# Highly-Automated 3D Segmentation of Femoral Bone from Hip MRI

**R. H. Dalvi[1], R. Abugharbieh[1], D. C. Wilson[2], and D. R. Wilson[2]**

[1]Department Of Electrical And Computer Engineering, University Of British Columbia, Vancouver, British Columbia, Canada, [2]Department of Orthopaedics, University Of British Columbia and Vancouver Coastal Health Research Institute, Vancouver, British Columbia, Canada

## Introduction

Clinical interest in detecting bone abnormalities of the proximal femur that may lead to osteoarthritis is emerging rapidly, and using MRI to detect these abnormalities requires segmentation of the bone from MR images. Manual segmentation of bone from hip MR data is labor intensive and time consuming. Automated segmentation methods such as texture-based geodesic active contours, model based segmentation, inclusion of phase information and modified watershed transforms have been previously proposed [1-4]. In studies of knee MR images, these automated techniques often either over or under segmented the data because cortical and trabecular bone tissues and the adjoining ligaments often have very similar intensity values in standard pulse sequences. In hip images, the problem is compounded by high noise and signal loss with depth. This paper presents a novel highly-automated 3D segmentation approach for femoral head hip data and presents a quantitative assessment of the sensitivity and specificity of the proposed technique validated on real MR scans. The presented method uses a combination of pre-processing steps including image non-uniformity correction and noise reduction techniques, with model based segmentation methods employing level sets.

## Methods

***Imaging:*** We scanned the hips of eight participants (age 19-40, 2 females and 6 males) using a Philips 3T Achieva scanner with a flexible surface coil. We used a transverse oblique TSE sequence cut parallel to the femoral neck axis with the following parameters: TR/TE = 700 ms/10 ms, FOV = 200 mm, matrix: 512 × 512, 2 mm slice thickness, 40 slices, scan time = 10:13. Femoral bone was segmented manually from each image (for validation purposes) using Analyze software (Analyze 6.0, BIR, Rochester, MN).

***Removal of image non-uniformity*:** Image non-uniformity was removed using the MNI non-parametric non-uniform intensity normalization technique (N3) [6].

***Noise removal:*** Noise was removed using curvature anisotropic diffusion filtering which is an edge preserving smoothing filer that minimizes loss of edge information due to smoothing by diffusing the image data along edges but not across edges[7]..

***Estimation of initial segmentation*:** The edge map of the original image, obtained using a Canny filter, was used to set the edge pixels in the image to an intensity of zero. This helped segmentation, both during the initial step (region growing) and the fine tuning step (level set) described next by explicitly stating known edges. Thresholding with an automatically computed threshold using the clustering method of Koontz et al [5] was then used to divide the image into two classes: namely, a high-intensity cluster, which contains the bone and a number of other tissues, and a low-intensity cluster, which mainly contained remaining tissues such as the muscle surrounding the bone and background. The class containing the bone was next morphologically eroded to ensure under segmentation at this stage. A single seed point was then manually specified in the central slice of the volume around which region growing was performed. An eroded version of this slice's segmentation result was next used as a set of seed points for similar segmentation of neighboring slices. This was continued until the whole volume is segmented.

***Level set segmentation:*** The under segmented initial estimate of the hip bone was then refined using level set segmentation, which evolved the 3D boundary surfaces by embedding them in a higher dimensional function (known as a level set function) using a differential equation that incorporates image data such as image edges and gradients to control the function evolution [8]. Laplacian level set segmentation as implemented under the ITK platform [7] was used.

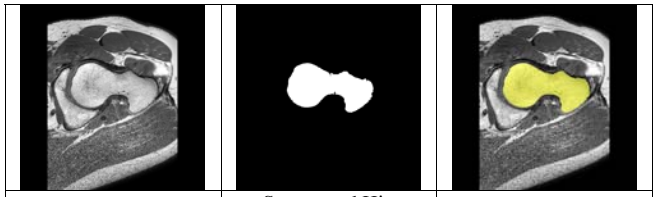


**Figure 1**: Slice 15 for the hip volume 8.

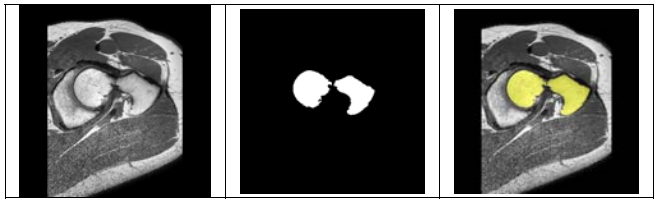


**Figure 2**: Slice 20 for the hip volume 7.

**Table 1**: Average sensitivity and specificity of our segmentation results on 8 hip volumes:

| Volume | Sensitivity (%) | Specificity (%) |
|---|---|---|
| 1 | 96.96 | 95.40 |
| 2 | 95.65 | 97.38 |
| 3 | 96.46 | 96.24 |
| 4 | 98.02 | 98.21 |
| 5 | 97.12 | 95.11 |
| 6 | 97.03 | 94.91 |
| 7 | 96.75 | 95.41 |
| 8 | 98.50 | 97.40 |
| Mean | 97.06+/-0.88 | 96.26+/-1.25 |

***Assessment:*** We compared regions identified as bone using the proposed automated method to regions identified using manual segmentation, which we considered as our reference standard. For each imaged hip we assessed mean sensitivity (percentage of pixels that are part of the bone but not recognized as such) and mean specificity (percentage of pixels that are not part of the bone but are recognized as such), i.e., *Sensitivity* = TP/(TP+FN), where TP=True Positives; FN=False Negatives and *Specificity* = TN/(FP+TN), where TN=True Negatives; FP=False Positives

## Results

The proposed automated segmentation method yielded consistent and robust results, with sensitivity consistently higher that 95% and specificity consistently higher than 94% (Table 1). The highest mean sensitivity and specificity were observed in volumes with high signal to noise ratio (volumes 4 and 8). The method performed well in challenging situations – for example, the segmented femoral head (the left part of the bone in Fig. 2) did not "leak" into the other, ligament region even though the edge between the bone segments and adjacent structures is quite blurry and has very weak edge information.

## Discussion

Our results suggest that the presented segmentation method has strong potential for automatically segmenting bone from MR images of the hip. The method may also have applicability for segmenting bone in other joints and for segmenting other tissues. Improving the speed of segmentation of bone from MR images of the hip through automation increases the potential scale of research studies and screening programs addressing bony abnormalities in the hip.

## References

1. T. Kapur *et al*. In Proc. IEEE Int'l Workshop on Model-Based 3D Image Analysis, pages 97--106, 1998. 2. L. Lorigo, *et al*.. In MICAI, October 1998. 3. V. Grau *et al*. IEEE Trans. Med. Imaging 23(4): 447-458 (2004). 4. Bourgeat, P *et al.* 3rd IEEE International Symposium on Biomedical Imaging: Macro to Nano, 2006. 742- 745. 5. W. L. Koontz, *et al*. IEEE Transactions on Computers, C-25, pp. 936-944, 1976. 6. http://www.bic.mni.mcgill.ca/software/N3/
7. http://www.itk.org/ 8. J.A. Sethian. Level Set Methods and Fast Marching Methods. Cambridge University Press, 1996.