A SUB-PIXEL AUTOMATED FEATURE-BASED ALIGNMENT FOR TOMOGRAPHY EXPERIMENTS *

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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.

INTRODUCTION

Synchrotron computed tomography (CT) has made significant progress concerning the spatial resolution achieving nanometric precision using conventional transmission CT. Nevertheless, determination of geometrical parameters with subpixel precision is becoming extremely challenging. Ideally, the projection of the center of rotation has to be collinear to the center of detector, which is a hard condition to be satisfied in a real experimental setup [1].

The two main factors to ensure the accuracy of the image reconstruction is the position and the perpendicularity of projected COR. Some authors showed that a deviation on COR bigger than 1 or even 0.4 pixels can cause artifacts in the reconstructed image [4, 6]. Figure 1 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 achieve this is necessary the correct positioning of the COR and also ensure its orthogonality.

Robust algorithms have already been created by several authors to find COR position before reconstruction [2, 5], however it differs from this work because our process is performed before the beginning of the experiment. Due to possible small sample movements during the experiment it is still interesting to perform the COR search before the reconstruction but this align method can drastically reduce the computational effort of this step.

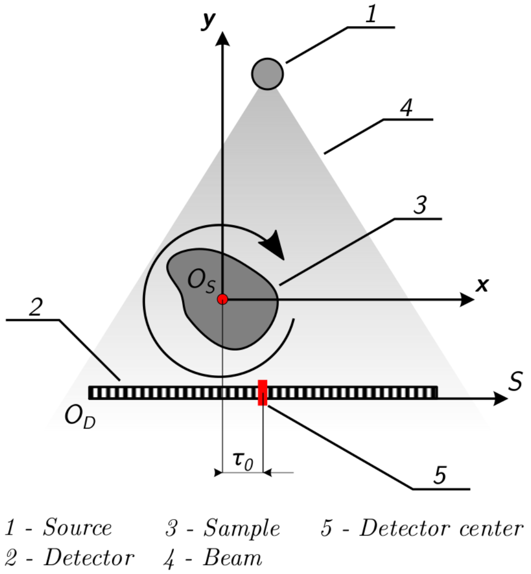

Figure 1: Illustration of a cone-beam tomography experiment.

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 COR projection must be exactly parallel to the detector plane. Thus, when a rotation is performed the heights of the sample features are not affected. Figure 2 illustrates sample projections at positions 0 and 180 degrees with a fully aligned COR and with sample within the field of view. 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.

$$\overline{\Delta Y} = \frac{\sum_{k=1}^{k=n} \Delta Y_k}{n} \tag{1}$$

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For the angle alignment it is preferable that the sample used contain large amount of features. After this process the optimal angles can be used for any other sample. The axis shown in Fig. 2 is not necessary for the angular alignment so it will be discussed in the linear alignment section.

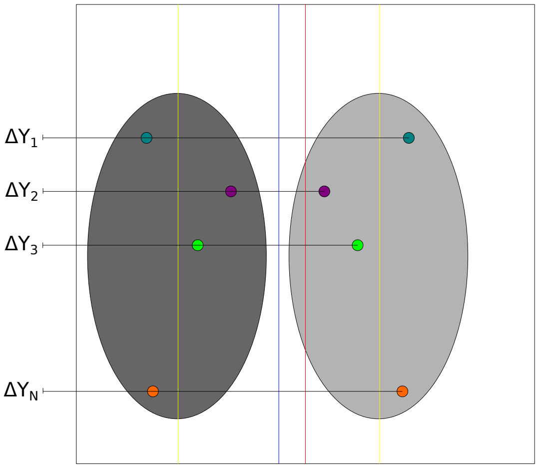

Figure 2: Difference between features heights for totally aligned sample.

Roll Misalignment Effect A misalignment in the roll angle causes variation in the height of the sample features when a rotational movement is performed. This effect is exemplified in Fig. 3. 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 horizontal shift of the sample 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.

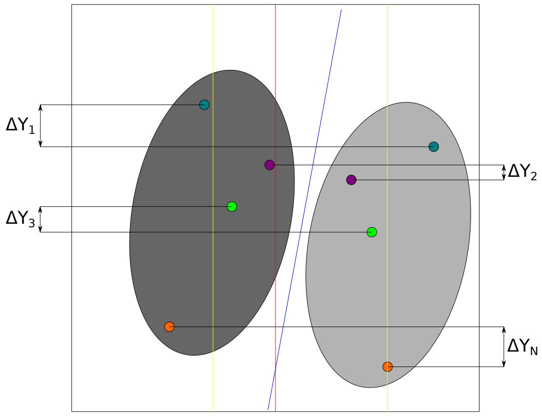

Figure 3: Difference between features heights for a sample with roll misaligned angle.

Pitch Misalignment Effect Pitch misalignment 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. Figure 4 illustrates this effect. In this case the projections of the sample center and COR are collinear to the detector center, so they were omitted from the figure.

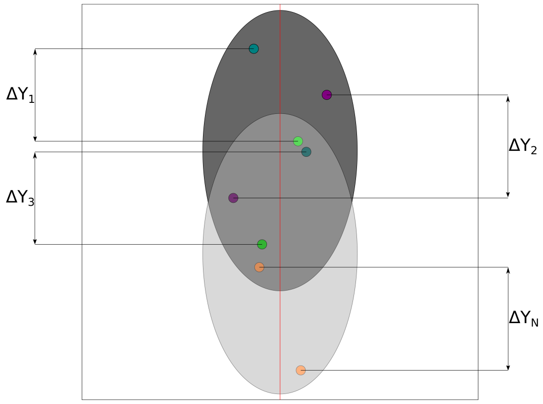

Figure 4: Difference between features heights for a sample with pitch misaligned angle.

Linear Alignment for COR Positioning

After angles alignment 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 COR projection also be collinear with the detector center to eliminate the existence of artifacts during the reconstruction. Therefore, for perfect alignment the three axes projections must be collinear.

METHODOLOGY

In this work the Z-axis is conventionally perpendicular to the plane of the detector, X is the horizontal axis relative to the detector plane and Y is the axis in the vertical direction with respect to the detector plane. In addition, the sample is subject to pitch, roll and yaw angle variations. The pitch angle is the movement around the horizontal axis in the direction of the Z axis and the roll is the movement around the horizontal axis perpendicular to the Z axis. The motion of yaw is the rotation about the Y axis, ie the rotational movement necessary to acquire deferents projections for the CT experiment, so it is not a directly parameter to be considered for alignment.

For a complete understanding of the methodology used in this work, it is necessary to know the basic setup of a CT beamline. Sample setup and detector setup make up a basic experimental setup. Sample setup will be considered with only six motion motors, which are stacked in the following order, from base to top: Pitch angle correction motor, roll angle correction motor, translational motor in X direction, rotational motor, motor high precision in the Z' direction and high precision motor in the X' direction. Normally there is also a translational motor in the Y axis, however, it has no direct impact on the alignment process and therefore will not be referenced in this work. Figure 5 illustrates the coordinates axes and the experimental setup of the imaging beamline (IMX), at The Brazilian Synchrotron Light Laboratory, located in the city of Campinas - Brazil, where the proposed method was applied. IMX is a parallel tomography beamline that has an electron source size of 391 μm x 97 μm and beam divergence of 808 μrad x 26 μrad and was designed to operate in either white beam or monochromatic beam.

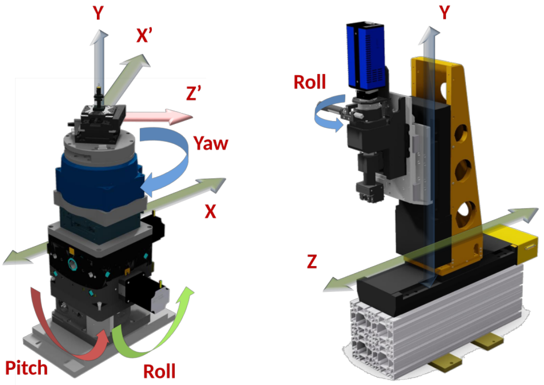

Figure 5: Illustration of the coordinates and experimental setup of the IMX beamline, at The Brazilian Synchrotron Light Laboratory (LNLS).

Feature Detection and Matching

In order for the alignment method to work automatically and reliably, it is necessary to use a robust method to locate the features in the images, that is, it is necessary to use robust image descriptor algorithms. Some of the most used object detection frameworks are: SURF, SIFT, AKAZE, ORB and FAST. In this work, the SIFT (Scale Invariant Feature Transform) algorithm is used because it is a fast and robust tool [3]. After extracting the features of two projections they are compared using brute force. The result of the comparison processing is a vector containing the compatible features and their respective locations. Figure 6 illustrates the matching result of a comparison between two projections of a mouse embryo.

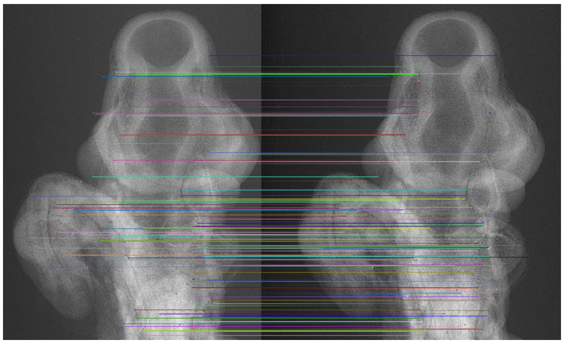

Figure 6: Feature matching illustration for a biological sample. The number of true matches in the image was reduced from 11604 to 200 for clear visualization.

Pitch and Roll Alignment Methodology

In order to minimize the $\overline{\Delta Y}$ error caused by the misalignment of the pitch and roll angles an iterative method of optimization is performed, so the angle of the motors is varied and the projections are analyzed. Features are filtered to eliminate false positives and matches from optics artifacts. Thus the value of $\overline{\Delta Y}$ error is compared with a stop value which when achieved guarantees an optimal alignment.

COR Alignment Methodology

The first step for alignment is performed by varying the sample at 0 and 180 degrees. The sample alignment method needs to find the center area of the object. For this, a normalized image is used, which is generated by using a background image and also a noise image, ie a x-ray projection with slits closed. This process removes undesirable artifacts. After normalization, the value of centroid is calculated using the image moments.

The center of rotation is calculated using the correlations of the features, being the average midpoint of the distances of each match. After this, the necessary translations are calculated to move the axes to the optimal position. This process is performed until the three main axes are collinear. This process is repeated for 90 and 270 degrees, ensuring that the sample is aligned on the two main directions.

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 7 illustrates the effect of misalignment of the pitch and roll angles 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 the artifacts are with the concavity facing upwards, while in the bottom part of the sample 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 shown in Fig. 8.

COR Alignment Results

The top square in Fig. 9 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 measurement was redone and the result is shown in the bottom square of Fig. 9. 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.

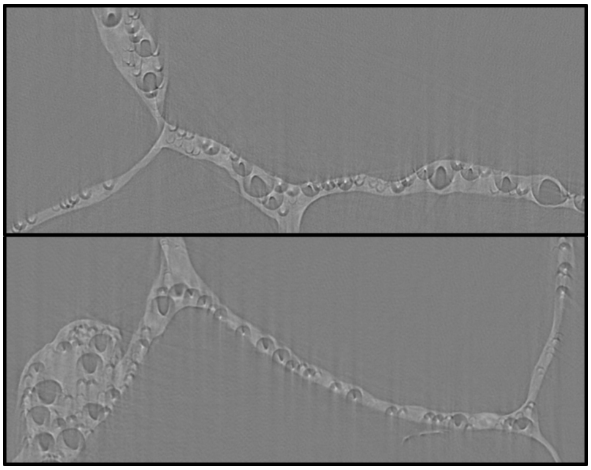

Figure 7: Artifacts from misaligned angles. Top image: Upper part of the sample (200 of 2048 slices). Bottom image: Bottom part of the sample (1848 of 2048 slices).

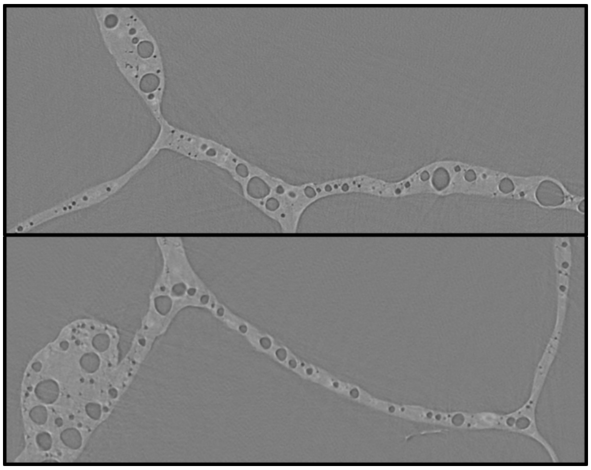

Figure 8: Reconstruction after angles alignment. Top image: Upper part of the sample (200 of 2048 slices). Bottom image: Bottom part of the sample (1848 of 2048 slices).

A Standard Sample Alignment Case on the IMX Beamline

To demonstrate the application of the automatic sample alignment a real experiment from IMX beamline 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 and start in the closest position at 0, 90, 180 or 270 degrees. In this case the position is closer 0 or 180 degrees so it initiate the iteration in those angles. Each line in Fig. 10 shows an iteration. It is observed that in the first iteration both COR and the sample center are moved, positioning they projections collinear in relation of the center of detector. At the second 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.

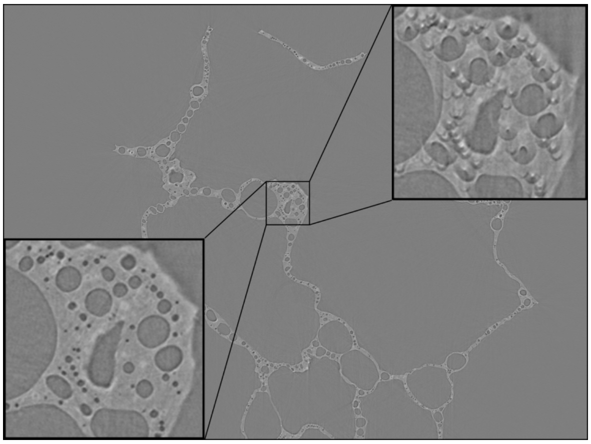

Figure 9: Artifacts from COR misalignment. Upper Square: Reconstruction with COR misaligned in 2 pixels. Bottom square: Reconstruction after alignment using the proposed process.

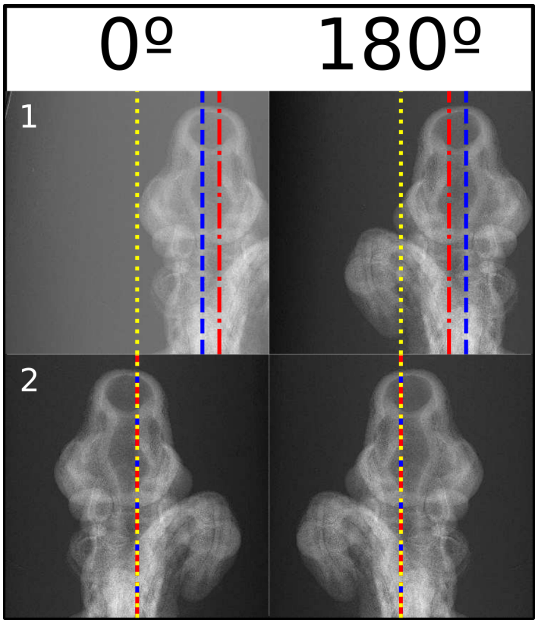

Figure 10: Iterations for sample alignment at 0 and 180 degrees. In yellow is the center of detector, blue is the axis of rotation and red is the center of the sample.

Figure 10 shows the next step in 90 and 270 degrees. Since the second step started with the COR aligned it only moves the sample center. When the code in any iteration of any step finds more features compared to the number of features that were used to align the center of rotation, it automatically calculates the new center of rotation and positions it more accurately. However, this variation is usually of the subpixel order. The whole alignment method takes about one minute without any user intervention. It is also showed that if the start projections are within the field of view, the process usually reaches the stopping criterion with only two iterations, as showed in Fig. 10.

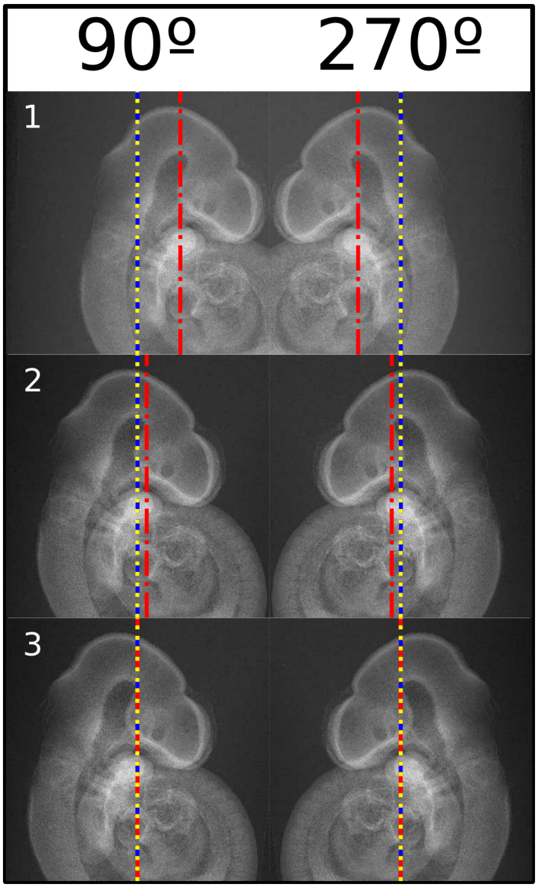

Figure 11: Iterations for sample alignment at 90 and 270 degrees. In yellow is the center of detector, blue is the axis of rotation and red is the center of the sample.

CONCLUSION

The method presented in this work uses only the image generated by the beamline detector for the alignment process. This is a great advantage as it excludes the need to acquire high resolution positioning sensors. Another advantage is the adaptation of alignment resolution according to the image resolution, that is, the same algorithm can be used for both micro and nano-tomography experiments. This methodology can also be applied in parallel and fan-beam beamlines.

Applying this alignment method to the IMX beamline has proven to be a great help to users since they spend less time in the alignment process and also do not need to manually search for the COR before reconstruction, so all experiment steps can be automated. The alignment method is also a guarantee for small deviations in the automatic sample exchange robot, providing reliability in experiments without the user presence. Pitch and roll alignment was done manually and was time consuming, now this methodology make it faster and automatic.

MOGNO is the future X-rays nano- and micro-tomography beamline of SIRIUS, the new Brazilian synchrotron light source. MOGNO is being designed to run and process experiments in just a few seconds, so all of these improvements are designed to provide the least unproductive time and allow easy adaptation of new users. The next step for this project is to use this approach to create automated alignment for 360 degree experiments.

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