THOMAS: Thalamus Optimized Multi-Atlas Segmentation

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Target Audience: Scientists interested in automatic segmentation of the thalamus and its nuclei, esp. for the study of atrophy or treatment targeting.

Purpose: The white matter nulled MP-RAGE (WMnMPRAGE) contrast at 7T has recently enabled detailed manual delineation of thalamic nuclei[1] by a trained neuroradiologist guided by the Morel atlas[2]. Unfortunately, such a labor-intensive procedure, typically requiring roughly 1 day of tedious manual tracing per subject, is difficult to scale to larger studies and applications. We present the development of an automated thalamic segmentation method that leverages the manual thalamic segmentations accomplished to date with WMnMPRAGE images by utilizing label fusion and nonlinear registration. Similar schemes have proven successful in other brain structures such as the hippocampus, brain stem, caudate, and putamen.[1,3,4]

Methods: After obtaining informed consent, 15 multiple sclerosis patients and 8 healthy subjects were scanned at 7T (Discovery MR950, GE Healthcare) using a 32 channel head coil (Nova Medical). WMnMPRAGE scan parameters: TS 6s, TI 680ms, TR 10ms, BW 12kHz, flip angle 4°, FOV 18cm, 180x180x200 matrix, slice thickness 1mm, ARC parallel imaging 1.5x1.5 (2D radial fanbeam), scan time 5.5 minutes.[5] Previously, a separate exploratory group of 6 controls were acquired with an unaccelerated, 1D-centric version of the WMnMPRAGE protocol (scan time 16 min). The whole thalami and 15 thalamic nuclei of these controls were manually delineated with a high degree of reproducility.[1] For the 23 accelerated subject scans, the whole thalami and only 12 nuclei were able to be manually traced. In this project, we consider the common set of 12 nuclei and pool the data from both studies. Automatic segmentation was achieved by using nonlinear registration to align prior manually delineated ROIs from an atlas group of subjects to an incoming image, forming a collection of candidate segmentations. Each collection was then combined into a single solution using a label fusion algorithm. We employed the PICSL multi-atlas label fusion for this work.[6] The combined pool of 29 subjects was divided into a training set of 20 (9C:11P) and validation set of 9 (5C:4P). The training set was used to optimize various stages in the segmentation pipeline with leave-one-out cross validation (20 permutations of 1 target and 19 atlas priors). In the registration stage, a crop of the whole thalamus was extracted from the target image and all atlas priors to reduce the size of the data as well as computation time. The region to crop was estimated by transforming the atlas group's whole thalami ROIs to the target with an affine registration, then taking the union across the collection to be conservative about where the thalamus could lie. ANTS was used with its default parameters to nonlinearly register the cropped thalamus from each of the priors to this cropped target region.[7] These warps were also applied to the prior traced thalamic nuclei to ready them for label fusion. The optimal choice of configuration parameters for PICSL MALF was found with cross-validation and a grid search over a range of values[5] for each nucleus. Dice's coefficient was computed across the cross-validation group and the sum of the trimean and worst case coefficient was maximized. With this optimized pipeline, the validation set of 9 subjects was automatically segmented using the entire training set as atlas priors. The results were then evaluated against manually delineated truth labels using Dice's coefficient.

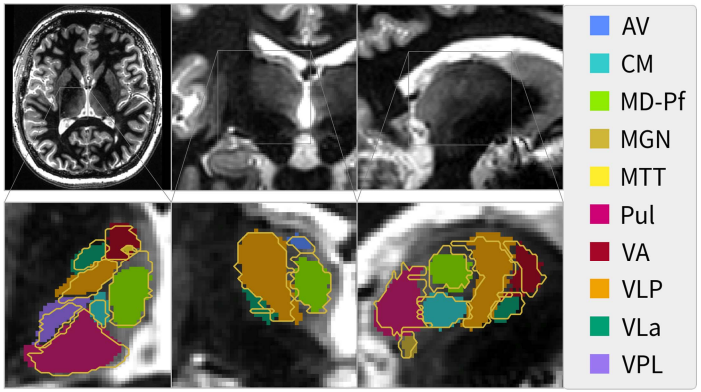

Fig. 1: Automatic segmentations (filled region) for whole thalamus and nuclei with the manual truth (bright outline) overlaid in the target patient. See [1] for the abbreviation glossary.

	Median Dice	Median Dice in [8]	Median Dice in [9]
Whole Thalamus	0.925	N/A	N/A
AV	0.774	0.736	N/A
VA	0.695	0.869	N/A
VLa	0.643		N/A
VLP	0.789		N/A
VPL	0.713		N/A
Pul	0.863	0.819	0.725
LGN	0.702	N/A	0.405
MGN	0.711	N/A	0.515
CM	0.778	N/A	N/A
MD	0.868	0.707	N/A
Hb	0.791	N/A	N/A
MTT	0.686	N/A	N/A

Table 1: Performance of the algorithm compared to a previous DTI and multi-modal techniques.

Results: Processing time for a single subject was 30-35 minutes on a 12-core 2.66 GHz Intel Xeon. The optimized parameters for PICSL MALF vary depending on the nucleus, ranging from (patch radius: 2x2x2, search radius: 1x1x1, beta: 1) for the smallest nucleus, MTT, to (patch radius: 5x5x5, search radius: 2x2x2, beta: 1) for the large VLP nucleus. Fig. 1 shows the results of the automatic segmentation with our method, where the truth is brightly outlined and the algorithm predicted the filled-in colored region. Table 1 displays the Dice coefficient performance for each of the regions of interest in the validation group. In particular, the median predictions for whole thalamus (0.92), pulvinar nucleus (Pul, 0.86), mediodorsal nucleus (MD, 0.87), and habenular nucleus (Hb, 0.79) were quite accurate. This is a substantial improvement over existing multi-modal methods that require longer and more complex acquisitions including DTI.[8,9]

Discussion/Conclusion: We demonstrate that label fusion with nonlinear registration using the WMnMPRAGE contrast is highly effective for achieving automatic segmentation of the whole thalamus as well as many of the larger thalamic nuclei in both MS patients and healthy controls. Smaller nuclei are estimated well enough to provide a good starting point for light manual revision. Machine learning techniques like adaptive boosting, perhaps with information supplied by other contrasts or quantitative mapping, may help improve performance as in [3]. Reliable automatic segmentation of the whole thalamus and its nuclei is critically required for any large-scale study of thalamic changes with disease. Our new method should also have significant applications in treatment planning, e.g. thalamic ablation for essential tremor, where there is a critical need for better localization of specific nuclei for targeting. The work presented here offers higher accuracy in more nuclei with a faster processing time than current state of the art techniques. Furthermore, our method uses the robust WMnMPRAGE acquisition protocol that is both faster and higher resolution than protocols used in previously published work. Ongoing work will evaluate segmentation performance using WMnMPRAGE images acquired at 3T.

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Acknowledgement: Research support from NIH P41 EB015891, NIH 1 S10 RR026351-01Al, GE Healthcare, BioX-Sanofi BIOSTAR program