



NA-MIC

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Slicer3 Tutorial: Registration Library Case 08

Serial PET-CT

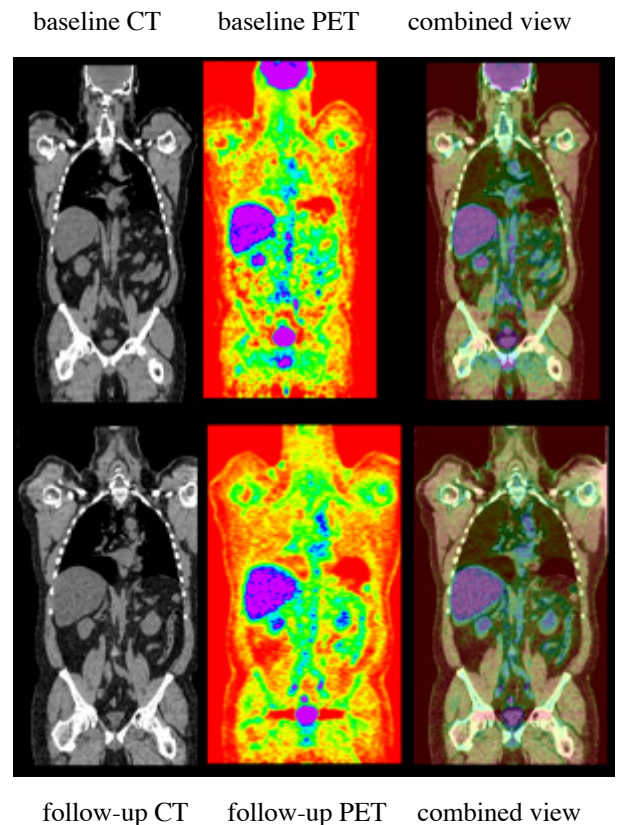
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Introduction / Scenario

- We have two sets of PET-CT scans, a baseline and follow-up scan.
- Both exams were obtained on a combined PET-CT scanner, hence the PET and CT within each exam are aligned already
- We want to align the follow-up exam with the baseline.
- Because we have two pairs of images, we have two sets of separate registrations we can perform and choose the better one: we can register CT-CT or PET-PET. Aligning CT of one exam with the PET of the other exam is unlikely to produce a better result than any of the first two.
- The images represent the same subject, hence we expect good alignment. However these are full body scans, hence unlike a brain scan there are many opportunities for relative motion within the image that are very difficult for a global registration to correct.





Modules Used

- To accomplish this task we will use the following modules:
 - Register Images
 - Deformable B-spline Registration
 - Resample Scalar/Vector/DWI Volume
 - Extract Subvolume ROI
 - Data Module
 - Volume Module



Prerequisites

- Slicer version 3.5 or later
- **Example Dataset:** download and extract the dataset for this tutorial: RegLib_C08_PET-CT.zip, which should contain this tutorial and all original and intermediate solution data files.
- **Tutorials to complete first:**
 - Extract Subvolume ROI
 - Slicer3Minute Tutorial
 - Loading and Viewing Data



1. Loading Example Dataset

To get the Example Dataset loaded into Slicer:

1. File Menu: File: Load Scene...

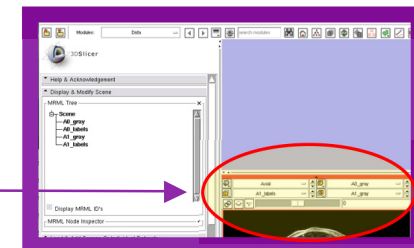
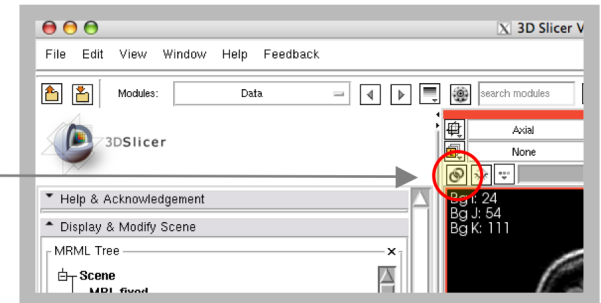
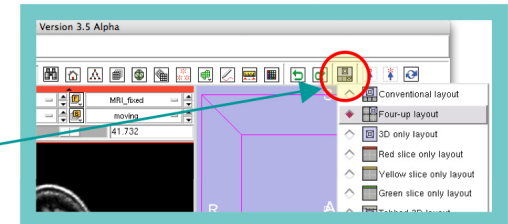
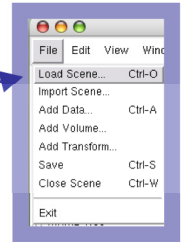
- Select the Slicer Scene file that comes with the downloaded example dataset, called: RegLib_..._SlicerScene.mrml
- This will load all the necessary images. If this fails, use the "Add Data..." menu to load the files in the data directory.

2. Select Layout: From the icon bar, click on the Layout menu and select "Conventional Layout".

3. Link Views: Click on the Ring Icon in any of the slice views to link all the views together. This will save you the work of making selections for each slice window separately.

4. Choose Foreground: S1_PET

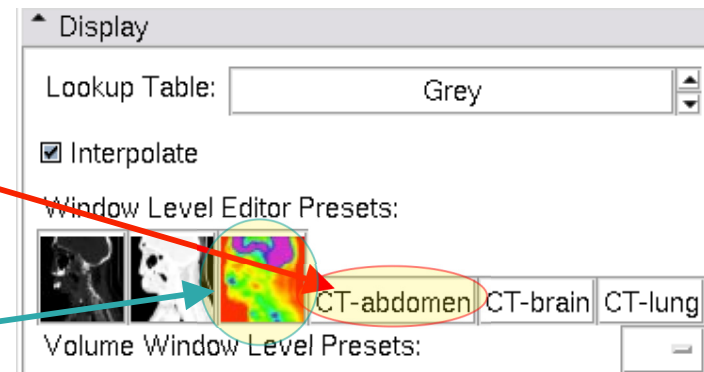
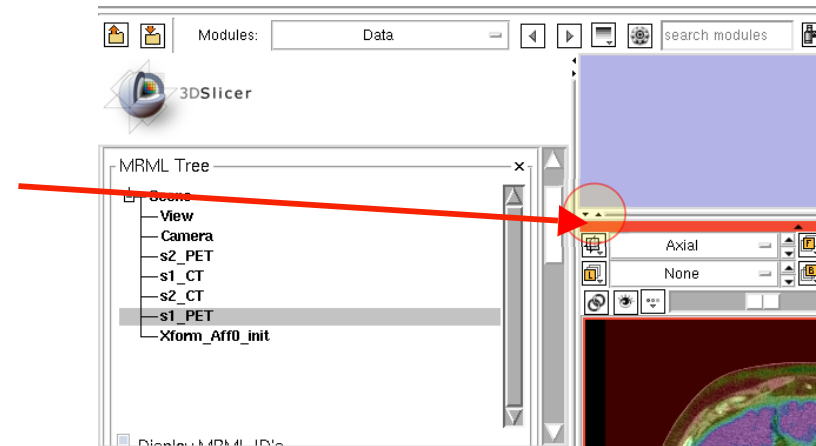
5. Choose Background: S1_CT





Adjust Views

1. Click on the little upward-facing triangle to collapse the 3D view.
2. If the images do not appear as shown on the right, adjust the window&level:
3. Go to the “Volumes” module and select s1_CT. Expand the “Display” tab.
4. For the CT scan images, click on the “CT-abdomen” button.
5. For the PET images, click on the “PET” icon.
6. This will adjust the dynamic range and colormaps.





Initial Alignment

1. The two exams are far apart initially, due to different coordinate origin settings in acquisition. We perform an initial alignment, for which we use CT-CT:

2. Go to the “Register Images Module”, and select the following parameters:

fixed image: s1_CT

moving image: s2_CT

Save transform: “Create New Transform”, then select rename and change to “Xform_Aff0_Init”

Initialization: Centers of Mass

Registration: Pipeline Affine

Metric: MattesMI

Expected offset magnitude: 50

Expected rotation, scale, skew magnitude: leave at default (see right)

Expected offset magnitude: 50

Expected offset magnitude: 50

“Advanced Affine Registration Parameters” Tab:

Affine Max Iterations: 10

Affine sampling ratio: 0.02

Modules:

Register Images

Register Images

Parameter set: RegPres...f0_Init

Status: Completed

IO

Fixed Image: s1_CT

Moving Image: s2_CT

Resample image: None

Registration Parameters

Load transform: None

Save transform: Xfo...it

Initialization: None Lan ImageC CentersC

SecondM

Registration: No Initial Rigid Affine

BS Pipeline Pipeline/ PipelineBS

Metric: MattesMI NormCorr MeanSqrd

Expected offset magnitude: 50

Expected rotation magnitude: 0.1

Expected scale magnitude: 0.05

Expected skew magnitude: 0.01

Advanced Affine Registration Parameters

Affine Max Iterations: 10

Affine sampling ratio: 0.02

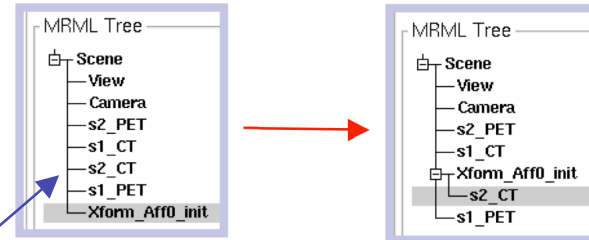
3. Click “Apply”



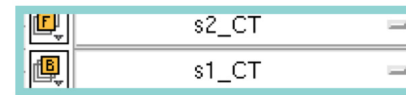
Initial Alignment (2)

- Algorithm should return within ~ 1 minute. To see the result we apply the result transform to the volume: Go to the data module.

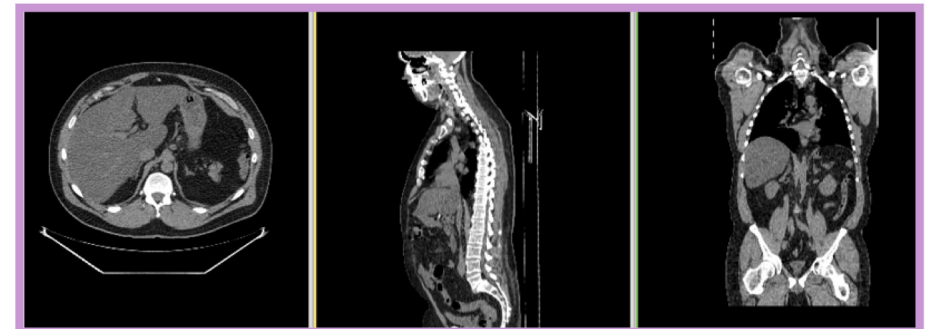
- Drag the node for “s2_CT” on top of the transform node “Xform_Aff0_init”. You should see the tree update as shown.



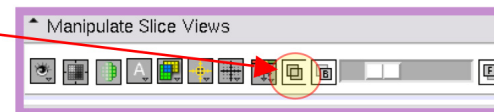
- Adjust the slice views to show the two CT scans:
background: s1_CT
foreground: s2_CT



- You should see the two images aligned as shown on the right. To see the effect use the toggle switch.



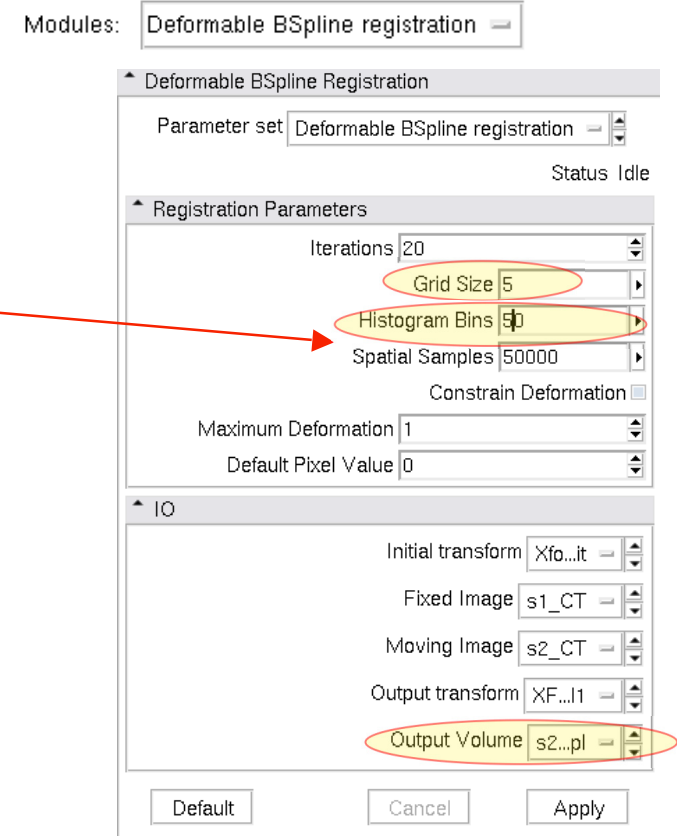
animated gif, view in presentation mode





Non-rigid alignment

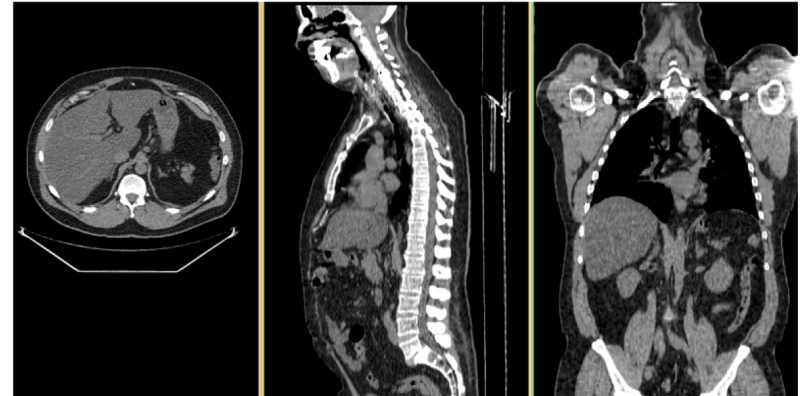
1. As apparent from the sagittal view, there are differences from posture and breathing that a global alignment cannot correct. We proceed to a non-rigid alignment to compensate for this: Go to the “Deformable B-spline registration” module
2. Select the following parameters: (if you loaded the scene file, you can also choose the parameter preset loaded that will set them for you):
Iterations: 20
Grid Size: 5
Histogram Bins: 50
Spatial Samples: 50000
Initial Transform: Xform_Aff0_Init
Fixed Image: s1_CT
Moving Image: s2_CT
Output transform: create new, rename to “Xform_BSp1”
Output Volume: create new, rename to “s2_CT_BSp1”
3. Click “Apply”. Registration should take ~ 2 minutes





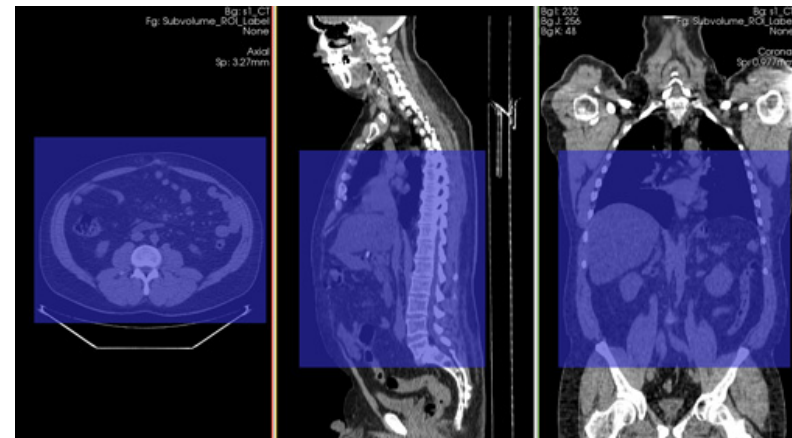
Non-rigid alignment (2)

- The result and deformation applied can be seen on the right. The differences in the chest region were reduced, however head position remains different. Because we care about the abdominal region, we proceed with further refinement by cropping the region of interest:
- Go to the “Extract Subvolume ROI” module. We clip both s1_CT and s2_CT between the 5th lumbar and the 5th thoracic vertebrae. For a separate tutorial on how to use the Subvolume module, see the slicer training compendium: To skip this step, load the ready-made cropped volumes from your example directory: s1_CT_crop , s2_CT_crop. Once loaded set the proper display in the Volumes module as described before on slide #x



animated gif, view in presentation mode

Modules:





Non-rigid alignment (3)

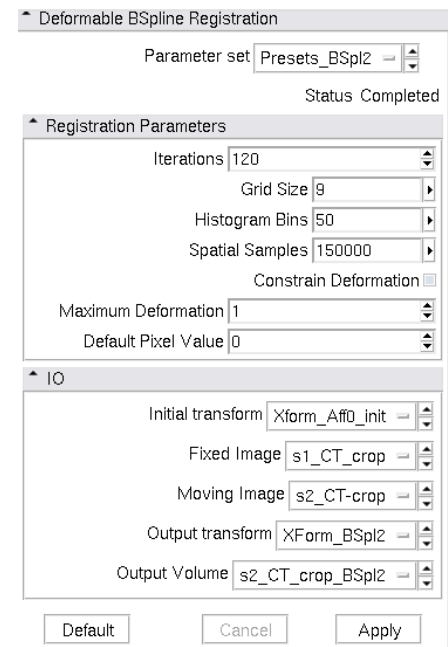
6. Now we repeat the B-spline registration process with the cropped volumes:

Iterations: 120
Grid Size: 9
Histogram Bins: 50
Spatial Samples: 150000
Initial Transform: Xform_Aff0_Init
Fixed Image: s1_CT_crop
Moving Image: s2_CT_crop
Output transform: create new, rename to "Xform_BSpl2"
Output Volume: create new, rename to "s2_CT_BSpl2"



7. Click "Apply". This will take ~ 1-2 min
8. Resulting alignment should look like shown on the right. Small residual misalignment remains in some areas, but the liver is mostly aligned
9. We now proceed to send the full CT and PET images through the same transforms. The sequence goes first through Xform_Aff0_Init and then through Xform_BSpl2. However, since we gave Xform_Aff0_Init as starting point for the B-spline, its transform already includes the affine portion. So we have to apply only 1 step for the resampling.

animated gif, view in presentation mode





Resample

Modules: sample Scalar/Vector/DWI Volum...

1. Go to the “Resample Scalar/Vector/DWI Volume” module.
2. Select the following:
Input Volume: s2_CT
Reference Volume: s1_CT
Output Volume: create new, rename to s2_CT_BSpl2
Transform Node: XForm_BSpl2
Transform order: output-to-input
Interpolation Type: ws (windowed sinc)
Interpolation window function: h (Hanning)

Modules: sample Scalar/Vector/DWI Volum...



3. Click “Apply”
4. Repeat the steps 2-3 above for: s2_PET as Input, s1_PET as reference volume, and s2_PET_BSpl2 as output.

Modules: sample Scalar/Vector/DWI Volum...

Resample Scalar/Vector/DWI Volume

Parameter set: Resample Scala...or/DWI Volume

Status: Idle

Input/Output

Input Volume: s2_CT

Reference Volume (To Set Output Parameters): T

Output Volume: s2_CT_BSpl2

Deformation Field

Resampling Parameters

Transform Parameters

Transform Node: X...m

Transforms Order: input-to-output output-to-input

Annual Transform (Only Used If No Transform Node Set)

Rigid/Affine Parameters

Interpolation Type

Interpolation: linear nn ws bs

Windowed Sinc Interpolate Function Parameters

Window Function: h c w l b

Modules: Volumes

5. Go to the Volumes module; in the “Display” tab select “CT_Abdomen” and “PET” as the display parameters for the 2 newly created volumes s2_CT_BSpl2 and s2_PET_BSpl2

Modules: Volumes

Display

Lookup Table: Grey

Interpolate

Window Level Editor Presets:

CT-abdomen CT-brain CT-lung

Volume Window Level Presets:

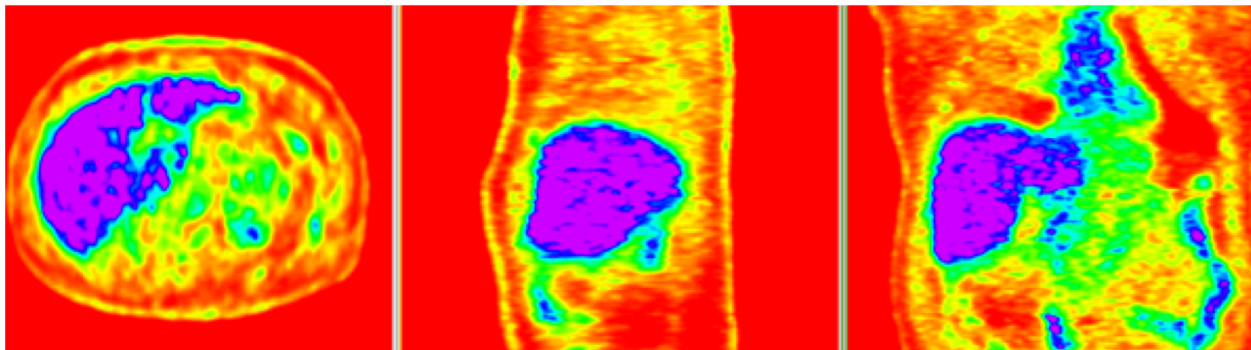
Modules: Volumes



View Results

We can now compare the aligned PET images:

1. Choose Foreground: S2_PET
2. Choose Background: S1_PET
3. Using the view toggle button switch back and forth between FG and BG to see the alignment. You should see something similar to the animation below.

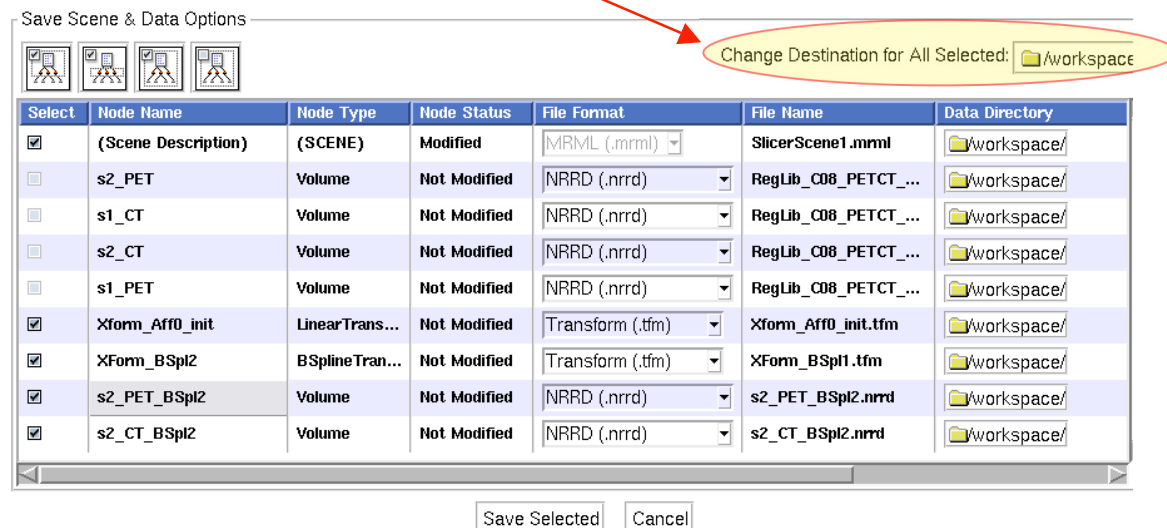


animated gif, view in presentation mode



Save

1. We now have all 4 images in the same aligned space.
2. From the File menu, select “Save”
3. In the dialog box, check the boxes for:
XForm_BSpl2
s2_CT_BSpl2
s2_PET_BSpl2
4. Choose desired output directory
5. Click on “Save Selected”.





What Next

- Try the Manual Registration Tutorial or one of the tutorials from the Registration Case Library.
 - <http://www.slicer.org/slicerWiki/index.php/Slicer3.4:Training>
 - <http://na-mic.org/Wiki/index.php/Projects:RegistrationDocumentation:UseCaseInventory>
 - http://www.slicer.org/slicerWiki/index.php/Slicer3:Registration#Registration_in_3D_Slicer|Main
- Feedback: anything amiss? If you have suggestions on how we can improve this and other documentation, please let us know: visit:
 - <http://na-mic.org/Wiki/index.php/Projects:RegistrationDocumentation>



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