Remastering the imperfect home-made CT projections data for further reconstruction

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Abstract. We developed and implemented a few strategies to recover the faulty, randomly shifted, off-axis rotation sequence of projections images for the home-made computed tomography. Features detection, homography and other image transformation and processing tools from the open-source free and non-free OpenCV libraries in C++ were used. The developed methods, routines and implemented strategies could be collected into the standalone library for any home-made CT software packages.

1. Introduction
Computed tomography is the imaging tool of choice in healthcare and non-destructive sample analysis. The free access to the components of the CT scanner, the availability of the high performance computers as well as the ever-increasing number of publications on reconstruction algorithms make it possible to produce the CT scanners in numbers. Despite the steady growth in this equipment diversity and availability the cost for the complete CT scanner solution is still high. That explains not only the growing number of companies offering the complete solutions for CT, PET, X-ray tools but also a big number of homemade CT implementations. Additional boost to this process is given by ever-increasing processing power of CPUs and GPUs. The later come, nowadays, preconfigured for the ray tracing and other computationally intensive image processing algorithms.

Investigator who builds these setups from scratch and equips them with his own processing software would like to identify the most common imaging artifacts and distortions, what caused them and how to fix them. Many of these artifacts are introduced as early as at the projection recording stage, some of them came later at reconstruction. This knowledge provides valuable feedback for the future experiments planning. The essentials of this topic were covered in multiple sources, see [1] and [2]. We discuss the immediate corrections that needed to be applied to the sequence of already recorded images to recover the collected data.

2. Methods
In this paper we used our homemade X-ray projections acquisition setup complimented with the previously developed 3D data reconstruction software for data acquisition and reconstruction [3, 4]. For backprojection, the most popular and easy to implement yet very flexible and robust
FDK algorithm was used. The method represents the reverse of acquisition procedure and is shown on Figure 1.

The multiple projections were taken while rotating the rigidly coupled X-ray source and detector panel around the sample on angle $\beta$ each time. $XYZ$ is the laboratory frame associated with an observer and fixed sample. Another two reference frames on the figure are the rotating frames $(t, s)$ and $(t', s')$ binding the source point $S$ and detector/projection $R_\beta (p, \zeta)$ together. The first frame is created from the central backprojecting ray $s$ and the $t$ axis crossed at the right angle on the rotation axis. The second one is constructed from the tilted from the central plane ray $s'$ and the similar $t'$ axis. Axes $t$ and $t'$ are parallel and defined by the level at which $s'$ and $s$ rays are crossing the $Z$ axis. These two frames are introduced to quantify the contribution of the different data points on projection $R_\beta (p, \zeta)$ to the reconstructed slice voxel pointed by a vector $r'$ during backprojecting.

To partially reconstruct an $f (x, y, z)$ slice, arbitrary oriented across the sample, the data from a single line of the $R_\beta (p, \zeta)$ projection, is smeared along the oblique fan $f (t', s')$. Performing an obvious change of variables $(t', s') \rightarrow (t, s)$, that is connecting the oblique plane $f (t', s')$ coordinates with the cardinal, in-plane system $(t, s)$, one can write an expression for the projection data contribution to the particular point $r'$ in reconstructed slice as

$$f (t, s) = \frac{1}{2} \int_0^{2\pi} \int_{-\infty}^{\infty} \frac{D^2}{(D - s)^2} R_\beta (p, \zeta) \cdot h \left( \frac{Dt}{D - s} - p \right) \frac{D}{\sqrt{D^2 + \zeta^2 + p^2}} dp d\zeta,$$

where $D$ is the distance from the source $S$ to the axis of rotation. The $p$ and $\zeta$ are the distance from the rotation axis and elevation pertinent to the fan rays crossing with the axis $t'$. The $h(p)$ is the inverse Fourier transform of $H (\omega)$ where the later is given by

$$H (\omega) = |\omega| b_\omega (\omega), \text{ where } b_\omega (\omega) = \begin{cases} 1, & \text{if } |\omega| < W \\ 0, & \text{if } |\omega| \geq W \end{cases},$$

and $W$ defines the window’s size for the high-pass filter $H (\omega)$ in the Fourier space of the spatial frequencies $\omega$, see [1].

Rotating coordinates $(t, s)$ are fixed with respect to the source-detector couple and related to the stationary laboratory coordinates $(r, \phi)$ by the following expressions

$$t = x \cdot \cos (\beta) + y \cdot \sin (\beta), \quad s = -x \cdot \sin (\beta) + y \cdot \cos (\beta),$$

$$x = r \cdot \cos (\phi), \quad y = r \cdot \sin (\phi).$$
The process is repeated with all projections in the sequence, and, at the end of summation, the complete \( f(x, y, z) \) slice of certain thicknesses and spatial orientation is assembled from these different projections contributions, representing the process of tomosynthesis.

### 2.1. Recording Conditions and Sample Description

Unlike with professional medical CT scanners, the lab conditions usually assume that the X-ray source and detector’s panel are securely fixed and immobile with respect to the lab equipment. Multiple X-ray projections are now taken by rotating the sample by means of the sample holder and rotation stage. The equations (1)-(3) are still valid with the simple modification of \( \beta \rightarrow -\beta \).

There is one potential problem with this arrangement, see Figure 2(a). We plan the experiment with the \( Z \) axis of rotation perfectly aligned with the detector’s panel and the source, and confirm it by taken a measurement at the initial sample placement, see the blue dashed line. In real life, when the manual rotation starts, one figures out that the rotation takes place about another axis \( Z' \), see the red line. But this become obvious not before we reconstruct the data, already crippled by this off-axis rotation.

The best efforts are made to place the sample and its real rotation axis \( Z' \) according to the plan of experiment, that is along the \( Z \) axis, and then supply the projections data to the reconstruction software. Nevertheless the \( Z \) and \( Z' \) axes are rarely aligned and all parts of the setup tend to be shifted rather randomly during rotation and exposition stage [5]. This causes a few typical artifacts which are able to completely destroy the scout set of data and is the topic of our further discussion.

The sample is the 3D printed human tibiofemoral joint. The height of the joint’s image, projected on the 42.7 cm by 34.4 cm detector, is about 180 mm and its width at the widest part is about 115 mm. The distances between the source to the sample and between the sample to the detector were 140 and 70 cm correspondingly. Taking into account the 1 : 2 magnification ratio introduced by the recording scheme, it is close to the regular male knee size, see [6]. The overall 113 projections were taken separated by the manual rotation of the sample on 2 degrees clockwise if seen from the top.

Figures 2(b) and (c) show two typical projections of our sample, treated for the brightness and contrast levels and trimmed for a better display. On the upper right part of the Figure2(b) one can clearly see the patella, also known as the kneecap, attached with two metal pins to the femur. The fibula is attached to tibia by a single pin, see the bottom right parts of the Figures 2(b) and (c). Two other pins are used to hold the two parts of the tibia together as a whole. The material of the sample corresponds to the regular polycarbonate 3D printer supplies.

The G-297 rotating anode X-Ray tube and PaxScan 4336W v4 flat panel detector, both from Varex Imaging, were used for this experiment. The hardware was salvaged from the airport security scanner.

Our implementation of the backprojection equation (1), assumes the CPU multithreading with MSMP libraries [3]. Conventionally, the CPU multithreading is included explicitly as a part of the CBCT package and implicitly in the specific image processing packages. Desktop PC with the 8-core Intel(R) Core(TM) i7 – 4790K CPU @ 4.00GHz and 32 Gb RAM was used to run reconstruction software.

### 3. Results

There are two most common acquisition errors caused by the manual sample rotation and positioning. The first is made when the sample or/and the detector panel are accidentally and randomly shifted back and forth or sideways with respect to the main line of view defined by the source. The second is made when the sample is rotated around some \( Z' \) axis which actual position is unknown and treated by reconstruction software as the different \( Z \) axis, see the previous discussions of Figure 2(a). Let us call the first “the random projection shifts” and
Figure 2: (a) Experimental setup and recording conditions, not drawn to scale; (b)-(c) Typical projections taken at 94 and 166 degrees rotation angles correspondingly.

On the next Figure 3 the imaging artifacts from these two acquisition errors are shown in combination and separately. On Figure 3(a) one can see the case when two of these errors are combined and reconstructed slice is completely unreadable. Isolated, that is without the off-axial rotation, the rotation axis shifts during the projections recording still completely destroy the reconstructed slice on Figure 3(b). The off-axis rotation, presented in the otherwise perfect image sequence, resulted in the reconstructed slice smeared in a spiral fashion, see Figure 3(c). Figure 3(d) shows the slice reconstructed from the projections sequence treated for both of theses errors.

In the first case, in order to compensate for the non-negligible sample projection’s shifts relative to the detector and not associated with rotation itself, we need to carefully choose the features which will be realigned with selected points in the reference image for each faulty projection. In our simple case the shifts happen in plane parallel to the detector and these features were chosen to be the edges of the sample holder. On Figure 4(a) they are marked with
the arrows of different color and length. The sample holder is the uniform metal cylinder and its projection keeps its basic shape irrespectively of the rotation angle which makes it the best candidate for the role.

OpenCV library provides the functions for proper ROI (region of interest) selection, image thresholding, image’s features detection algorithm etc. We used the Harris corner detection algorithm as `cv::cornerHarris(strip_roi, corners, blockSize, apertureSize, k, BORDER_DEFAULT)` which works perfectly well in simple ROIs for the edge detection as well. The `strip_roi` is taken to be the compact rectangular strip area including the cylinder sample holder only and the typical values for the `blockSize, apertureSize` and `k` are 10, 21 and 0.04 correspondingly. Here the `cv::Mat corners` object is to be filled with the image of detected corners and `BORDER_DEFAULT` is the pixel extrapolation method, see [7] for the full description of method.

After the edges of the sample holder’s shade in the misplaced and pivot projections were found this information is used to calculate the back-shift of the current projection in order to match it with the pivot, see Figure 4(b). The first projection in series was selected as the pivot or the reference image.

\[ h = \text{findHomography}(\text{srcPoints, dstPoints, method}) \]

\[ \text{warpPerspective} (\text{src, dst, h, OutputImageSize}) \]

Figure 4: (a) Two typical projections are randomly displaced in the detector’s plane before the alignment; (b) The same projections after the alignment. The edge features used for calculated shift are indicated by different color arrows. The most left projection, marked with the red arrows, is used as the pivot. The size of the images corresponds to the size of the detector. One can see that only the portion of its surface is occupied by a projection.

The similar results could be achieved by using homography transformation. This tool should be considered if the trajectory of the rotating sample in space is quite complex and includes the sample moving back and forward from the detector significantly. In this case the size and orientation of the reference feature are changed as well.

For the small, parallel to the detector, shifts of the sample, the homography transformation is again extracted from the sample holder’s image only. After finding the homography `h` transformation for the selected reference feature, using `h = findHomography(srcPoints, dstPoints, method)`, the transformation data is applied to the whole projection, i.e. to the `src` image, using the `warpPerspective(src, dst, h, OutputImageSize)` function. As the output we get the `dst` image aligned with the pivot. Before all these, the matching features, i.e. `srcPoints, dstPoints`, between the pivot (reference) and current (to be
corrected) images should be found using the ORB class implementing the keypoint detector and descriptor extractor, see the manual pages in [8] for other parameters explanation. This method produces roughly the same results as before, see Figure 5(a)-(b).

Some scaling takes place because the sample, together with the sample holder, does move farther and closer to the detector, resulting in different sizes and orientations of its projection, and this is compensated by homography transformation. This effect of homography transformation may be observed as an appearance of the shaded strips around the image after transformation telling us that some shrinking or perspective transformation took place, see Figure 5(b).

However, this method should be used with caution, because if we expand the ROI for homography transformation search over the whole sample, it will transform the whole image, completely destroying the rotation information. On Figure 5(c) one can see how this happens and the images of the rotated metal pins have been perfectly converged to each other, though for the correct backprojection these images should not be completely realigned.

![Figure 5: (a) Two different, taken at different angles, randomly shifted projections; (b) The same projections treated with homography transformation computed from the sample holder’s image displacement only; (c) The same projections treated with homography transformation calculated from the whole image.](image)

Multiple free and non-free feature detectors like SIFT (nonfree module), SURF (nonfree module), FAST, STAR, MSER, Dense and BRISK, the same name descriptor extractors plus BRIEF and FREAK, the descriptors matchers like BruteForce, BruteForce-Hamming etc., are offered in OpenCV beside the ORB. Usually, the non-free only means that the developer should obtain these libraries by himself and deal with the potential patent issues in his country if he builds this software for commercial use. Otherwise they are free to download and use in your applications.

The second error came from the off-axial rotation. That is when the sample is rotated around the $Z'$ axis which different from the $Z$ axis that was included in the experiment design and supplied to the reconstruction software. In the simple case of the parallel $Z$ and $Z'$ axes, it is treated straightforwardly by introducing the 2D displacement vector for the misaligned coordinate systems $XYZ$ and $X'Y'Z'$ in the numerical version of the Equation (1) of the reconstruction software. In fact, this may be much easier than to aim for the perfect $Z$ and $Z'$ axes alignment. The arbitrary tilted $Z'$ case requires slightly more complex coordinates transformation through the Euler’s angles and is not considered in our paper. The arbitrary
tilted $Z'$ axis is rarely the case and needed to be considered only for the sake of generality and is the case of a bad experiment planning.

The FOV shift, which inevitably appears in the reconstructed slice as a result of the axis misalignment compensation, is corrected at the final stage of the reconstruction by correcting the $x$ and $y$ values assumed to be present in the left, $f(t,s)$ part of the equation (1). Together with this option, our software package provides the means to choose the slice thickness, its orientation and image filtering techniques.

The limited number of expositions, that is the 133 projections with 2 degrees step, did produce a decent image quality assuming all the corrections were made to compensate for the image jitter and off-axis rotations.

There were multiple intermediate image preprocessing and postprocessing steps provided by OpenCV including but not limited by the following:

- Original image brightness and contrast correction through the regular expression $g(i,j) = \alpha f(i,j) + \beta$. Though its written as a voxelwise expression the operations are done with the complete matrices $g$ and $f$ at once. Optimization and calculation speed up is provided by the OpenCV library.
- Cutting and pasting the ROI (region of interest) from original image with cv::Rect() and cv::copyTo() functions.
- Color scheme conversion cv::convertTo().
- Thresholding of the reconstructed slice with severe contrast deterioration caused by a metal object and by other acquisition artifacts using cv::inRange() and similar functions and image matrix expressions. On Figure 6(a) and (c) one can see the classical example of this artifact when the limited range of the brightness values is dominated by the heavy absorbing object like a metal pin. In order to reveal the modest variations in our bone sample’s density, one could assign to the area of the metal pin the average brightness of the sample or the zero values, effectively shifting the dynamic range of the brightness levels to the actual bone structure and to make visible the minor variations in sample density.

![Figure 6: (a)-(c) Coronal and sagittal slices of the sample before the thresholding, (b)-(d) The same slices after the proper dynamic range adjustment has been introduced.](image)

The last group of pictures from Figure 7, represents a series of coronal slices taken one by one starting from the bottom of the sample, all the way up to its top. On the last pictures of the top and bottom rows, one can also notice the the inner structure of the sample substituted with the 3D printed square mesh like structure. Pictures 2 and 7 have been thresholded to exclude the metal pins artifacts.

4. Conclusions

We explored the most common artifacts met in the homemade CT experiment and made during the experiment planning, acquisition stage/image data collection and reconstruction. Recording
Figure 7: Coronal slices from a sample of equal thickness and different locations, taken from bottom to top, are shown in a successive order left-to-right and top-to-bottom. Several slices have been thresholded to remove metal objects shadows from an image.

and processing the artificial, 3D printed human tibiofemoral joint sample projections sequence, we demonstrated the working solution for how to fix the original, non-perfect X-ray images sequence before the slice reconstruction and during the backprojection stage to get a perfectly readable and informative slice data. The simple set of procedures allows us to salvage the otherwise lost data and helps to plan a better experiment in the future.

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