

# A 2D Matching Method for Reconstruction of 3D Proximal Femur using X-ray Images

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**Abstract:** The femur shape reconstruction from a limited number of 2D X-ray images is a challenging task but it is desired as it lowers both the acquisition costs and the radiation dose. The aim of this paper is to use a small number of 2D X-ray images to reconstruct a 3D proximal femur surface without any prior knowledge of the shape model. The proposed method combines a 2D binary contour points coordinates and their normals to find the best matching between 2D point pairs. The obtained results are promising. The estimated error shows that it is possible to rebuild the proximal femur shape from a limited number of radiographs.

## 1 INTRODUCTION

Three dimensional patient bone models play an important role in pre-operative surgery planning and improved guidance during surgery, modeling and simulation. The pre-operative reconstruction of 3D anatomical models can be achieved using the direct 3D imaging modalities such as Computed Tomography (CT) (Gamage et al., 2011). However, the use of such imaging is restricted to a minor specific procedures; due to constraints placed by cost, availability and radiation risk. Thus, the diagnostics and planning of many interventions still rely on two dimensional (2D) radiographic images, where the surgeon has to mentally visualize the 3D anatomy of interest. A direct 3D imaging must be developed, as an alternative to current pure 2D radiographs, in order to assist the clinicians on their medical tasks (Gamage et al., 2011).

Literature on pre-operative reconstruction of proximal femur based on information collected through 2D imaging modalities can be divided into two subgroups. The first group methodology is based on 2D images and can be considered as Silhouette Intersection for 3D model reconstruction (Caponetti and Fanelli, 1993). The second group contains methods based on a prior knowledge of the anatomical structure as well as 2D images (Gamage et al., 2011).

A majority of studies require prior knowledge of the 3D anatomy model to guide the reconstruction process and to compensate the lack of information in 2D imaging modalities (Gamage et al., 2011). This information can be provided by the integration of one generic geometrical surface of the considered bone structure (Laporte et al., 2003; Le Bras et al., 2004), or by Statistical Shape Models (SSM) (Baka et al., 2011; Zheng et al., 2009; Whitmarsh et al., 2011).

Our aim is to study the accuracy of the 3D femur reconstruction without using any 3D prior information. Only, the mathematical projection model and a limited number of 2D X-ray images are employed for this purpose. Two successive projections are used to compute the coordinates of a 3D contour.

The proposed scheme works as follows: after extracting the contour of the proximal femur on the 2D X-ray images, comes the matching process. This stage is a very important step for the 3D reconstruction, because it impacts the accuracy of the computed 3D coordinates. There exists several works for contours matching (Park and Han, 1998; Frenkel and Basri, 2003; Cui et al., 2009). For this work we examine contour points matching using merely the position and normal as features to establish correspondences. The matching between the points of two contours is performed with the

Euclidian 2D spatial distance then, the normals of each point pairwise are used to filter the outliers. This method is simple and relatively efficient allowing a good trade-off between accuracy and computation complexity, which is important for our application. The estimated point pairs are then used to set up a set of 3D points. Since we are using binary images, the correspondence of the contour 1 towards the contour 2 is not symmetric and may give different results if contour 2 is used towards contour 1, thus the 3D reconstruction result may be different. Here, we will discuss this issue and study its influence on the 3D reconstructed models.

The obtained results, through the proposed methodology, are benchmarked against real 3D CT scan data to assess the accuracy of reconstruction. The cadaver proximal femur was used as the anatomy of interest throughout this study.

The paper is organized as follows: Section 2 presents the data. Follows the method and experiments section that presents, the contours extraction, contours matching, and estimating the 3D coordinates.

## 2 MATERIALS

For this work we have used, a cadaver proximal femur scanned with a resolution of  $200\mu\text{m}$  by the VISCOM X8060 NDT scanner. The bone was placed on a rotating platform, between the x-ray source and the sensor, and then 450 radiographs, with a size of  $1024 \times 1024$  pixels, were acquired on 360 degrees. Examples of the ex vivo proximal femur radiographs are shown in Figure 1. Thanks to these radiographs, and with the help of modern computed tomography, the 3D mode allowed the reconstruction of complete volumetric model of  $911 \times 806 \times 711$  voxels. Figure 2 shows the 3D model of the reconstructed proximal femur. This model serves as a ground truth to compare the performances of the proposed algorithm.

In this study, eighteen 3D contours were computed to reconstruct the 3D femur shape. Each 3D contour was estimated using 2 successive X-ray images spaced by an angle of  $8^\circ$ . The step  $8^\circ$  was chosen to realize the trade-off between the precision and the matching process. In fact, if the two projections are too close, this will generate more errors for 3D coordinates estimation. And if the projections are too far, a good matching between the two contours will not be possible.

The next pair of X-ray radiographs was spaced from the precedent one by an angle of  $20^\circ$ . This

way, we ensure including in the reconstruction a minimum of information reflecting the different forms of the proximal femur. The step  $20^\circ$  between two pairs of projections was chosen based on the number of radiographs we wanted to use and to improve the quality of the reconstruction.

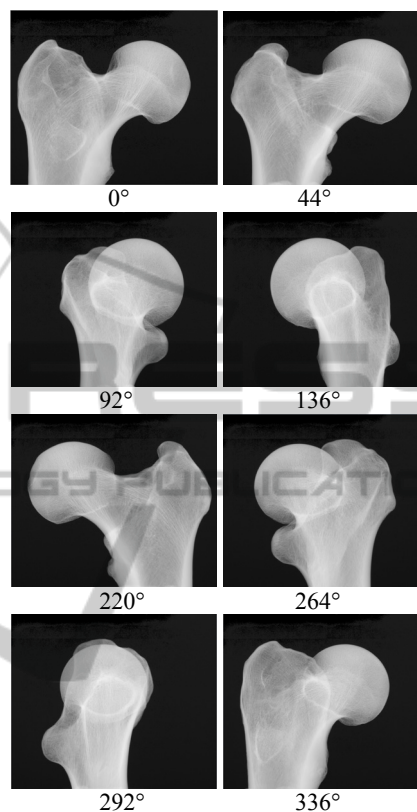


Figure 1: X-ray images of the ex vivo proximal femur at different angles.

## 3 METHOD AND EXPERIMENTS

Given few 2D X-ray images, our task is to establish correspondence between the two input images. For a given point of the edge identified in the first X-ray image, the goal is to associate it to a point of the edge identified in the second X-ray image. This matching between points, on two different contours, is realized using two criteria:

- The spatial distance: both associated points have to be as close as possible to each other.
- Normals to the contours: the normals for both associated points have to be in the same direction.

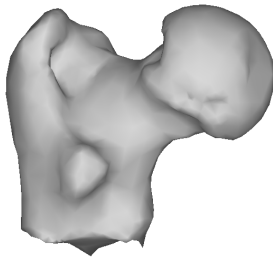


Figure 2: 3D ground truth of proximal femur used for the test and reconstructed from 450 radiographs using X-ray tomography reconstruction.

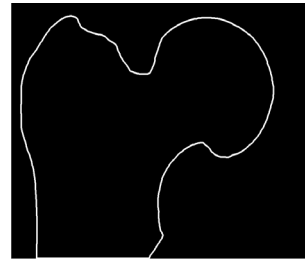


Figure 4: Extracted edge corresponding to the image of Figure 1.(0°) after applying the closing operation.

### 3.1 Bone Edge Extraction

The edge extraction is the first step of the 3D reconstruction procedure. Despite that the good contrast between the background and the femur in the X-ray images, the accurate edge extraction is not always a simple task. The nature of the x-ray imaging makes the border fuzzy difficult to define the real position of the edges. Whereas, the edge localization determines the precision of the 3D coordinates estimation. For that, various authors have proposed semi-automatic or interactive solutions to solve this problem (Laporte et al., 2003; Le Bras et al., 2004).

To accurately detect the contour of a given proximal femur, a morphology method is applied on binarized X-ray images. The binarization step aims at separating bone tissue (lighter) from pore and background (darker) pixels. A standard binarization method is applied (Chappard et al., 2008). This method consists in determining a threshold based on the local minimum between the two modes of the histogram of each image.

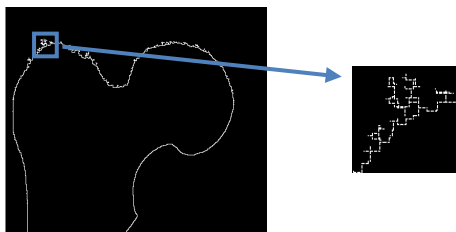


Figure 3: Extracted edge corresponding to the image of Figure 1.(0°) before applying the closing operation and a zoom on the squared area in blue.

A morphological closing operation is then applied to eliminate small contours considered as noise of the segmentation step. The structuring element is a disk-shaped of radius of 3 pixels. Figure 4 depicts an example of the edge extraction.

### 3.2 2D Matching Process

Let us denote the detected edge pixels in image1 (red edge, see Figure 5) as  $I1 = \{I^1_i, i=0, 1... M-1\}$  and the detected edge pixels in image2 (green edge, see Figure 5) as  $I2 = \{I^2_j, j=0, 1, ..., N-1\}$ , where M and N are the number of the edge points detected in image1 and in image2, respectively. Each point has two features: the 2D coordinates  $(x, y)$  and the normal vector at that position. The matching process consists first in finding for each point in  $I1 = \{I^1_i, i=0, 1... M-1\}$ , the closest one in  $I2$ , by computing the Euclidean distance  $d$  as (1).

$$d(x, y) = \sqrt{(x^1_i - x^2_j)^2 + (y^1_i - y^2_j)^2} \quad (1)$$

The matching result is shown in Figure 5.

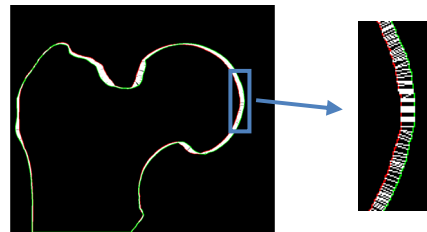


Figure 5: Matched points using the spatial distance and the points coordinates.

As can be seen on Figure 5, many pairs of associated points on the two contours have been found. To improve the detection process, we propose to use an additional criteria. For each retained pair of points, the normals are estimated. If the normals are in the same direction, these two points are retained, otherwise they are rejected.

Figure 6 shows that using the distance and the normals enable reducing the number of outliers candidates pairs for the 3D reconstruction.

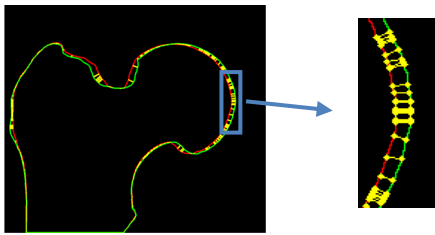


Figure 6: Matched points using the spatial distances and the normals.

As mentioned in the introduction, since we are dealing with binary images, the detected corresponding points using the matching may differ depending on the way of using the contours towards each other. The matching is not symmetric. Therefore, there are three cases of matching directions:

- (i) contour I1 toward contour I2,
- (ii) contour I2 toward contour I1,
- (iii) the intersection between the two directions.

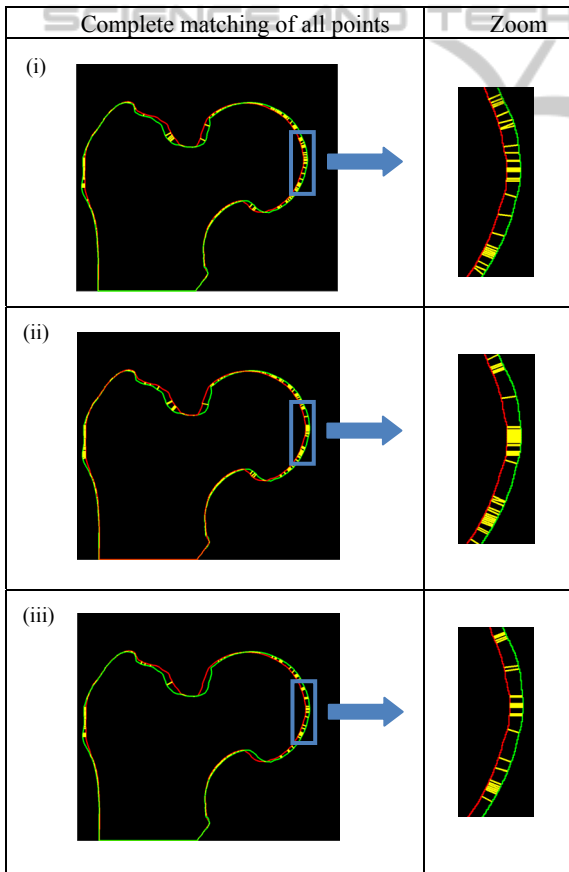


Figure 7: Matching after calculation of the distance and the normals for the three cases. (i) edge I1 toward edge I2, (ii) edge I2 toward edge I1, (iii) Intersection between (i) and (ii).

The aim of the intersection technique is to keep the pairs of points that are common in both matching directions.

Figure 7 summarizes the obtained results for the three cases.

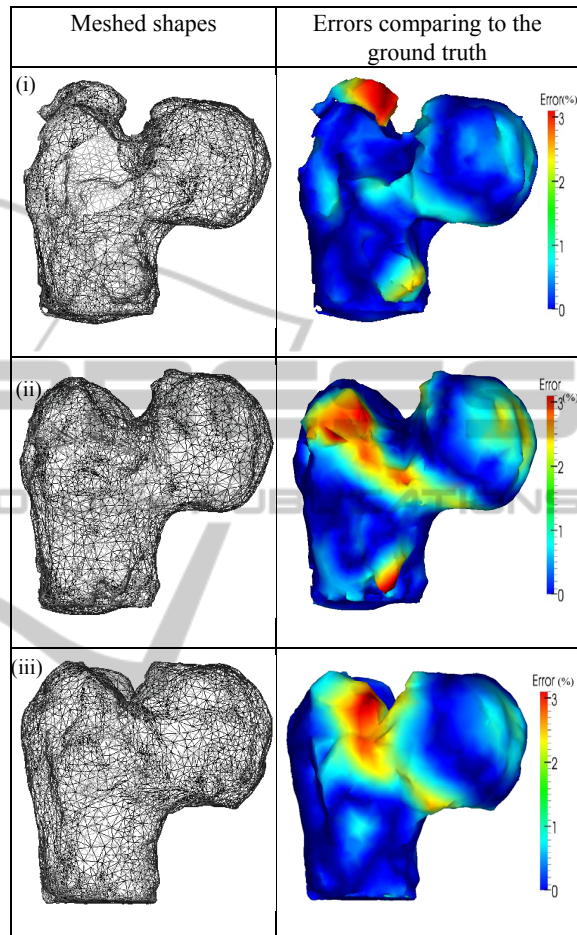


Figure 8: Meshed shapes and corresponding errors to the ground truth. (i) edge I1 toward edge I2, (ii) edge I2 toward edge I1, (iii) Intersection between (i) and (ii).

Figure 8 presents the meshed shapes of the proximal femur obtained from the reconstructed contours for the three cases presented in Figure 7.

The estimated errors obtained in comparison to the ground truth are presented too. These errors were evaluated using the Metro tool for measuring error on simplified surfaces (Cignoni et al., 1998). The red and blue colors in the 3D reconstructed shapes represent respectively the high and the low error values. Errors are minimal in the case (c) where the matching is performed in the two directions. This demonstrates that the filtering of the outliers helps to reduce the errors and increase the reliability of the 3D reconstruction technique.



## 4 CONCLUSIONS

This work shows that it is possible to recover the 3D shape of the proximal femur from relatively small number of X-ray projections. This was possible thanks to x-ray stereo model, contour points matching and combination of a round-trip scan to exploit the different possibilities of estimating the 3D contours. As a prospect to this work, we would like to reduce furthermore the number of the X-ray images and improve the accuracy by exploring new matching techniques as the Chamfer matching. The incorporation of this whole system will help providing enhanced 3D images for orthopedic procedures and intra-operative assistance.

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## REFERENCES

- Baka, N., Kaptein, B. L., de Bruijne, M., van Walsum, T., Giphart, J. E., Niessen, W. J., Lelieveldt, B. P. F., 2011. 2D-3D shape reconstruction of the distal femur from stereo X-ray imaging using statistical shape models. In *Medical Image Analysis*. 15(6):840-50.
- Caponetti, L., Fanelli, A. M., 1993. Computed-aided simulation for bone surgery. In *IEEE Comput Graph Appl*. 13:86-92.
- CGAL, Computational Geometry Algorithms Library. <http://www.cgal.org>.
- Chappard, C., Marchadier, A., Benhamou, C. L., 2008. Side-to-side and within-side variability of 3d bone microarchitecture by conventional micro-computed tomography of paired iliac crest biopsies. *Bone*, Vol. 43, No. 1, Pages 203-208.
- Cignoni, P., Rocchini, C., Scopigno, R., June 1998. Metro: measuring error on simplified surfaces. In *Computer Graphics Forum*, Blackwell Publishers, vol. 17(2), pp 167-174. Available at <http://vcg.sf.net>.
- Cui, M., Femiani, J., Hu, J., Wonka, P., Razdan, A., January 2009. Curve matching for open 2D curves. In *Journal Pattern Recognition Letters*. Volume 30 Issue 1, Pages 1-10.
- Frenkel, M., Basri, R., 2003. Curve matching using the fast marching method. Energy Minimization Methods in Computer Vision and Pattern Recognition. *Lecture Notes in Computer Science* Volume 2683, 2003, pp 35-51.
- Gamage, P., Xie, S. Q., Delmas, P., Xu, W. L., 2011. Diagnostic radiograph based 3D bone reconstruction framework: Application to the femur. In *Comput Med Imaging Graph*. 35(6):427-37.
- Laporte, S., Skalli, W., De Guise, J.A., Lavaste, F., Mitton, D., 2003. A biplanar reconstruction method based on 2D and 3D contours: application to the distal femur. In *Comput Methods Biomech Engin* 6(1): 1-6.
- Le Bras, A., Laporte, S., Bousson, V., Mitton, D., De Guise, J.A., Laredo, J.D., Skalli, W., 2004. 3D reconstruction of the proximal femur with low-dose digital stereoradiography. In *Comput Aided Surg* 9(3): 51-7.
- Park, J., S., Han J., H., 16 March 1998. Contour matching: a curvature-based approach. In *Image and Vision Computing*, Volume 16, Issue 3, Pages 181-189.
- Whitmarsh, T., Humbert, L., De Craene, M., Del Rio Barquero, L., M., Frangi, A., F., December 2011. Reconstructing the 3D Shape and Bone Mineral Density Distribution of the Proximal Femur From Dual-Energy X-Ray Absorptiometry. In *IEEE Transactions on Medical Imaging*, Vol. 30, No. 12.
- Zheng, G., Gollmer, S., Schumann, S., Dong, X., Feilkas, T., 2009. A 2D/3D correspondence building method for reconstruction of a patient-specific 3D bone surface model using point distribution models and calibrated X-ray images. In *Medical Image Analysis*. Volume 13, Issue 6, Pages 883–899.