Tutorials of ZIB Projects: Slice Registration *(SliceRegistration)*

This tutorial explains how to find the position of a 2D image in a 3D image. The workflow as well as some of the modules used in the workflow were developed in collaboration with the Max Planck Institute of Colloids and Interfaces. In its original application, the 2D image is an ESEM scan of a cross section of a bone (for example, of a rat or a mouse) and the 3D image results from a CT scan of the whole bone. The following figure shows a possible result.

![Image](image.png)

*Left: OrthoSlice of the ESEM image, Middle: Volume Rendering of the CT, Right: Final solution (OrthoSlice of ESEM with Colorwash)*

The process to find this position is called **image registration**. In the terminology of registration processes, the ESEM image is the **model** and the CT is the **reference**. The goal is to find a transformation of the model such that the transformed model and the reference match as good as possible.

There are various methods to solve the image registration problem. In Amira, the **AffineRegistration** module can be used for this task. This module starts a local optimization around the current model position. Unfortunately, this method fails if the model is only a 2D image (and not 3D) and the starting position is not near the searched solution. Thus, for this application, a more complex approach is needed, which is described in this tutorial.

The idea of this approach is to find some good initial model positions and to use them as starting points for multiple local optimizations. To find good initial positions, we use the **GeneralizedHoughTransform** module. These positions are then refined using multiple affine registrations. This step is carried out using the **AffineRegistrationOnMultipleTransforms** module which internally uses the **AffineRegistration** module for all given model positions resulting from the Generalized Hough Transform. After the optimizations for all initial positions have been carried out, the user can visually explore all results and take the most pleasing one, or she can take the one with the best metric value.

The whole pipeline consists of the following steps:

1. Preparation of the ESEM image
2. Template creation (the resulting template is the input of the Generalized Hough Transform)
3. Preparations for the Generalized Hough Transform
4. Execution of the Generalized Hough Transform
5. Execution of the Affine Registrations

Another way to solve the registration problem is to find a good initial model position manually and use the **SliceIntegrator** script. This is an alternative way to achieve the registration and is not explained in this tutorial.

If you want to use the example data set of this tutorial please download the CT data using the following link: [https://amira.zib.de/releases/demodata/sliceregistration/sliceregistration_data_v1.tar.gz](https://amira.zib.de/releases/demodata/sliceregistration/sliceregistration_data_v1.tar.gz). Copy the archive file to your Amira folder and extract it. After this has been done, you can use the example networks from this tutorial.

1 Prepare the ESEM image

The first step includes removing parts of the ESEM image (model) that might prevent a successful registration. Furthermore, we need to take care of the background.

- Load the ESEM image and be careful to use the right voxel sizes and to set the **Channel conversion** to **Luminance**. If you use the example data sets. Then load the file data/slice-registration/esem_before_preparation.am and set the voxel sizes for x, y and z to 0.00416801.
- Crop the image to remove unnecessary parts of the image, for example extra image information on the bottom. Do it with the help of the **Crop Editor**.
- If there is white background, use the Arithmetic module to make it black. The background has to be dark. Attach the Arithmetic module to the image and set the **Expression** for example to (A<255)*A (all values >=255 get the value 0). Press **Apply** to start the computation. The example ESEM has white background so you have to use the Arithmetic module.
- Save the result.

This network contains all these steps.

2 Create the template for the Generalized Hough Transform (GHT)

The GHT enables the detection of an arbitrary shape within an image. It needs landmarks and normal vectors for all landmarks to describe this template shape, and the gradient field of the search space. The landmarks define the boundary of the ESEM bone and the vectors point to the bone. There is a script **TemplateCreation** to support the template creation.

- Load your ESEM file from step 1 or load data/slice-registration/esem.am if you want to use exactly the same file as in the example.
The next part is to use the CreateAutomaticLandmarks module to create the landmarks. This module tries to create landmarks on edges of the ESEM image automatically. You should use the Segmentation Editor to separate the bone boundaries from the background and from parts inside the bone. The CreateAutomaticLandmarks module can use this segmentation, that is the landmarks are only created inside the masked area. This step reduces the number of outliers when creating the template.

- Switch to the Segmentation Editor.
- Select the original ESEM, create new label data and use the brush to mark the area where you want template points. Add the marked area to Inside. If your image is just black, check whether the camera is too close and try to zoom out.
- Switch back to the pool area.
- Connect the created label field to the mask connection port of the CreateAutomaticLandmarks module.
- Select the CreateAutomaticLandmarks module.

Note that a landmark is only created if the value is larger than the value of the threshold port. The second OrthoSlicc module helps you to find a good threshold value (picture). In most cases, the default value should be good enough. Alternatively, you can create the landmarks manually with the help of the landmark editor (without using CreateAutomaticLandmarks).

- Set a suitable threshold value. Example data: Use 6000 as threshold value and 60 as neighbourhood size.
- Press Apply to start the computation.
- Hide the second OrthoSlicc. You should see the whole data set, not just the boundary. Start the Landmark Editor of the landmarks data set. Now you can see your result.
- Remove and move landmarks with the help of the Landmark Editor as you like. In particular, remove wrong landmarks that clearly do not belong to the boundary.

Now you have created a landmark set. The CreateArbitraryTemplate module uses them to create the template.

- Connect the created landmarks to the SamplePoints connection port of the CreateArbitraryTemplate module.
- Press Apply to start the computation.

The created template consists of the normal vectors and a surface containing the landmarks. To check the quality of the template, add a Vectors module to the template normals and check whether the vectors point mostly to the inside of the bone. If you are not pleased with the result, you can delete or move some landmarks using the landmark editor and apply the CreateArbitraryTemplate module again. If the landmarks are too close to each other, go back to the landmark creation and increase the value of the Neighbourhood size port of the CreateAutomaticLandmarks module.

The resulting network should look like this.

- Save the template and the template normals and make sure not to delete the template points from the surface when saving the data set.

### 3 Prepare GHT

It is necessary to limit the size of the CT data set and to exclude the background of the CT due to performance issues. This will be explained in following section.

- Load the ESEM, the CT, the template points and the template normals. Use esem.am, ct.am, Template.surf and TemplateNormals.am in the folder data/slice-registration if you want to use the example data sets.
- Attach the HoughTransformPreparation script to the template points. (under SliceRegistration)
- Connect the ESEM, the CT and the normals to the HoughTransformPreparation script.
- Select the script.

First you have to deal with the resampling. The HoughTransformPreparation script contains the Resample factor port. A factor of value 3 means that a data set with X x Y x Z points will get a size of X/3 x Y/3 x Z/3. A total size around 500 x 500 x 300 seems a good size.

- Set the resample value. The default value should be good enough (do not change the value for the example data).
- Press Apply.

The next task is the exclusion of the background from the 3D image. All points with values below the Mask threshold will be excluded. The Volren module can help you to find a suitable value. You should see the main parts of the bone and not to much background. If you have some very high values (outliers) in your CT then it is possible that you can not see anything with the default value. Lower the VolumeRendering value until you see the bone.

- Set the threshold value. Use 500 for the example data set.
- Press Continue, not Apply.

The GHT performs rotations of the template around the global X, Y and Z axes. In the given problem, one wants to rotate 360 degrees around the bone as rotation axis and to do just little rotations in the other directions. This means that it is necessary to align the CT bone to a global axis. It is suggested to use the Z axis, because in all given data sets the CT bone was already aligned to the Z axis. In this case, nothing has to be done with the CT. Furthermore, we need to align the ESEM bone with the CT bone.

The HoughTransformPreparation script offers some functionality to do this alignment. Align CT bone to Z axis computes the first principal component with the help of a Principal Component Analysis (PCA) and aligns it to the Z axis. This first principal component should be the bone direction. Align ESEM bone to CT bone does the same for the ESEM bone but aligns it to the CT bone. Regarding the rat data sets, it
was only necessary to align the ESEM. If you are not happy with the results because the PCA fails, then you can do the alignment manually (move the original CT or ESEM). But notice that you only move the CT or ESEM, not the CT gradient field or the template. So you have to use Move template to model position or Move CT gradient to CT to align them too.

It is also important that the ESEM is flipped in the right direction. You can use the flip port to change the orientation. If you are not sure which flip is the right one, then you can take one orientation, then do a GHT which only rotates 360 degrees around the Z axis (not around X or Y axis). That should be really fast and you can normally see whether the result is completely wrong or seems to be reasonable. If it is completely wrong, then you had probably the wrong orientation. Do another flip and continue to step 4.

It is useful to use a Colorwash module for visualization. Add it to the OrthoSlice of the ESEM and you can see the ESEM and the CT in one image.

- Align the ESEM and the CT. Use an OrthoSlice with a Colorwash module on the ESEM to see its position. It is useful to start with Align ESEM bone to CT bone. Example data: Press Align ESEM bone to CT bone.

The resulting network should look like this.

4 Apply GHT

The GeneralizedHoughTransform module was created in step 3. Using the default values, the GHT does a rotation with 360 degree around the Z axis and small rotations around the X and Y axes.

- Select the GeneralizedHoughTransform module.
- Press Apply to start the GHT.

You can switch between the results with the help of the Sorted transforms port. You can reach a better visualization with the Colorwash module. Simply add it to the OrthoSlice of the model and connect the data connection port to the CT. Save the results into a Transforms module (with Create transforms). You can use the ApplyTransforms (under Compute) script to switch between the transformations inside a Transforms object.

- Press Create transforms -> Set multiple to save the first ten transformations.
- Save the Transform. These are your initial positions for the local image-based optimizations.
- Use the ApplyTransforms script on the transformations. Use a Colorwash and Volume Rendering to see your results.

What if your results are not good enough? First, it is possible that, due to errors in the data sets, there is no good matching. Other possibilities are: the alignment of ESEM and CT was not correct (see step 3), the landmarks are not good enough describing the bone shape (see step 2) or the search space of the GHT was too small. You can try the other orientation to solve the first problem. Second problem: Check the bad results (with the Colorwash module) to see if there are regions with too much or too less points. Third problem: Adjust the GHT options, for example use a wider rotation range around the X and Y axes.

5 Apply affine registrations

The last step is to perform affine registrations that start from the previous computed initial positions (results from the GHT). These affine registrations optimize the mutual information as metric value between model and reference. For details see the AffineRegistration module.

- Load the ESEM image, the CT and the transformations from the previous step. Be sure that there is no transformation on the CT.
- Attach the AffineRegistrationOnMultipleTransforms module (under SliceRegistration) to the transformations.
- The module tries to set useful parameters, for parameter description see AffineRegistrationOnMultipleTransforms.
- Press Apply to get the final transformations object.

The final transformations are sorted by their metric values. The first transformation is the best one. You can use the ApplyTransforms (under Compute) script to switch between the results. You can reach a better visualization with the Colorwash module. Simply add it to the OrthoSlice of the model and set the data port to the CT.

The resulting network should look like this.

- Save your final results.
- Use the ApplyTransforms script on the transformations. Use a Colorwash and VolRen to visualize your results.

What if your results are not good enough? First, it is possible that, due to errors in the data sets, there is no good matching. On the other hand you can try to find better parameters for the AffineRegistrationOnMultipleTransforms module. Try a smaller initial stepsize for Optimizer step, or use no resampling (Coarsest resampling to 1 1 1), or set a better data range for ESEM and CT (Histogram range reference and Histogram range model). The min value should remove the background values, you can use an OrthoSlice or VolRen to determine good values. You can also perform registrations on the results of the previous registrations.