between the MM and QM structures for each conformer. The largest values are seen for conformer 4 and conformer 1, and some of the maximum values are larger than the cutoff used in the MacroModel conformational search for elimination of redundancies. However, the significance of these differences depends on the application for which the conformers are being generated: if the geometric tolerance is 1 Å, then the change in structure on reoptimization with Jaguar might not be significant.

# Transition States

In this set of exercises, you will search for the transition state of the hydrolysis of an amide, examine its vibrational modes, and generate an intrinsic reaction coordinate. The hydrolysis involves breaking two bonds, an OH bond in water and a CN bond in the amide, and forming two bonds, an NH bond and a CO bond. The job takes about 30 minutes on a 2GHz processor.

## 5.1 Locating the Transition State

In this exercise you will set up and run a job to locate a transition state. You will use a QST-guided search, which is the recommended method for most transition state searches. The structures have already been prepared, so you can import them from the tutorial directory.

1. Click the Import button on the Project toolbar.



2. The Import file selector opens.
3. Import the file `amide-ts.mae` from your working directory into Maestro.

This file contains three structures: a reactant structure, a product structure, and a guess at the transition state structure. These three structures all have the same atom naming scheme, which allows Jaguar to identify the corresponding atoms in each structure.

If you build your own structures for a transition state search, you should copy and modify one structure (such as the reactant) to build the other two structures. This ensures that you have a consistent atom naming scheme, which is required for transition state searches.

4. Choose Applications → Jaguar → Transition State Search in the main window.
5. Click Reset, and click Yes in the dialog box that is displayed.

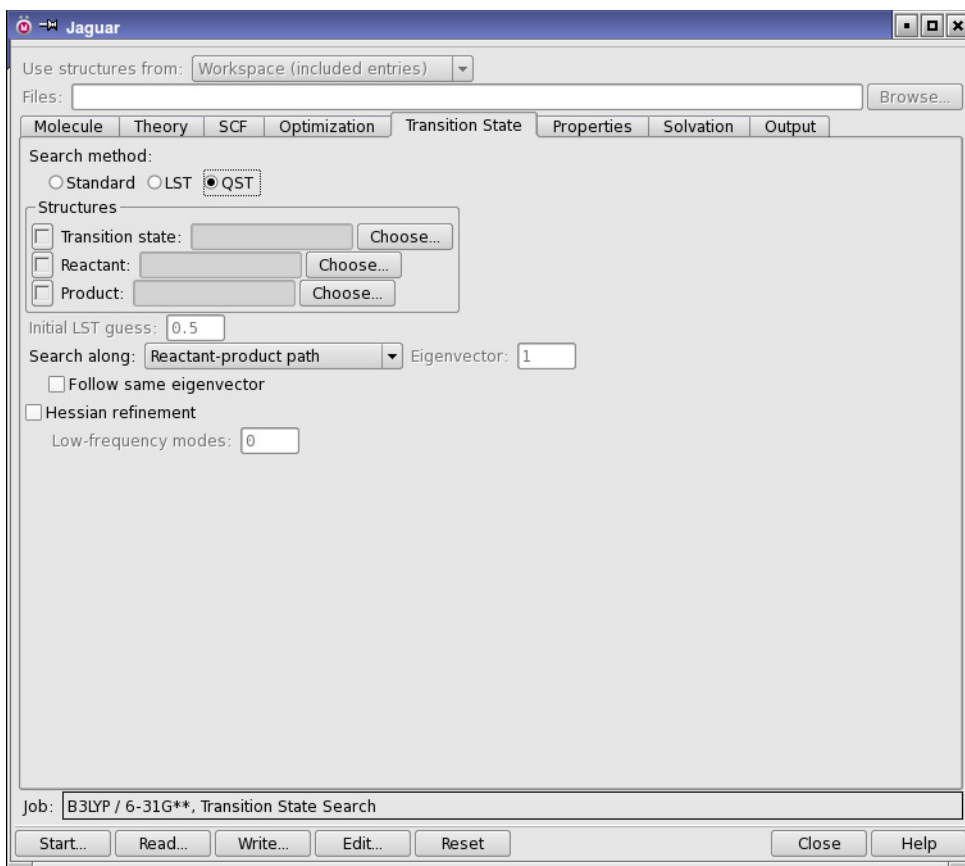
The settings in the Molecule and Theory tabs can be left at their defaults.

6. In the SCF tab, choose Ultrafine from the Accuracy level option menu.

This choice ensures that accurate gradients are generated.

7. In the Optimization tab, for Initial Hessian choose Quantum-mechanical.

Starting with a computed Hessian ensures that you have the best description of the curvature in the potential energy surface.



**Figure 5.1. The Transition State tab.**

8. In the Transition state tab (see [Figure 5.1](#)), under Search method, select QST.

The Transition state, Reactant, and Product rows in the Structures section are now available, and the choice for Search along is set to Reactant-product path.

9. In the Transition state row, click Choose.

The Choose Entry dialog box opens.

10. Select TS from the list, then click Choose.

The dialog box closes, and the Transition state text box now contains the entry number and TS, showing that this entry has been chosen for the transition state.

11. In the Reactant row, click Choose.

The Choose Entry dialog box opens.

12. Select reactant from the list, then click Choose.

The dialog box closes, and the Reactant text box now contains the entry number and reactant, showing that this entry has been chosen for the reactant.

13. In the Product row, click Choose.

The Choose Entry dialog box opens.

14. Select product from the list, then click Choose.

The dialog box closes, and the Product text box now contains the entry number and product, showing that this entry has been chosen for the product.

Next, you will add a **connect** section to the input file. This section contains information about atoms that are considered to be connected. In a transition state search, it is important to identify the bonds that are broken and formed in the reaction to guide the optimization process, by adding them to this section. To identify the appropriate atoms, they will be labeled.

15. Ensure that the transition state entry is included in the Workspace (the box should be filled in).
16. From the Label All button menu on the Labels toolbar, choose Atom name.



The atoms are labeled with the name, which consists of the element symbol and a sequential number.

17. In the Jaguar panel, click Edit.

The Edit Job dialog box opens.

18. Ensure that the Edit option is Input file.
19. At the end of the file, add the following text:

```
&connect
&
```

20. Between these lines, include one line for each atom pair in the bonds that are broken or formed in the reaction, with two atom names on each line.

The lines in the **connect** section should be as follows (the order does not matter):

```
C2 O13
N4 H14
C2 N4
O13 H14
```

These pairs involve the carbonyl carbon (C2), the amide nitrogen (N4), the water oxygen (O13), and the water hydrogen (H14). The atom names are given in parentheses here: you should check that they match what is in the Workspace.

21. Click OK to close the Edit Job dialog box.

Finally, you will add a frequency calculation at the end of the job, to verify the transition state, and then start the job.

22. In the Properties tab, select the check box for vibrational frequencies, and clear any other check boxes.
23. Click Start.

The Start dialog box opens.

24. (*optional*) In the Job section, choose a host from the Host option menu.
25. Set the name to amideTS.
26. Choose Append new entries individually from the Incorporate option menu.
27. Click Start.

Convergence should be reached in about 13-15 geometry steps. When the job finishes, the results are incorporated into the Project Table as a new entry.

## 5.2 Examining Vibrational Frequencies

In this exercise, you will examine the vibrational frequencies of the transition state you found in the previous exercise and view an animation of the frequencies in Maestro. The job from the previous section generates a .vib file that Maestro uses for animation of frequencies. When the results are incorporated, a V is added to the Title column in the Project Table for the incorporated entry.

1. Click the V button in the Title column of the Project Table for the incorporated entry.

The Vibration panel opens.

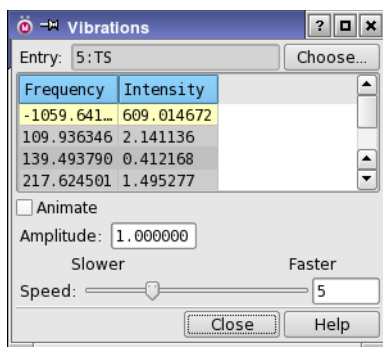
2. Select the first frequency in the list, then select Animate.

This is the imaginary frequency that corresponds to the transition state. The frequency is animated in the Workspace as if it were real. The structure can be rotated in the Workspace to view the animation from an optimal angle.

3. Click on other frequencies in the list to animate them. Experiment with the speed and amplitude.

You do not need to deselect Animate to change to a different frequency.





**Figure 5.2. The Vibration panel.**

The file `amideTS.out` contains a list of frequencies and normal modes below the heading start of program `freq`. Below the frequencies is information on the zero point energy, entropy, and other thermodynamic quantities.

## 5.3 Intrinsic Reaction Coordinate Calculation

In this exercise you will use the results of the transition state search and frequency calculation from the previous exercises to perform an intrinsic reaction coordinate scan, and visualize the reaction in Maestro with the ePlayer.

1. In the Jaguar panel, click Read.

The Jaguar Read dialog box is displayed. If you do not have the Jaguar panel open, choose Applications → Jaguar → Single Point Energy in the main window.

2. Select Geometry and settings from the Read As option menu.
3. Read the restart file `amideTS.01.in` from the transition state exercise.

The transition state structure is displayed in the Workspace and incorporated into the Project Table.

IRC scans require a Hessian, which must be read or generated. In this case the Hessian is read from the restart file.

4. Choose Applications → Jaguar → Reaction Coordinate in the main window.

You must choose the task after reading the input file because reading an input file with its settings sets the Jaguar task to the task defined by the **gen** section of the input file.

5. In the Properties tab, clear the Vibrational frequencies check box.

6. In the IRC tab, ensure that Use mass-weighted coordinates is selected.

The Structures section should already be set with the structures you read in (because the settings are kept in the panel). If they are not, select the structures by clicking Choose in each row of the Structures section in turn, and choosing the appropriate project entry.

7. Click Start.

The Start dialog box opens. You may choose a host from the Host option menu in the Job section, if you want.

8. Set the name to amide-irc, choose Append new entries as a new group from the Incorporate option menu, and click Start.

When the job finishes, 13 new entries are incorporated into the Project Table as an entry group named amide-irc, and are selected. The first entry corresponds to the transition state structure, the next six are the geometries found moving in the forward direction, and the last six are from the backward direction. To view the reaction in the ePlayer, the entries must first be sorted. It is also useful to display the structures in Ball & Stick representation.

9. In the Project Table, include all 13 output structures in the Workspace. (To do this, click the In column for the first entry and shift-click the last entry.)

10. Double-click the Ball & Stick button on the Representation toolbar.



11. Clear the Workspace.
12. In the Project Table, right-click the heading of the Rxn coord column and choose Sort → Selected Entries.
13. Choose ePlayer → Show Toolbar.

The ePlayer toolbar is displayed at the top of the panel.

14. Click the Play forward button on the toolbar to start cycling through the entries.



The OH and CN bonds break and the NH and CO bonds form.

15. From the Loop button menu on the toolbar, choose Oscillate.



16. Click the Play forward button.

The sequence of structures is played in the forward direction, then the reverse direction, and continues this pattern. (If you stopped on the last structure, the sequence starts playing in the reverse direction.)

17. Click the Stop button.



You can change the speed of the ePlayer and set other options in the ePlayer Options panel, which you open from the ePlayer menu.



# Molecular Spectra

## 6.1 Generating a VCD Spectrum

In this exercise, you will run calculations to generate the data for a vibrational circular dichroism (VCD) spectrum. Experimental spectra are usually an average over the low-lying conformations of the molecule. To compare with experiment, it is therefore necessary to perform a conformational search and generate the spectrum for each conformer.

The exercises in this section can take a substantial amount of computing time. The output files from each time-consuming exercise have been provided in the distribution so that you can import them into Maestro without running the exercises. However, it is recommended that you at least perform the exercises up to the point of starting the job, to gain familiarity with the procedure.

### 6.1.1 Running a Conformational Search

In this exercise, you run a conformational search on the target molecule, alanine, which is capped with NMA and ACE.

To perform this exercise, you need a MacroModel license as well as a Jaguar license.

1. Clear the Workspace.



2. Choose Edit → Build → Fragments.

The Build panel opens with the Fragments tab displayed.

3. From the Fragments option menu, choose Amino acids.

4. Select ALA (alanine).

This amino acid is selected by default.

5. Click in the Workspace.

An alanine molecule is placed, with NMA and ACE caps.

6. Click Create Entry on the Workspace toolbar.

7. Enter the name `ala` in the Title text box, and click **Create**.

A new entry is created with the title `ala`.

8. Choose **Applications** → **MacroModel** → **Conformational Search**.

The Conformational Search panel opens at the Potential tab.

9. From the Solvent option menu, choose CHCl3.

VCD spectra are usually measured in a solvent, such as CCl4, CHCl3 or CS2, which can affect the conformations that are present.

10. Click **Start**.

11. In the Output section, choose **Incorporate** → **Append new entries as a new group**.

12. Name the job `ala_conf_search`, and click **Start**.

The job finishes in less than a minute. Six entries are added to the Project Table.

## **6.1.2 Optimizing Conformers and Eliminating Redundancies**

In this exercise, you optimize each of the conformers generated by MacroModel, and eliminate the redundant or high-energy conformers.

The optimization of the conformers takes 1–2 hours per conformer, of which there are six. If you do not want to run this exercise, you can skip to the next exercise and read in the unique conformers from your working directory (from the files that were copied from the installation).

1. Choose **Applications** → **Jaguar** → **Optimization**.

2. Click **Reset**, and confirm the action in the dialog box that opens.

This clears any settings from previous jobs, and selects the defaults.

3. From the Use structures from option menu, choose **Project Table (selected entries)**.

The entries should already be selected from the MacroModel job incorporation. If not, click on the row for the entry group to select all the entries in the group.

4. In the Solvation tab, choose **PBF** from the Solvent model option menu.

5. From the Solvent option menu, choose **Chloroform**.

6. Click **Start**.

If you have access to multiple processors, you can distribute the job. Since there are six entries, you can use up to six processors for the job.

7. Name the job `ala_optimize`, and click **Start**.

When the job finishes, a new entry group is added to the Project Table with six entries.

8. Choose **Applications** → **MacroModel** → **Redundant Conformer Elimination**.
9. From the **Use structures from** option menu, choose **Project Table (selected entries)**.
10. Click **Heavy Atoms** in the **Define comparison atoms** section.
11. From the **Source of energy** option menu, choose **Jaguar**.
12. Click **Start**.
13. Name the job `ala_eliminate`, and click **Start**.

The job returns four out of the six conformers. Two of the conformers produced by MacroModel optimized to the same state as other conformers.

### 6.1.3 Calculating the VCD Spectra

In this exercise, you calculate the VCD spectral data with Jaguar. You can start the exercises at this point by importing the file `alanine_conformers.maegz` from your working directory.

1. Ensure that the four optimized alanine conformers are selected in the Project Table.

This should be the case whether you are continuing from the previous exercise, or you imported them from file.

2. Choose **Applications** → **Jaguar** → **Single Point Energy**.
3. In the **Properties** tab, click the **Calculate** check box for **Vibrational Circular Dichroism**.
4. In the **Solvation** tab, ensure that the solvent is **Chloroform** and the solvent model is **PBF**.
5. Click **Start**.

If you have access to multiple processors, you can distribute the job. Since there are four structures, you can use up to four processors for the job. The time taken per structure is about 30–40 minutes. You can also run each individual structure in parallel if you run them sequentially.

6. Name the job `vcd`, and click **Start**.

### 6.1.4 Calculating Weights for Averaging the Spectra

To compare with experimental spectra, it is usually necessary to create a weighted average, for example assuming a Boltzmann distribution of the populations. In this exercise you will calculate the Boltzmann weights from the Jaguar energies.

You can start the exercises at this point by importing the file `vcd_spectra.mae` from your working directory.

1. Ensure that the four structures with VCD spectra are selected in the Project Table.

This should be the case whether you are continuing from the previous exercise, or you imported them from file. These entries should have a V button in the Title column (to indicate that they also have vibrational data).

2. Choose Scripts → Project Table → Calculate Boltzmann Populations.

The Boltzmann Populations panel opens.

3. Ensure that Use structures from is set to Project Table (selected entries).
4. From the Source energy property option menu, choose Solution Phase Energy.
5. Check that the Source energy unit is set to hartrees and that the temperature is 298.15 K.
6. In the Population property text box, enter Boltz Weight.
7. Click Calculate, then click Close.

The property is added to the Project table. The property values are normalized percentage Boltzmann populations.

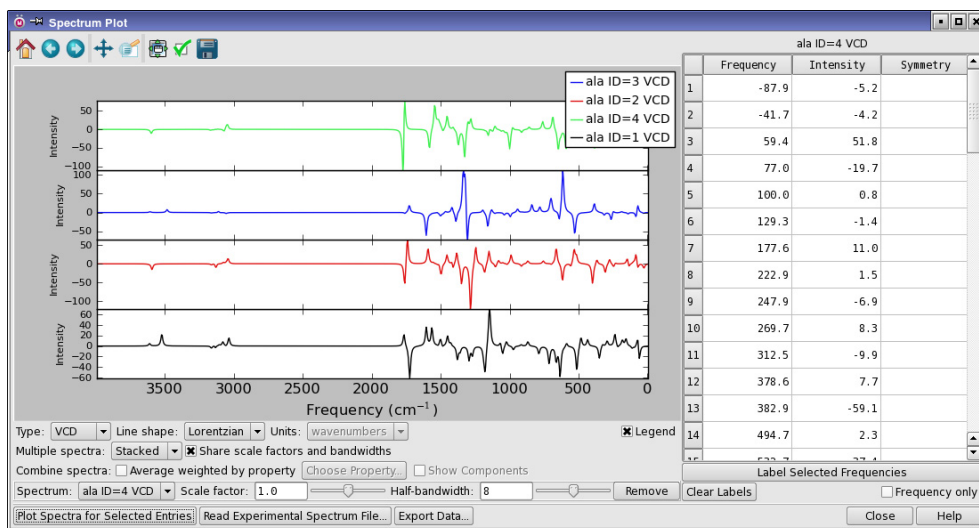
### 6.1.5 Displaying the VCD Spectra

In this exercise you display the VCD spectrum in Maestro, using the weights calculated in the previous exercise.

1. Ensure that the four structures with VCD spectra calculated are selected in the Project Table.
2. Choose Applications → Jaguar → Plot Spectra.
3. The Spectrum Plot panel opens.
4. From the Type option menu, choose VCD.
5. From the Multiple spectra option menu, choose Stacked.

This option plots spectra in a vertical “stack”, one for each structure, so you can see how different the spectra are.





**Figure 6.1. The stacked VCD spectra of the four conformers.**

6. Click Plot Spectra for Selected Entries.

When you click this button, a sequence of file selectors opens, so that you can import the spectrum file for each entry. Spectrum files are not imported automatically.

7. In each file selector, navigate to the spectrum file, `vcd_N_vcd.spm`, and click Open.

You should import the spectra in ascending order of  $N$ . When all the files are imported, the spectrum is displayed.

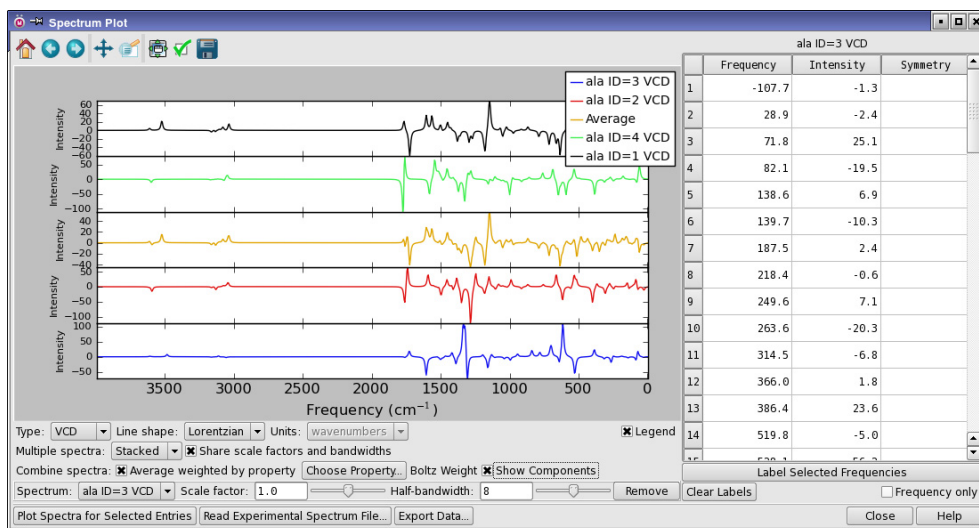
The spectra differ substantially from each other, both in terms of peak positions (vibrational frequencies) and in terms of the peak amplitudes. For molecules that have two or more conformers with similar energies, the experimentally observed spectrum would not be expected to closely match the calculated spectrum for a single conformer. For this reason it is advisable to calculate the spectra for all important conformers and average them using Boltzmann weighting of their energies. The weights can be calculated from the Jaguar energies (as done in the previous exercise).

8. Select Average weighted by property.

Initially, no property is selected, so the weights are equal.

9. Click Choose Property.

A property selector opens.



**Figure 6.2.** The stacked VCD spectra including the averaged spectrum.

10. Select the Boltz Weight property from the list, and click Accept.

The spectrum is averaged with weights determined by the Boltzmann factors for the free energy. This spectrum more closely resembles an experimental spectrum.

11. Select Show components.

The spectra for the components are shown individually along with the averaged spectrum. You can see by visually comparing the spectra which conformers have the most weight.

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# Getting Help

Information about Schrödinger software is available in two main places:

- The `docs` folder (directory) of your software installation, which contains HTML and PDF documentation. Index pages are available in this folder.
- The Schrödinger web site, <http://www.schrodinger.com/>, particularly the Support Center, <http://www.schrodinger.com/supportcenter>, and the Knowledge Base, <http://www.schrodinger.com/kb>.

## Finding Information in Maestro

Maestro provides access to nearly all the information available on Schrödinger software.

### To get information:

- Pause the pointer over a GUI feature (button, menu item, menu, ...). In the main window, information is displayed in the Auto-Help text box, which is located at the foot of the main window, or in a tooltip. In other panels, information is displayed in a tooltip.

If the tooltip does not appear within a second, check that **Show tooltips** is selected under **General → Appearance** in the Preferences panel, which you can open with CTRL+, (⌘,). Not all features have tooltips.

- Click the **Help** button in a panel or press F1 for information about a panel or the tab that is displayed in a panel. The help topic is displayed in your browser.
- Choose **Help → Online Help** or press CTRL+H (⌘H) to open the default help topic in your browser.
- When help is displayed in your browser, use the navigation links or search the help in the side bar.
- Choose **Help → Manuals Index**, to open a PDF file that has links to all the PDF documents. Click a link to open the document.
- Choose **Help → Search Manuals** to search the manuals. The search tab in Adobe Reader opens, and you can search across all the PDF documents. You must have Adobe Reader installed to use this feature.

### For information on:

- Problems and solutions: choose Help → Knowledge Base or Help → Known Issues → *product*.
- Software updates: choose Maestro → Check for Updates.
- New software features: choose Help → New Features.
- Scripts available for download: choose Scripts → Update.
- Python scripting: choose Help → Python Module Overview.
- Utility programs: choose Help → About Utilities.
- Keyboard shortcuts: choose Help → Keyboard Shortcuts.
- Installation and licensing: see the *Installation Guide*.
- Running and managing jobs: see the *Job Control Guide*.
- Using Maestro: see the *Maestro User Manual*.
- Maestro commands: see the *Maestro Command Reference Manual*.

## Contacting Technical Support

If you have questions that are not answered from any of the above sources, contact Schrödinger using the information below.

E-mail: [help@schrodinger.com](mailto:help@schrodinger.com)

USPS: Schrödinger, 101 SW Main Street, Suite 1300, Portland, OR 97204

Phone: (503) 299-1150

Fax: (503) 299-4532

WWW: <http://www.schrodinger.com>

FTP: <ftp://ftp.schrodinger.com>

Generally, e-mail correspondence is best because you can send machine output, if necessary. When sending e-mail messages, please include the following information:

- All relevant user input and machine output
- Jaguar purchaser (company, research institution, or individual)
- Primary Jaguar user
- Installation, licensing, and machine information as described below.

## Gathering Information for Technical Support

This section describes how to gather the required machine, licensing, and installation information, and any other job-related or failure-related information, to send to technical support.

### For general enquiries or problems:

1. Open the Diagnostics panel.
  - **Maestro:** Help → Diagnostics
  - **Windows:** Start → All Programs → Schrodinger-2012 → Diagnostics
  - **Mac:** Applications → Schrodinger2012 → Diagnostics
  - **Command line:** `$SCHRODINGER/diagnostics`
2. When the diagnostics have run, click Technical Support.

A dialog box opens, with instructions. You can highlight and copy the name of the file.
3. Attach the file specified in the dialog box to your e-mail message.

### If your job failed:

1. Open the Monitor panel in Maestro.

Use Applications → Monitor Jobs or Tasks → Monitor Jobs.
2. Select the failed job in the table, and click Postmortem.

The Postmortem panel opens.
3. If your data is not sensitive and you can send it, select Include structures and deselect Automatically obfuscate path names.
4. Click Create.

An archive file is created in your working directory, and an information dialog box with the name of the file opens. You can highlight and copy the name of the file.
5. Attach the file specified in the dialog box to your e-mail message.
6. Copy and paste any log messages from the window used to start Maestro (or the job) into the email message, or attach them as a file.
  - **Windows:** Right-click in the window and choose Select All, then press ENTER to copy the text.
  - **Mac:** Start the Console application (Applications → Utilities), filter on the application that you used to start the job (Maestro, BioLuminate, Elements), copy the text.

### If Maestro failed:

1. Open the Diagnostics panel.

- **Windows:** Start → All Programs → Schrodinger-2012 → Diagnostics
- **Mac:** Applications → Schrodinger2012 → Diagnostics
- **Linux/command line:** \$SCHRODINGER/diagnostics

2. When the diagnostics have run, click Technical Support.

A dialog box opens, with instructions. You can highlight and copy the name of the file.

3. Attach the file specified in the dialog box to your e-mail message.

4. Attach the file `maestro_error.txt` to your e-mail message.

This file should be in the following location:

- **Windows:** %LOCALAPPDATA%\Schrodinger\appcrash  
(Choose Start → Run and paste this location into the Open text box.)
- **Mac:** Documents/Schrodinger
- **Linux:** Maestro's working directory specified in the dialog box (the location is given in the terminal window).

5. On Windows, also attach the file `maestro.EXE.dmp`, which is in the same location as `maestro_error.txt`.



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