

Automated processing of series of micro-CT scans

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Abstract

For some applications of high-resolution X-ray Tomography (micro-CT) scanning, a large set of similar samples is to be analyzed in order to obtain statistically significant results. The complete process, including the micro-CT scan itself, the reconstruction and the analysis is almost identical for every sample. However, in a typical workflow every step is manually performed for every individual sample. This could be optimised by automation of this process, which results in less human intervention and thus a smaller cost and a lower risk to human error. We developed a reliable method to semi-automatically scan several stacked samples and automatically reconstruct the resulting series of data sets. The reconstruction step includes the manual reconstruction of one data set in order to optimize the reconstruction parameters, which can then be used for the rest of the batch. In future work, the automatic handling of the next step in the micro-CT workflow, 3D analysis, will also be improved.

Introduction

At the 'Centre for X-ray Tomography' of Ghent University (UGCT; www.ugct.ugent.be) a wide variety of samples is imaged at different state-of-the-art home built micro-CT systems. For some applications, a large number of similar samples need to be scanned in order to obtain statistical relevant results (Mader *et al.*, 2011). This is quite common in (bio-)medical applications, where for example specific parts of small animals are imaged. Conventionally, these samples must be properly positioned, scanned and reconstructed one by one. Given the desired resolution and the sample size, the sample has to be positioned accurately on the rotational axis, which requires human intervention due to the variation between samples. This causes a large number of delays in the scanning procedure, and makes scanning without human supervision impossible. After acquisition, the raw projection data needs to be reconstructed, yet most software packages do not allow for batch processing. The goal of this research was to limit the amount of human intervention in CT scanning and processing and to even be able to scan and process multiple samples without intervention of the operator and without the presence of an automated sample mounting system (Mader *et al.*, 2011).

Methods and results

A simple method to improve efficiency without complicated automated sample mounting is by vertical stacking. In this method, multiple samples are mounted on top of each other and subsequently scanned one by one. However, precision positioning systems mounted on the rotation stage often have no absolute positioning, hence automatic centering based on this can not be separately performed for each sample. To overcome this issue, we have developed several methods to perform the centering for

stacked objects without absolute positioning. This is easily implemented at the home built scanners at UGCT, because they are controlled by in-house developed software, which gives the opportunity to modify the acquisition schemes.

Before scanning a batch of stacked samples, the vertical position of each sample has to be specified and two reference images for each sample, separated in angle by 90°, are made. During the execution of the scanner script, the sample is moved to the correct height and a test image is made at the first rotational position. By comparing the test image with the reference image, the sample is moved to obtain a better agreement. This procedure continues until the test images corresponds sufficiently with the reference image. At that moment the x-position of the sample is optimised. The same methodology is done at the second angular position using the second reference image to optimize the y-positioning. If needed, this procedure can be executed iteratively in order to optimize the result.

For the comparison of the test image and the reference image, two possible techniques are investigated. The first method is based on the calculation of the centre of mass of the images, for example a horizontal strip. The method is designed to be able to adjust the horizontal position of the sample, so only the horizontal component of the centre of mass is relevant. Therefore the grey values of all the pixels within one column are summed, column by column. The centre of mass (COM) is defined as

$$COM = \frac{\sum_{columns} im_i}{\sum_{columns} m_i},$$

with i , the index of each column and m_i the mass of every column, defined as $m_i = -\ln(\text{columnvalue}_i)$. By neglecting the vertical component, the computing time is significantly reduced. Figure 1 shows the centre of mass of several normalized projection images. It is important to note that this centre of mass depends on the amount of material which is out of the field-of-view.

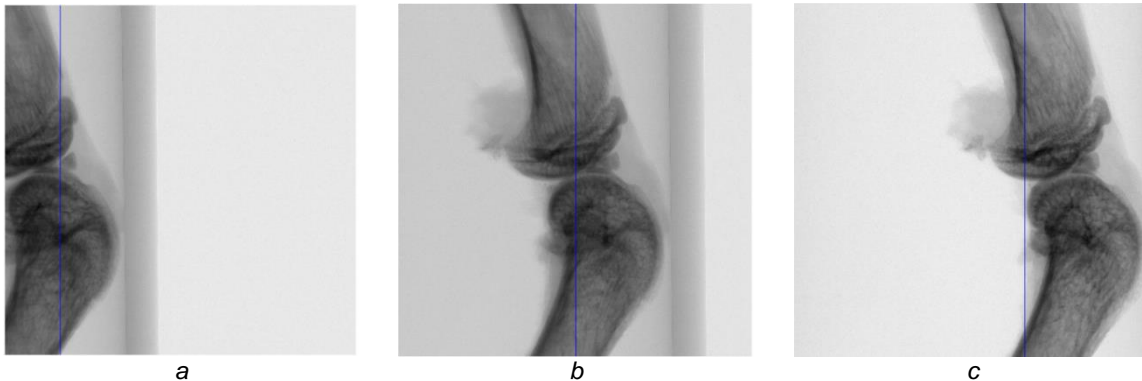


Fig. 1. The blue line indicates the x-component of the centre of mass of normalised projection images.

The difference between the centre of mass of the two images gives an indication of how far the sample is situated from its ideal position and whether the correction needs to be done in positive or negative direction. To speed up the correction, the distance between the centre of mass of both images is used as input to the relative movement, yet this is not necessary for the proper operation of the method. If the object under

investigation is prone to a mass being outside the field-of-view, the script foresees in an automated reduction of the geometrical magnification.

The second method is to compare the obtained image at a specific location with the reference image by summing the square of the differences (SD) between each pixelvalue. This also gives a good idea of the deviation between the two images but gives no information of the direction in which the sample has to be moved to improve the sample location. This effect is clearly shown in figure 2. Therefore, the first method is the one currently used at UGCT.

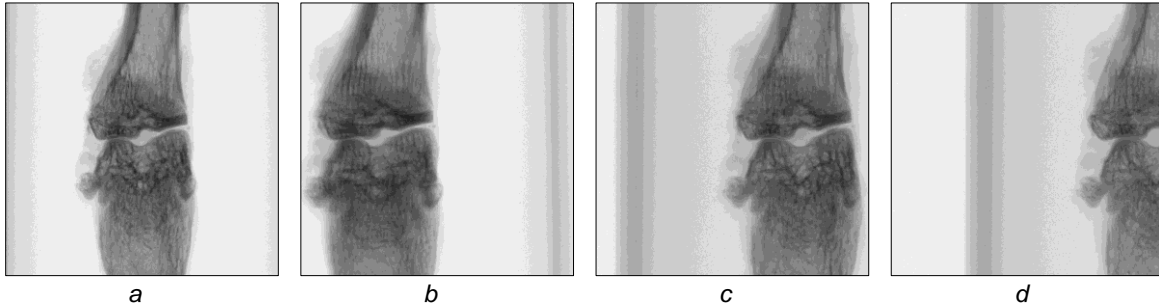


Fig. 2. Figure a is the reference image. Figures b, c & d have similar SD values, (respectively, $SD = 60282$, $SD = 62138$ and $SD = 61028$), but they all are located on different positions, which makes it almost impossible to use this method to adjust the sample position.

To avoid infinitely repositioning and diverging movements, the number of steps to obtain the ideal position is limited to a user-defined number.

Another issue with a large number of similar scans is the reconstruction and analysis. Previously, the data was reconstructed per scan using Octopus Reconstruction (Inside Matters, www.octopusimaging.eu). This allowed for a high degree of optimization, but is a time-consuming and tedious method. Additionally, this is prone to human error. We used the Software Development Kit (SDK) of Octopus Reconstruction to develop a framework to automate this process. This framework allows for setting the optimization parameters determined using the Octopus Reconstruction Graphical User Interface (GUI), hence the reconstruction quality can remain similar. The GUI of the batch reconstruction tool is shown in figure 3. The reconstruction of the first scan needs to be done manually. The parameters used for the first reconstruction, such as tilt, skew and beam hardening correction, are the input parameters for every following sample.

For future research, the automation of the analysis of the scans will be investigated. This will drastically reduce the human time spent on 3D analysis, and reduce the operator dependency in repeated studies.

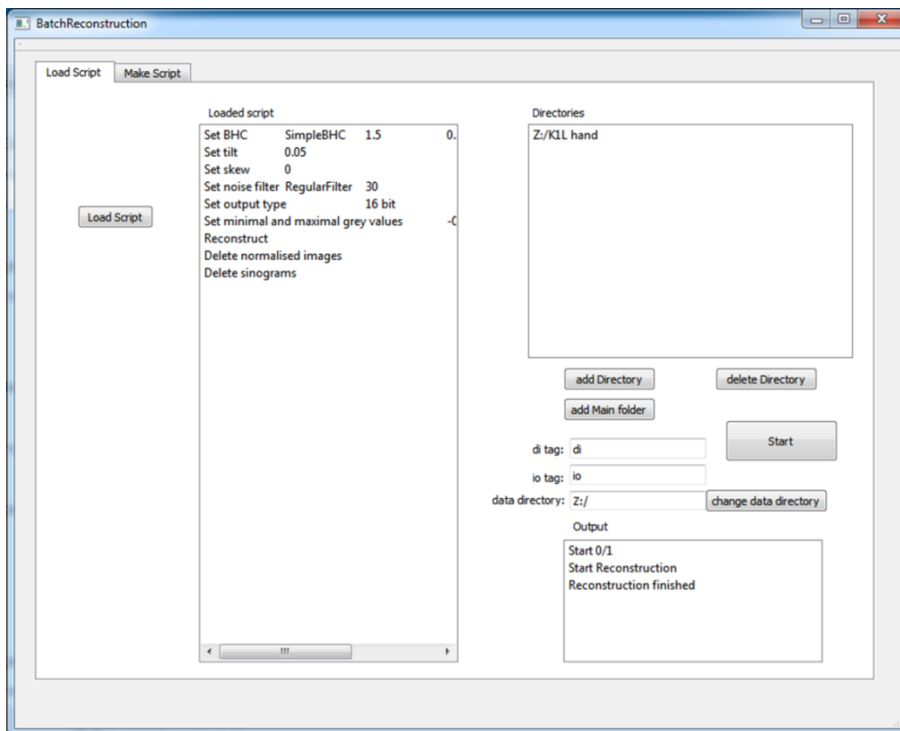


Fig. 3. *Gui of the batch reconstruction tool*

Conclusion

A part of the complete scanning process of a large set of similar samples has been semi-automated. Multiple samples are vertically stacked and sequentially properly positioned and scanned. The amount of samples that can be scanned during one run is limited by the available vertical stacking space. Next to the scanning itself, the reconstruction has also been semi-automated. The first dataset of a batch is manually reconstructed and the obtained parameters are used for the automatic reconstruction of the remaining data sets.

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