



Comparison of Two Statistical Shape Models for the Femur Segmentation in MRI

Zoheir Dib ^{1,3}, Tinashe Mutsvangwa ^{1,4}, Guillaume Dardenne ^{1,2}, Chafiaa Hamitouche ^{1,4}, Valérie Burdin ^{1,4} and Eric Stindel ^{1,2,3}

¹LaTIM, INSERM, UMR 1101, SFR IBSAM, Brest, 29200, France.

²CHU Brest, Brest, 29200, France.

³ Université de Bretagne Occidentale, Brest, 29200, France.

⁴IMT-Atlantique, Dpt ITI, Brest, 29200, France.
guillaume.dardenne@chu-brest.fr

Abstract

Active Shape Models (ASM) have been widely used in the literature for the extraction of the tibial and the femoral bones from MRI. These methods use Statistical Shape Models (SSM) to drive the deformation and make the segmentation more robust. One crucial step for building such SSM is the shape correspondence (SC). Several methods have been described in the literature. The goal of this paper is to compare two SC methods, the Iterative Median Closest Point-Gaussian Mixture Model (IMCP-GMM) and the Minimum Description Length (MDL) approaches for the creation of a SSM, and to assess the impact of these SC methods on the accuracy of the femur segmentation in MRI. 28 MRI of the knee have been used. The validation has been performed by using the leave-one-out cross-validation technique. An ASM_{MDL} and an $ASM_{IMCP-GMM}$ has been built with the SSMs computed respectively with the MDL and IMCP-GMM methods. The computation time for building both SSMs has been also measured. For 90% of data, the error is inferior to 1.78 mm and 1.85 mm for respectively the $ASM_{IMCP-GMM}$ and the ASM_{MDL} methods. The computation time for building the SSMs is five hours and two days for respectively the IMCP-GMM and the MDL methods. Both methods seems to give, at least, similar results for the femur segmentation in MRI. However (1) IMCP-GMM can be used for all types of shape, this is not the case for the MDL method which only works for closed shape, and (2) IMCP-GMM is much faster than MDL.

1 Introduction

Active Shape Models (ASM) have been widely used in the literature for the segmentation of organs, and more specifically in orthopedics for the extraction of the tibial and femoral bones from MRI (Fripp, 2006) (Davies, 2010) (Zhu, 2011) (Tümer, 2013). These methods use Statistical Shape Models (SSM) to drive the deformation and make the segmentation more robust against artefacts or intensity inhomogeneities.

The SSM plays a major role in the ASM since the segmentation result can be directly impacted by the quality of the SSM. A SSM can be built thanks to a database containing several shapes of the object of interest and is composed of (1) a mean shape and (2) a number of deformation modes. In order to build a SSM, a very important step is needed: the shape correspondence, which consists in finding, for all points of the model, the equivalent points in all shapes coming from the database.

Several shape correspondence methods have been described in the literature (Heimann, 2009). Among them, the mesh-to-mesh registration (MMR) which directly uses the different meshes of the database to compute the correspondences, and the population-based optimization (PBO) which consists in mapping all the shapes in a common base domain and making the points correspondence in this domain.

The Minimum Description Length (MDL) (Davies, 2010) and the very recent Iterative Median Closest Point-Gaussian Mixture Model (IMCP-GMM) (Jacq, 2008) (Mutsvangwa, 2014) are two methods belonging respectively to the PBO and the MMR approaches. While the MDL method is widely used in the literature, the recent IMCP-GMM method seems to be very promising.

The goal of this paper is therefore to compare both IMCP-GMM and MDL methods for the creation of a SSM, and to assess the impact on the accuracy of the femur segmentation in MRI.

2 Materials and Methods

28 MRI of the knee, coming from the MICCAI SKI10 challenge, have been used for the validation. These data have been previously manually segmented by experts. The validation has been performed by using the leave-one-out cross-validation technique which consists in computing the ASM_{MDL} and the $ASM_{IMCP-GMM}$ thanks to 27 MRIs and in validating both ASMs with the 28th data. The ASM_{MDL} and the $ASM_{IMCP-GMM}$ have been obtained with the SSMs computed respectively with the MDL and the IMCP-GMM methods.

The segmentation error is defined as the RMS error of the point-to-surface distance between the femur model coming from the manual segmentation, and the femur model obtained with the ASM.

The computation time for building a SSM with both methods has been also measured with an Intel Core I5 computer and 4Go of RAM.

3 Results

Figure 1 shows the error concerning the segmentation of the femur in MRI with the ASM_{MDL} and the $ASM_{IMCP-GMM}$ approaches. In this figure, the middle line represents the median, the central rectangle spans from the first quartile to the third quartile and the vertical line extends from the first decile to the ninth decile. Minimum and maximum values are displayed as separated points.

For 90% of data, the error is inferior to 1.78 mm and 1.85 mm for respectively the $ASM_{IMCP-GMM}$ and the ASM_{MDL} methods. The maximum error is 4.8 mm and 4.2 mm for respectively $ASM_{IMCP-GMM}$ and ASM_{MDL} .

The computation time for building a SSM with 27 data is five hours and two days for respectively the IMCP-GMM and the MDL methods.

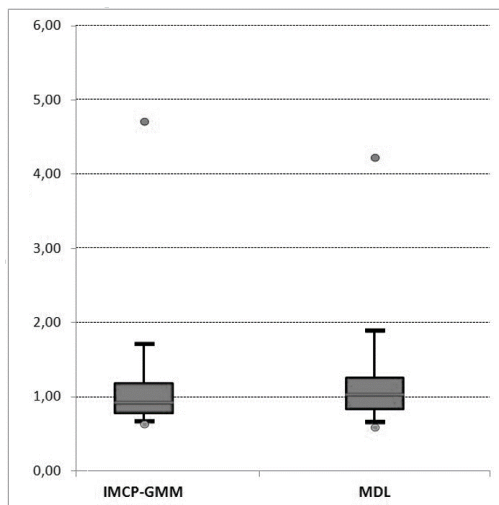


Figure 1: Error (mm) of the ASM_{MDL} and the $ASM_{IMCP-GMM}$ approaches

4 Discussion

The maximum error has been observed on one MRI data and is due to a bad initialization of both ASM methods.

For the femur segmentation in MRI with ASM, the IMCP-GMM methods (Mutsvangwa, 2014) for the creation of the SSM seems to give, at least, similar results as the MDL method. But (1) IMCP-GMM can be used for all types of shape, this is not the case for the MDL method which only works for closed shape, (Heimann, 2009), and (2) the IMCP-GMM method is much faster than the MDL method.

References

- Davies, R. (2010). Building 3-D statistical shape models by direct optimization. *IEEE Transactions on Medical Imaging*, 29(4).
- Fripp, J. (2006). Automatic segmentation of the knee bones using 3D active shape model. *Pattern recognition*, 167-170.
- Heimann, T. (2009). Statistical shape models for 3D medical image segmentation: a review. *Medical Image Analysis*, 13, 543-563.
- Jacq, J. (2008). Performing accurate joint kinematics from 3D in vivo image sequence through consensus-driven simultaneous registration. *IEEE Trans. on Biomedical Engineering*, 55(5), 1620-1633.
- Mutsvangwa, T. (2014). An automated statistical shape model developmental pipeline: application to the human scapula and humerus. *Biomedical engineering*, 1098-1107.
- Tümer, N. (2013). Statistical Shape and Appearance model of bones. *Bone*, 60, 129-140.

Zhu, Z. (2011). Constuction of 3D human distal femoral surface models using a 3D statistical deformable model. *J. Biomech*, 29(3).