

JOINT INSTITUTE FOR NUCLEAR
RESEARCH

DZHELEPOV LABORATORY OF NUCLEAR PROBLEMS

FINAL REPORT ON THE SUMMER STUDENT PROGRAM

Calculation of the rotation axis
projection in X-ray μ CT

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1 Abstract

The reconstruction problem in X-ray μ CT is studied. Reconstruction program based on the open-source library RTK is developed. Different methods are proposed to calculate RAP (rotation axis projection) using radiotomographic images. Speed and output image quality determined by the contrast are compared. Program that simulates CT scan is developed and deployed on a cluster to gain ability to compare ideal experimental setup with real conditions.

2 Introduction

GaAs group of the Laboratory of Nuclear Problems is studying semiconductor detectors based on GaAs, Medipix electronics and its application in medical and geological problems. MARS (Medipix All Resolution System) scanner is used to produce tomographic images of the studied objects.

The MARS scanner incorporates the Medipix detector chip, a new generation x-ray detector[1]. It has been developed by the Medipix3 Collaboration, which comprises CERN in Geneva and 18 research institutions worldwide. CT (computed tomography) scanner makes a series of radiographic two-dimensional images taken around axis of rotation. Digital geometry processing is used to generate a three-dimensional image of the inside of the object.

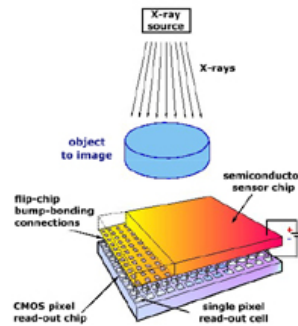


Figure 1: X-ray μ CT scanner

During the practice I was engaged in 3 tasks:

1. Development of the reconstruction program based on the open-source software RTK.
2. Research of methods for determining one of the reconstruction parameters using only projection images.
3. Simulation of the CT scan using Geant4 toolkit.

3 Reconstruction

The Reconstruction Toolkit (RTK)[2] is an open-source and cross-platform software for fast circular cone-beam CT reconstruction based on the Insight Toolkit (ITK). RTK is developed by the RTK consortium. RTK provides basic operators for reconstruction, multithreaded CPU and GPU versions, preprocessing of raw data.

RTK uses its own geometry format based on the international standard IEC 61217[3] that has been designed for cone-beam imagers on isocentric radiotherapy systems, but it can be used for any 3D circular trajectory. All previously used reconstruction programs were based on different geometry format. Our main problem was to calculate the required parameters using the measured values of the scanner geometry.

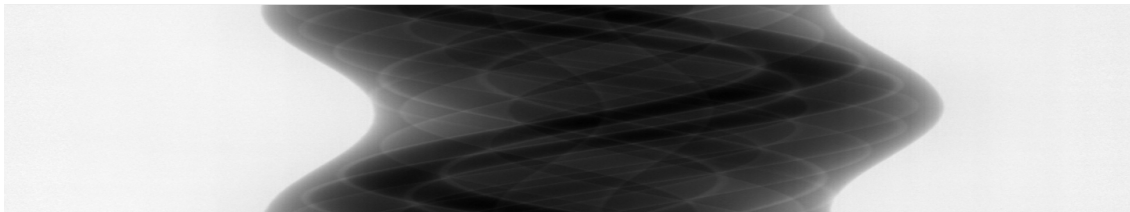


Figure 2: Example of a sinogram

The core of our reconstruction is written on C++, python scripts are used to generate geometry configuration files and deal with file management. RTK provides several algorithms for CT reconstruction. Algorithm FDK[4] was chosen because its different implementations worked previously, in future it is expected to use different methods of reconstruction[5].

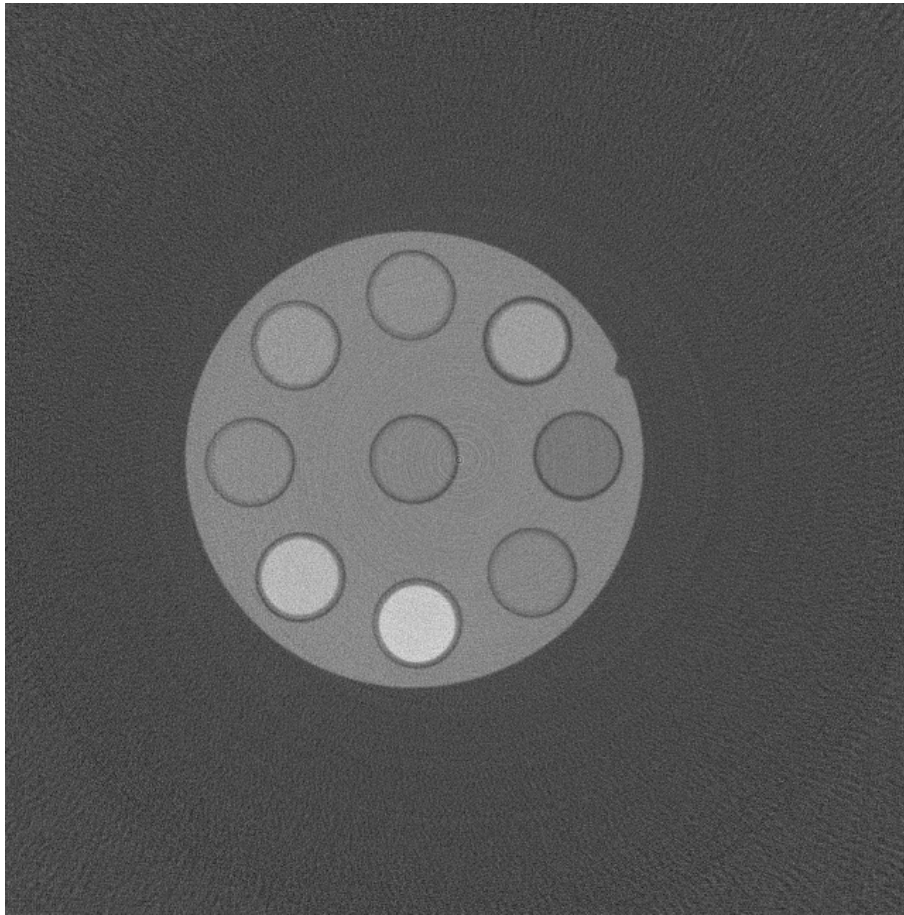


Figure 3: Example of a slice of reconstructed volume

4 RAP determination

RAP = Rotation Axis Projection - is one of the parameters used by reconstruction algorithms. Quality of the output image is highly sensitive to the correct selection of this value. For good contrast and sharpness it is required to set RAP to within tenth of pixel, while its value is of the order of hundreds of pixels.[6]

The great value has the task of determining the RAP using only projections or sinograms from CT scanner without any direct measurement. Several concepts of solving this problems were proposed and implemented. All of them

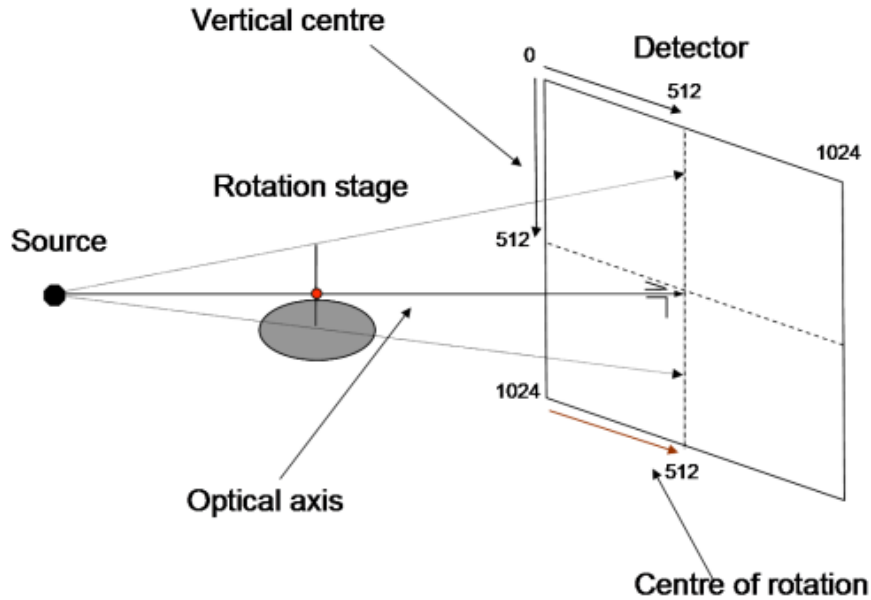


Figure 4: Geometry of CT scan

used sinogram profile - sum of the values of pixels on each column of the sinogram. As a result, profile is an array of numbers of a length equal to the width of sinogram.

First two proposed methods share the same concept of background cut and analyzing the object part of sinogram. Sinogram is filtered to eliminate noise contribution. Background level is determined to distinguish object from everything else. First way to find RAP value is to evaluate the middle point of the object. Another proposed method expects to determine RAP by computing the center of mass of the object using the values of the profile points as weights.

Detailed description of the algorithm "Middle of the object":

1. Filter the profile:
Divide the profile by small groups consisting of 10 points. Fit each group using fifth-order polynomial. Calculate root mean square of the differences between values of the profile and values calculated using

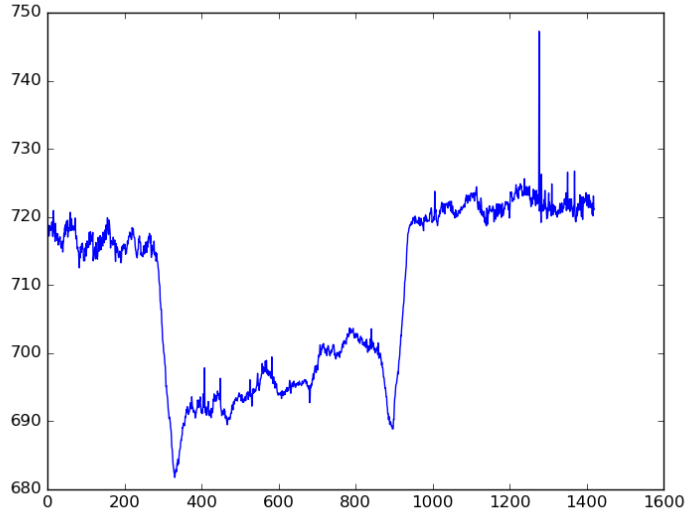


Figure 5: Profile with considerable noise

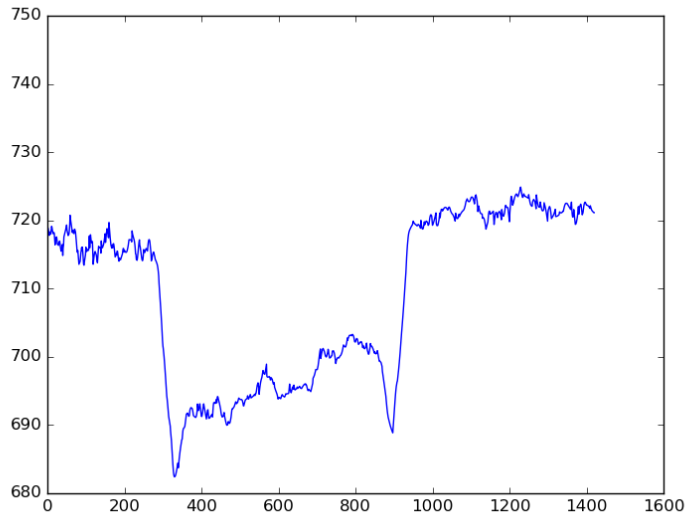


Figure 6: Profile after filtration

fitting polynomial. All points that differ from the fit function more than this threshold are considered to be noise and are removed.

2. Calculate the background value:
Make a linear interpolation of the first 10 and last 10 points of the filtered profile. In our case fit line has relatively small slope coefficient in comparison with intercept value. This intercept coefficient is further used as background level.
3. Subtract the background level from all values of the profile.
4. Calculate standard deviation of the values of the profile. Further it is used as object threshold.
5. All profile points with value module greater than object threshold are considered to belong to the object. Find the most left and right points of the object and calculate the average of the positions of these points. This value is further used as RAP approximation.

Detailed description of the algorithm "Center of mass":

1. Do the stages 1 - 4 of the algorithm "Middle of the object" and locate object points in profile.
2. Compute the center of mass of the object using the positions of its points and their values as wights. Use this value as RAP approximation.

The other method is connected with the symmetry of the sinogram. There is no exact symmetry in the sinogram but some point can be roughly considered as the symmetry axis. We measured symmetry using the differences between values in points that are equidistant from the studied point. This method gave us the best approximation of RAP but required far more time. Symmetry maximization was performed using Python library SciPy.

Detailed description of the algorithm "Center of symmetry":

1. Divide the profile by small groups consisting of 10 points. Fit each group using fifth-order polynomial. This allows to compute the value of any point with rational position.

2. For every point of the profile build a grid of points with step of 1 pixel covering the whole profile. Coordinates of the points can be rational, in this case polynomial approximation is used.
3. Calculate the differences between equidistant points on the grid that are located on the left and right sides of the given point. Sum the squares of these differences. This sum is further called nonsymmetry of the point. Obviously nonsymmetry equals zero for the center of symmetry if it exists because values of the equidistant points are equal.
4. Use any minimization algorithm to find the point of the profile with least nonsymmetry. Center of the profile can be used as initial value. Our program used COBYLA (Constrained Optimization BY Linear Approximation) algorithm from SciPy.

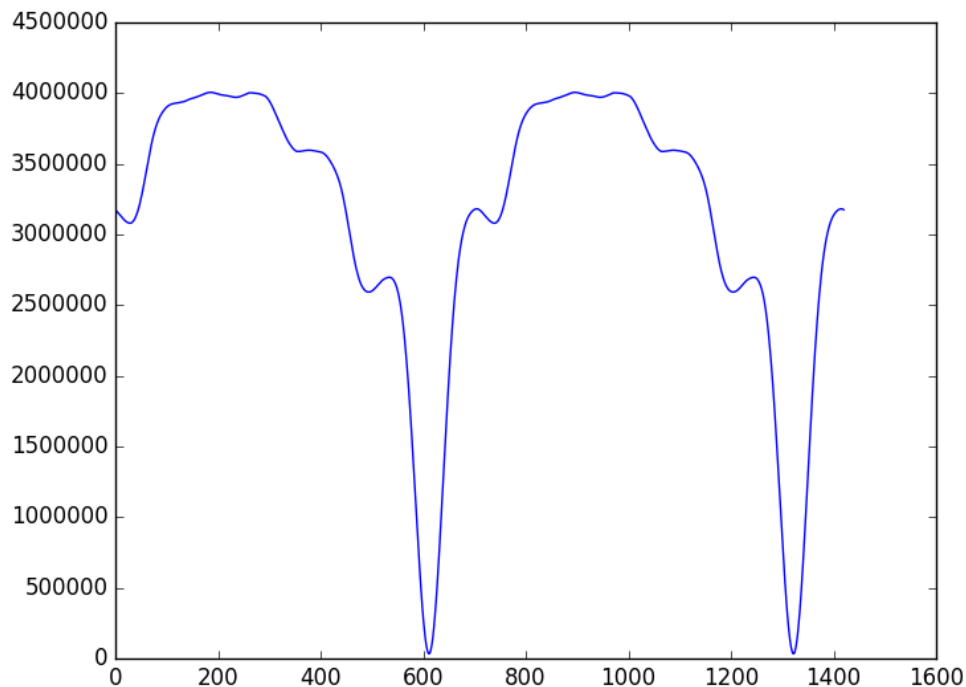


Figure 7: Nonsymmetry as a function of profile point

Our main goal was to test all proposed methods and make a comparison in speed and quality. Contrast of the output image was used as quality measure. Contrast was defined as standard deviation of the pixels of the image[7]:

$$Contrast = \sqrt{\frac{1}{MN} \sum_{i=0}^{N-1} \sum_{j=0}^{M-1} (I_{ij} - \bar{I})^2}$$

where intensities I_{ij} are the i-th j-th element of the two-dimensional image of size MxN. \bar{I} is the average intensity of all pixel values in the image.

Our final way to determine RAP is to maximize the image contrast. Obviously, this method requires much more time because it calls reconstruction algorithm dozens of times but it provides the best result if there are only small image artifacts.

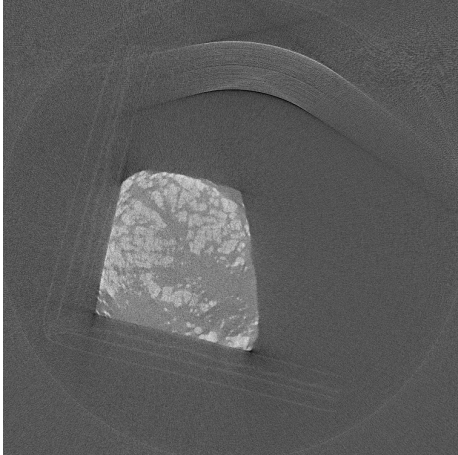


Figure 8: Contrast = 0.0409

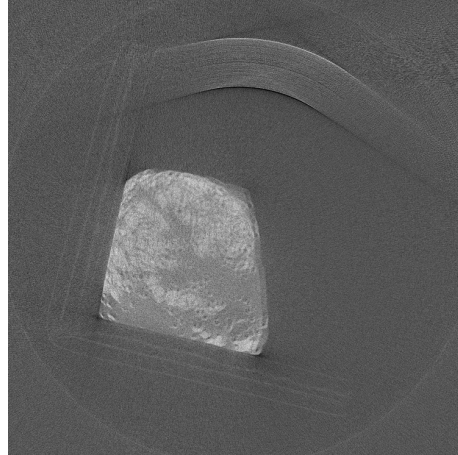


Figure 9: Contrast = 0.0403

All RAP calculation algorithms were tested on 6 scans. The final results of the comparison:

1. Two algorithms with object selection are the fastest. Calculation of the center of mass requires a bit more time, results are similar. Symmetry maximization demands from five to ten times longer.

2. Symmetry maximization usually provides the best RAP approximation (except method using contrast). Nevertheless, for a number of scans it gave not the best result.
3. With correct geometry parameters the best RAP value is different from the symmetry approximation no more than a pixel. But if some geometrical values are not accurate, best RAP might be considerably different to compensate errors of the geometry config.

Scan number		1	2	3	4	5	6
Width		716	1567	2196	2292	1232	1952
Center of mass	Time by 1 sin, s	0,237	0,507	0,761	0,826	0,434	0,399
	RAP	267,847	682,185	994,834	1087,19	514,311	1029,54
	Contrast	0,0188	0,01637	0,02538	0,03517	0,03894	0,01142
Middle of the object	Time by 1 sin, s	0,236	0,509	0,663	0,705	0,381	0,345
	RAP	275,5048	682,558	995,266	1089,44	514,383	1030,03
	Contrast	0,0187	0,01632	0,02537	0,03473	0,03896	0,01141
Center of symmetry	Time by 1 sin, s	1,131	2,051	3,018	4,101	1,614	2,458
	RAP	260,876	682,208	995,208	1089,59	515,225	1030,09
	Contrast	0,0191	0,01639	0,02537	0,03469	0,03912	0,01141
Contrast maximization	RAP	261,838	685,419	996,649	1087,73	518,276	1007,91
	Contrast	0,0192	0,01651	0,02548	0,03527	0,03984	0,01222

Table 1: Comparison of different methods

5 Simulation

The other important task was to make a simulation of CT scan. Our simulation program is written in C++ language using the Geant4 toolkit to simulate passage of γ rays through the matter[8]. Execution of this program demands huge computational resources. Because of this, it was essential to run it on a DLNP cluster.

Our program simulates the real scan of the multi-contrast phantom for material decomposition, calibration and quality assurance. This object is a cylinder containing 9 tanks with different liquids: solutions of gold, calcium, gadolinium, iodine, lipid and water. Each liquid is placed on Eppendorf tube - 0.2 ml polypropylene PCR (polymerase chain reaction) tube.

Simulation produces projections of the object like the real CT scanner.

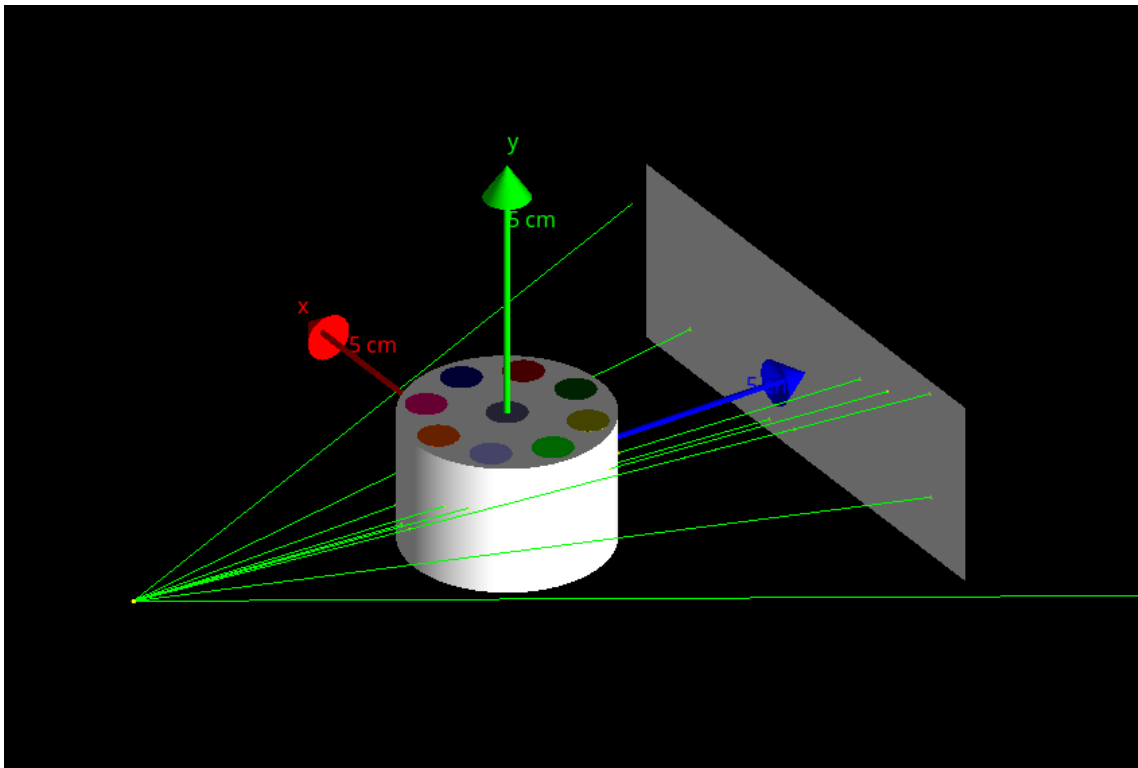


Figure 10: Simulation of the scanning procedure

Volume of the simulated phantom was reconstructed using RTK. It represents ideal scanner without any X-ray tube defects, ideal energy resolution

etc. This result can be used to analyze the impact of real life defects in the reconstructed volume.

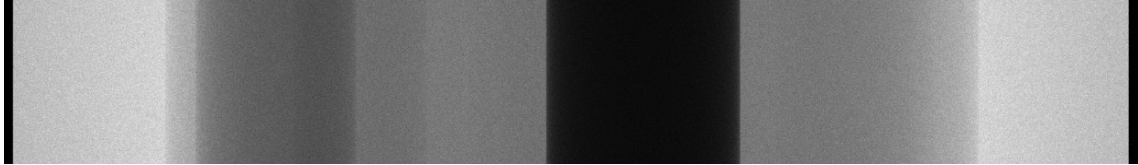


Figure 11: Example of simulated projection image

6 Conclusion

Reconstruction program was developed and tested on the data provided by our MARS scanner. It is both fast and open-source unlike proprietary software that was used before. In future it is planned to test other algorithms of volume reconstruction.

Several methods of RAP calculation were developed, tested and compared. This task is of great importance because most of the open-source reconstruction software doesn't provide you any methods to determine parameters such as RAP without direct measurements. At the same time, manual measurement is often inaccurate and difficult to implement. Algorithm "Center of symmetry" gives the best RAP approximation while other two are fast and can be used for initial RAP value for iterative search based on contrast. Simulation task was completed and its results are ready for analysis and comparison with real experimental data.

7 Acknowledgments

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