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Abstract

Three-dimensional image reconstruction in X-ray computed tomography (XRCT) is a mathematical process that entirely depends on the alignment of the object of study. Small variations in pitch and roll angles and translational shift between center of rotation and center of detector can cause large deviations in the captured sinogram, resulting in a degraded 3D image. Most of the popular reconstruction algorithms are based on previous adjustments of the sinogram ray offset before the reconstruction process. This work presents an automatic method for shift and angle adjust of the center of rotation (COR) before the beginning of the experiment removing the need of setting geometrical parameters to achieve a reliable reconstruction. This method correlates different projections using Scale Invariant Feature Transform algorithm (SIFT) to align the experimental setup with sub-pixel precision and fast convergence.

Main Objectives

Figure 1A illustrates a typical fan-beam CT. The main objective of this work is to create an alignment method to minimize τ_0 in each horizontal line of the detector to eliminate the existence of artifacts in the reconstruction process. For this it is necessary the correct positioning of the COR and also ensure its orthogonality.

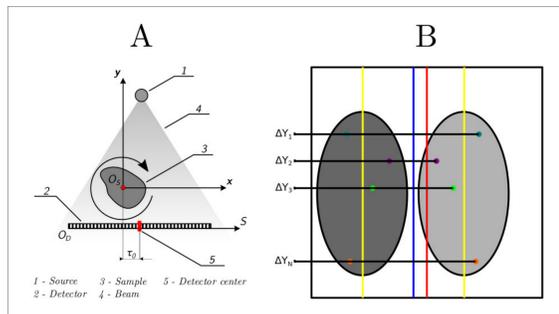


Figure 1: A. Illustration of a typical fan-beam CT. B. Rotation of a full aligned sample.

Alignment process

The alignment process is performed in two steps. The first one is related to the variation of pitch and roll angles and the second one is related to the linear position of the sample in relation to the detector. Ideally pitch and roll should be aligned only when sample or detector stages are translated and the sample should be aligned always before any experiment.

Pitch and roll alignment

For perfect alignment of the pitch and roll angles the axis of rotation of the sample must be exactly perpendicular to a plane orthogonal to the detector. Thus, when a rotation is performed the heights of the sample features are not affected. The figure 1B illustrates the sample projections at positions 0 and 180 degrees with a fully aligned axis and within the field of view of the detector. The light gray ellipse represents a projection of the sample at zero degrees position and the dark gray ellipse represents a projection of the sample at 180 degree. Colored circles represent sample features. The red axis represents the center of field of view, ie the center of detector. The yellow axis represents the center of sample and blue is COR. The objective function to be minimized in this case is the average of the absolute variation of the feature heights, given by equation 1. Where n is the number of true matches.

$$\overline{\Delta Y} = \frac{\sum_{k=1}^{k=n} \Delta Y_k}{n} \quad (1)$$

Roll misalignment effect

A misalignment in the roll angle causes variation in the height of the sample features when the rotational position is moved. This effect is exemplified in the figure 2A. Sample position at 0 and 180 degree results in a more evident height variation of

these characteristics, so they are the angles used to correct this misalignment. The shift of the sample horizontally relative to the plane of the detector also maximizes this height variation, so this step is also performed with the sample shifted to the border of field of view.

Pitch misalignment effect

Pitch misalignment also causes a variation of height of the sample features, however, this effect is maximized with rotational stage positions at 90 and 270 degrees. In addition, a sample shift normal to the detector is also interesting for maximizing the effect. The figure 2B illustrates this effect. The center of the sample and the center of rotation were omitted from the figure because in this case their projections are collinear to the axis of the center of detector.

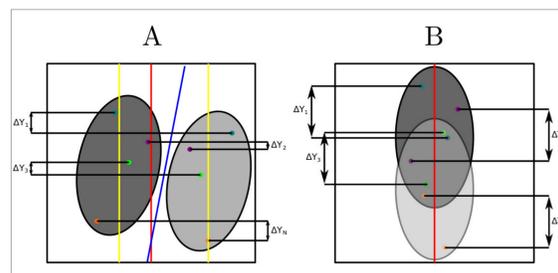


Figure 2: Difference between features heights for misaligned samples. A. Roll misalignment effect. B. Pitch misalignment effect

Linear alignment for COR positioning

After correction of the angles the beamline is ready to receive the sample to be measured. In this step, the objective is to place the sample fully within the field of view. For this, it is necessary that the projection of the center of the sample be collinear with the center of the detector. Further, it is desirable that the rotation axis projection also be collinear with the central axis of the detector to eliminate the existence of artifacts during the reconstruction. Therefore, for perfect alignment the three axes must be collinear.

Results

Reconstructions before and after the alignment process are compared to analyze the result achieved. A common case of sample alignment performed in the IMX beamline is also detailed.

Pitch and roll alignment results

Figure 3A illustrates the effect of pitch and roll misalignment on the reconstruction. It is clear the existence of artifacts with semi-circle shapes in all reconstructed slices, which modify their direction as the slice varies. In the upper part of the sample, showed in the upper line of the figure 3, the artifacts are with the concavity facing upwards, while in the lower part of the sample, showed in the bottom line, they are with concavity facing down. In the central part its intensity decreases. After use the alignment proposed in this work, the experiment was redone and artifacts eliminated, as showed in figure 3B.

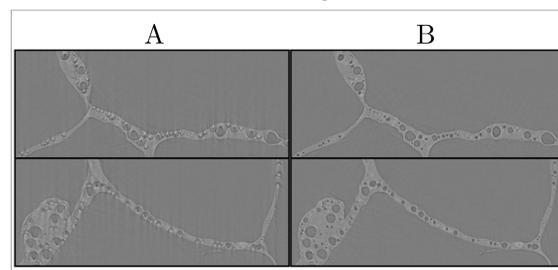


Figure 3: Reconstruction artifacts caused by misaligned angles. A. Reconstruction before the alignment process. B. Reconstruction after the alignment process.

COR positioning results

The top square in the figure 4 illustrates the effect of COR shift on reconstruction. It is observed the existence of artifacts with

semi-circle shapes in all the reconstructed slices, however, unlike the angular misalignment, the artifacts presents the same intensity and direction in any slice of the reconstruction. After the alignment using the methodology proposed in this work, the experiment was redone and the result is shown in the bottom square of the figure 4. Again, the artifacts are completely removed. In this case, the COR shift relative to the center of the detector was only 2 pixels but its sufficient to create visible artifacts.

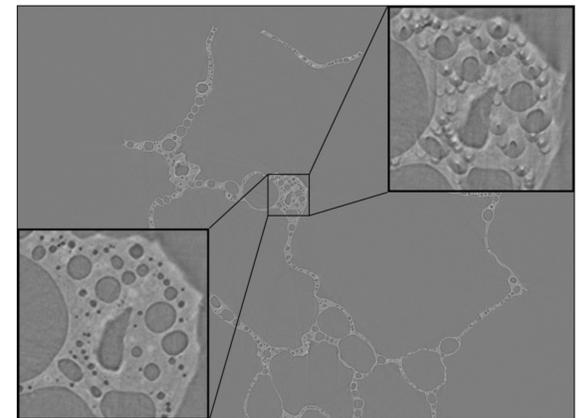


Figure 4: Artifacts from COR shift. Upper Square: Reconstruction with COR shifted in 2 pixels. Bottom square: Reconstruction after alignment using the proposed process.

A standard sample alignment case on the IMX beamline

To demonstrate the application of the automatic sample alignment a real experiment from IMX beamline users was chosen. After placing the sample in the experimental setup the alignment code is started and it first verify the angle that the rotational stage is positioned. In this case, the position is closer 90 or 270 degrees, so it initiate the iteration in those angles. Each line in the figure 5 shows an iteration. It is observed that in the two first 90 and 270 iteration both COR and the center of sample are moved, positioning they projections collinear in relation of the center of detector. At the third 90 and 270 iteration the algorithm verifies that it has reached the criteria of stop. The criteria stop is less than 1 pixel of difference between the center of sample and the center of detector and also less than 1 pixel of COR shift relative the center of detector. So the next step is the alignment of the sample in 0 and 180 degrees. Since the alignment at 0 and 180 degrees started with the COR shift aligned and both start projections are within the field of view, the process usually reaches the stopping criterion with only two iterations.

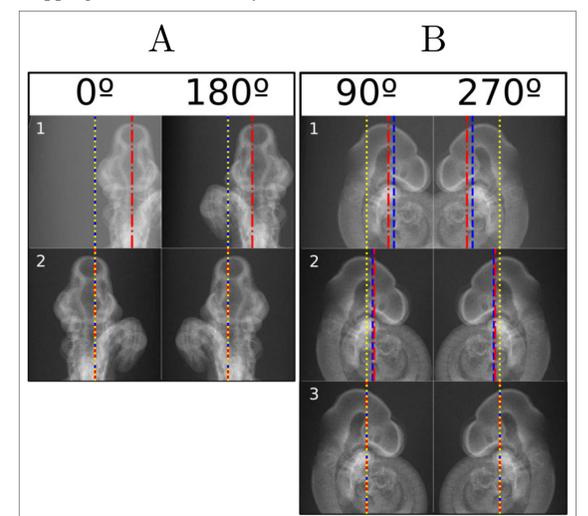


Figure 5: Iterations of a standard sample alignment case on the IMX beamline. In yellow is the center of detector, blue is COR projection and red is the center of the sample.

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