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.

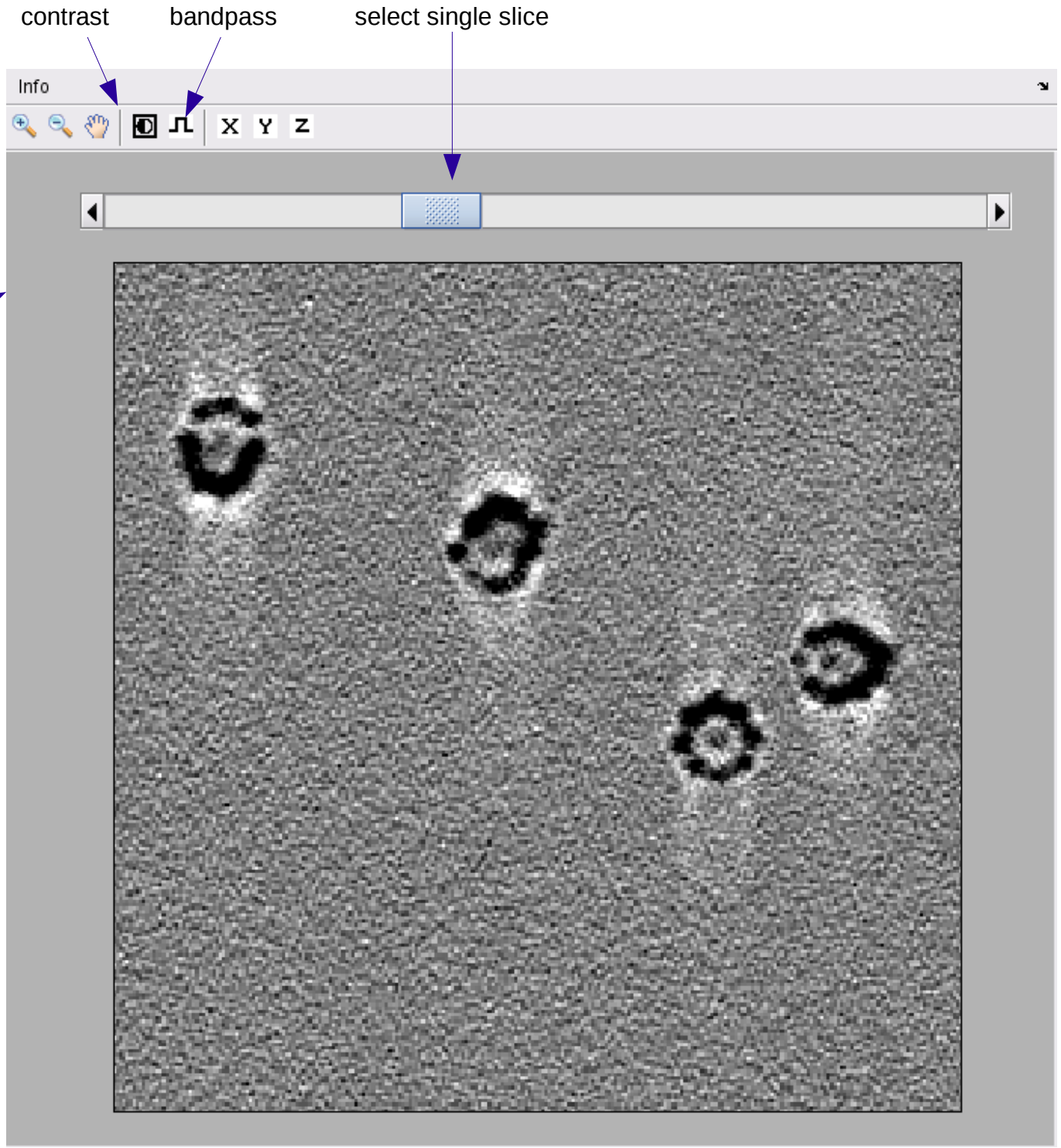
Using the stand-alone version of Dynamo (the Dynamo console) you might need to adapt the syntax preceding the command with "\"

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

```
>> dTomogram.createExample('l',256);
[dTomogram] Metadata accesses 8 particles.
[dTomogram] Compatibility check: not yet implemented.
[dTomogram] Volume 256 x 256 x 256 linked to object.
-----------------------------------------------------------
>> ls phantom_dTomogram_temp
coarse.tbl  models  tables  templates  tomograms  volumelists

>> dtmshow phantom_dTomogram_temp/tomograms/tomogram_01.em
Preloading file phantom_dTomogram_temp/tomograms/tomogram_01.em into memory.
>>
```

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 tomogrm, the information will be read from disk.

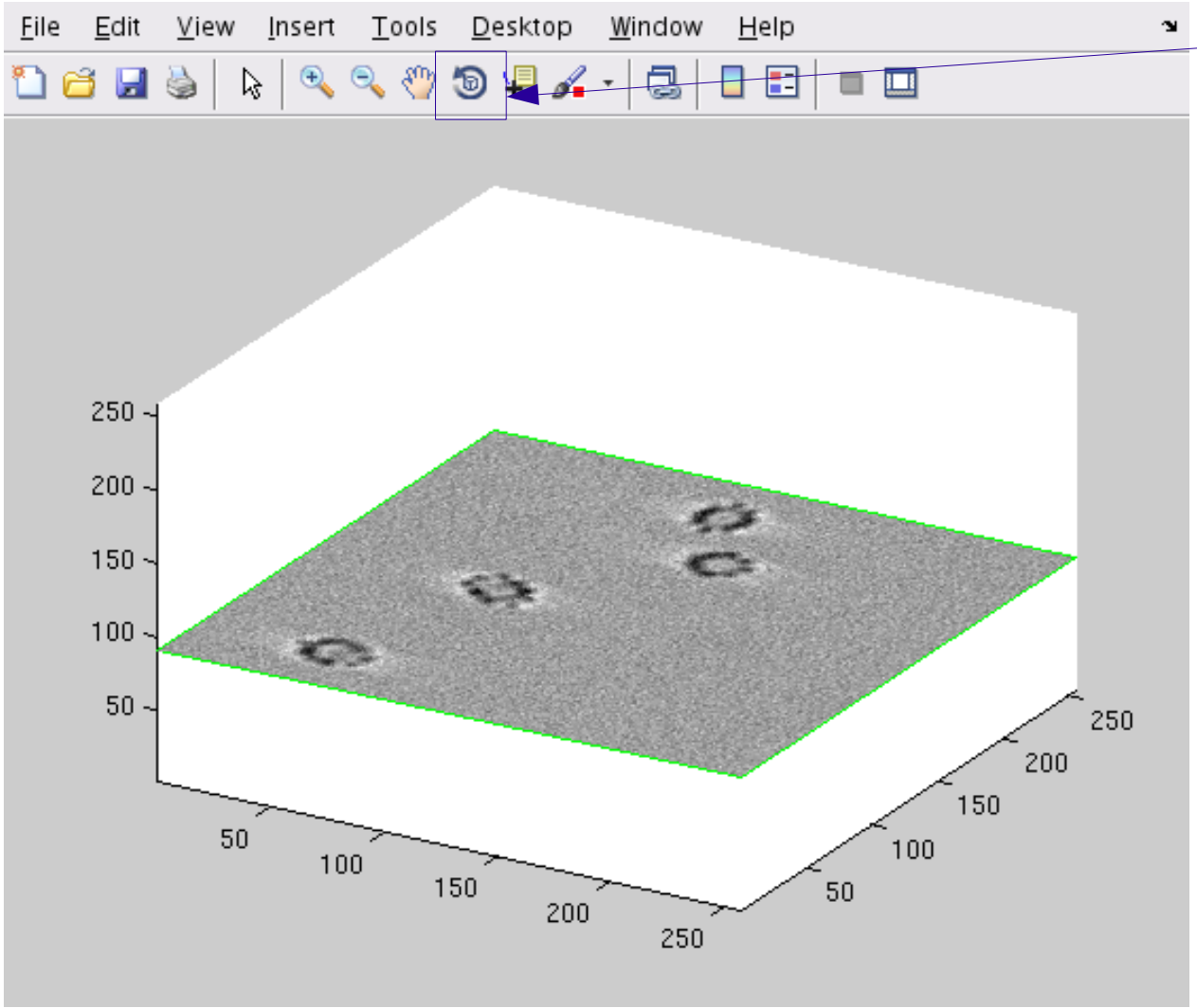


In on-line modus (direct read from disk), z-slices are read much faster than y or x slices, because all the voxels belonging to a single slice are in contiguous positions in disk.

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:

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

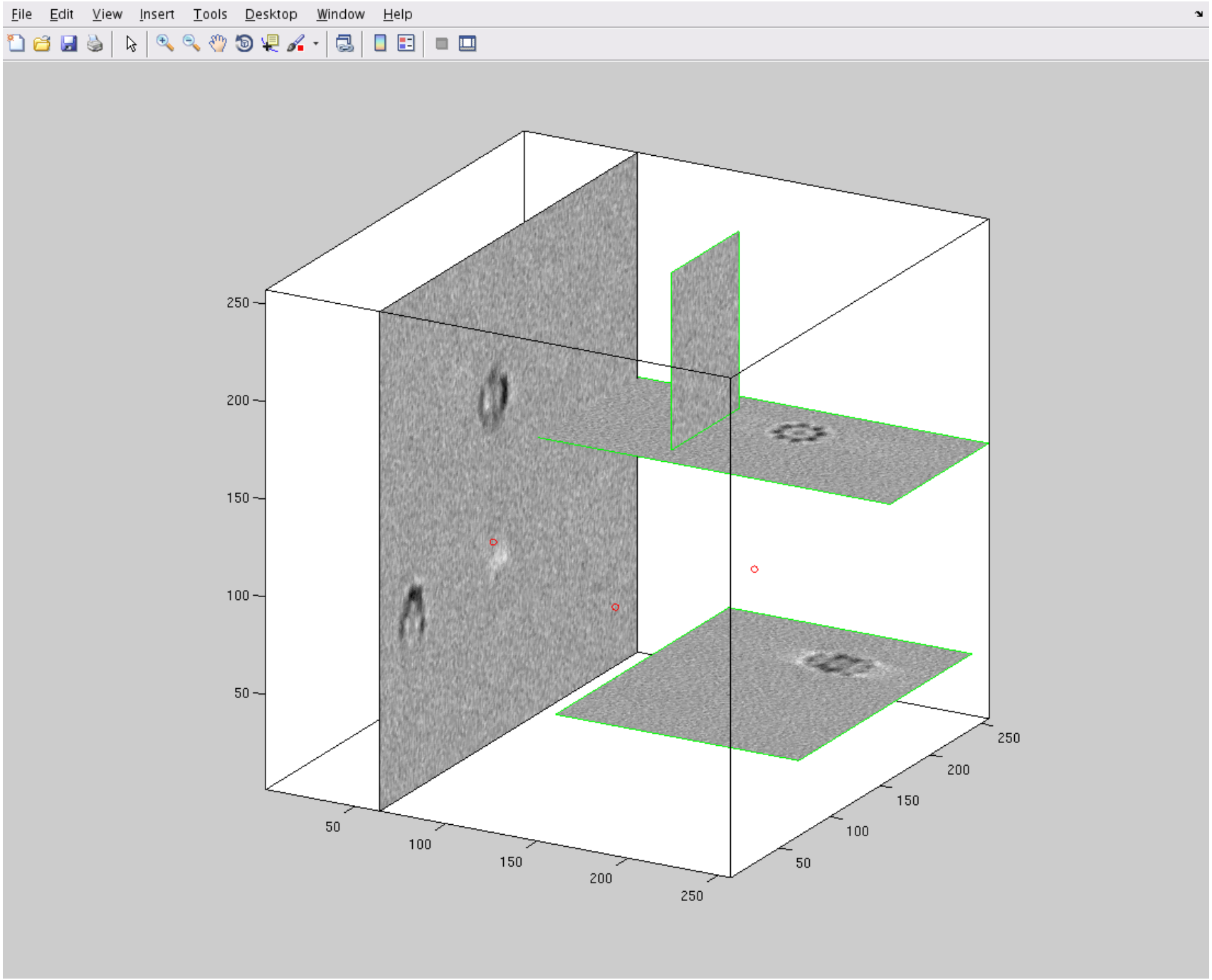


Matlab control for perspective

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)`

```
default.ctlg
>> dpreview phantom_dTomogram_temp/tomograms/tomogram_01.em
Database updated in memory (to 1 volumes) with volume "unlabelled_volume"

  In this folder the catalogue "default" is not defined
  A catalogue will be created, and your input file will be inserted as first t

 [identify]:
   Tomogram file NOT in catalogue.
     * file      : "/home/casdanie/work/dynamo/mtutorials/click_particles/phan
     * catalogue : "default"
    Entering file into catalogue "default"
    * assigned label : "unlabelled_volume"
    * assigned index : "1"
[dpreview] No catalogue specified as option for dpreview, using "default"
[read_header] File tomograms/tomogram.map does not exist.
Click on the name of a file or or catalogue entry to adjust the range.
>>
```

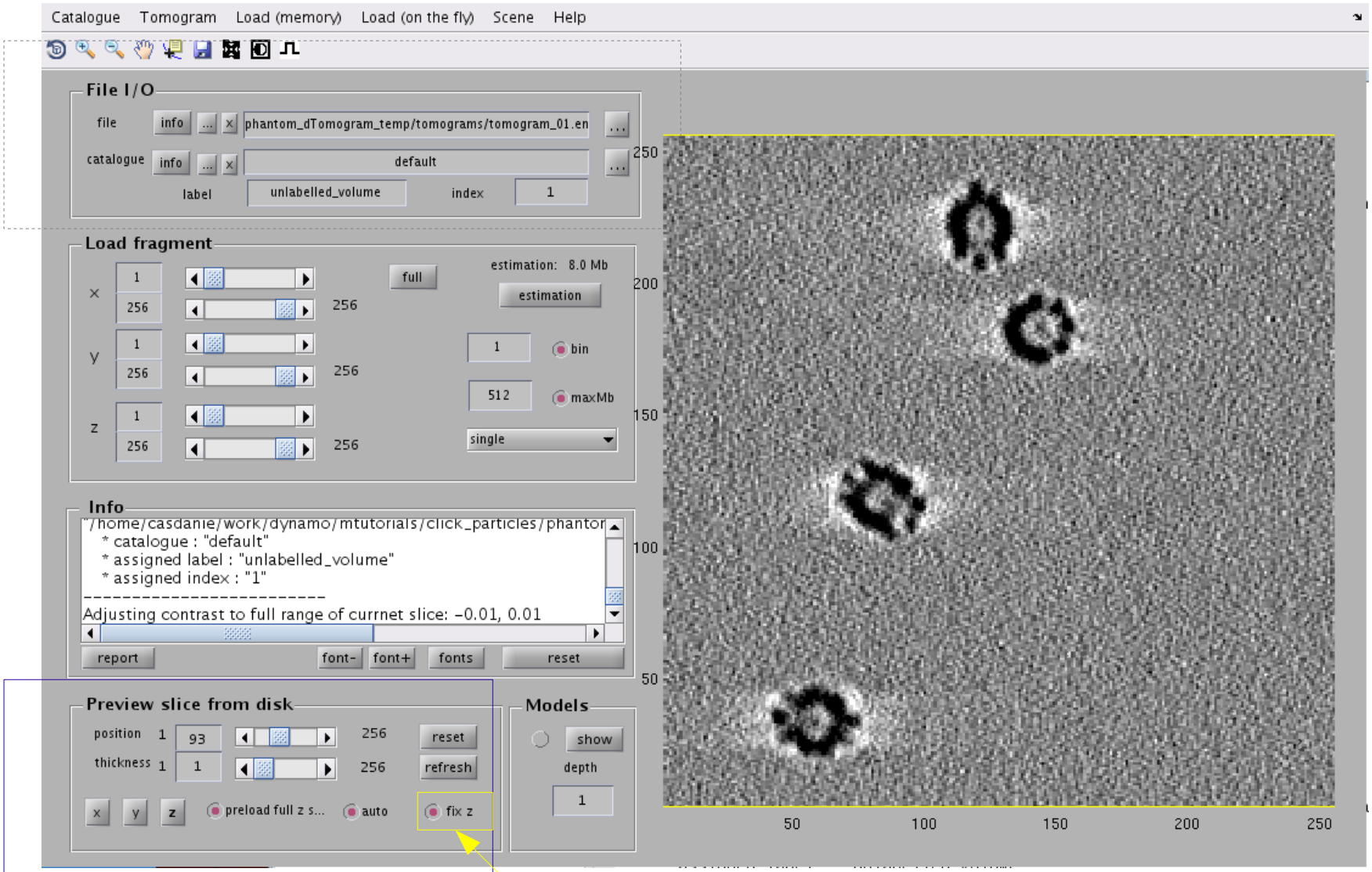
Note that dpreview (exactly as dtmview) will register the tomograms that you visit into a “catalogue”.

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 defautl 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/

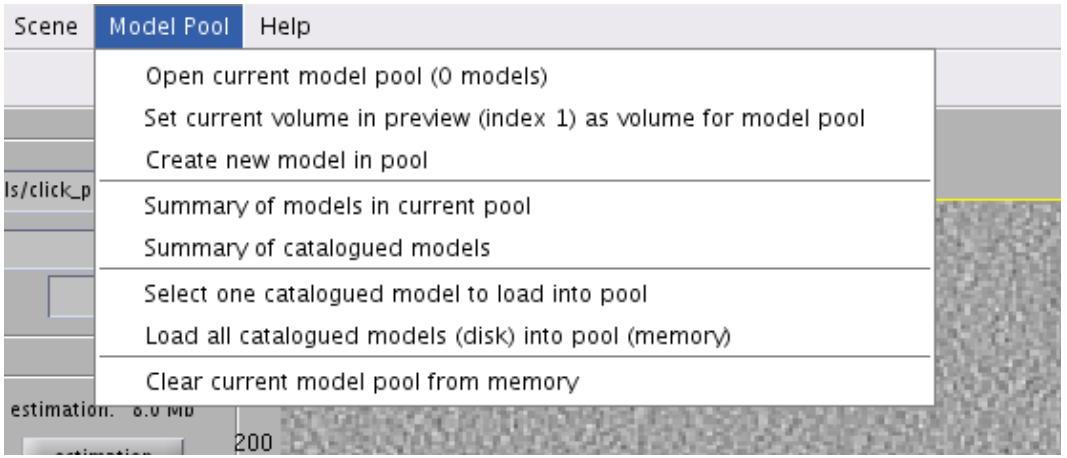
1) Open the model pool

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.

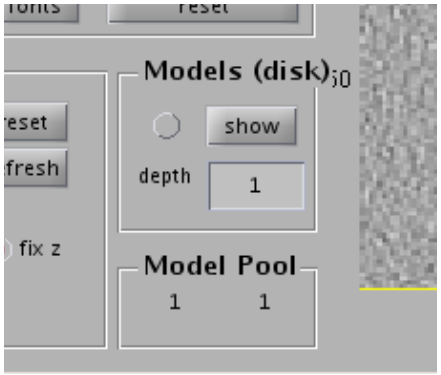
(use backspace to get rid of the last selected particle)

Select:
create a new model

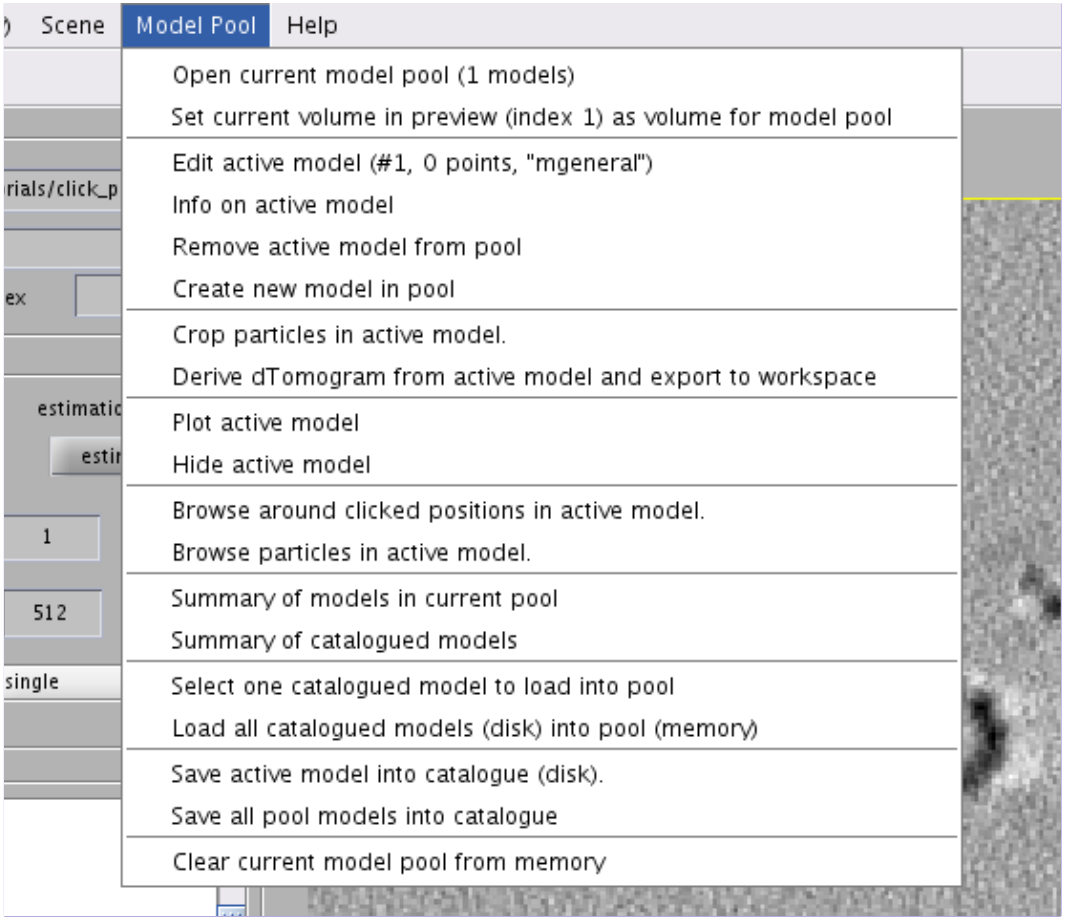


After creating a model:

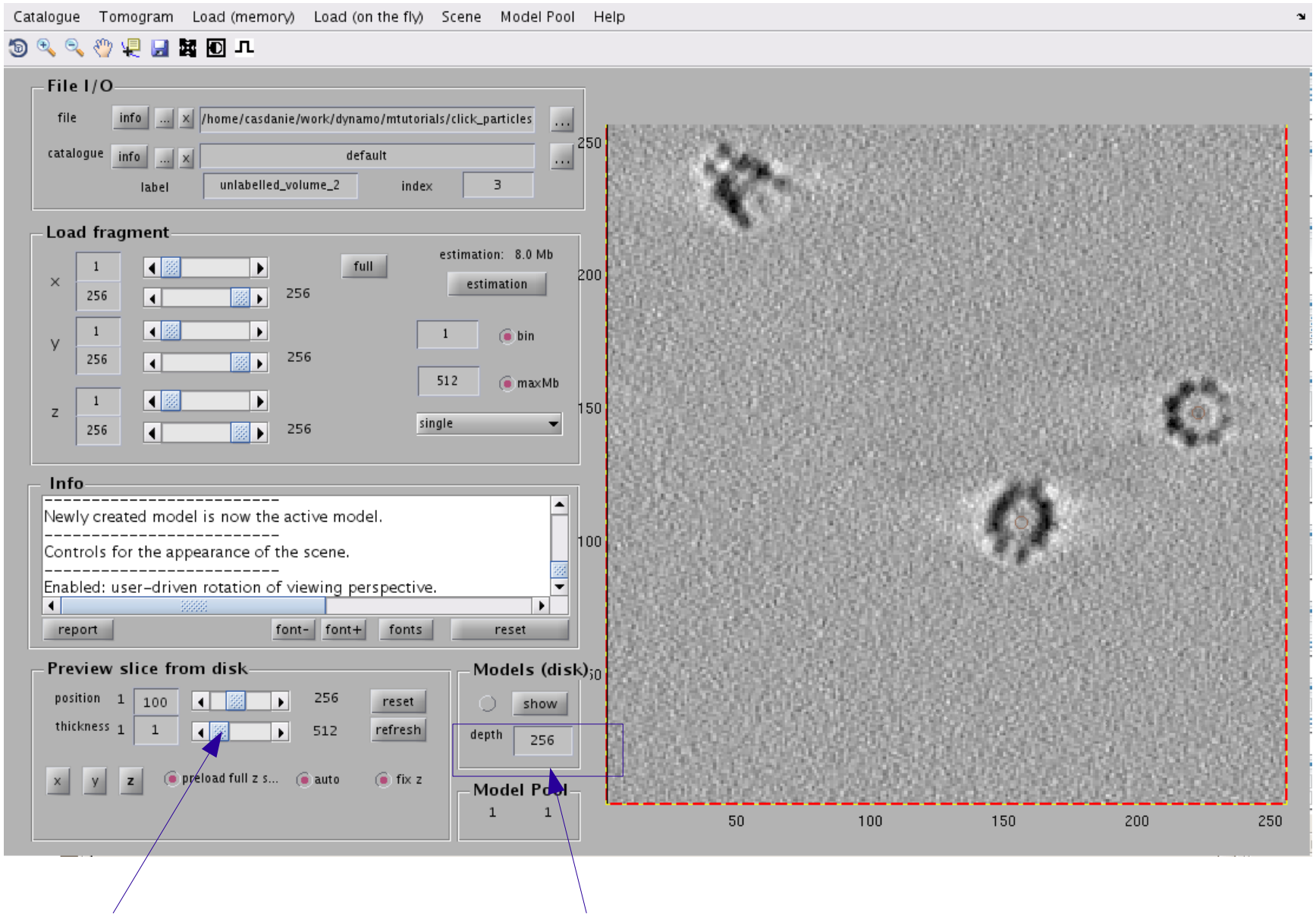
* there is a model in memory
* the active model is number 1



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.

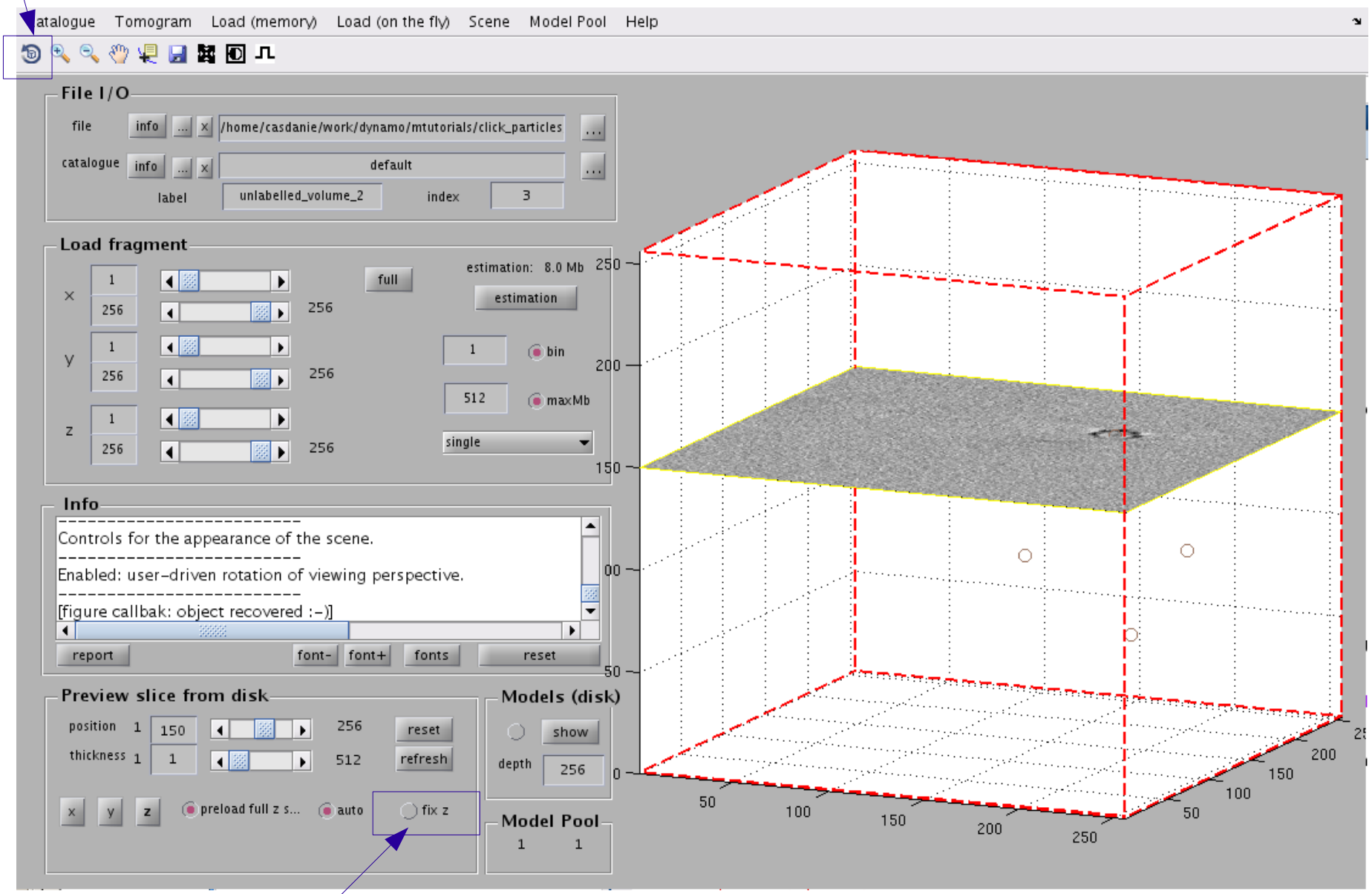


navigates the volume

sets how far away from the slice can be the model markers and still be visible

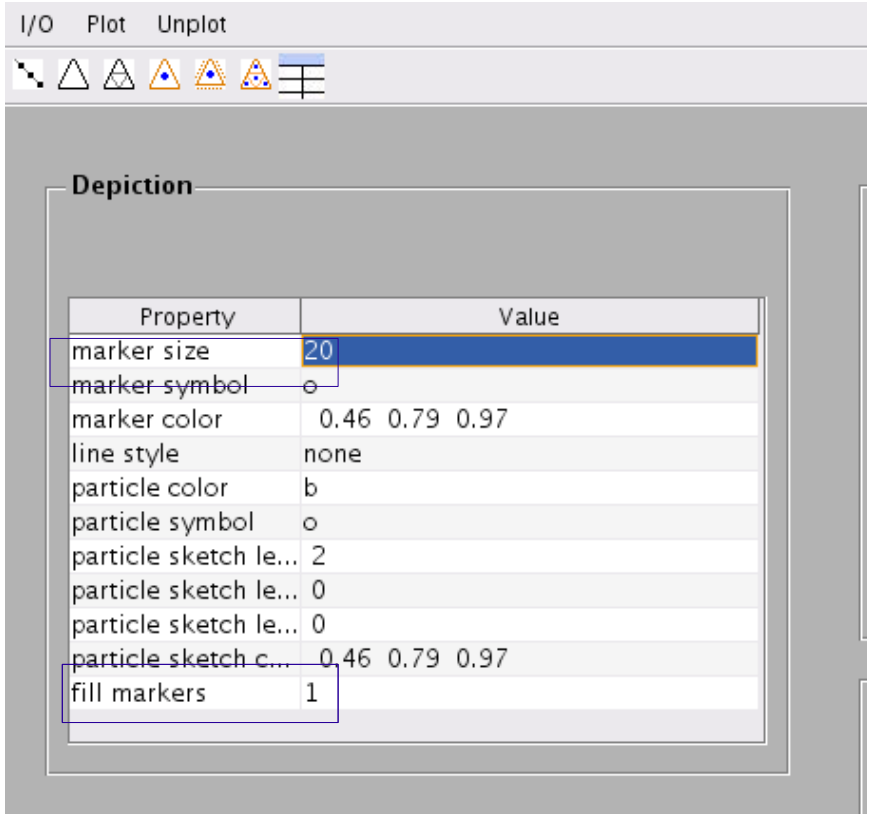
You can also see the volume in perspective and slide the slice to click there the particles

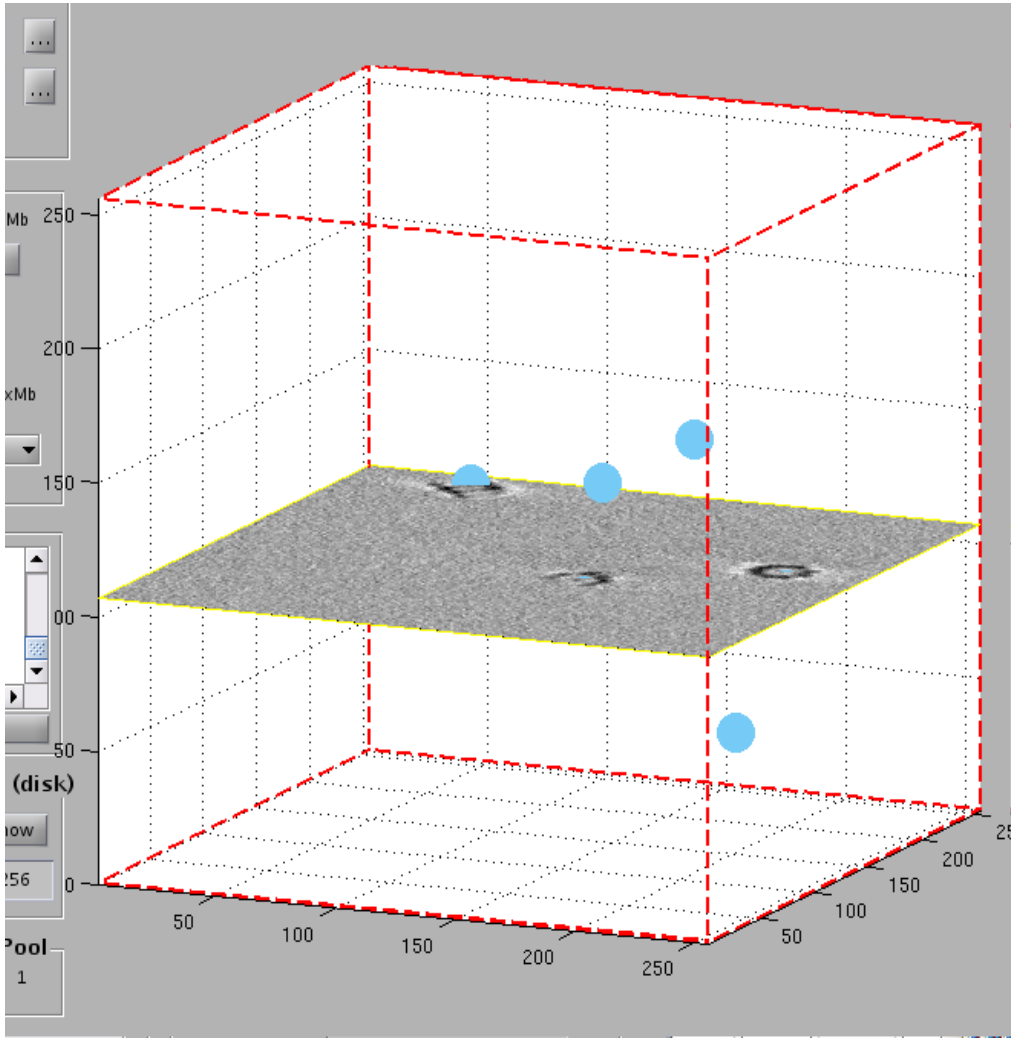
activates rotation



switch off to allow perspective view

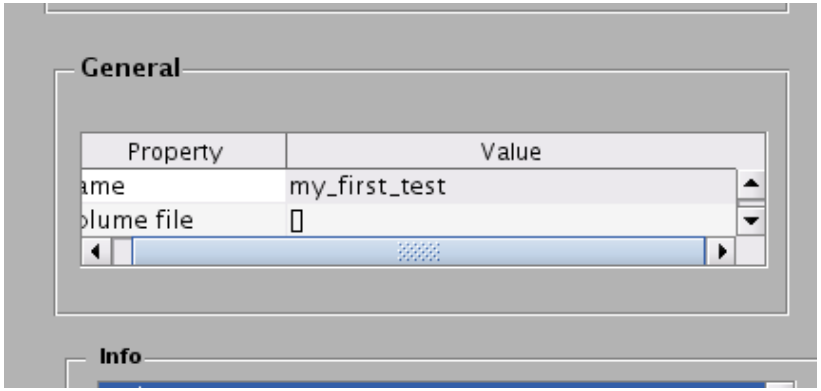
You can edit the model to change the appearance of the markers:





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.

the "default" catalogue ("c") was automatically created

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

we choose the volume index ("i") 1 inside the chosen catalogue

we want to list ("l") the models ("m") inside the chosen volume

```
>> dcm -c default -i 1 -l m
/home/casdanie/work/dynamo/mtutorials/click_particles/default/tomograms/volume_1/models/testing_model.omd
>>
```

Picking particles with `dynamo_tomoview`

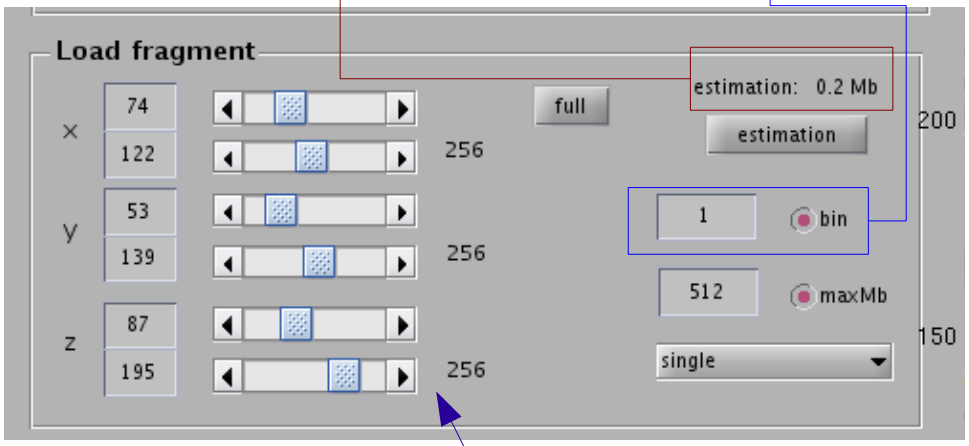
`dynamo_tomoview` works in a different way than `dynamo_preview`.

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.

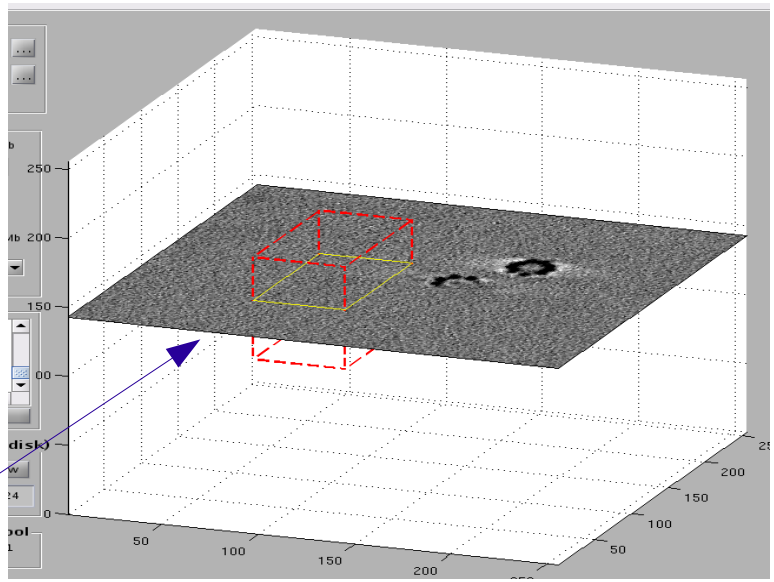
most probably you want to use some binnig when inspecting the tomogram in memory

you can set a maximum to ensure that you do not crowd your system's memory accidentally.

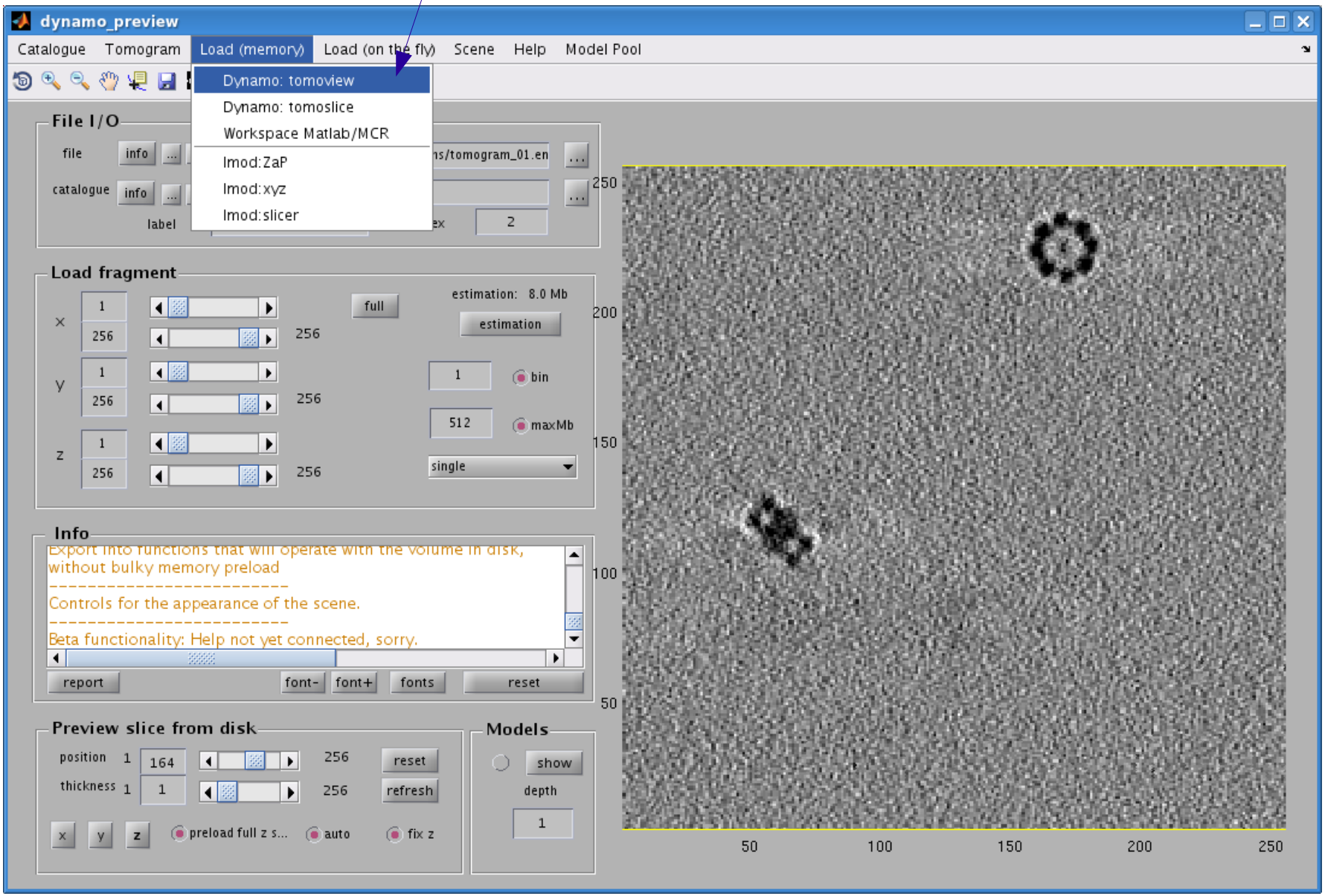
Memory that you would consum if you download the chunk with current settings into dtmview



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

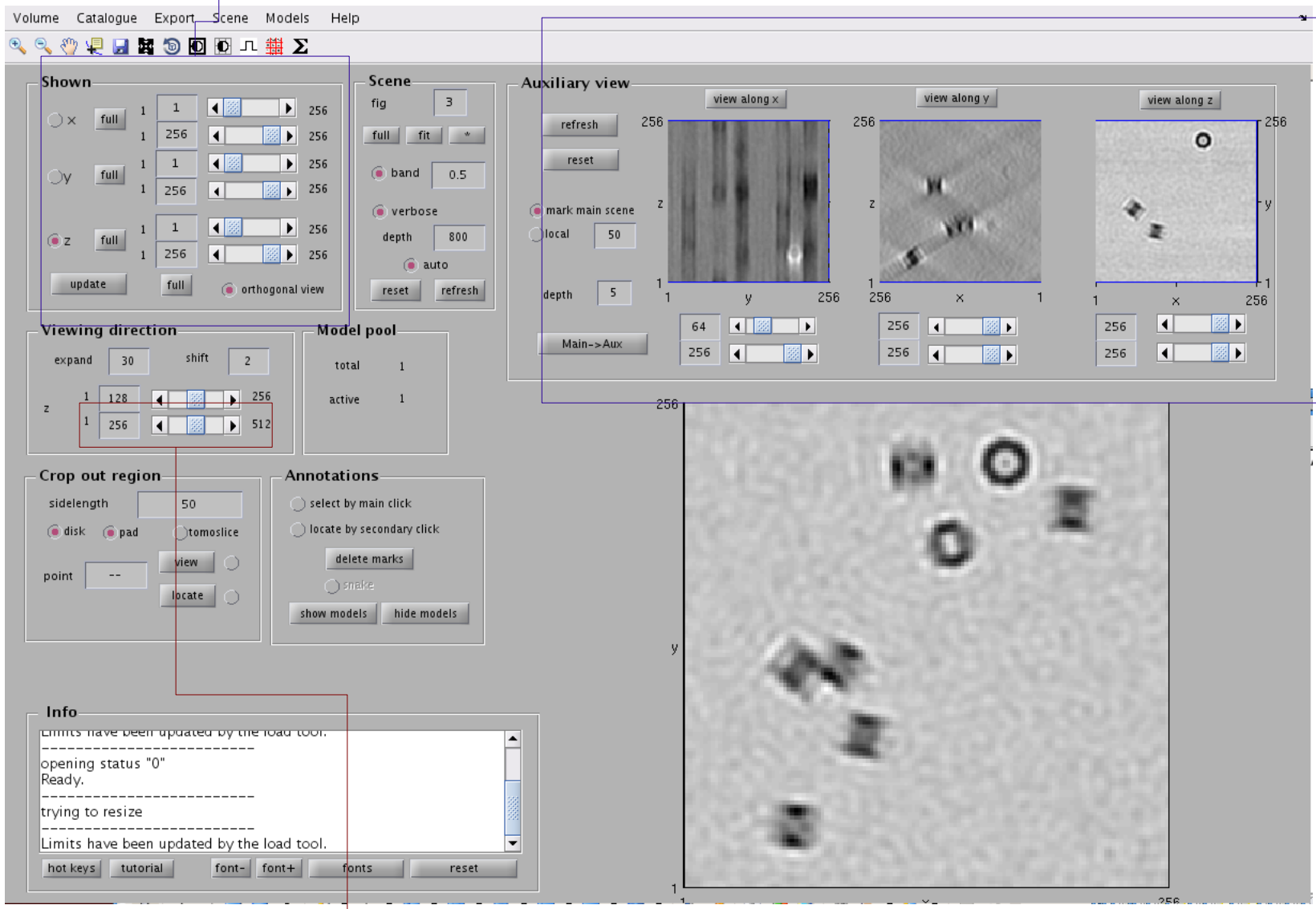


The fragment currently chosen can then be sent into `dtmview`.
In this case of small tomogram we send the whole fragment
(by default, catalogue information is also sent)



Three auxiliary views to see different simultaneous perspective of the scene. They will play different roles in different particle pciking scenarios.

controls the extent of the shown scene

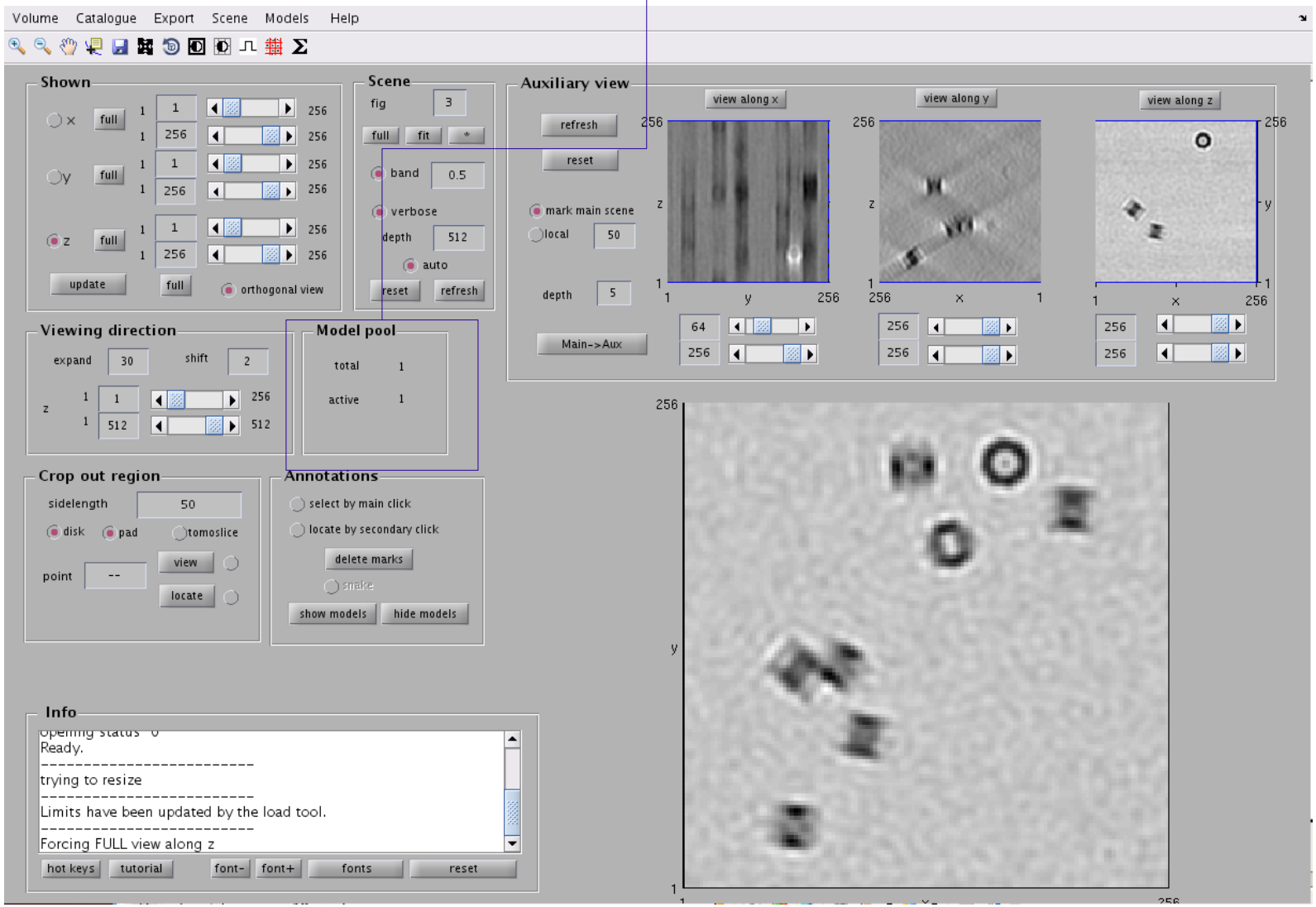


number of projected slices averaged in the main scene.

Model pool in dtmview

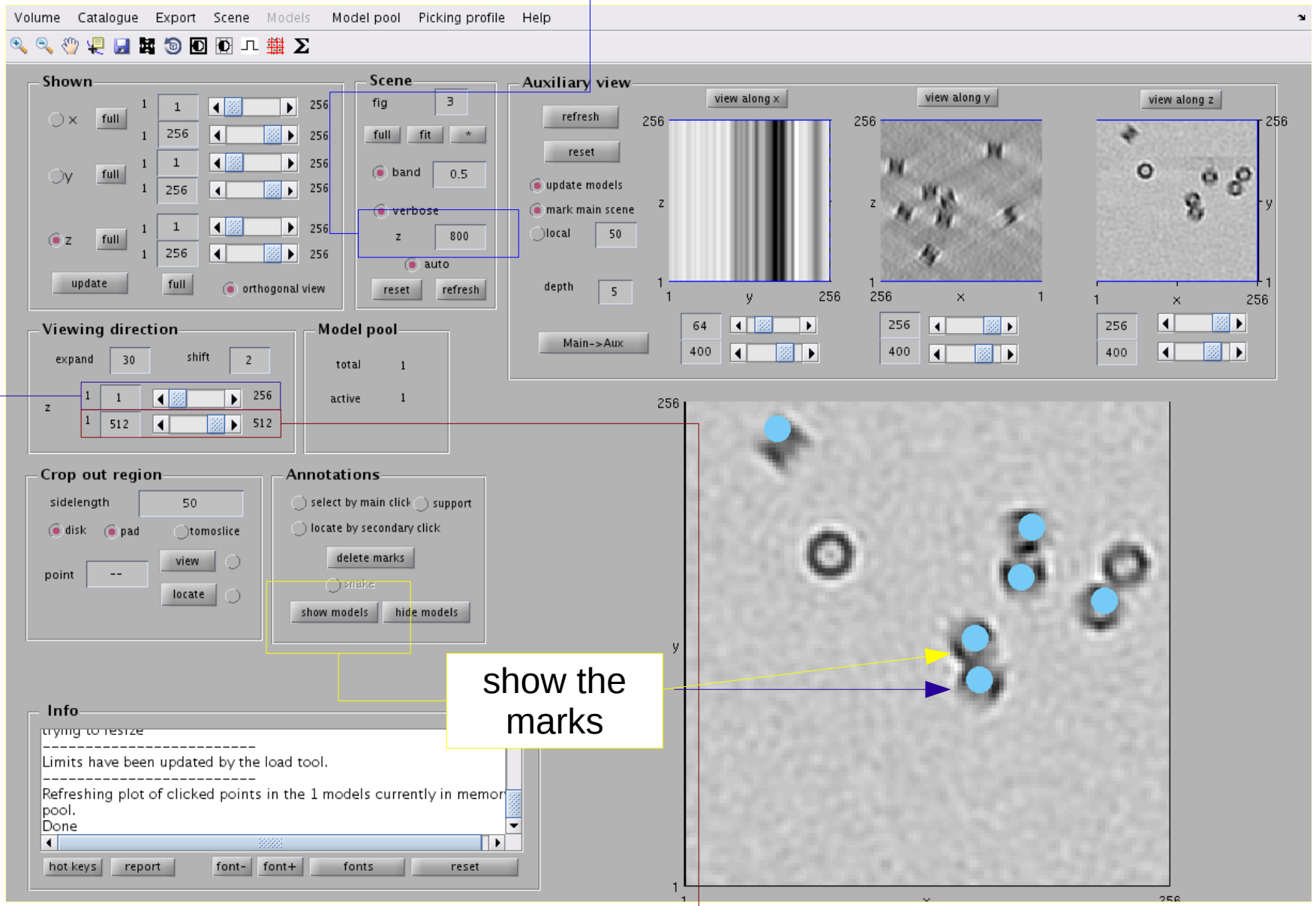
It follows the same logic than `dpreview`: there is a pool of models in memory that can be edited. These models can be then directly saved into disk, landing in *catalogue* positions.

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 fare away from the slice

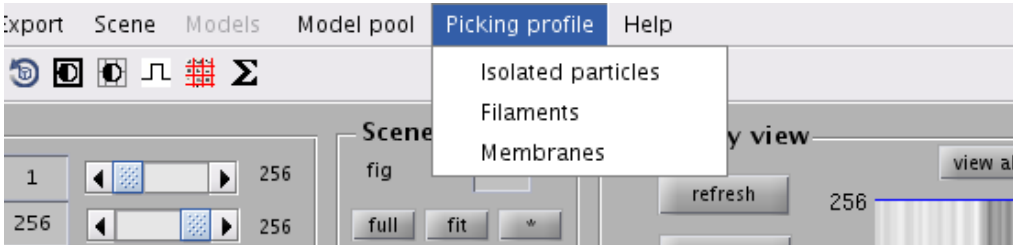


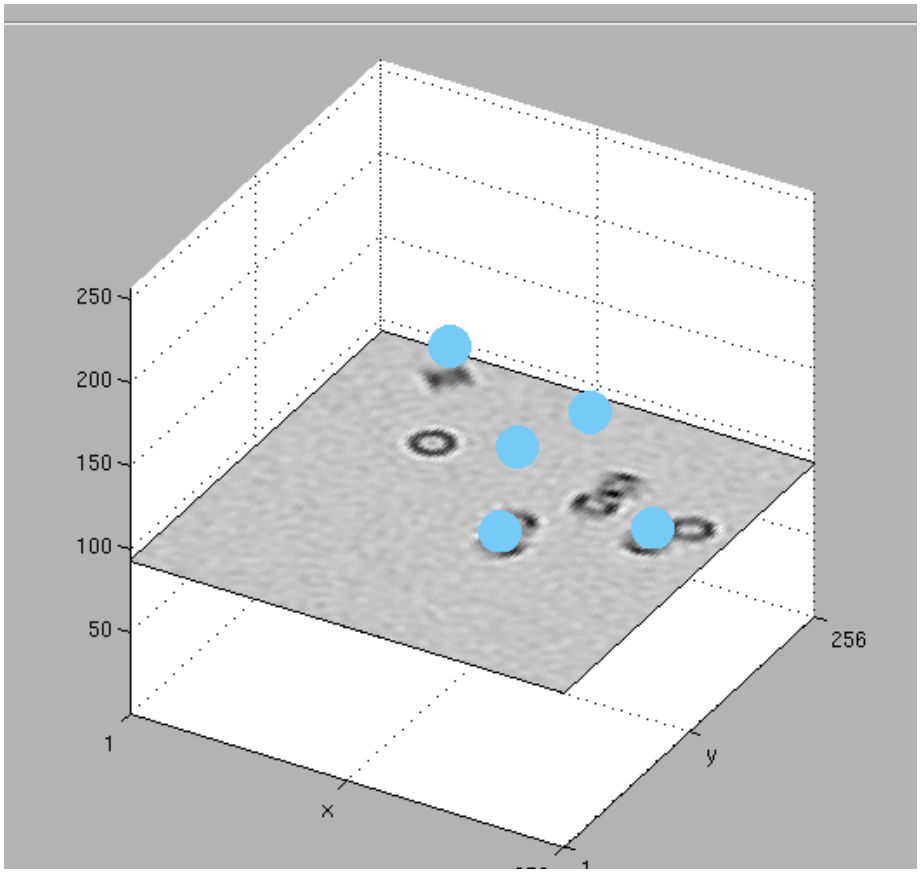
2) Put the viewed slice in the bottom of the tomogram

3) and project the whole tomogram

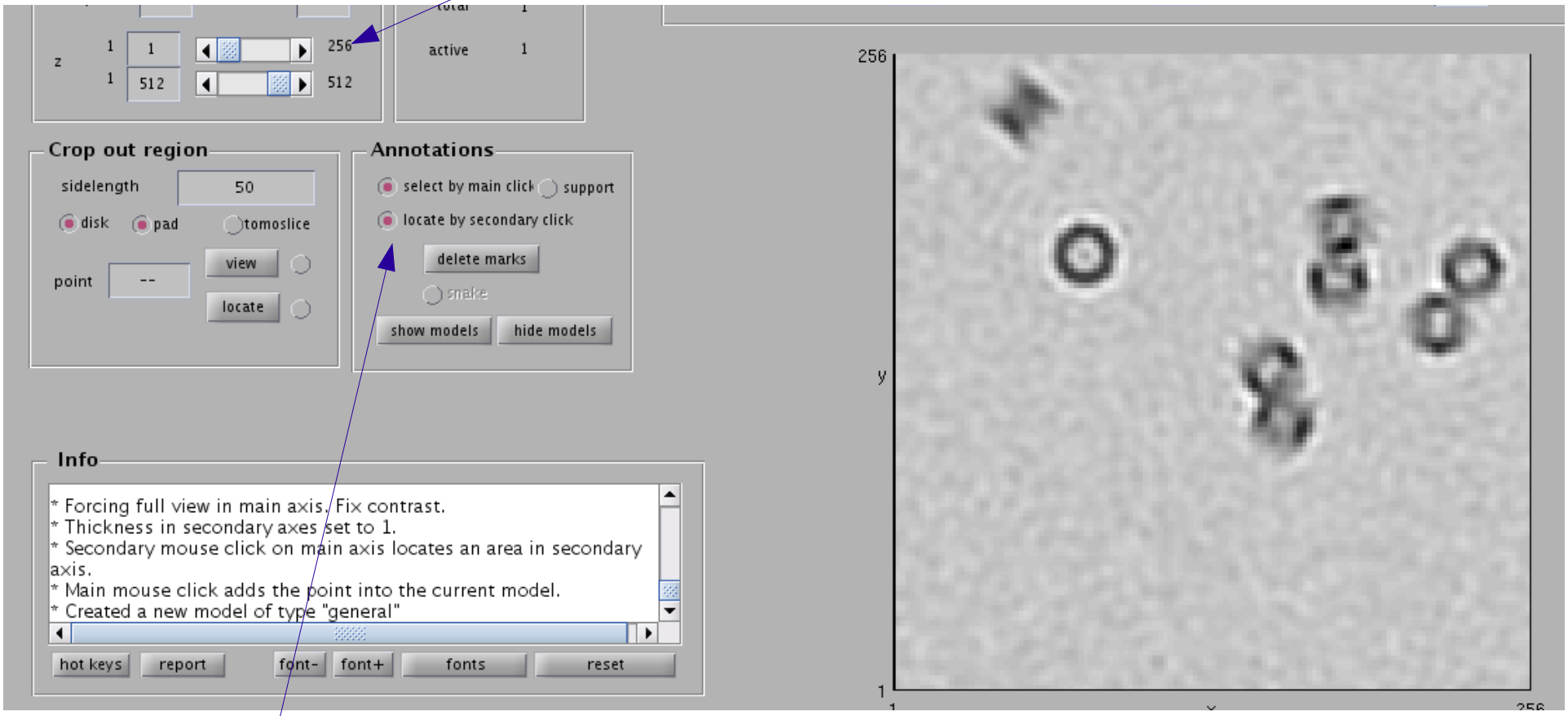
While you can use the perspective view also here, the depth of globular objects while picking is best controlled using the auxiliary views.

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.



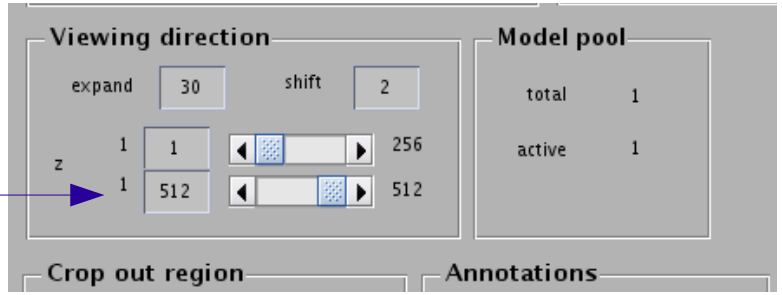
But the most salient important feature here is that the mouse controls are tuned to pick 3d particles quickly:

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

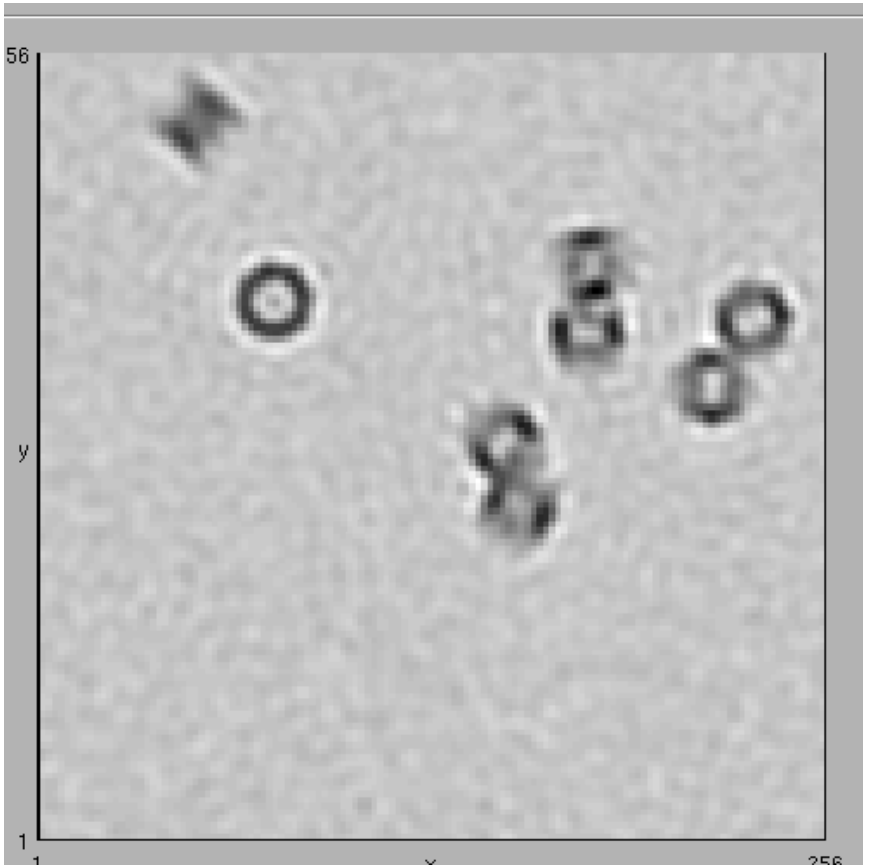
2- with the main mouse click you can then click particles depicted on a single projection slice.

Remember the motivation:

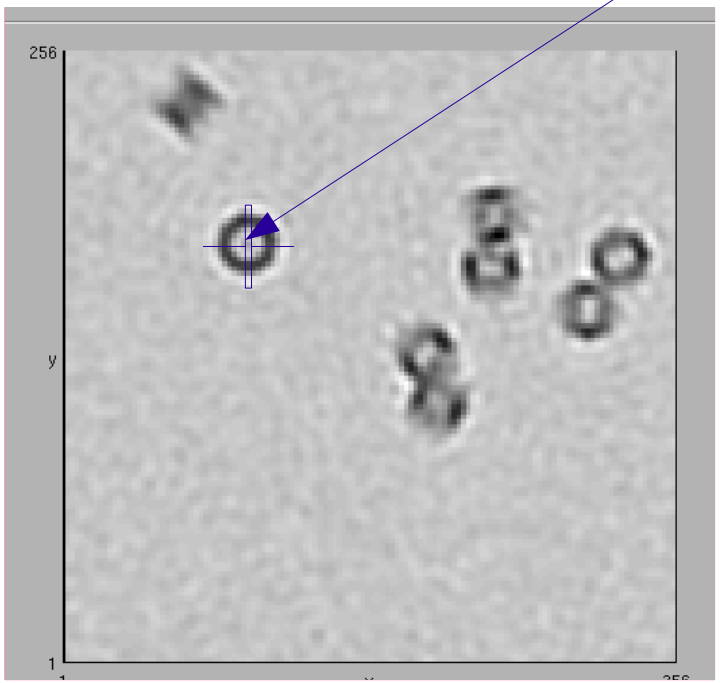
we are showing a main scene with full view of rverything in tomogram:



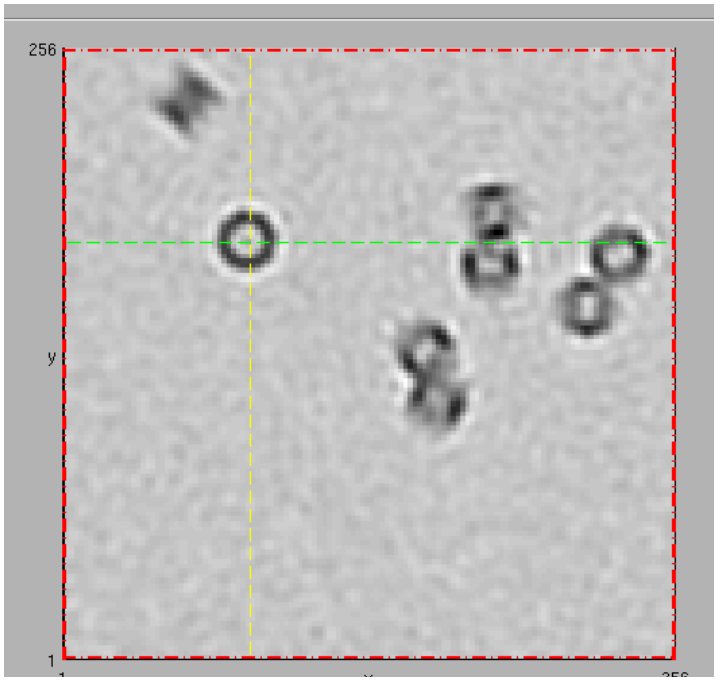
This configuration is useful to see what you have, but prevents you from directly clicking on the scene, as the height in z would be undetermined.



If you click with the secondary button here...

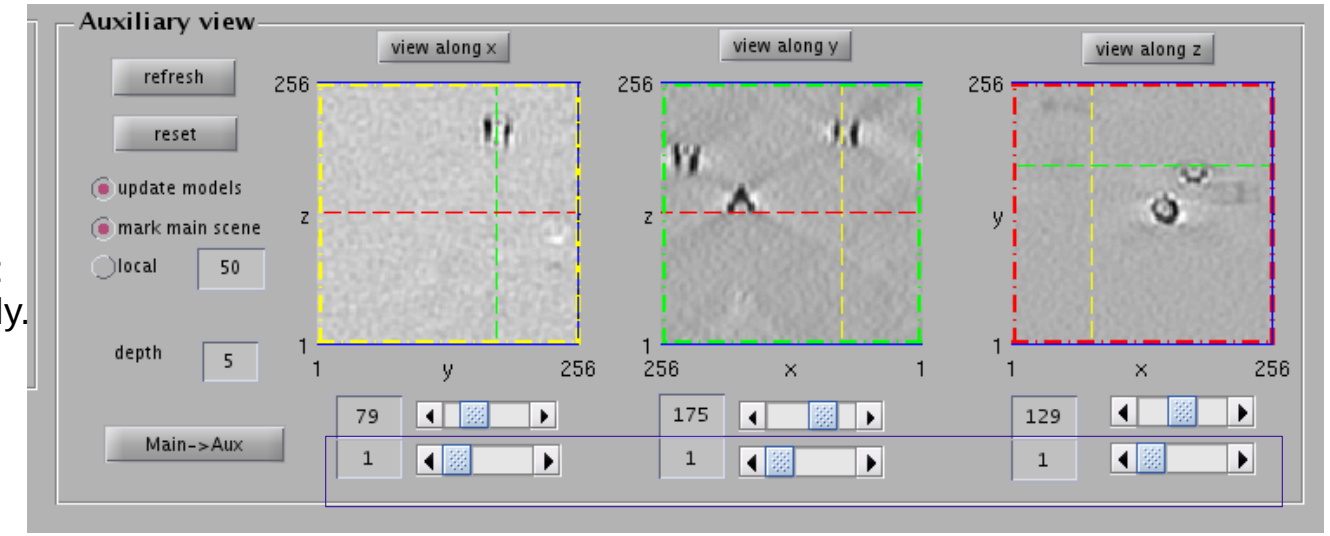


... you'll get locate three planes in different colors

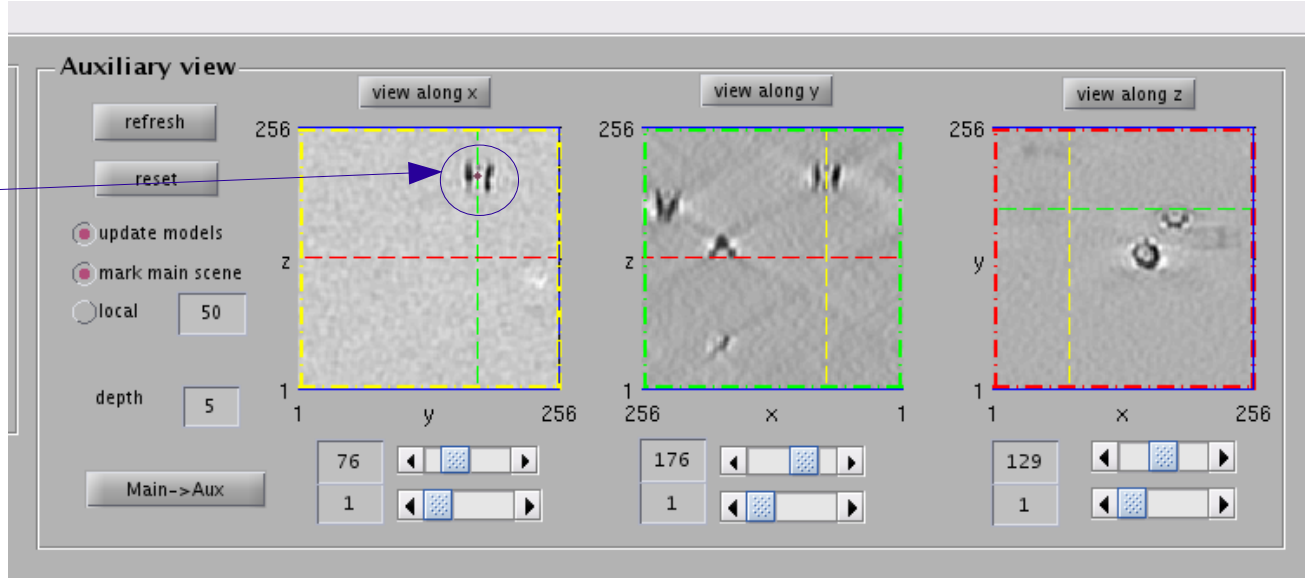


... with the same color code in the auxiliary views....

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.

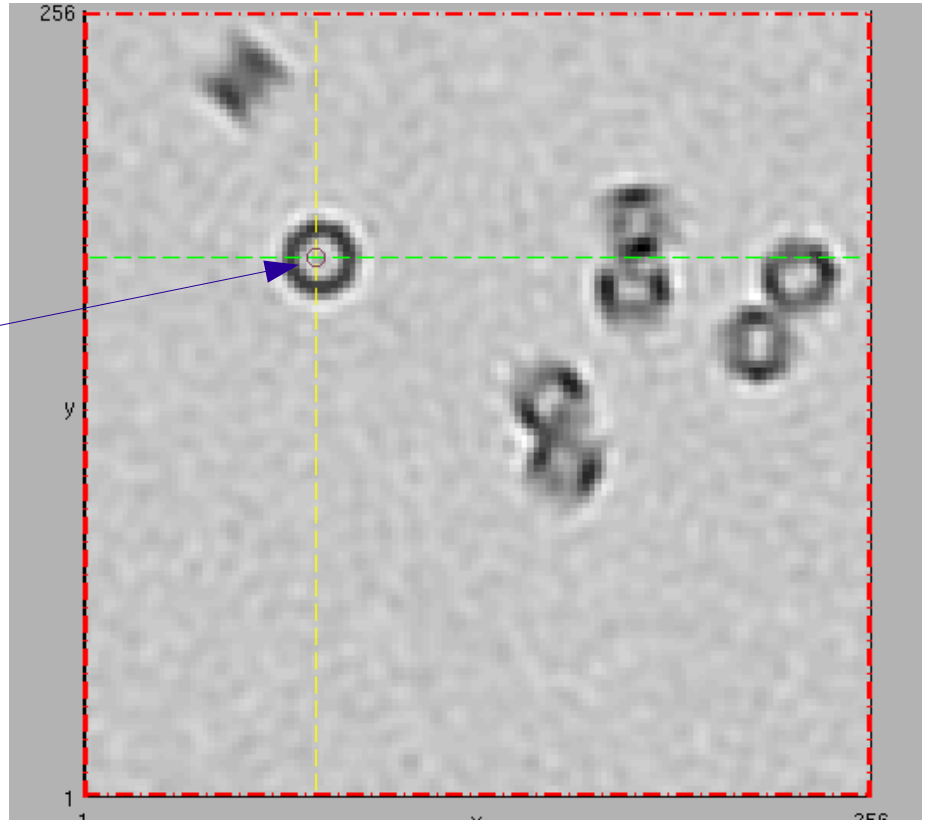


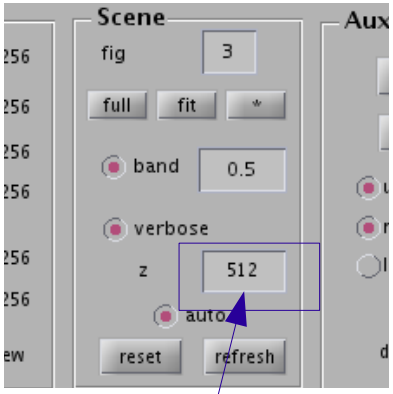
So, you can just use the main click on points defined on these slices.



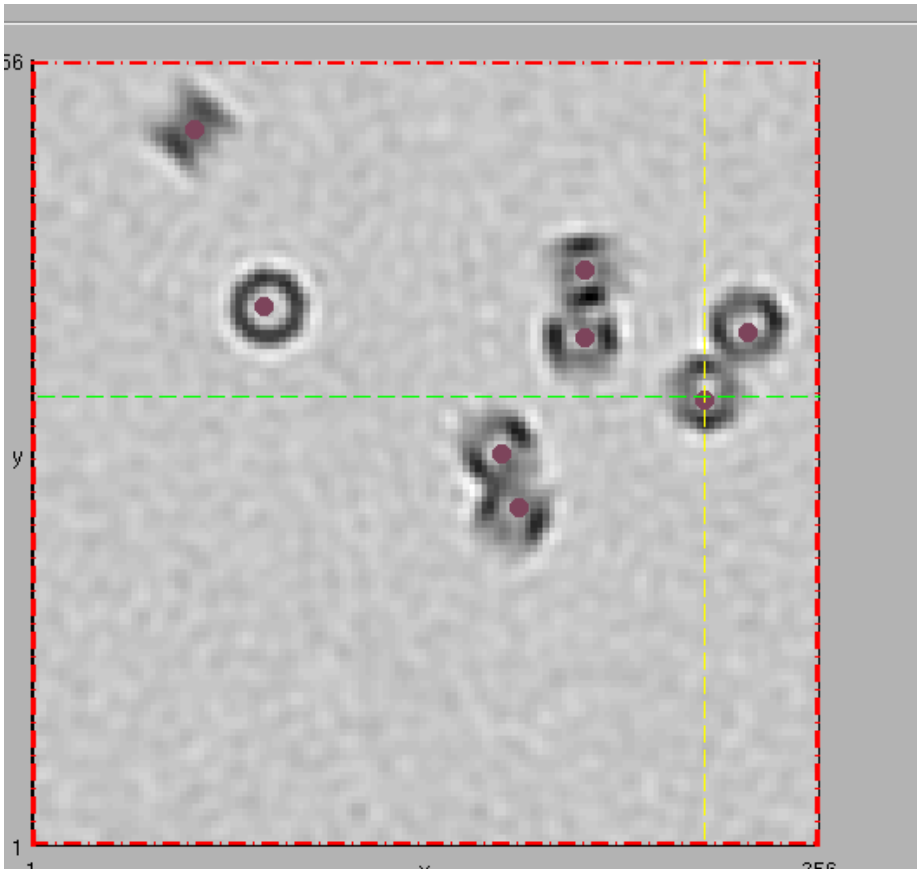
The point will land in in the current model in pool.

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





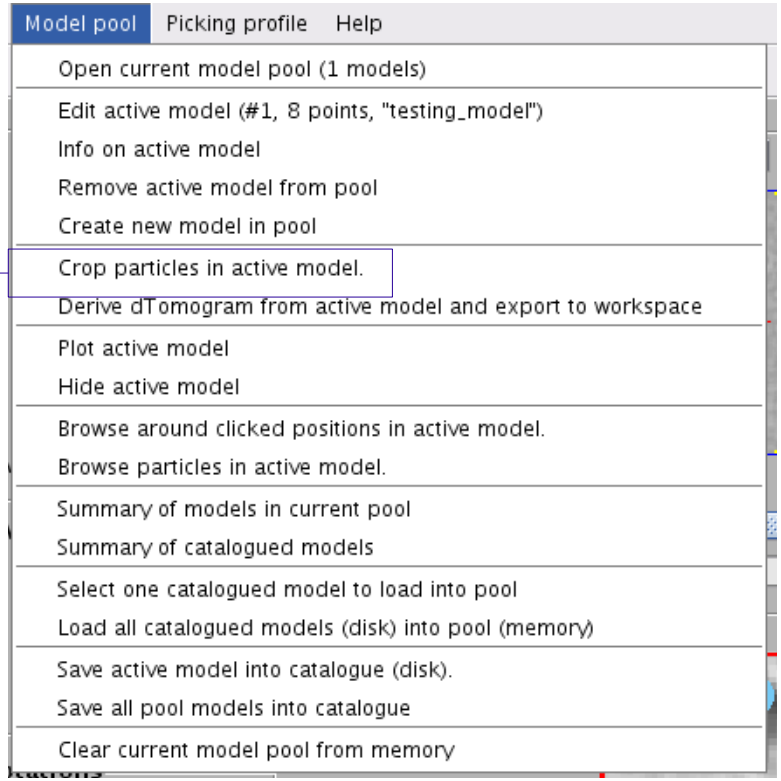
a big “depth” ensures that all the clicked particles are visible in the main scene.



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.

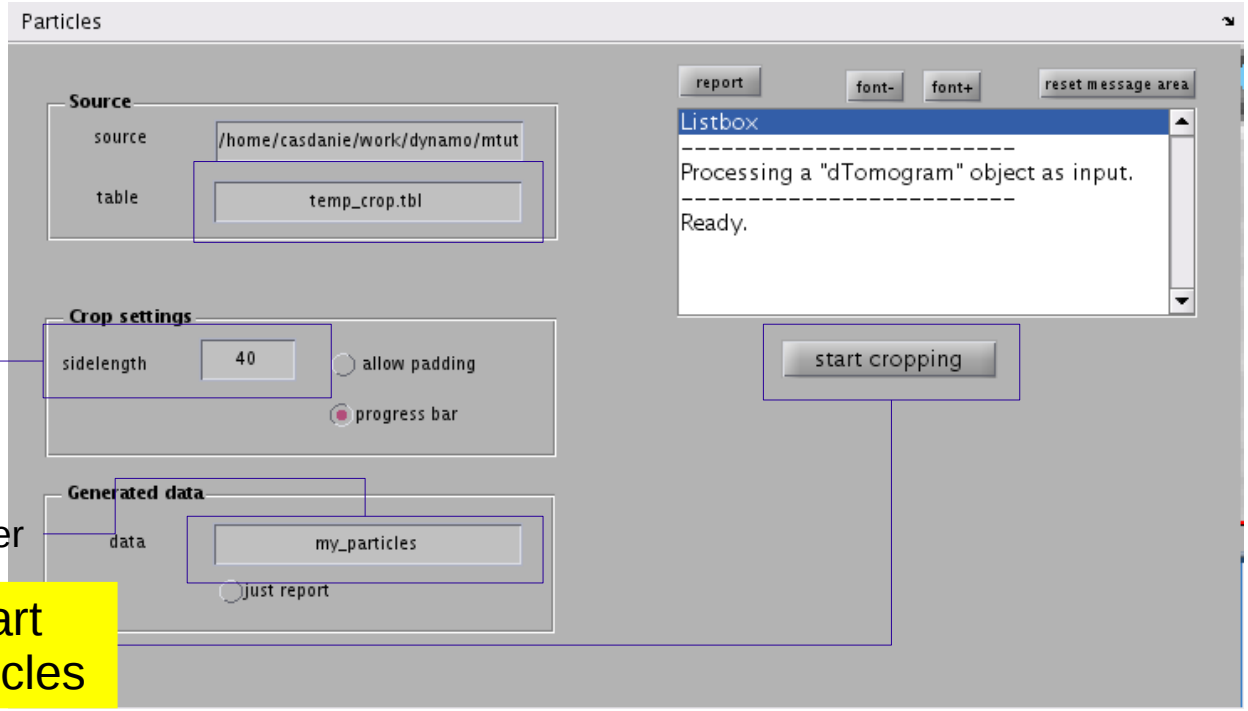


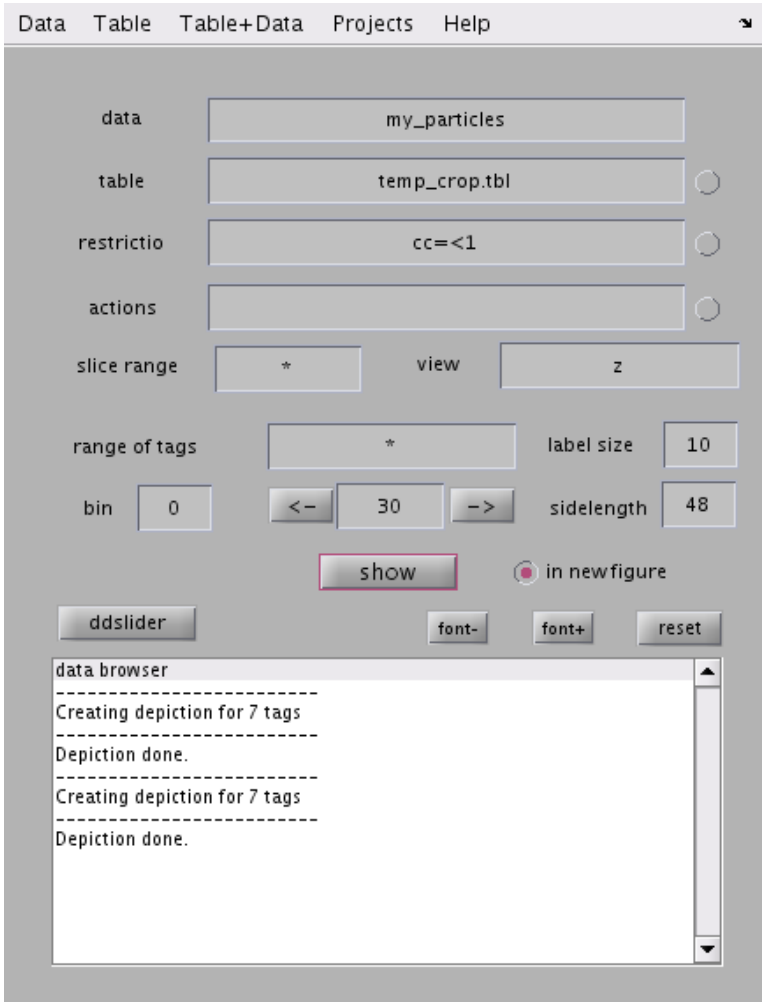
A temporary table file is generated automatically.

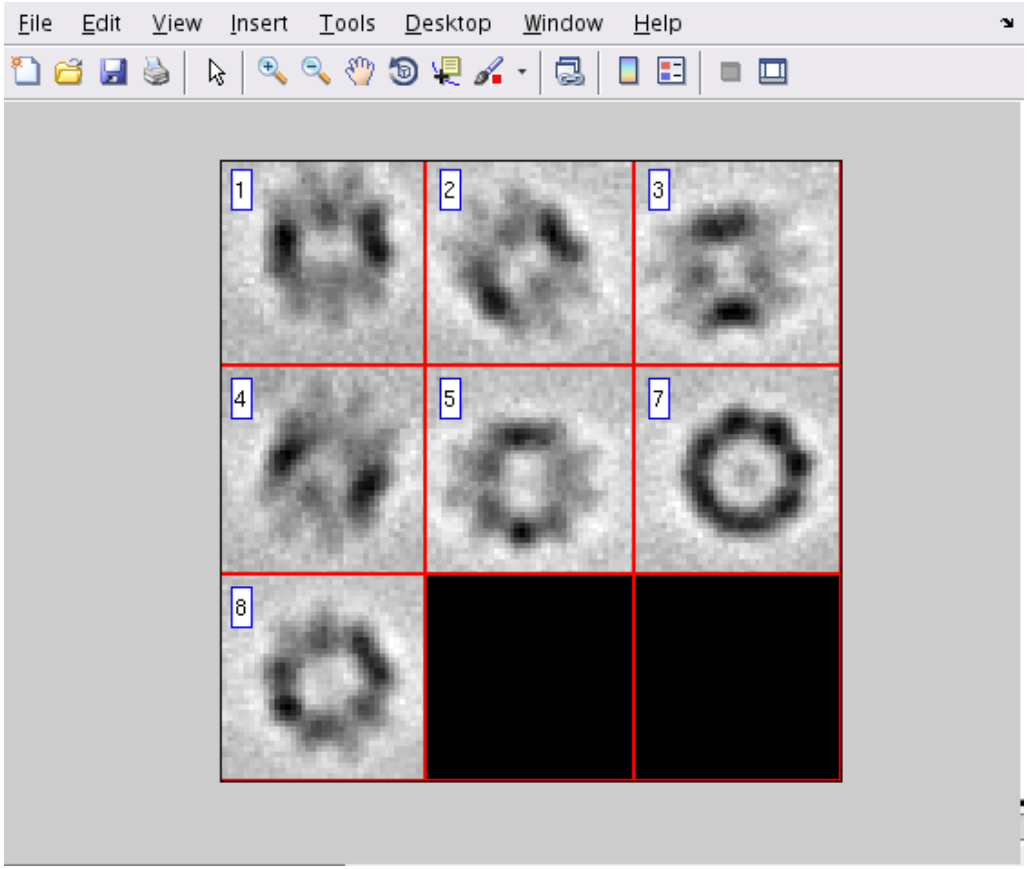
indicate a sidelength for the particle boxes

indicate a target data folder

and press to start cropping the particles







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

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