Constraining the molecular geometry

We will consider a Pd complex that co-crystallizes with ½ equivalent of ethyl acetate; figure on the right. The solvent molecule is disordered over an inversion center and should be refined with part -1.

Files disorder 3.res and disorder 3.hkl are needed to follow the steps below.

1. Begin by deleting the solvent molecule and refining the structure.
   a) To select the EtOAc molecule double click on it, and press the delete key to delete it.
   b) Under Work→Refine select the desired refinement program, refinement method, number of least-squares cycles and click on the Refine bar to run a refinement.

2. The refinement reveals, among other things, four residual peaks higher than the rest:

3. Optional: the four residual peaks can be repositioned to be closer together in two ways:
   a) typing `compaq -c`
   b) clicking on the button under Work→Refine→Toolbox Work.

In the GUI make sure only the Pd complex and the four highest Q peaks are shown. The Q peaks can be hidden or shown by rotating the mouse wheel. Type `grow` to generate the symmetry related Q peaks:
4 Prepare an idealized geometry of the molecule of choice (ethyl acetate in this case). It should look like a typical FRAG/FEND command:

```
FRAG 17
O1  3 -0.787135 1.361478 -1.826069
O2  3 -1.250238 2.162490 0.179184
C1  1 -0.072846 0.126000 0.077980
C2  1 -0.733637 1.268944 -0.645662
C3  1 -1.903975 3.293234 -0.386436
C4  1 -2.401190 4.153250 0.753379
FEND
```

Many DFT-optimized molecular geometries are available free at [http://xray.chem.wisc.edu/Projects/IdealizedMolecularGeometry.html](http://xray.chem.wisc.edu/Projects/IdealizedMolecularGeometry.html). Of course one can use a reasonable geometry from the Cambridge Structural Database or any other reliable source.

This just in. The link to this web site is in the OLEX2’s GUI: Tools→Disorder→Ilia’s fragment library.

5 Copy the entire frag/fend list (including the frag and fend command) for ethyl acetate and paste them with CTRL-V into the GUI.

The idealized molecule will be inserted in a green(ish) color (on the right in the diagram below) and OLEX2 goes into the MATCH mode (the cursor is no longer an arrow).

The inserted molecule can be superimposed on the Q peaks in the MATCH mode. Prior to that it may be beneficial to move the inserted molecule closer to the Q peaks manually as follows:
Left click on the molecule and keep the left button depressed to rotate the molecule. Hold down the SHIFT key to drag the molecule with a depressed left button. You can rotate the entire structure as usual if you click elsewhere on the GUI.

Once the inserted molecule is close to the proper place its position can be fine-tuned in the MATCH mode, by pairwise matching of the atoms and Q peaks (use no more than three atom pairs):

To exit from the MATCH mode either keep hitting the ESC button until you exit the mode (the cursor becomes an arrow again) or type mode off:

Because the solvent molecule is disordered over an inversion center it should be refined with PART -1 and occupancy of 50%.

First, we will assign part -1 to the solvent molecule. Double click on the solvent molecule to select it. Then type part -1
The latter command serves to prove that the atoms belong to PART -1. The part numbers are displayed next to the atoms that are in a PART:

![Diagram]

**Olex2 dictionary:**

*part number [occupancy]*

assigns the part number and occupancy (optionally) to the selected atoms. The occupancy involve a free variable.

Example.

To assign part number 2 to atoms C1 and C2:

*select* atoms C1 and C2 and type

```
part 2
```

Now atoms C1 and C2 belong to part 2.

To assign the selected atoms to part 3 with occupancy of 40% type

```
part 3 10.4
```

To assign the selected atoms to part 1 with occupancy defined by the third free variable:

```
part 1 31
```

Next, the solvent molecule should be given the proper occupancy.

One way to do so is to select the molecule by double-clicking on it and then type

```
fix occu 0.5
```

Another way to select the molecule and type

```
part -1 10.5
```

Another way is to select the molecule by double clicking on it and then click on the “atom edit” button to modify the instructions in the context menu:

Prior to modification:

```
FVAR 0.38625
PART -1 ! the line to be modified
AFIX 6
```
O7  O  0.98336  0.46279  0.43296  11.00000  0.05000  
O8  O  0.98510  0.56586  0.51732  11.00000  0.05000  
C7  C  1.10254  0.28937  0.50910  11.00000  0.05000  
C8  C  1.01760  0.44680  0.48150  11.00000  0.05000  
C9  C  0.90473  0.72118  0.49622  11.00000  0.05000  
C10  C  0.88189  0.83477  0.54498  11.00000  0.05000  

AFIX 0

Only the occupancy must be modified, and that is achieved by addition 10.5 to the PART line:
Upon modification:
FVAR 0.38625
PART -1 10.5  ! modified line
AFIX 6

O7  O  0.98336  0.46279  0.43296  11.00000  0.05000  
O8  O  0.98510  0.56586  0.51732  11.00000  0.05000  
C7  C  1.10254  0.28937  0.50910  11.00000  0.05000  
C8  C  1.01760  0.44680  0.48150  11.00000  0.05000  
C9  C  0.90473  0.72118  0.49622  11.00000  0.05000  
C10  C  0.88189  0.83477  0.54498  11.00000  0.05000  

AFIX 0

Click OK and run a refinement. If the resultant structure looks “strange” and some solvent atoms are missing - type fuse. A proper view should be restored.

Refine the structure anisotropically:

The refinement indicators have improved, but the ellipsoid of the carbonyl atom looks somewhat enlarged. In this case it is a good idea to remove the idealized geometry constraint: -double click on the solvent molecule to select it.
-type afix 0.

Run a refinement. Then position H atoms on this molecule and run another refinement:

![Molecule Image]

The solvent molecule looks much better and the overall refinement is stable. The R factor is 2.04%.

To remove the “-1” labels from the GUI type labels.

To ensure the SFAC/UNIT cards of the INS files correctly reflect the content of the unit cell, type fixunit. The structure composition is printed in the console output.

**Olex2 dictionary:**

- **fixunit [Z’]**
  updates the formula based on the content of the asymmetric unit. The Z’ value is unity by default. If the symmetry independent unit contains a number of molecules different from unity the Z’ should be specified. It will be updated on the ZERR line in the INS file.
  The OK button works similarly.

Example: the asymmetric unit contains one half of a molecule. To update the formula with the correct Z on the ZERR line type

`fixunit 0.5`

---

**When a solvent cannot be modeled**

Sometimes a solvent molecule can be neither identified nor modeled. In such cases option SQUEEZE of Ton Spek’s PLATON can be used. The SQUEEZE procedure accounts for diffuse electron density. People interested in the void algorithm of PLATON ("CALC SOLV") are
referred to the following presentation:
http://www.cryst.chem.uu.nl/spek/ppp/PLATON-SQUEEZE.pdf
(pages 6-12). An application in microporous crystals can be found in:

[Solvent accessible voids can be displayed with Mercury. For an introduction to crystal porosity I recommend “Crystal porosity and the burden of proof” by Len Barbour, Chem. Commun., 2006, 1163-1168. But I digress.]


Let us proceed with the previous example Disorder3 with ethyl acetate. In this case it is known what the solvent is and thus the structure is a good test.

1. Delete the ethyl acetate solvent molecule and run a refinement.
2. Go to Tools→Maps→Mask and click on the Mask button to run a computation with the default parameters. The program draws the solvent accessible voids in the GUI (unit cell drawing below) and generates a numerical output (also available in file name-mask.log) the bottom portion of which is copied here:

<table>
<thead>
<tr>
<th>Void</th>
<th>Vol/Ang(^3)</th>
<th>#Electrons</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>152.2</td>
<td>51.7</td>
</tr>
<tr>
<td>2</td>
<td>152.2</td>
<td>51.7</td>
</tr>
</tbody>
</table>

OLEX2 has identified two voids of 152.2 Å\(^3\) with 51.7 electrons in each. Ethyl acetate contains 48 electrons and the estimated volume of the molecule is 124 Å\(^3\). For comparison, PLATON (with the default settings) estimated the volume of each of the two voids at 145 Å\(^3\) with 48 electrons in each. Similarly to this case, in my experience PLATON’s algorithm frequently works somewhat better than OLEX2’s. With electron counts, anyway.

To proceed with the refinement return to the Work menu (F5), expand the Refine menu, mark the “Use solvent mask” checkbox and run a refinement. You can also elect to “Recompute mask” by checking its box.

You can proceed to completion in this fashion, or you can select file name-mask.hkl from the Work→Refine→Reflection file and uncheck the “Use solvent mask” and “Recompute mask” boxes.

It goes without saying that this type of refinement should be documented in the experimental.
Hydrogen bonding interactions

We proceed with the same example and with the solvent molecule mapped out.

To document the H-bonding interactions in the structure the appropriate HTAB and EQIV cards should be inserted in the INS file. OLEX2 generates them automatically if you type

htab

In this case this command generates two bonds:

Processing HTAB with max D–A distance 2.9 and minimum angle 120
HTAB O5 O2$_1$ d=2.631
HTAB O5 O4$_1$ d=2.635

and the following lines are inserted in the INS file:

EQIV $1 1.5$X,–0.5$Y,1.5$Z
HTAB O5 O2$_1$
HTAB O5 O4$_1$

OLEX2 dictionary

htab [dist] [angle] [switch]

analyzes the atomic connectivity list and inserts HTAB (and/or RTAB) and EQIV cards in the SHELXL instruction file in order to tabulate the hydrogen bonding interactions in the LST and CIF files with proper standard uncertainties. (Note that if the H atoms are in the idealized positions there will be no s.u.’s on the donor–H…acceptor angles.)

Defaults for the distance and angle are 2.9 Å and 150° and the default elements for the H–bond detection are N,O,F,Cl,S.

switches:

–t: adds extra elements that should be comma-separated
–g: if any of the detected H–bonds are generated by symmetry transformations, the structure is grown using those symmetry operations

If the htab command is issued multiple times only unique results will be added to the INS file.

Examples:

htab
will insert HTAB cards (and the necessary EQIV cards) for the detected hydrogen bonds in the INS file.

To survey more interactions one may use

htab 3.2 120

where 3.2 is the donor–acceptor distance in Angstroms, 120 is the donor–H…acceptor angle in degrees.

switch –t allow the use of additional elements in the hydrogen bond searches:

htab 3.2 –t=Br,I
will ensure that in addition to the default donor/acceptor atoms all Br and I atoms will also be considered and all H-bonding interactions shorter than 3.2 Å will be listed.

```
htab -g
```

produces an expanded structure if any hydrogen bonds are generated with a symmetry operation.

If too many bonds are generated and inserted into the instruction file and a removal of some of them is desirable, the HTAB commands should be edited out manually from the INS file.

Let us proceed with the generation of a hydrogen-bonded network.
View→Symmetry Generation→Packing→Expand Short contacts (Hydrogen bonds)

Click on the slider of the Expand Short Contacts bar and drag it until you see four pink dashed lines, indicators of the potential H-bonding interactions:

Note that the cursor is now in a “mode” as indicated by its change from an “arrow” to a “hand”.

Click on a dashed line to generate a hydrogen bonded molecule. The hydrogen bonding interaction are drawn with dotted lines.