Bone segmentation using discrete tomography

E. Van de Casteele¹, K.J. Batenburg¹,², P. Salmon³, and J. Sijbers¹

¹ IBBT-Vision Lab, University of Antwerp, Universiteitsplein 1, 2610 Wilrijk, Belgium,
² Centrum Wiskunde & Informatica, Science Park 123, 1098 XG Amsterdam, The
Netherlands
³ SkyScan, Kartuizersweg 3B, 2550 Kontich, Belgium

Aims
Bone studies in X-ray micro-computed tomography (CT) are targeted towards analyzing a
stack of virtual slices and calculating bone parameters in order to assess the differences in
structures between, for example, control and diseased animals. Due to the small number of
different materials under investigation, bone studies are ideal for discrete tomography, which
is a new reconstruction technique. This method can be applied if the scanned object is
known to consist of only a few materials; the prior knowledge on the grey values of each of
these materials is then exploited to obtain a reconstruction that contains only these values.
Reconstructing a stack of images with only a discrete set of grey values avoids the subjective
segmentation step of global thresholding, mostly used in bone studies. A second advantage
is that discrete tomography generally requires fewer projection images due to the use of prior
knowledge. This is important when dose constraints determine the image quality, which is
the case for in-vivo small animal studies.
The aim of this work is to present the first results on a real 3D dataset using the Discrete
Algebraic Reconstruction Technique (DART). A comparison is made of the calculated
trabecular morphometric parameters on the datasets obtained with the standard
reconstruction and segmentation methods and with discrete tomography, both using 100%,
50% and 25% of the commonly used number of projection images.

Method
Sample material:
In this study, the sample under investigation is the distal femur of a control mouse. The soft
tissue was removed from the bone as much as possible, after which the bone was stored in
70% alcohol. When scanning the sample, it was wrapped in saline-soaked gauze to avoid
drying.

Micro-CT scanning:
The bone was scanned using a SkyScan 1172, a high resolution desktop X-ray micro-CT
system. As a consequence of the cone beam geometry of the system, the distance of the
sample to the source determines the magnification, which was set so that the bone stayed
within the field of view of the detector for the full rotation cycle. By using camera binning, i.e.
4 by 4 pixels taken together giving 1000 pixels on a detector row instead of 4000, an
isotropic pixel resolution of 4.98µm was obtained. In order to have an optimal contrast in the
images, the source voltage was set at 40kV. Furthermore, a 0.5mm aluminium filter was
used to restrict the X-ray spectrum to a more monochromatic range reducing the beam
hardening effect. A frame averaging of 2 and a rotation step of 0.5º, covering a view of 180º,
were chosen to minimize the noise. The scan took 13 minutes.
Reconstruction:
The most commonly used method for the reconstruction of X-ray cone beam data is the algorithm described by Feldkamp, David and Kress (FDK). Although FDK is an approximate reconstruction method, the errors resulting from small cone angles are rather small and often acceptable. Additionally, FDK is computationally highly efficient and can thus offer very fast reconstruction speeds. For these reasons, FDK (often referred to as filtered back projection, FBP) is nowadays still the most used method.

Next to analytical reconstruction, there exist alternative approaches such as iterative reconstruction methods, which consider the reconstruction process as the optimization of a discrete representation of the object function in order to satisfy a system of equations that describes the imaging modality. If only a limited number of projections is available, if the sampling of the projections is not equiangular, or if certain orientations are missing, iterative methods can even provide reconstructions of higher quality than with FDK. Another advantage is their better noise handling. However, the main reason why they are not or only rarely used in X-ray μCT is the high computational burden. Currently these iterative techniques are accelerated using several GPU’s.

Within the field of Discrete Tomography, a new reconstruction algorithm, called the Discrete Algebraic Reconstruction Technique (DART) has recently been proposed with very promising results. DART is a reconstruction method based on iterative reconstruction techniques that includes prior knowledge on the grey values representing the materials under investigation. It directly reconstructs segmented images for further analysis. In other words the subjective step, used in e.g. bone studies, of selecting a threshold value can be avoided. This new reconstruction method has shown to achieve high quality reconstructions, even with a small number of projections. This is particularly interesting for small animal imaging using X-rays since the dose submitted to the animal imposes an important scanning constraint. In order to minimize the dose, researchers need to make a compromise in image quality due to the limitation on the scan time. With DART, fewer projection images can be used so that it would be possible within the same scan time to go to a higher frame averaging, thereby reducing the noise, or to choose a smaller pixel size obtaining a better resolution.

The following reconstructions were made:

<table>
<thead>
<tr>
<th>Parameters</th>
<th>FDK</th>
<th>DART</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>NRecon parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Beam hardening correction</td>
<td>30%</td>
<td>30%</td>
</tr>
<tr>
<td>Smoothing</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Ring artefact correction</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td><strong>Iterations</strong></td>
<td>NA</td>
<td>Initial SIRT = 100</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Update edges = 50</td>
</tr>
<tr>
<td></td>
<td></td>
<td>DART = 10</td>
</tr>
<tr>
<td><strong>Number of projection images &amp;</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>corresponding rotation step</strong></td>
<td>376 (0.5°), 188 (1°),</td>
<td>376 (0.5°), 188 (1°),</td>
</tr>
<tr>
<td></td>
<td>94 (2°)</td>
<td>94 (2°)</td>
</tr>
</tbody>
</table>

The NRecon reconstruction parameters were applied on the sinograms exported from NRecon and used for the iterative reconstruction. The DART algorithm (flow chart shown in Figure 1) alternates iteratively between a “continuous” update step where SIRT was used and discretization steps incorporating the prior knowledge of the grey values of the image. This prior knowledge was obtained from an initial SIRT reconstruction.
Parameter calculation:
For the quantitative analysis morphological parameters\textsuperscript{6,7} are calculated using CTAn. Several parameters are in common with histomorphometry: relative bone volume (BV/TV), trabecular thickness (Tb.Th), trabecular separation (Tb.Sp), trabecular number (Tb.N), and surface-to-volume ratio (BS/BV). Other parameters have been developed from micro-CT analysis of bone which are fundamentally 3D quantities and have no equivalent in 2D-based histomorphometry. These include for example the structure model index (SMI) which indicates the relative prevalence of plates and rods in trabecular bone and calculation of open and closed pores and number of objects in 3D.

Two steps are required for morphometric analysis of the reconstructed datasets: (1) binarisation and (2) the selection of the volume of interest.

The most widely used method in bone research for binarisation is the simple and quick method of global thresholding. This technique is generally adequate for obtaining morphometric data where the bone images are of sufficient quality. However the selection of the grey value for thresholding is crucial since it is directly related to the thickness of the binarized structures. Often this threshold value is chosen using calibrated thickness measurements, which is done by scanning a micro-CT phantom composed of four aluminium foils of 20, 50, 100, 250\textmu m embedded in a PMMA cylinder\textsuperscript{8}.

The selection of the region of interest (ROI) is the starting point of the morphometric analysis. An important and common example is the selection of the volume of trabecular bone at a standard trabecular site in a rodent bone, such as the distal femur metaphysis as investigated in this paper. The ROI was selected containing trabecular bone and marrow only, starting 393\textmu m above the growth plate and covering a region of 1.25mm in height (see Figure 2 (a) and (b)). The region of interest, on which the parameters were calculated, was kept the same throughout the different reconstructed datasets. 3D models were made for visualisation purposes using surface rendering (Figure 2 (c)).
Results and discussion

In Table II, the calculated trabecular morphometric parameters of the mouse distal femur for the six different reconstructions are shown.

Table II: Trabecular morphometric parameters in the mouse distal femur

<table>
<thead>
<tr>
<th>Number of projection images</th>
<th>Standard FDK</th>
<th>DART</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameter</td>
<td>Symbol (unit)</td>
<td>376</td>
</tr>
<tr>
<td>Percent bone volume</td>
<td>BV/TV (%)</td>
<td>5.76</td>
</tr>
<tr>
<td>Bone surface</td>
<td>BS (mm$^2$)</td>
<td>9.79</td>
</tr>
<tr>
<td>Bone surface to volume ratio</td>
<td>BS/BV (mm$^3$)</td>
<td>77.25</td>
</tr>
<tr>
<td>Trabecular Thickness</td>
<td>Tb.Th (mm)</td>
<td>1.05</td>
</tr>
<tr>
<td>Trabecular Separation</td>
<td>Tb.Sp (mm)</td>
<td>0.37</td>
</tr>
<tr>
<td>Trabecular number</td>
<td>Tb.N (mm$^3$)</td>
<td>1.05</td>
</tr>
<tr>
<td>Structure model index</td>
<td>SMI</td>
<td>2.46</td>
</tr>
<tr>
<td>Number of objects</td>
<td>Obj.N</td>
<td>175</td>
</tr>
<tr>
<td>Number of closed pores</td>
<td>Po.N(cl)</td>
<td>4</td>
</tr>
</tbody>
</table>

When comparing the results for FDK and DART using the full set of projection images, it can be seen that most parameters are similar. Differences are found in the bone surface, bone surface-to-volume ratio, and the number of objects. These differences can be visualized using 3D surface rendered models which are shown in Figure 3. The green DART model is shifted down over 5 pixels in comparison with the yellow FDK model in order to show the differences more clearly. The arrow in Figure 3 gives an example of the differences that are found at the thinner structures. These differences are due to the constraints used for obtaining the segmented images. With a global thresholding method, one threshold value was chosen with the assumption that every material above this threshold is bone. In order to
select smaller structures (having a lower grey value), the threshold value is lowered resulting in a thickening of the other structures. For discrete tomography however the prior knowledge on the grey values gives a much harder constraint. The selected value for bone gives a good segmentation for structures where no differences in grey values or partial volume effects are present. This explains the larger value for the number of objects and smaller BS and BS/BV for DART in comparison with FDK while the bone volume was the same.

![Figure 3: Comparison between the FDK reconstruction (yellow) and the DART result (green, shifted downward) both using 376 projection images for the reconstruction.](image)

The results using fewer projections show that BV, BS and Tb.N decrease for DART, while the number of objects increases, indicating a further loss in connections on the smallest trabeculae. However, for the FDK reconstructions, more parameters are influenced and the differences are often larger, especially using only a quarter of the projection images. For the standard reconstruction technique the BS, BS/BV, Tb.N, Obj.N and the amount of closed pores increase, while the Tb.Th and Tb.Sp decreases. The latter only when using 25% of the images, indicating an increase in noise. Iterative reconstruction techniques are known for their advantage in handling in a better way noisy data or data obtained from fewer projections explaining the larger differences for FDK in comparison with DART. The increase in noise for FDK 94 can also be seen in Table II with the dramatic increase in number of objects and in closed pores.

**Conclusion**
Discrete tomography is a promising new method for bone research especially for in-vivo small animal imaging where dose constraints are important. This paper presents the first results on a 3D dataset and proofs the strength and robustness of DART using e.g. only a quarter of the projection images in comparison with the standard reconstruction method. In ongoing research the DART algorithm is further improved to make it more resilient to partial volume effects, which will potentially allow to resolve small structures with high accuracy.
References: