

3D to 3D microCT registration

Introduction

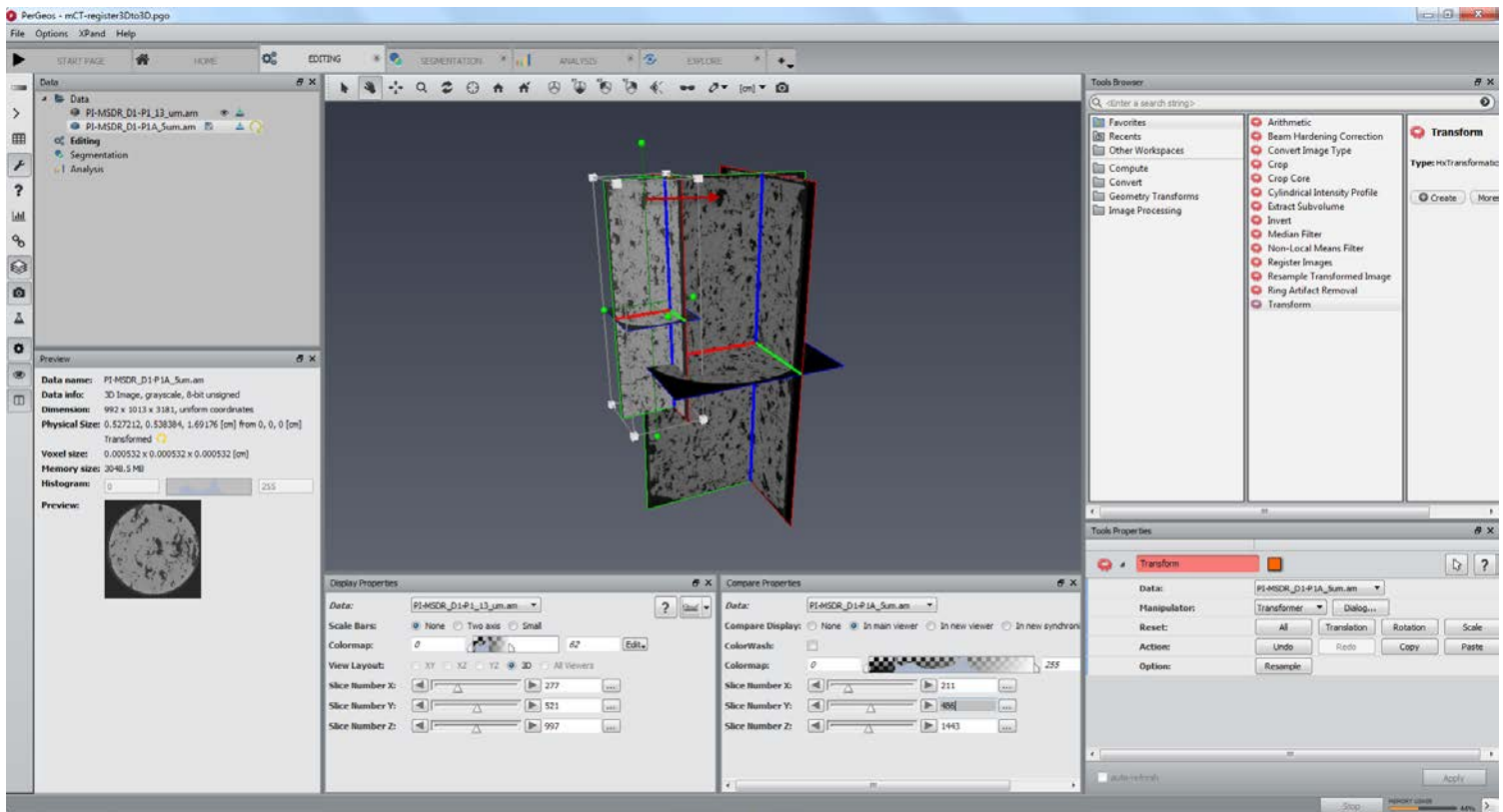
This tutorial is part of the PerGeos Training course, and will detail how to register 2 microCT scans of the same rock sample acquired at two different resolutions, and having different physical sizes.

The dataset are courtesy of Mustapha Jouiad, MASDAR institute of Science and Technology, Abu Dhabi.

A small sample scanned at 5 μm needs to be registered into a bigger one scanned at 13 μm .

1. Pre-align the 2 samples

Using a Transform object, approximatively place the 5 μm sample in the center top region of the 13 μm sample. The big pore shown in the image can be used as a reference.



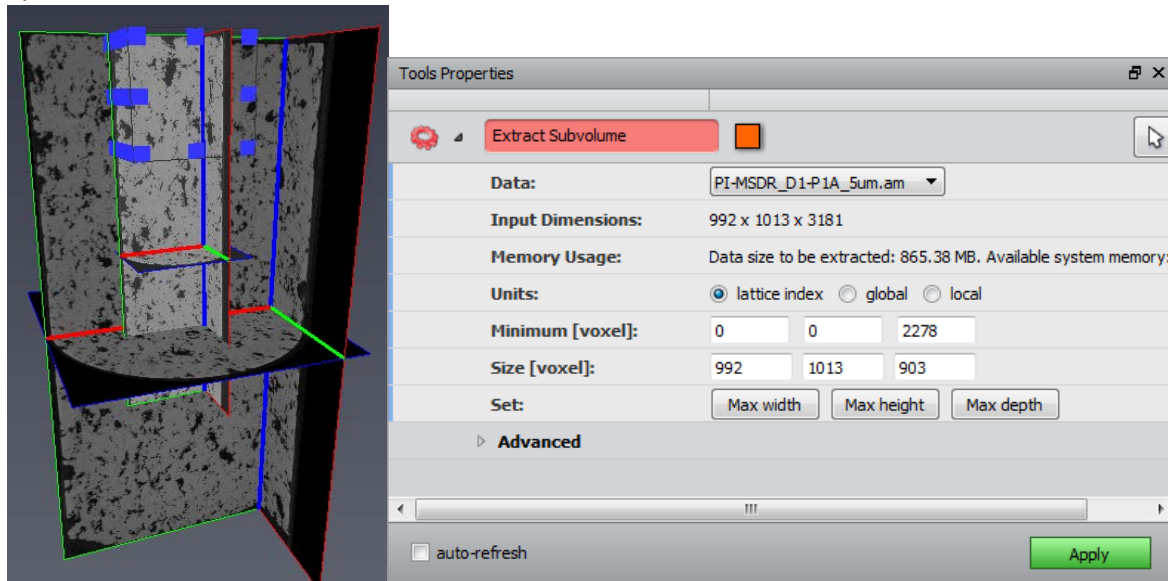
Note : It is highly recommended to transform only one sample, since a resampling step is often needed after a data has been transformed.

2. Extract a subset of both samples

In order to maximize the registration precision and lower the computation time, it is recommended to extract a subset of both samples before applying the registration module.

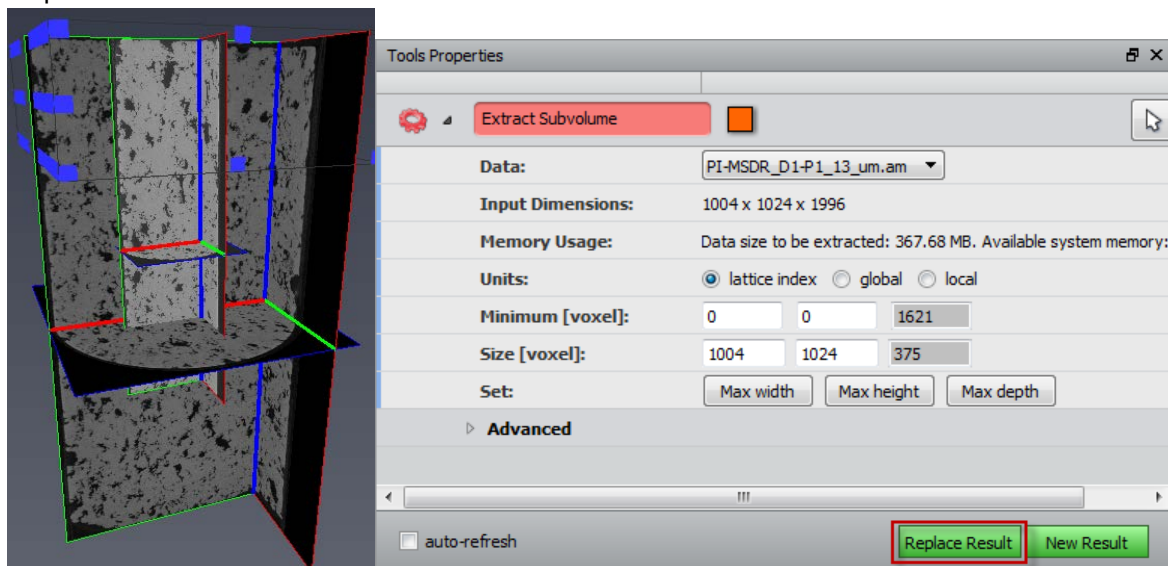
Apply 2 successive *Extract SubVolume* modules on both 5µm and 13 µm samples taken from the top part.

5µm:



Note: the transformation applied during step 1 is kept in the extracted 5µm subset

13 µm:



3. Set registration parameters

As the model, set the 5 μ m subsample containing the transformation, since the registration process will lead to a transformation (a modification of the existing one).

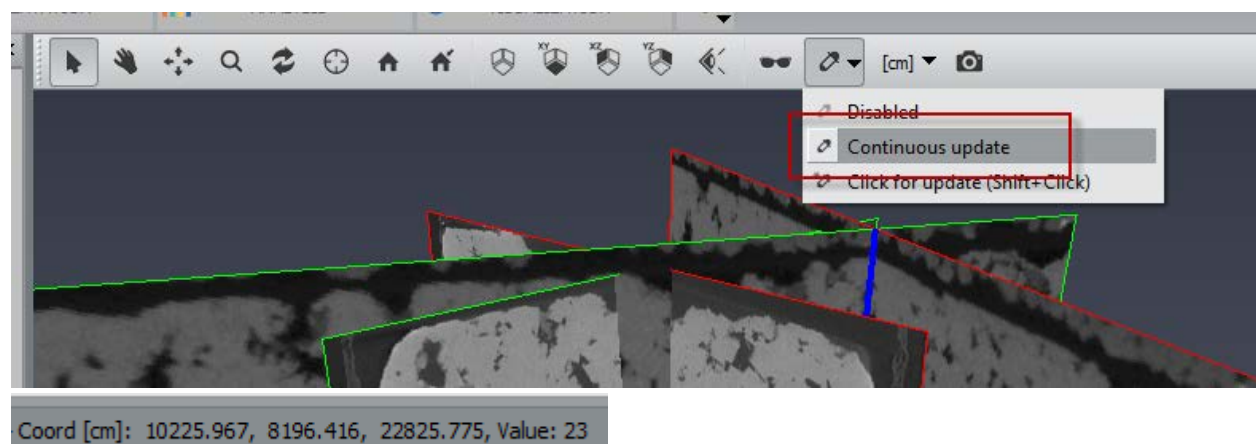
The reference is the 13 μ m subsample.

As both histograms are different, we'll use the *Normalized Mutual Information* metric.

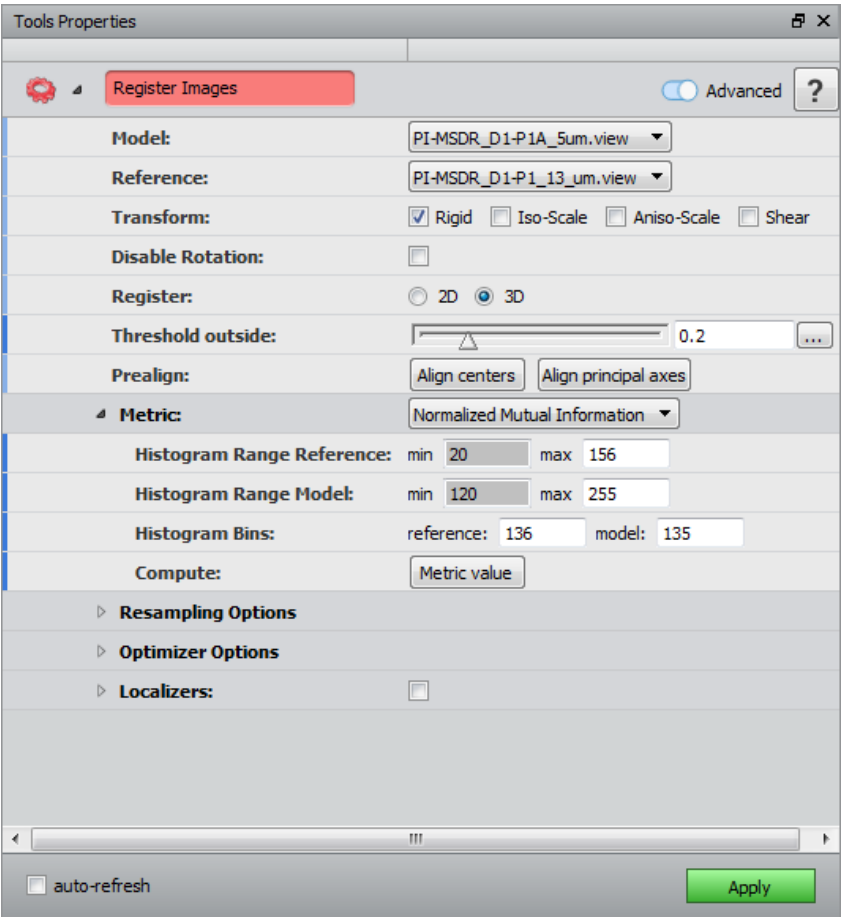
Also, as the 5 μ m sample contains outside space whereas the 13 μ m one may not, we indicate the histogram ranges under the Metric options such as only the mineral pixels are taken into account:

Metric:	Normalized Mutual Information	
Histogram Range Reference:	min 20	max 156
Histogram Range Model:	min 120	max 255
Histogram Bins:	reference: 136	model: 135
Compute:	Metric value	

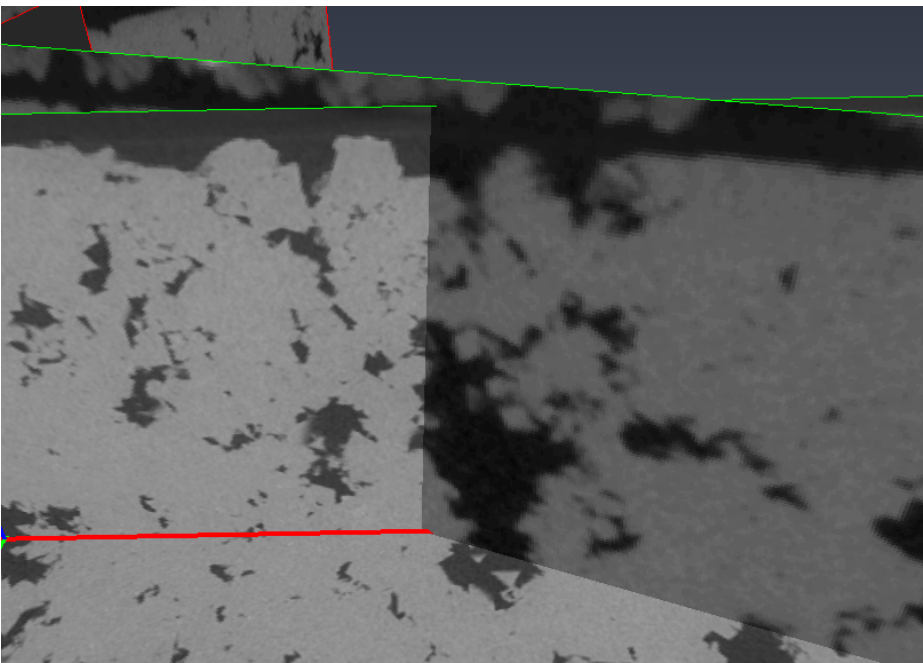
Note : these values were obtained quickly by using the probing tool of the viewer toolbar



4. Register the samples



When pressing the Apply button, the best transformation to apply to the 5µm subsample in order to minimize the error according to the metric is computed.



5µm sample (left) registered to 13µm sample

5. Copy the transformation to the original sample

Using *Copy Transformation*, copy the transformation of the 5µm subsample to the 5µm sample

Copy Transformation	
Data:	PI-MSDR_D1-P1A_5um.am ▼
Reference:	PI-MSDR_D1-P1A_5um.view ▼

The 5µm and 13µm samples are now correctly registered