

# Simultaneous Segmentation and Registration of MR Images

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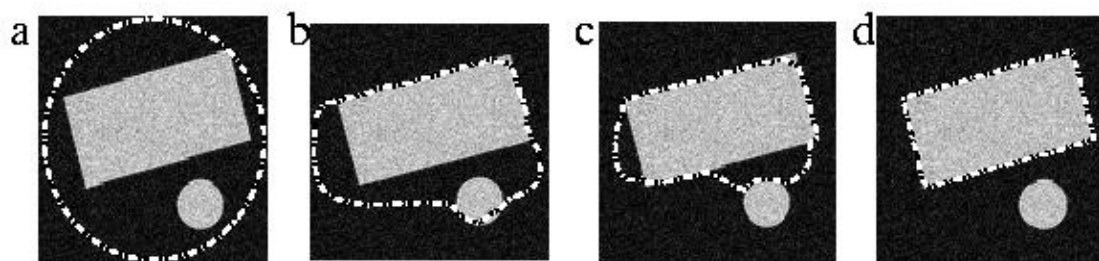
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## Introduction

In medical imaging studies that analyse the evolution of structures through time, measurements of anatomical parameters must be preceded by a registration and a segmentation process, to provide the location correspondence of equivalent structures on different images, and the selection of the object of interest, respectively. Clearly both processes have a strong dependency between each other. For example, in MRI scans of articular joints, a single rigid-body registration cannot be applied, since the relative movements among bones provide additional degrees of freedom. Thus, a rigid-body registration can only be done analysing each articular structure independently, and therefore, image segmentations are needed in advance. Several authors [1]-[4] have successfully developed joint segmentation and registration schemes, however, those techniques provide geometrically distorted segmentations due to their pixel-based characteristics, or are 2D schemes without 3D extensions. We present here an alternative approach that successfully integrates segmentation and registration based in Simplex Mesh Diffusion Snakes, in 2D and 3D with sub-pixel accuracy.

## Methods

The Simplex Mesh Diffusion Snakes (SMDS) technique is an explicit deformable model in which curves and surfaces are parametrised with Simplex Meshes, and the deformation process is partially driven by a region-based image functional (Mumford-Shah functional [5,6]). Additionally, the SMDS contains a shape dissimilarity functional, which favours the segmentation of a shape prior [6]. Since "shape" is invariant to Euclidean similarity transformations, the SMDS shape dissimilarity functional needs to be evaluated removing pose and scaling factors. The SMDS account for this invariance through a Procrustes analysis [7], resulting in an algorithm that keeps correspondence between equivalent structure locations in different images throughout the entire deformation process, so that segmentation and registration outputs are computed simultaneously [8]. To evaluate the accuracy of the SMDS performing simultaneously 2D and 3D registrations and segmentations, synthetic and real MR images have been obtained in which the objects size and pose are known *a priori*. Synthetic images have been created sampling (in *k*-space) simple geometrical shapes with known analytical Fourier Transforms. Size and pose are therefore defined *a priori* applying the Fourier Transform properties for scaling, shift and rotation independently to each of the objects contained in the image. These phantoms were also corrupted adding Gaussian noise (in *k*-space) to the scaled, rotated and shifted analytical Fourier expressions. For real 2D MRI scans, pose of the object of interest (a patella) was controlled keeping still the knee of a volunteer and changing the location of the FOV of the scans (images were acquired in a Philips T5 Intera). Translations, rotations and scaling factors were chosen between -40% and +40% of the FOV, -25° and +25° and 90% and 110%, respectively. The accuracy was measured by the absolute error of the global registration parameters (translation and rotation on each axis and scaling factor), and by the mean and standard deviation of the Euclidean distance between the segmented contour on a reference image and on images with different pose and scaling parameters. All the experiments were done with identical initial contour (circles or spheres) without any rotation or node renumbering.



**Fig.1** Sequential process of simultaneously segmentating and registering a synthetic rectangle. From left to right: a) Initial contour. b) The contour quickly converges to the nearest boundaries. c) The contour "overtakes" the circle's boundary, because the deforming contour does not match the reference shape. d) Final Contour.

## Results

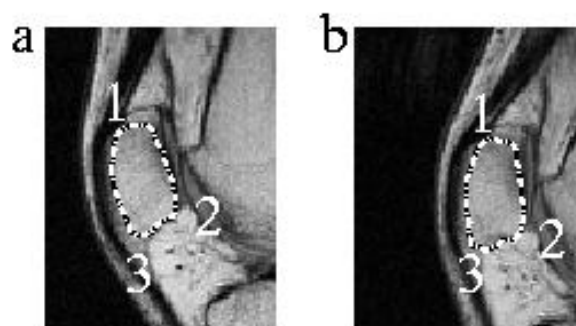
For all the 2D and 3D experiments, the estimated global registration parameters were less than 1 pixel (translation), less than 2° (rotation), less than 2% (scaling), and the Euclidean distance was less than 1 pixel. Since the deformable model is partially driven by a shape dissimilarity functional, it can perform not only the registration and segmentation process simultaneously, but also it can decide which is a "valid" boundary and which is not. Fig.1 shows how the initial contour (Fig.1 a) quickly converges to the nearest boundary (Fig.1 b), however, do to the fact that some boundaries leads to a shape that is not consistent with the segmented shape obtained from the reference image, the deforming contour has the ability to "overtake" invalid boundaries (Fig.1 c), resulting in a segmentation that finally match the shape prior (Fig.1 d). Fig. 2 shows that the algorithm can deal with rotations and translations in more complex structures such as an in-vivo patella; even though the pose of the FOV on each image is not the same, the algorithm can segment the patella keeping correspondence of equivalent points with sub-pixel accuracy.

## Conclusion

The obtained results show a reasonable level of accuracy for both synthetic 2D and 3D MR images and 2D real MR images. The technique must be evaluated in 3D for real MRI scans as well; however, the obtained results show a strong evidence to suggest that the SMDS algorithm can perform simultaneously segmentations and registrations of 3D clinical MRI scans.

## References

- [1]Wyatt et al. Med Im Anal 7: 539-552, 2003. [2]Xiaohua et al. Proc. MICCAI'04: 663-670, 2004. [3]Young et al. Math Bioscience and Engineering, 2: 79-96, 2005. [4]Pizer et al. IEEE TMI 18:851-865, 1999 [5]Mumford et al. Comm Pure and App Math 42: 577-685, 1989. [6] Tejos et al. Proc. IEEE EMBS, 1648-1651, 2004 [7]Dryden et al. Statistical Shape Analysis, Wiley, Chichester, 2002. [8]Tejos. Segmentation of Articular Cartilage from MRI using Simplex Mesh Diffusion Snakes. PhD thesis, University of Cambridge, 2005.



**Fig.2** Segmentation and registration of a patella. Control points (1, 2 and 3) show that the contour keeps correspondence between images "a" and [0] "b".