3d modeling with the MRI Object Modeling Workbench

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Step 1 – Renaming images

The 3d input image must be series of tiff files. To not mix up the order of the images the files should be numbered in a format like this:

```
rat001.tif
rat002.tif
...
rat408.tif
```

If for example the original image names are like this:

```
lame7-1.tif
lame7-3.tif
lame7-4.tif
lame8-1.tif
```

the images should be renamed. This can be done with the freeware tool Lupas Rename. Lupas Rename can be found at:

```
http://rename.lupasfreeware.org/download.php
```

Copy the original series into a new folder and rename the images using Lupas Rename.

Step 2 – Loading the renamed images

Run MRI Cell Image Analyzer and open the Object Modeling Workbench by clicking the « OMW » button.



Choose « open series » from the « File » menu of the OMW. This will open a list editor. Press the « add button » of the list editor to open a file dialog. Go to the folder containing the renamed images and select all of them, then press the open button. Close the list editor window. You can now display images of the series by clicking on a row in the table at the left. You can scroll the list up and down using the scroll bar on the right side of the list.

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Open the toolbox from the MRI Cell Image Analyzer launcher window.

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Click on the magnifying glass in the tool box. You can now zoom in by left-clicking into the image and zoom-out by right-clicking. You can move the image in the workspace by using the scrollbars on the bottom and on the right side.



Step 3 – Converting the series to greyscale

In the OMW select Process>apply operation... Select the operation « convert image type » in the dialog window. Press the button « apply operation to series... ». In the file dialog window create a new folder « 8bit », enter the newly created folder and press the « save » button.





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When the convertion finished load the converted images into the OMW using File>open series... Change the selected image to see a greyscale image.

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Step 4 – Calculate alignments

Run « Process>calculate translations quickly » to align the images in the series. A dialog will ask for the step width. The lower the step width, the longer the calculation will take and the better the result will be. Press the « ok » button. The translations will be saved into a text file. Press the « save » button in the file dialog and wait until the calculation finished. The calculation may take a long time.



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After the calculation finished, open the translations in the OMW using « File>open translations... ». In the file dialog select the file translations.txt and press open.



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The translation in x and y direction and a score will be displayed for each slide. The lower the score the better the alignment.

Step 5 – Manually correct the alignments

Select the first slice and click on the red button on the tool box. The image will now be displayed red instead of grey. Selet the second slice and click on the green button in the toolbox. The second image will be displayed in green. Right click on the second list entry and select display options. Set the opacity of the second slice to 50 percent. The image will become transparent. Now select the two first images. Click on the first list entry, then shift-click on the second. You see now an overlay of the two images.

If the alignment is not satisfactory you can now manually correct it. First click one time in the empty space around the image or directly in the image. If you click in the image select a tool that doesn't change the image display, like for example the rectangular selection tool in the toolbox. You can now use the arrow keys on your keyboard to move the second image around. Notice the the image accelarates while you keep an arrow key pressed. The translation and the score of the actual position are displayed on the bottom of the MRI Cell Image Analyzer window.

When you found the best alignment press ctrl+enter. You will be asked if you want to accept the alignment for all following slices. Answer « yes ».

Continue in the same way for all alignments that need enhancement. Once you finished, save the new alignments with « File>save translations as... ».



For the following steps you can either continue to work with the greyscale images or you can load the color images and continue to work with them.

Step 6 – 3d data extraction

Open the « 3d object manager » from the menu « Model ». Create an object for each 3d object that you want to model. To create an object press the « add object... » button and enter the name of the object.

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add selections	
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Select the object you want to begin with in the list. Select the first slice on which the structure you are interested in appears. Trace the structure with one of the selection tools from the toolbox, for example the freehand selection tool.



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When a selection is finished press the « add selections button » to add it to the selected object or press ctrl+space. Select the « show » checkbox to display the objects in the image. Trace all objects on all slices you are interested in.

You can use the « hide » and « show » buttons to hide and show selected objects. When there are many objects the display might become slow. In this case you can only show the objects you are interested in at the moment.

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To get an idea of what the 3d result will look like, you can create a stack of a part of the slices and objects and calculate a 3d view. Select some slices in the OMW window and some objects in the « 3d object manager ». Call « create stack » from the menu model of the « 3d object manager ». If you want you can reduce the size of the stack either by cropping the image or by scaling it or both.

To crop the image make a rectangular selection around the area you are interested in. Make sure that the objects are within the area on all slices by using the slider on the bottom of the stack window. Open the ImageJ launcher window by clicking on the microscope icon on the MRI Cell Image Analyzer launcher. Call the crop function from the menu Image>Crop.

To scale the image use Image>scale from the ImageJ window and enter the scaling factor in the dialog.



You can create a 3d projection by using Stack>projection>3d projection. Enter the slice spacing in the dialog to get the right z to x ratio and check interpolate. To adjust the brightness of the result use the brightness/contrast adjuster from View>adjust>brightness/contrast from the MRI Cell Image Analyzer window. To smooth the result select the window press shift+s or use the menu Process>smooth.



Step 7 – Saving and exporting the extracted 3d data

To save the model you created by outlining objects in a way that you can continue to work on it later on, use File>save... in the « 3d object manager ». You should create a folder and save your model into it, since it consists of multiple files. Enter a name and use the extension .3do.

If later you want to load the model use File>open... from the « 3d object manager » and select the .3do file.

To export your data in a way that it can be loaded with a program for 3d rendering select the slices in the OMW and the objects in the « 3d object manager », then use either « Model>save one series per object » or « Model>save series... ». Create a new folder for the series, enter a name and press ok. In the first case one series of images will be written for each object. In the second case all objects will be in the same image series. The image series can then be imported into a 3d rendering software.