A Fully Automated White Matter / Gray Matter Segmentation of Mice Spinal Cord on DTI Images

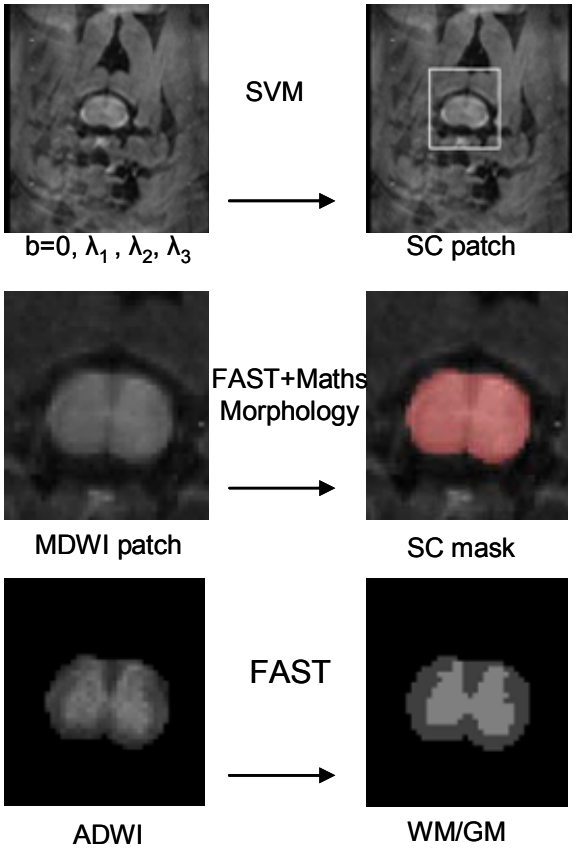
M. Sdika[1], V. Callot[1], M. Hebert[1], G. Duhamel[1], and P. J. Cozzone[1]
[1]CRMBM/CNRS UMR6612, Faculté de médecine, Université de la Méditérranée, Marseille, France, France

Introduction

Diffusion Tensor Imaging (DTI) provides important information on tissue structure and changes resulting from pathology are widely used, along with anatomic imaging (T2w) to study mouse spinal cord (SC) diseases [1]. Very high fields ($B_0 \geq 9.4T$), allowing significant increase in SNR, are now commonly used for small animal studies. However, at these field strengths, delineation of structures on T2w images is difficult due to contrast loss [2], making DTI a good candidate for an accurate segmentation. In this work, a fully automated method is proposed to segment mice SC white matter (WM) and gray matter (GM) tissues on DTI images.
Fully automated segmentation is of great importance as it removes a tedious part during the analysis of the data as well as the intra/inter operator variations of manual segmentation. The method proposed in this abstract applies to DTI images of mice. A SC mask is first delineated on each slice, the WM and GM are then segmented within this mask. The images are assumed to be axial slice, and, as the resolution is highly anisotropic, the processing is performed slice by slice.

Method

The proposed segmentation process consists in three steps. A small patch containing the SC is first detected using a machine learning procedure. A mask of the SC is then computed on a Mean Diffusivity Weighted Image (MDWI). The WM/GM segmentation is then performed on an image weighted by the diffusion along the SC axis. The complete process is illustrated on the figure hereinafter.



SC Patch Detection: A patch containing the SC is detected using a linear support vector machine (SVM) [3]. The features used to define the object in the patch are value of the b=0 image and the three eigenvalues of the tensor at each pixel in the patch. These pixels in the patch are normalized by subtracting the mean intensity and dividing by the standard deviation for each image. To detect the spinal cord on a slice of a new subject, the output of the SVM is computed for each patch of each slice. The SC patch of each slice is the one with the highest SVM output value. A few multislice DTI images of different mice are used as training dataset. Rotated versions of the training images are added to the training dataset to ensure rotation invariance.

SC Mask Segmentation: To segment the spinal cord, the MDWI image is computed as $MDWI = S_0 e^{-bMD}$. Pixels in the SC patch of this image are classified in three classes using the FSL segmentation software FAST [4]. To detach the SC from other tissues, the class of highest intensity is eroded; the largest connected component is then identified and dilated .

SC Axis Estimation: Once the SC mask is obtained, it is used to estimate the tangent to the axis of the spinal cord. This tangent is found by registering SC of adjacent slices with the moment method: the displacement in the plane is estimated by the difference of the center of gravity of the SC mask of adjacent slices.

WM/GM Segmentation: In the SC, the diffusion in the GM is preferentially directed perpendicular to the spinal cord axis whereas in the WM, the diffusion is preferentially along this axis. To segment WM and GM in the SC mask, the diffusion weighted image along the spine axis is computed as $ADWI = S_0 e^{-bu^T Du}$, where u is the tangent to the spine axis found previously. FAST is then run on this image to separate WM and GM pixels within the SC mask.

Results and Discussion

A total of 18 mice were used to evaluate the method. The DTI images (7 slices) of the mouse SC were acquired on a 11.75T Bruker MR system (see [5] for details). Five mice were used as a training group for SVM and the method was tested on the 13 remaining mice.
A recognition rate of 100% was achieved for the first step of the procedure: the SC patch was detected on all the slices. Two experts evaluated independently the SC mask and the WM/GM segmentation by visual assessment. Slices were classified in three categories according to their segmentation results: C1 for accurate results (<5 pixels mismatch), C2 when few pixels (<10 pixels) were misclassified and C3 when a gross error was visible. Results in percent of the total number of tested slice are given in Table I.

Table I: Results in percent of the visual assessment evaluation

	SC mask			WM/GM		
	C1	C2	C3	C1	C2	C3
Expert1	88	8	4	54	38	8
Expert2	75	23	2	58	25	15

Table I shows that more than 80% of the SC masks are very good (C1 group). This percentage drops below 60% when considering WM/GM segmentation. This was however mainly explained by a systematic error encountered in the dorsal GM /dorsal WM interface One can also note that 85% to 92 % of the slices do not have gross errors in their WM/GM segmentation.
In term of CPU time, the full process lasts about 45s and 60s for images of size 256x128x7.

Conclusion

In this abstract a complete framework for a fully automated WM/GM segmentation of the mouse SC on DTI images is presented. The proposed method, evaluated by visual assessment of two experts, seems to be very promising and should offer a huge gain of analysis postprocessing time. Future works will include adaptation of the process to pathological mice or to human data.

References

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