Desmond 4.2

Quick Start Guide

Schrödinger Press

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Contents

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	`$SCHRODINGER/maestro`	File names, directory names, commands, environment variables, command input and output
Italic	*filename*	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].

Introduction

Desmond is an advanced application developed by D. E. Shaw Research that allows you to conduct molecular dynamics (MD) simulations on proteins and other complex molecular systems. Using Desmond, you can perform simulations of small molecules, proteins, nucleic acids, and membrane systems, and visualize the trajectories in Maestro. You can also simulate the interactions of proteins with other proteins and ligand molecules.

This tutorial provides exercises in the basic tasks of setting up a Desmond MD simulation in Maestro and analyzing the results. Because MD simulations are very CPU intensive, the simulation exercises are on simple systems that give results in a reasonable time; the time taken is still around 24 hours of CPU time. It is therefore advisable to run the simulations on a multiprocessor host if you can.

Desmond calculations must be run on a Linux host. However, you can prepare and submit your jobs from Windows if you have remote job submission set up. See Chapter 7 of the *Installation Guide* for instructions on setting up job submission.

If you work through the entire tutorial, you do not need to copy the input files. If you want to start with a particular exercise, you can copy the input files from the installation as described in Section 1.2.

A basic knowledge of molecular mechanics and molecular dynamics is assumed. It is also assumed that you have a basic familiarity with Maestro.

1.1 Tutorial Outline

Chapter 2 deals with protein preparation. In this chapter you will prepare two proteins for later use, 1bel and 2qdz.

Chapter 3 contains exercises on building a model system. The exercises cover building a system for a small molecule (butane), for a protein (1bel), and for a protein with a membrane (2qdz).

The exercises in Chapter 4 demonstrate basic MD simulations. The first is for butane, which will be minimized first, and the second is for 1bel, which is relaxed as part of the simulation.

1.2 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 `desmond` zip file from the `tutorials` directory of your installation into your working directory.

On Linux, youYou 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-2015-2 → Maestro.

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

  If it is not on the dock, drag it there from the SchrodingerSuites2015-2 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 Desmond 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.

Note: Copying the tutorial files is not strictly necessary, but is convenient if you want to run a particular exercise.

Preparing Proteins

Structures imported from the PDB are not usually suitable for molecular mechanics or dynamics calculations, because they have no hydrogen atoms, and include crystal water molecules. They might also have ill-defined bond orders, protonation states, formal charges, tautomerization states, disulfide bonds, and so on. All of these issues must be resolved before simulations can be performed.

This chapter provides exercises in preparing proteins. Two proteins will be prepared: 1bel and 2qdz. Both of these proteins will be used to build a model system.

2.1 Preparing 1bel

In this exercise, you will import the protein structure 1bel (hydrolase phosphoric diester) from the PDB and prepare it for building a model system, using the Protein Preparation Wizard. This structure contains two disulfide bonds (Cys 26 – Cys 84 and Cys 65 – Cys 72), which are correctly assigned by the Protein Preparation Wizard; it also contains sulfate ions and methanol. The latter are remnants of crystallization and will be removed.

You can import structures with the Import panel, but the Protein Preparation Wizard panel provides a convenient facility for importing proteins.

1. Choose Applications → Protein Preparation Wizard, or click the Prep Wiz toolbar button.

   

   The Protein Preparation Wizard panel opens.

2. Enter `1bel` into the PDB text box, and click Import.

   The PDB file for 1bel is downloaded (from a local copy of the PDB if it is available, otherwise from the Web) into your working directory and imported into Maestro.

3. Select the following options and clear any others:

   - Assign bond orders
   - Add hydrogens
   - Create zero-order bonds to metals
   - Create disulfide bonds
   - Cap termini
   - Delete waters beyond N Å from het groups.

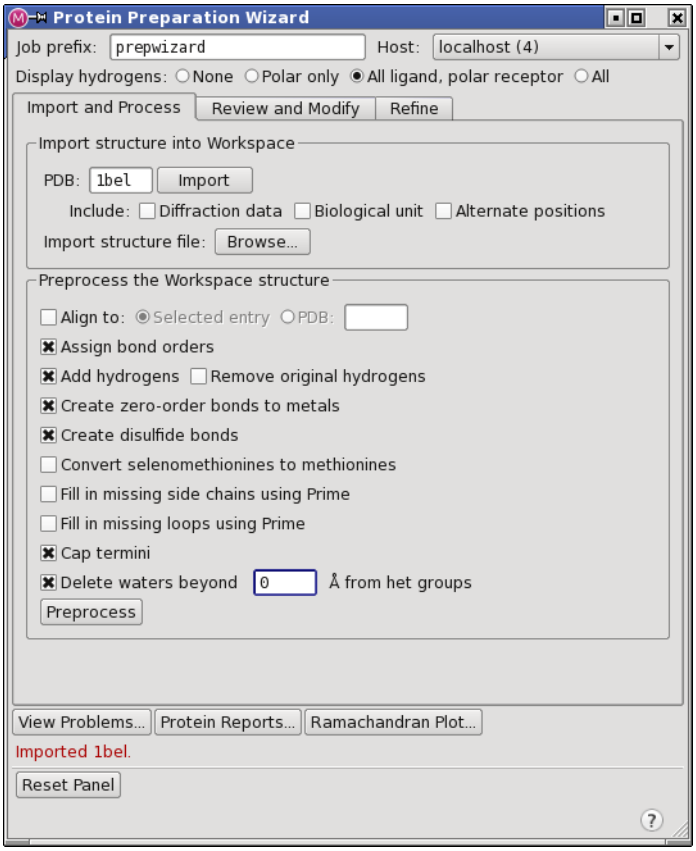

Figure 2.1. The Protein Preparation Wizard panel.

4. Enter `0` in the Delete waters beyond text box.
5. Click Preprocess.

   The structure is preprocessed to correct the bonding information, add hydrogen atoms, cap the termini with NME and ACE, and delete water molecules. At the same time, the tables in the Review and Modify tab are filled in. Note that there are no waters listed because they were all deleted.
6. In the Review and Modify tab, select all sulfate ions (SO4) and methanol molecules (MOH) in the Het group table, and click Delete.

   You might want to deselect Fit on select before you do this so that the Workspace view does not zoom in on each group that you select.

7. In the H-bond assignment section of the Refine tab, click Optimize.

   This task optimizes the hydrogen bonding network in the protein, which includes orientation of hydroxyl and terminal amide groups in various residues. The job is run with the host selected at the top of the panel, and should only take a minute or so.

   When the job finishes, a message is displayed at the foot of the Protein Preparation Wizard panel. The optimized structure is imported as a new entry into the Project Table and displayed in the Workspace. It is labeled with the results of the optimization operation: Flip or No flip for hydroxyl and amide orientations, and the residue name for histidines, whose charge state and protonation location may have been changed. Normally, you would check the labeled residues to ensure that they have been assigned correctly, by clicking Interactive Optimizer and using the panel that opens.

8. From the Label All button menu on the Labels toolbar, choose Delete Labels.

   

   The labels are deleted.

If you do not want to proceed to the next exercise at this time, close the Protein Preparation Wizard panel. If you want to continue with the preparation of a model system for this protein, go to Section 3.2 on page 10.

2.2 Preparing 2qdz

In this exercise, you will import the protein structure 2qdz (FHAC: a member of the OMP85/TPSB transporter family) from the PDB and prepare it for building a model system, using the Protein Preparation Wizard. This structure contains two fairly large gaps, which you will cap with NMA and ACE. If these gaps are critical to the simulation you want to perform, you could run a Prime loop prediction. There are no waters in this structure, and no disulfide bonds.

1. If the Protein Preparation Wizard panel is open, click Reset Panel. If it is not open, then choose Applications → Protein Preparation Wizard or use the Prep Wiz toolbar button

2. Enter `2qdz` into the PDB text box, and click Import.

   The PDB file for 2qdz is downloaded (from a local copy of the PDB if it is available, otherwise from the Web) into your working directory and imported into Maestro.

3. In the Preprocess the Workspace structure section, check that the following options are selected:

   - Assign bond orders
   - Add hydrogens

- Create zero-order bonds to metals
- Cap termini

4. Deselect Delete waters.
5. Click Preprocess.

   The structure is preprocessed to correct the bonding information, add hydrogen atoms, and cap the termini with NME and ACE. At the same time, the tables in the Chains, waters, and het groups section are filled in. In this case, there is only one chain, chain A, and no waters or het groups.

   When this process is done the Protein Preparation - problems dialog box is displayed, because the structure has missing residues.

6. Click OK to dismiss the Protein Preparation - Problems dialog box.
7. In the H-bond assignment section of the Refine tab, click Optimize.

   This task optimizes the hydrogen bonding network in the protein, which includes orientation of hydroxyl and terminal amide groups in various residues. The job is run with the host selected at the top of the panel, and should only take a minute or so.

   When the job finishes, a message is displayed at the foot of the Protein Preparation Wizard panel. The optimized structure is imported as a new entry into the Project Table and displayed in the Workspace, labeled with the results of the optimization operation.

8. From the Label All button menu on the Labels toolbar, choose Delete Labels.

   

   The labels are deleted.

9. Close the Protein Preparation Wizard panel.

If you want to continue with the preparation of a model system for this protein, go to Section 3.3 on page 13.

Building a Model System

This chapter contains exercises for three model systems. The first two will be used in the next chapter to perform MD simulations. The third is an exercise in preparing a model system for a membrane protein. Simulations for this system would take much longer than the others, so it is not included as a simulation exercise.

The System Builder generates a solvated system that includes the solute (protein, protein complex, protein-ligand complex, protein system immersed in a membrane, etc.) and the solvent water molecules with counter ions to neutralize the system and a salt to set the ionic strength, if requested.

In this chapter, you will need to use the Fragments, Representation, and Workspace toolbars. If they are not displayed, click the relevant button on the Manager toolbar, or choose Window → Toolbars → *toolbar*.

3.1 Building a Model System for Butane

In this exercise, you will build the butane molecule in the Workspace, and then use it to prepare a model system for simulation.

1. If the Workspace is not empty, click the Clear button on the Workspace toolbar.

   

2. Click the Methyl fragment on the Fragments toolbar, then click in the Workspace.

   

   A methane molecule is placed in the Workspace.

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

   A methyl fragment is added to the methane molecule, to form ethane.

4. Click on the terminal hydrogen of the fragment that was just added.

   Another methyl fragment is added, to form propane.

5. Click on the terminal hydrogen of the fragment that was just added.

   Another methyl fragment is added, to form butane. If you rotate the structure, you will see that the trans form of butane has been built.

6. Choose Applications → Desmond → System Builder in the main window.

   The System Builder panel opens with the Solvation tab displayed. For this molecule, we do not need to change any of the defaults. However, if you have used this panel previously in the current Maestro session, choose Reset Panel from the Settings button menu.

   

7. Click Minimize Volume.

   The solute is reoriented relative to the coordinate axes to minimize the box volume.

8. Set the job name to `butane_setup`.

9. Click Run.

   On Windows, you should instead click the Settings button, choose a remote Linux host in the Job Settings dialog box, and click Run. For subsequent jobs, you can click Run. This is because Desmond does not run locally on Windows.

   When the job finishes, a new entry group is added to the Project Table, labeled butane_setup-out1. It contains only a single entry, which includes the entire model system. The model system consists of a cubic box containing the butane molecule and enough water to fill the box, which has sides that are 10 Å from the butane molecule.

To continue with the simulation exercise for this system, go to Section 4.1 on page 19.

3.2 Building Model Systems for 1bel

In this exercise, you will use the System Builder panel to build a model system for the protein 1bel, which was prepared in Section 2.1 on page 5, in a 0.15 M NaCl solution. If you have not completed the exercise in that section, you can import the file `1bel_prep.maegz`. You will prepare two model systems, one for the protein before optimizing the H-bond network, and one for the protein after the optimization.

1. If the System Builder panel is not open, choose Applications → Desmond → System Builder.

   The System Builder panel opens with the Solvation tab displayed.

   If the System Builder panel is already open, choose Reset Panel from the Settings button menu.

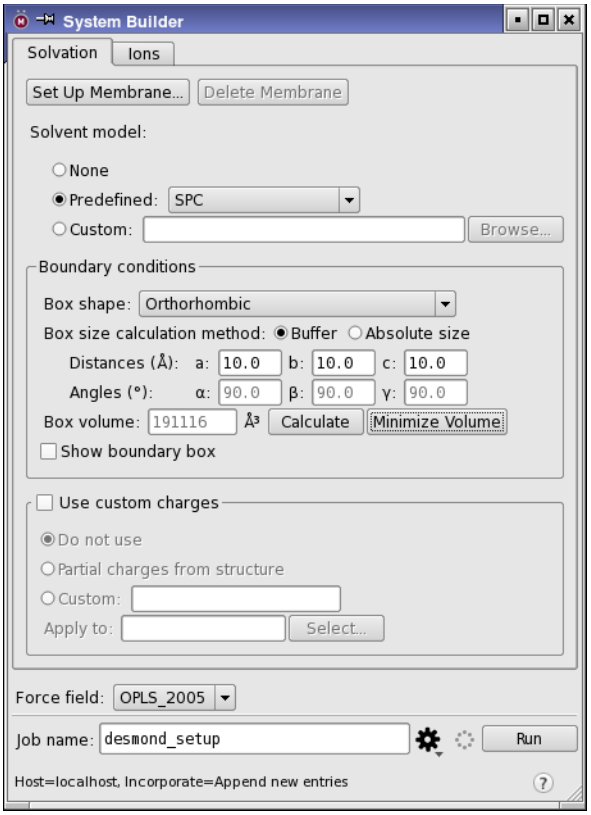

Figure 3.1. The Solvation tab of the System Builder panel.

2. Include the second of the three 1bel entries in the Workspace.

   This is the structure before H-bond optimization. The first is the raw protein structure; the third is the optimized structure.

3. Ensure that Predefined is selected under Solvent model, and that SPC is chosen.

   This is the default, so you should not need to change it.

4. From the Box shape option menu, choose Orthorhombic.

   This is the shape that best fits the 1bel protein structure, and is the default.

5. Ensure that Buffer is selected for the Box size calculation method, and that all three Distances text boxes contain 10.0.

   Again, these are the defaults, so no change should be needed.

6. Click Minimize Volume.

   The protein is reoriented to minimize the volume of the box.

7. In the Ions tab, ensure that Neutralize by adding is selected.

   The prepared structure is charged, so it needs to be neutralized with counter ions.

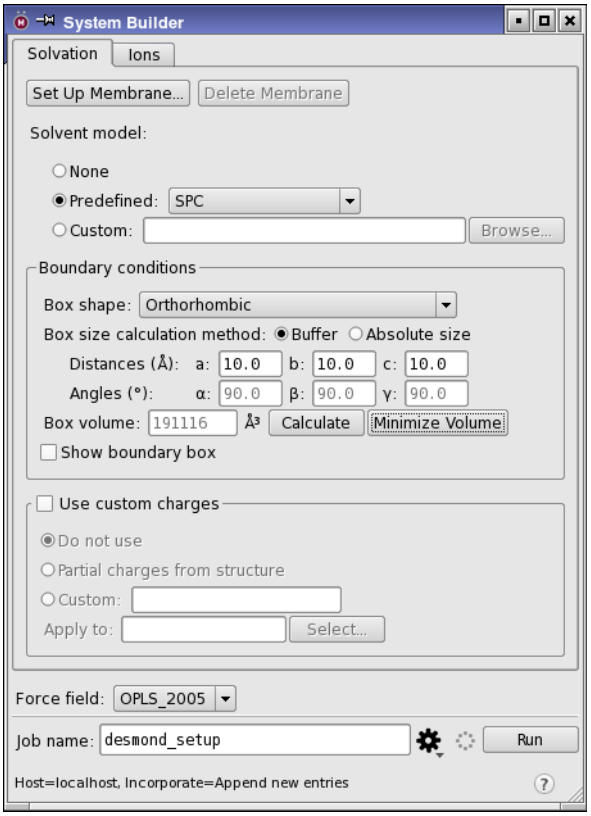

Figure 3.2. The Ions tab of the System Builder panel.

8. Click Recalculate.

   The text and menu should show 4 Cl- ions for the second 1bel structure. When you repeat the setup with the third 1bel structure, the text and menu should show 5 Cl- ions.

9. Select Add salt.

10. In the Salt concentration text box, enter `0.15`.

Ions will be added to the simulation box that represent background salt at physiological conditions. By default, sodium chloride is added, but you can choose a variety of positive and negative ions for the salt.

11. Change the job name to `1bel_setup_1`.
12. Click Run.

    The job should not take more than a minute. When it finishes, a new entry group is added to the Project Table, labeled 1bel_setup_1-out1. It contains only a single entry, which includes the entire model system.

13. Include the third of the three 1bel entries in the Workspace.
14. Repeat Step 3 through Step 12 for this entry, changing the job name to `1bel_setup_2`.

To continue with the simulation exercise for this system, go to Section 4.2 on page 23.

3.3 Building a Model System for 2qdz

In this exercise, you will use the System Builder panel to build a model system for the membrane protein 2qdz in a 0.15 M NaCl solution with a membrane.

1. Include the prepared 2qdz protein from Section 2.2 on page 7 in the Workspace.

   There are several entries generated by the Protein Preparation Wizard, with the same name. The last of these is the fully prepared protein structure. If you did not do the exercise, you can import the file `2qdz_prep.maegz`.

2. From the Ribbons button on the Representation toolbar, choose Show ribbons for all residues.

   

   The protein is displayed in ribbon representation, making it easy to identify the "beta barrel" portion of the protein that goes in the membrane.

3. If the System Builder panel is not open, choose Applications → Desmond → System Builder or Tasks → Molecular Dynamics → System Setup.

   The System Builder panel opens with the Solvation tab displayed.

   If the System Builder panel is already open, choose Reset Panel from the Settings button menu.

4. Click Set Up Membrane.

   The System Builder - Set Up Membrane panel opens.

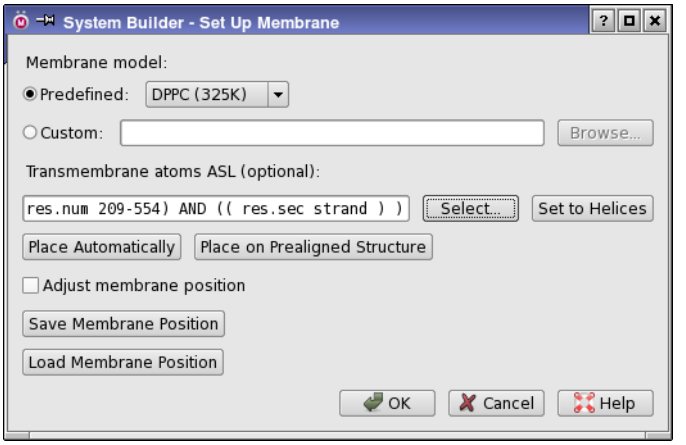

Figure 3.3. The System Builder - Set Up Membrane panel.

5. Choose DPPC is for the membrane model.
6. Click Place Automatically.

   The membrane is placed, represented by two red slabs. The actual membrane molecules are not inserted until the system builder job is run.

The membrane is not placed in the correct position, because the default placement takes account of the alpha helices rather than the beta "barrel". However, the parts of the protein that should be in the membrane can be selected, which you will do next.

7. Click Select.

   The Atom Selection dialog box opens.

8. In the Residue tab, choose Residue number from the list on the left.
9. Enter `209-554` in the Residue number text area.
10. Click Add.

    The ASL text box in the lower part of the panel displays `res.num 209-554`.

11. Choose Secondary structure from the list on the left.
12. Select Strand from the Secondary structure options.

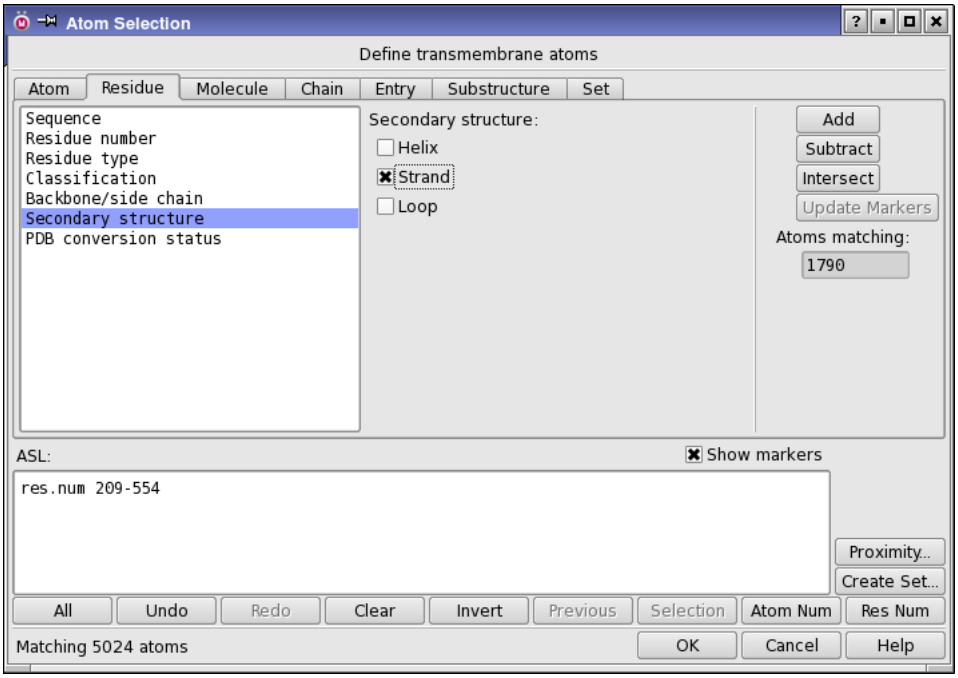

Figure 3.4. The Atom Selection dialog box, before clicking Intersect.

13. Click Intersect.

    The ASL expression now reads `(res.num 209-554) AND (( res.sec strand ) )` This expression indicates that the atoms to be selected are those that are in the given residue range and have a strand secondary structure.

14. Click OK.

    The Atom Selection dialog box closes, and the ASL expression appears in the Transmembrane atoms ASL text box in the membrane setup panel.

15. Click Place Automatically.

    The membrane is placed again, this time in the correct position around the “beta barrel”. If some finer adjustments to the membrane orientation are needed, you could select Adjust membrane, and rotate the structure (middle mouse) to improve the alignment.

16. Click OK.

    The Set Up Membrane panel closes. The membrane markers are no longer displayed in the Workspace, but the membrane will be added when you run the job. The Add Membrane button in the System Builder panel has changed to Edit Membrane.

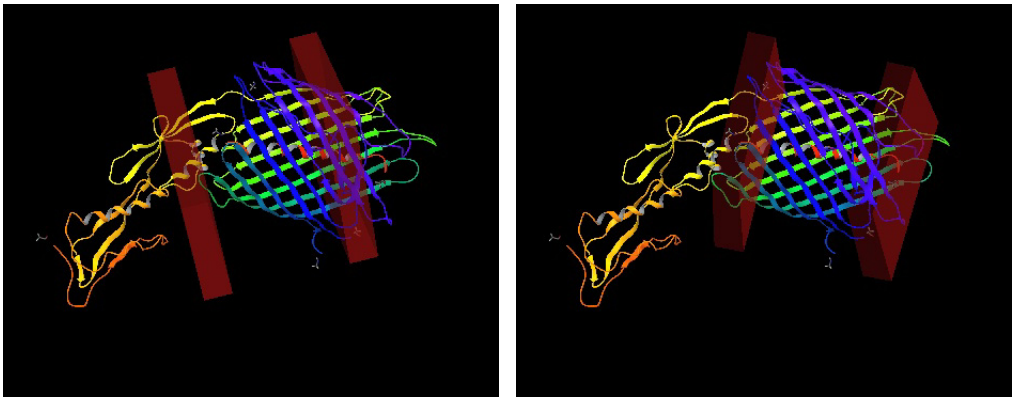

Figure 3.5. The default membrane alignment (left) and the ASL-directed alignment (right)

17. In the Ions tab, ensure that Neutralize is selected, and click Recalculate.

    The prepared structure is charged, so it needs to be neutralized with counter ions.

18. Select Add salt.

19. In the Salt concentration text box, enter 0.15.

    Ions will be added to the simulation box that represent background salt at physiological conditions. By default, sodium chloride is added, but you can choose a variety of positive and negative ions for the salt.

20. Change the job name to `2qdz_setup`.

21. Click Run.

    The job should not take more than a few minutes. When it finishes, a new entry group is added to the Project Table, labeled 2qdz_setup-out1. It contains only a single entry, which includes the entire model system.

22. Close the System Builder panel.

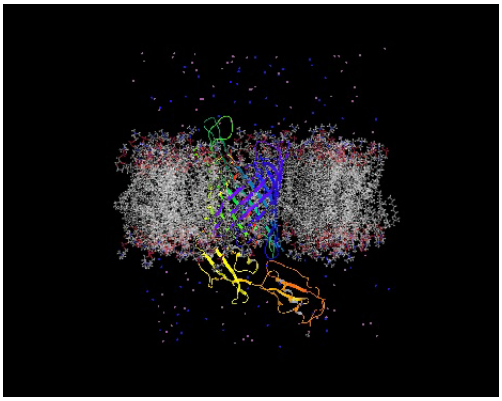

Figure 3.6. The 2qdz model system with waters undisplayed.

Molecular Dynamics Simulations

This chapter provides exercises on performing molecular dynamics (MD) simulations for two systems that were built in Chapter 3. If you have not completed the system building exercises, you should do so now.

You will use various toolbars in these exercises. If any of the toolbars is not displayed, click its button on the Manager toolbar, or use Window → Toolbars → *toolbar*.

4.1 MD Simulations for Butane

In this exercise, you will run a MD simulation on the butane system that you prepared earlier, and examine the trajectory. Before running the simulation, you will perform a minimization of the system to relax it. The model systems built by the System Builder are not optimal, and need to be relaxed before the simulation. You can perform the relaxation as part of the MD task, or you can perform it separately. In this exercise, you will perform the relaxation separately. When the results are returned, you will view the trajectory.

4.1.1 Running the Simulation

1. Include the butane model system in the Workspace.
2. In the main window choose Applications → Desmond → Minimization.

   The Minimization panel opens.
3. In the Model system section, ensure that Load from Workspace is chosen in the option menu, and click Load.

   A scratch entry is created in the Workspace containing the model system, and the project entries are excluded.

   The defaults for the minimization parameters are adequate, so no changes are needed.
4. Change the job name to `butane_min`.
5. Click the Settings button.

   

   The Job Settings dialog box opens.

6. Choose a host.

   On Windows, you must choose a remote Linux host.

7. Click Run.

The job finishes in about a minute, and the output from the minimization is included in the Workspace.

8. Close the Minimization panel.
9. In the main window choose Applications → Desmond → Molecular Dynamics.

   The Molecular Dynamics panel opens.

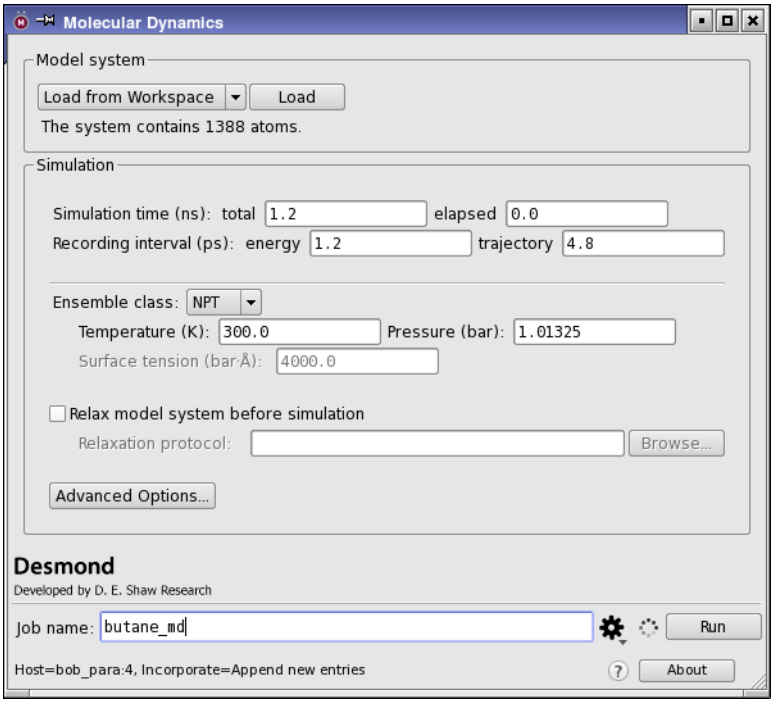

Figure 4.1. The Molecular Dynamics panel.

10. In the Model system section of the Molecular Dynamics panel, ensure that Load from Workspace is chosen in the option menu, and click Load.
11. Deselect Relax model system before simulation.

    The system has already been relaxed in the minimization calculation.

12. Click the Settings button.

    

    The Job Settings dialog box opens.

13. Change the job name to `butane_md`.

14. Set the number of processors, and choose a host.

    On Windows, you must choose a remote Linux host.

    Desmond MD simulations are CPU-intensive, and run very efficiently in parallel. This simulation takes about 2 hours CPU time, so if you can, you should distribute it over multiple processors. As the box size is fairly small, you should use at most 4 processors.

15. Click Run.

    The job is started and the Job Settings dialog box closes. When the job finishes, the results are imported into the Project Table and the last structure in the simulation is displayed in the Workspace.

16. Close the Molecular Dynamics panel.

4.1.2 Viewing the Trajectory

The next part of this exercise is to view the trajectory for just the butane molecule. The display is set up first, then the trajectory viewer is opened from the Project Table panel.

1. From the Undisplay button menu on the Display Atoms toolbar, choose Waters.

   

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

   

3. In the Entry List panel, click the T button for the butane simulation output entry.

   There should be only one such button. The Trajectory panel opens.

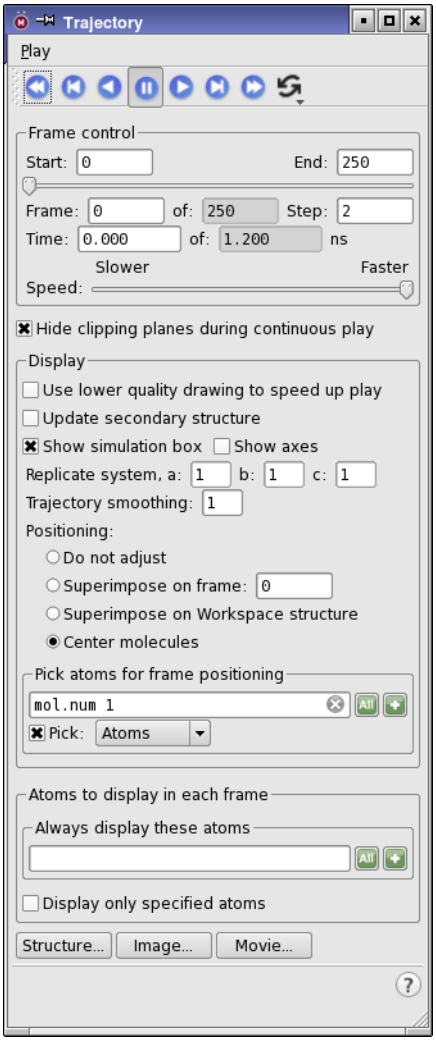

Figure 4.2. The Trajectory panel.

4. In the Frame control section, enter `1` in the Step text box.
5. Adjust the Speed slider to about the middle.
6. In the Display section, deselect Show simulation box and Show axes.
7. Select Superimpose on frame, and enter `1` in the text box.

   By default, the first molecule (the solute) is selected to superimpose: the ASL expression reads `mol.num 1`. Here, we will choose two atoms.

8. In the Pick atoms for frame positioning section, click the Clear button.
9. Ensure that Pick is selected, and pick the second and third carbon of the butane molecule.
10. Click the Play forward button.

You should see the butane molecule switch to the gauche and to the cis conformation during the course of the trajectory. If the play is too fast or too slow, adjust the Speed slider.

4.2 MD Simulations for 1bel

In this exercise, you will run MD simulations on the 1bel systems that you prepared earlier, and examine the trajectories. The trajectories for these two model systems demonstrate the effect of optimizing the H-bond network in the protein. In the unoptimized case, the ring in Tyr 115 flips to a new orientation. In the optimized case, this does not happen. The simulations each take about 48 hours, so you should run them in parallel on a suitable multiprocessor host.

4.2.1 Running the Simulations

1. Include the first 1bel system built in Section 3.2 on page 10 in the Workspace

   The entry group for this system is 1bel_setup_1-out1.

2. In the main window choose Applications → Desmond → Molecular Dynamics.

   The Molecular Dynamics panel opens.

3. In the Model system section of the Molecular Dynamics panel, ensure that Load from Workspace is chosen in the option menu, and click Load.

4. Select Relax model system before simulation.

   The model systems built by the System Builder are not optimal, and need to be relaxed before the simulation.

5. Click Advanced Options.

   The Advanced Options dialog box opens.

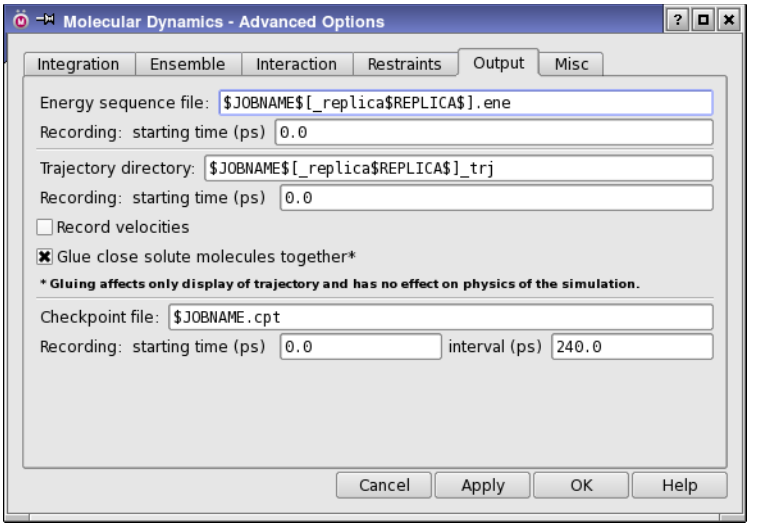

Figure 4.3. The Output tab of the Advanced Options dialog box.

6. In the Output tab, change the interval for the checkpoint file to 1200 ps.

   This choice improves the turnaround time for the simulation.

7. Click OK.

   The Advanced Options dialog box closes.

8. Click the Settings button.

   

   The Job Settings dialog box opens.

   As the simulation takes about 48 hours CPU time, you should use at least 8 processors if you can. The number of processors is displayed next to the host name on the Host option menu. Because of the way the work is distributed by Desmond, the number of processors should be a multiple of 2, 3, or 5.

9. Change the job name to `1bel_md1`.

10. Set the number of processors and choose a host from the Host option menu. On Windows, you must choose a remote Linux host.

11. Click Run.

    When the job finishes, the results are incorporated as a new entry in the Project Table, with a T button in the Title column to indicate the presence of a trajectory.

12. Include the second 1bel system built in Section 3.2 on page 10 in the Workspace.

    The entry group for this system is 1bel-setup_2-out1.

13. Repeat Step 3 through Step 7 for this model system, in Step 9.

    Many of the selections that you made for the first simulation are still selected, so you might only need to check the settings.

14. Set the job name to `1bel_md2`.

15. Click Run.

    The same host and number of processors as the previous run are used for this job.

16. Close the Molecular Dynamics panel.

4.2.2 Setting Up the Display

With a large number of atoms in the Workspace, it is difficult to see specific changes. To best view the changes in the orientation of Tyr 115, the display needs to be set up. Tyr 73 is close to Tyr 115, and starts with a hydrogen bond to it which is broken and briefly reformed during the simulation. You might not see this hydrogen bond when you are setting up the display.

1. Include the 1bel_md2-out entry, using the Entry List panel.
2. From the Display Only button on the Display Atoms toolbar, choose Select.

   

   The Atom Selection dialog box opens.

3. In the Residues tab, choose Residue number from the list.

   Tools for selecting by residue number are displayed in the center of the panel.

4. Enter `115` in the Residue number text box and click Add.
5. Choose Residue type from the list.
6. Choose TYR from the Residue type list and click Intersect, then click OK.

   The Atom Selection dialog box closes, and Tyr 115 is the only residue displayed in the Workspace.

7. From the Ball & Stick button on the Representation toolbar, choose Residue, and pick an atom in the Tyr 115 residue in the Workspace.

   

Tyr 115 should now be clearly distinguished from the other residues.

8. From the Within button on the Display Atoms toolbar, choose Custom.

9. In the dialog box that is displayed, enter `10.0` and click OK.

   Residues around Tyr 115 are displayed, including waters. The waters will be undisplayed in the next step.

10. From the Undisplay button on the Display Atoms toolbar, choose Waters.

   The water molecules are undisplayed, leaving only the protein residues near Tyr 115.

11. From the Ball & Stick button on the Representation toolbar, choose Residue, and pick an atom in the Tyr 73 residue in the Workspace.

   The residue name and number are displayed in the Status bar when you pause the cursor over an atom, so you can check that you have the correct residue before you pick. You could also use the Find tool or the sequence viewer to find Tyr 73.

12. Click the H-Bonds button menu on the Measurements toolbar, and select Other.

   The Edit H-Bonds Definition dialog box opens.

13. In the Atom set 1 section, choose Residues from the Pick menu, and pick an atom in Tyr 115.

14. In the Atom set 2 section, choose Residues from the Pick menu, and pick an atom in Tyr 73.

   The hydrogen bond (if it is present) is displayed as a yellow dashed line.

15. Click the Fit button on the Workspace toolbar.

The view zooms out so that the displayed residues occupy most of the Workspace. You might also want to rotate the structure to get a better view of Tyr 115. Note that any changes you make to the display are applied throughout the playing of the trajectory.

16. Repeat the above instructions for the other trajectory, 1bel_md1-out.

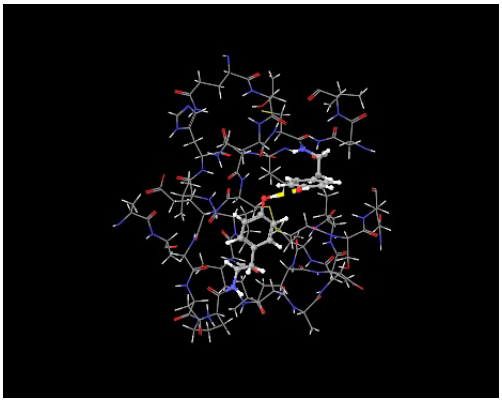

Figure 4.4. The first 1bel system set up for viewing the trajectory.

4.2.3 Viewing the Trajectory

Now that the display is set up, you can proceed to the viewing of the trajectory.

1. Include the 1bel_md1-out entry in the Workspace and click the T button in the Title column.

   The Trajectory panel opens.

2. In the Frame control section, enter `1` in the Step text box.
3. In the Display section, deselect Show simulation box and Show axes.
4. In the Trajectory smoothing text box, enter `5`.
5. Click the Play forward button.

   

   Observe the behavior of the H-bond and of the Tyr 115 ring. You might have to rotate the structure to observe the ring.

6. Repeat the setup in Section 4.2.2 and the viewing instructions above for the 1bel_md2-out entry, and observe the behavior of the H-bond and of the Tyr 115 ring.

Note the different behavior of the H-bond, which breaks and reforms several times, and the ring, which swings out into the solvent. The behavior depends on the preparation, but in a fairly short simulation it is difficult to tell whether the differences are really due to the preparation of the hydrogen bonds. Longer simulation times may be needed to settle this issue.

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/, In particular, you can use the Knowledge Base, http://www.schrodinger.com/kb, to find current information on a range of topics, and the Known Issues page, http://www.schrodinger.com/knownissues, to find information on software issues.

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 the lower right corner of 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 the Help panel. The button may have text or an icon:

  

- Choose Help → Online Help or press CTRL+H (⌘H) to open the default help topic.
- When help is displayed in the Help panel, use the navigation links in the help topic or search the help.
- Choose Help → Documentation Index, to open a page that has links to all the 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*.
- New software features: choose Help → New Features.
- 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.

Web:	http://www.schrodinger.com/supportcenter
E-mail:	help@schrodinger.com
Mail:	Schrödinger, 101 SW Main Street, Suite 1300, Portland, OR 97204
Phone:	+1 888 891-4701 (USA, 8am – 8pm Eastern Time)
	+49 621 438-55173 (Europe, 9am – 5pm Central European Time)
Fax:	+1 503 299-4532 (USA, Portland office)
FTP:	ftp://ftp.schrodinger.com

Generally, using the web form is best because you can add machine output and upload files, if necessary. You will need to include the following information:

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

Gathering Information for Technical Support

The instructions below describe how to gather the required machine, licensing, and installation information, and any other job-related or failure-related information, to send to technical support. Where the instructions depend on the profile used for Maestro, the profile is indicated.

For general enquiries or problems:

1. Open the Diagnostics panel.
   - **Maestro:** Help → Diagnostics
   - **Windows:** Start → All Programs → Schrodinger-2015-2 → Diagnostics
   - **Mac:** Applications → Schrodinger2015-2 → 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. Upload the file specified in the dialog box to the support web form.

   If you have already submitted a support request, use the upload link in the email response from Schrödinger to upload the file. If you need to submit a new request, you can upload the file when you fill in the form.

If your job failed:

1. Open the Monitor panel, using the instructions for your profile as given below:
   - **Maestro/Jaguar/Elements:** Tasks → Monitor Jobs
   - **BioLuminate/MaterialsScience:** Tasks → Job Monitor
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, and an information dialog box with the name and location of the file opens. You can highlight and copy the name of the file.
5. Upload the file specified in the dialog box to the support web form.

   If you have already submitted a support request, use the upload link in the email response from Schrödinger to upload the file. If you need to submit a new request, you can upload the file when you fill in the form.

6. Copy and paste any log messages from the window used to start the interface or the job into the web form (or an e-mail 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-2015-2 → Diagnostics
   - **Mac:** Applications → SchrodingerSuite2015-2 → 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. Upload the file specified in the dialog box to the support web form.

   If you have already submitted a support request, use the upload link in the email response from Schrödinger to upload the file. If you need to submit a new request, you can upload the file when you fill in the form.
4. Upload the error files to the support web form.

   The files should be in the following location:

- **Windows:** `%LOCALAPPDATA%\Schrodinger\appcrash`
  (Choose Start → Run and paste this location into the Open text box.)
  Attach `maestro_error_`*`pid`*`.txt` and `maestro.exe_`*`pid_timestamp`*`.dmp`.
- **Mac:** `$HOME/Library/Logs/CrashReporter`
  (Go → Home → Library → Logs → CrashReporter)
  Attach `maestro_error_`*`pid`*`.txt` and `maestro_`*`timestamp_machinename`*`.crash`.
- **Linux:** `$HOME/.schrodinger/appcrash`
  Attach `maestro_error_`*`pid`*`.txt` and `crash_report_`*`timestamp_pid`*`.txt`.

If a Maestro panel failed to open:

1. Copy the text in the dialog box that opens.
2. Paste the text into the support web form.

120 West 45th Street
17th Floor
New York, NY 10036

101 SW Main Street
Suite 1300
Portland, OR 97204

245 First Street
Riverview II, 18th Floor
Cambridge, MA 02142

8910 University Center Lane
Suite 270
San Diego, CA 92122

155 Gibbs St
Suite 430
Rockville, MD 20850-0353

Dynamostraße 13
D-68165 Mannheim
Germany

Zeppelinstraße 73
D-81669 München
Germany

Potsdamer Platz 11
D-10785 Berlin
Germany

Quatro House
Frimley Road
Camberley GU16 7ER
United Kingdom

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