Clicking particles inside a tomogram

General case: models for globular particles
In this tutorial, we will see the basics of extracting particles from a tomogram.

* Opening and visualizing a tomogram (dpreview, dtmview)

* Defining “models” attached to a tomogram.

* Clicking positions inside a tomogram using models

* Create subtomogram averaging projects on the clicked particles.
First of all we need a tomogram.

For this tutorial we will just create a small synthetic data set:

the class dTomogram incorporates several methods to handle tomographic data
In this case we just use a build in tool that creates a decoy tomogram.
With the default parameters, it will create 8 thermosome decoys floating in noise.

Using the stand-alone version of Dynamo (the Dynamo console)
you might need to adapt the syntax preceding the command with "\"

A directory has been created.
Besides the tomogram many auxiliary tools are also created, we just ignore them right now...

dtmshow is the simplest program to open tomograms and take a look on them.
With this syntax you will explore the tomogram “on the fly”, i.e., when you depict a section in the tomogram, the information will be read from disk.
In on-line modus (direct read from disk), z-slices are read much faster than y or x slices, because all the voxels belonging to a single slice are in contiguous positions in disk.
Another useful way of looking “on the fly” into tomograms in a simple way is with class `dSlice`

Plots generated with this class are fully embedded in regular Matlab graphical windows, but incorporate tools that are activated through clicking onto the image:

```matlab
>> dSlice phantom_dTomogram_temp/tomograms/tomogram_01.em
```

Matlab control for perspective

Click on the section to get a menu of actions:

* colormap

* restriction of range on x,y,z

* add new slices into plot

* move slices

New controls should pop for each clicked option
Both with command line or just interacting on screen it is relatively easy to create depictions of several orthoslices.
After having seen these two simple ways to peek into a volumetric file, we move now to some other tools which offer more options: dpreview (dynamo_preview) and dtmview (dynamo_tomoview).

Note that dpreview (exactly as dtmview) will register the tomograms that you visit into a “catalogue”.

We can ignore this by now, as these catalogues are not strictly needed for operating in single tomograms, they just make life much easier when coping with projects with many tomograms.

In this case, as no catalogue identifications were passed, Dynamo just created a default catalogue in the current disk location and put the tomogram inside this catalogue, assigning to it a default label.
Looking at single slices in tomogram:

Options to navigate inside a catalogue, choosing different tomograms not really needed right now

Selects the slice currently viewed

switch off to allow the use of 3d perspective to see the slice inside the volume
dpreview: Clicking particles

dpreview is not the most flexible tool for picking particles, but it offers some basic functionalities useful for a quick start/

1) Open the model pool
   The "model pool" is a set of models (Dynamo objects that describe sets of points) kept in memory at each given moment. Different GUIs in Dynamo can talk to the model pool

2) Select with [c] the position in the slice that you want to include in the active model.
   (use backspace to get rid of the last selected particle)

Select:
create a new model
After creating a model:

* there is a model in memory
* the active model is number 1

You get more options to operate onto the currently active model.
Now that we have a model (a "drawer" to put points), we can explore the tomogram.
You can also see the volume in perspective and slide the slice to click there the particles activates rotation

switch off to allow perspective view
You can edit the model to change the appearance of the markers:

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>marker size</td>
<td>20</td>
</tr>
<tr>
<td>marker symbol</td>
<td>o</td>
</tr>
<tr>
<td>marker color</td>
<td>0.46 0.79 0.97</td>
</tr>
<tr>
<td>line style</td>
<td>none</td>
</tr>
<tr>
<td>particle color</td>
<td>b</td>
</tr>
<tr>
<td>particle symbol</td>
<td>o</td>
</tr>
<tr>
<td>particle sketch le...</td>
<td>2</td>
</tr>
<tr>
<td>particle sketch le...</td>
<td>0</td>
</tr>
<tr>
<td>particle sketch le...</td>
<td>0</td>
</tr>
<tr>
<td>particle sketch c...</td>
<td>0.46 0.79 0.97</td>
</tr>
<tr>
<td>fill markers</td>
<td>1</td>
</tr>
</tbody>
</table>

Clicking on the name of a property produces a short description of its effect in the information window inside the model edit GUI.
To save the models, you probably want to change first the name assigned by the program. You can do this again in the model editor.

Now, you can save the active model into the disk catalogue (option is inside [Model Pool] menu tab).

The model has been stored as a model file that can be used later to extract the positions of the particles in the [Tomogram] menu tab you can check how many model files have been stored.

Note that you can check the status of the catalogue also from the command line with command: `dynamo_catalogue_manager (dcm)`: 

```
>> dcm -c default -i 1 -l -m
/home/casadie/work/dynamo/tutorials/click_particles/default/tomograms/volume_1/models/testing_model.omd
```
Picking particles with `dynamo_tomoview`

`dynamo_tomoview` works in a different way than `dynamo_preview`.

The point is that you use `dynamo_preview` to select a subvolume of your file and load it into memory. Once in memory you, `dynamo_tomoview` has a wider range of tools to navigate inside the loaded tomogram fraction, and pick particles or perform other manipulations.

You can manually set bounds in the area of interest in your tomogram.

Memory that you would consume if you download the chunk with current settings into `dtmview`.

Most probably you want to use some binning when inspecting the tomogram in memory.

You can set a maximum to ensure that you do not crowd your system's memory accidentally.
The fragment currently chosen can then be sent into dtmview. In this case of small tomogram we send the whole fragment (by default, catalogue information is also sent)
Three auxiliary views to see different simultaneous perspective of the scene. They will play different roles in different particle picking scenarios.

controls the extent of the shown scene

number of projected slices averaged in the main scene.
Model pool in dtmview

It follows the same logic than dpreview: there is a pool of models in memory that can be edited. These models can be then directly saved into disk, landing in catalogue positions.

The same model pool that appears in dpreview is accesible through dtmview. Thus, we find here the model that we had already defined.
An effective way of seeing which particles are already in the model is with these settings:

1) Set the depth of view to a big value, so you can see model marks far away from the slice.

2) Put the viewed slice in the bottom of the tomogram.

3) And project the whole tomogram.
While you can use the perspective view also here, the depth of globular objects while picking is best controlled using the auxiliary views.

This is best controlled with the “picking profiles” foreseen for different geometries:
If you select the option “isolated” particles under “Picking profiles”, some adjustments will occur. Some of them are just about the viewing: depth and viewed slice are set so that you can see at a glance on the main scene everything contained in the loaded chunk: all slices are projected.

But the most salient important feature here is that the mouse controls are tuned to pick 3d particles quickly:

1- with the secondary click you can locate all the views of the same particle projecting a single slice along x y z.

2- with the main mouse click you can then click particles depicted on a single projection slice.
Remember the motivation:

we are showing a main scene with full view of everything in tomogram:

This configuration is useful to see what you have, but prevents you from directly clicking on the scene, as the height in $z$ would be undetermined.
If you click with the secondary button here...

... you'll get locate three planes in different colors

... with the same color code in the auxiliary views.

But here, you can set the projected thickness to a single slice, so that you can directly click points in the depiction: the height will be defined unambiguously.
The point will land in the current model in pool.

The graphic windows that are connected with the pool will get updated automatically, for instance the main scene.

So, you can just use the main click on points defined on these slices.
a big “depth” ensures that all the clicked particles are visible in the main scene.
Getting cropped particles

The easiest way to prepare a data folder that can be used directly in the subtomogram averaging routines of Dynamo is the command `dynamo_table_crop`.

While you can consult the documentation (`help dtcrop` or `doc dtcrop`) to find out the syntax of this order when used through the command line, you can also use the GUI to get an user interface.

A temporary table file is generated automatically.

Indicate a target data folder, indicate a sidelength for the particle boxes, and press to start cropping the particles.
you can then navigate the extracted data set with the usual tools as `dynamo_data_browse`, `dynamo_data_slider` or `dynamo_gallery`. `ddbrowse` has a direct link from the particle extraction GUI.

remember that secondary clicking on the individual particles will give you the possibility of accessing them and their metadata.