

Thalamic nuclei segmentation from T1weighted MRI: unifying and benchmarking state-of-the-art methods

Article

Supplemental Material

Williams, B. ORCID: https://orcid.org/0000-0003-3844-3117, Nguyen, D., Vidal, J. P. and Saranathan, M. (2024) Thalamic nuclei segmentation from T1-weighted MRI: unifying and benchmarking state-of-the-art methods. Imaging Neuroscience, 2. pp. 1-16. ISSN 2837-6056 doi: https://doi.org/10.1162/imag_a_00166 Available at https://centaur.reading.ac.uk/116049/

It is advisable to refer to the publisher's version if you intend to cite from the work. See <u>Guidance on citing</u>.

To link to this article DOI: http://dx.doi.org/10.1162/imag_a_00166

Publisher: MIT Press

All outputs in CentAUR are protected by Intellectual Property Rights law, including copyright law. Copyright and IPR is retained by the creators or other copyright holders. Terms and conditions for use of this material are defined in the <u>End User Agreement</u>.

www.reading.ac.uk/centaur



CentAUR

Central Archive at the University of Reading

Reading's research outputs online

1 Supplementary methods

2 **THOMAS pipeline and its variants**: The original THOMAS method that was developed and optimized for WMn-MPRAGE uses a set of 20 WMn-MPRAGE datasets (p1-p20) as priors which 3 4 have been manually segmented using the Moral atlas as guide. The 20 priors are mutually 5 registered and averaged to create a WMn template. The input image is first cropped and 6 registered to a cropped WMn template image using ANTs nonlinear registration (R). The 7 precomputed prior-to-template space warps (W_{piT}) are combined with R⁻¹ to warp the 20 prior 8 labels to input space. These labels are then combined using a joint-fusion algorithm to generate 9 a single parcellation in subject space. The WMn-MPRAGE sequence is neither part of standard 10 clinical imaging protocols nor part of extant databases such as ADNI and OASIS. To adapt 11 THOMAS for T1w data, one approach was to replace the cross-correlation (CC) metric with a 12 mutual information (MI) metric in the ANTs nonlinear registration step of THOMAS and replace 13 the joint fusion (JF) with majority voting (MV) in the label fusion step of THOMAS. We refer to this 14 variant as T1-THOMAS. To leverage the improved intrathalamic contrast of WMn-MPRAGE, a 15 polynomial synthesis method (box labelled HIPS) was used to first synthesize WMn-MPRAGE-16 like images from T1w images before applying the THOMAS algorithm. Note that the WMn-like 17 input enables the use of the more accurate CC metric for nonlinear registration as well as the 18 more sophisticated JF algorithm compared to MV for label fusion. We call this method HIPS-THOMAS. The original THOMAS method and the T1-THOMAS and HIPS-THOMAS variants are 19 20 shown in Supplemental Figure 1 below, using green, red, and cyan colours to differentiate the 21 three methods.



Supplementary Figure 1. Schematic of THOMAS and the two variants- T1-THOMAS and HIPS THOMAS. T1-THOMAS (grey text) uses a mutual information metric for nonlinear registration of
 input to template and a majority voting algorithm to combine the labels. HIPS-THOMAS (cyan
 text) uses a cross-correlation metric for more accurate nonlinear registration of input to template

and a joint fusion algorithm for label fusion.

28 Supplementary results



Supplementary Figure 2. Violin plots of left hemisphere nuclei with significantly different Average Hausdorff Distances for nuclei segmented from Human Connectome Project data using FreeSurfer, HIPS-THOMAS, CNN-SCS, and T1-THOMAS approaches. Posthoc t-test results (Bonferroni corrected) are presented to show pairwise difference between segmentation approaches for each nucleus (**p<0.01, ***p<0.001).



Supplementary Figure 3. Violin plots of right hemisphere nuclei with significantly different Average
 Hausdorff Distances for nuclei segmented from Human Connectome Project data using
 FreeSurfer, HIPS-THOMAS, CNN-SCS, and T1-THOMAS approaches. Posthoc t-test results
 (Bonferroni corrected) are presented to show pairwise difference between segmentation
 approaches for each nucleus (**p<0.01, ***p<0.001).



Supplementary Figure 4. Violin plots of left hemisphere Dice overlap using Freesurfer as a
 reference space for THOMAS-variants with Human Connectome Project data. Posthoc t-test

44 results (Bonferroni corrected) are presented to show pairwise difference between segmentation

45 approaches for each nucleus (*p<0.05, **p<0.01, ***p<0.001).



Supplementary Figure 5. Violin plots of right hemisphere Dice overlap using Freesurfer as a
 reference space for THOMAS-variants with Human Connectome Project data. Posthoc t-test
 results (Bonferroni corrected) are presented to show pairwise difference between segmentation

50 approaches for each nucleus (*p<0.05, **p<0.01, ***p<0.001).



Supplementary Figure 6. Violin plots of left hemisphere Average Hausdorff Distance using
Freesurfer as a reference space for THOMAS-variants with Human Connectome Project data.
Posthoc t-test results (Bonferroni corrected) are presented to show pairwise difference between
segmentation approaches for each nucleus (*p<0.05, **p<0.01, ***p<0.001).



Supplementary Figure 7. Violin plots of right hemisphere Average Hausdorff Distance using
Freesurfer as a reference space for THOMAS-variants with Human Connectome Project data.
Posthoc t-test results (Bonferroni corrected) are presented to show pairwise difference between
segmentation approaches for each nucleus (*p<0.05, **p<0.01, ***p<0.001).



- 62 Supplementary Figure 8. Density plots for volumes of segmented thalamic nuclei for data from
- 63 healthy controls (HC), early minor cognitive impairment (EMCI), late minor cognitive impairment
- 64 (LMCI), and Alzheimer's disease (AD) using the 4 segmentation methods. Vertical lines for each
- 65 density plot represent quantiles.

R	eeSufer						
Left hemisphere	Right hemisphere						
AV VA VLa VLp VPL LGN MGN Pul CM MD-PF	AV VA VLa VLp VPL LGN MGN Pul CM MD-Pf						
10 155 130 155 130 155 340 350 350 370 500 510 520 520 520 750 700 770 780 780 80 80806840858866870 200 210 220 84 88 92 14075 1500 1525 220 235 240 245 875 980 155 1500	15 10 115 40 46 110 335340445050555600565 530 646 550 750 700 700 80 800 800 800 216 216 202 225 07 5 100 110 2515554051405482 200 225 240 8756008256609701						
I all headshow	+ ITD/MAS						
Lots tempstere	rogin emispinee AV VA V						
AV VA VLA VLP VPL LGN MGN PU CM MD-PT	AV VA VL3 VLD VPL LINN MIGN PU CM MDPT						
	24 - 24 - 24 - 24 - 24 - 24 - 24 - 24 -						
nó ró alo zác zác zác zác zó zá nó al ar no rác nó	e oka ska ska ska ska ska ska ska ska ska s						
SCS-CNN							
S	2S-CNN						
S Left hemisphere	S-CNN Right temisphere						
S Left hemisphere AV VA VLa VLp VPL LGN M/GN P/I CM M/D-PF	S-CN AV VA VLa VLp VPL LGN MGN PI CM MDPT						
S Left henisphere AV VA VLa VLp VPL LGN MGN P4 OM MD-P7 KC 4 KC 4	SSON						
S Left hemisphere NV VLa VLp VPL LGN MGN Put CM MD/F KC K _	M VL VL VL VL VL VL MCM Put CM MDP et						
S Left hemisphere AV VA VLa VLp VPL LGN MCN Pul CM MD-Ff KC K	SCM CM VLp VE LGN MGN Pul CM MDP' 40						
S Uch hemisphere AV VLa VLp VPL LGN MGN Put GM MD-F K	SON SOM Right hemisphere ac						
S AV VA VLa VVP LGN MGN PJ OM MDPR AV VA VLa VVP VPL LGN MGN PJ OM MDPR RC #	SOM SOM AV VA VLp VPL LGN MGN PL CM MDP ac						
AV VA Max Mp VP LCN MCN Pd CM MDF RC	SOM Right hemisphere AV VA VLa VLp VPL LGN MGN Pd CM MDP/ 60						
S	SON Use Use						
AV VA VA<	SCN SCN SCN SCN SCN SCN SCN SCN						
S Left hemisphere AV VA VLa VLP VPL LGN MGN Put CM MD-Pr 60 40	SON Son A/ VA VLa VLp VPL LCA MCA Pul CM MDP 6 4						
S AV VA VLa V.p VPL LGN MGN Pu OM MD/F KC +	SOM SOM AV VA VLa VLp VPL LGN MGN Pd CM MDP av 4<						
S AV VLa VLp VPL LGN MGN Put CM MD.Pr K6	SOM Right hemisphere AV VA VLa VLp VPL LGN MGN Pd CM MDP/ ac						
I cel hemisphere NV VA VLa VLp VPL LGN MGN Put CM MDM ec	SCN SCN AV VA						
Intel hemisphere AV VLa VLp VPk LGN MCN Pu CM MCAP 60 400	SON SQM Intrinsphere AV VA VLp VPL LGN MGN Pd CM MDP/ ac						
I cel hemisphere AV VA VLa VLP VPL LGN MGN Put CM MDP ec	SCNV SCNVV SCNVVV SCNVVV SCNVV SCNVVV SCNVVV SCNVVV SCNVVV SCNVVV SCNVVV SCNVVV SCNVVV SCNVVV SCNVVVV SCNVVV SCNVVVV SCNVVV SCNVVVV SCNVVVV SCNVVVV SCNVVVV SCNVVVVV SCNVVVV SCNVVVVVVV SCNVVVVVVVVVV						
S NV VA VLa V.p VPL LGN MGN Pu CM MDPf 60 4 6 4 6 4 6 4 6 4	SCN						

67 Supplementary Figure 9. Estimated marginal means for volumes of segmented thalamic nuclei 68 for data from healthy controls (HC), early minor cognitive impairment (EMCI), late minor cognitive 69 impairment (LMCI), and Alzheimer's disease (AD) using the 4 segmentation methods. Estimated 70 marginal means were calculated from ANCOVAs used to compare nuclei volumes for each

71 segmentation method

66

72 Supplementary table 1. Two-way ANOVA results for HCP dataset analysis in subject space for

each nucleus. Significant main effects of segmentation approach (dataset) and hemisphere
(side), and interactions were found for all nuclei except for VPL, which did not show a main effect
of side.

Effect	DFn	DFd	F	р	p<.05	ges	segmentation
Dataset	2.56	251.05	138.753	3.06E- 48	*	0.333	AV
side	1	98	156.403	5.10E- 22	*	0.196	AV
Dataset:side	1.9	185.8	110.71	2.50E- 31	*	0.199	AV
Dataset	1.35	132.2	596.277	1.24E- 57	*	0.719	VA
side	1	98	286.446	7.60E- 31	*	0.213	VA
Dataset:side	1.83	179.69	100.781	1.75E- 28	*	0.126	VA
Dataset	2.11	206.35	85.01	1.30E- 28	*	0.31	VLa
side	1	98	79.947	2.40E- 14	*	0.059	VLa
Dataset:side	1.97	192.81	166.994	2.08E- 42	*	0.251	VLa
Dataset	1.56	153.36	184.886	1.79E- 36	*	0.498	VLp
side	1	98	18.759	3.59E- 05	*	0.016	VLp
Dataset:side	1.47	143.99	55.408	3.26E- 15	*	0.08	VLp
Dataset	1.72	168.96	75.557	5.91E- 22	*	0.275	VPL
side	1	98	0.692	0.407		0.000709	VPL
Dataset:side	1.79	175.34	56.634	2.78E- 18	*	0.1	VPL
Dataset	2.74	268.54	407.59	1.34E- 95	*	0.593	LGN
side	1	98	357.482	1.83E- 34	*	0.267	LGN
Dataset:side	2.57	252.24	92.152	1.79E- 36	*	0.202	LGN
Dataset	1.25	122.32	188.742	5.26E- 30	*	0.515	MGN
side	1	98	698.738	2.18E- 46	*	0.35	MGN
Dataset:side	1.47	143.66	126.936	3.58E- 27	*	0.2	MGN
Dataset	2.07	202.89	490.928	1.16E- 79	*	0.531	Pul

side	1	98	268.92	7.54E- 30	*	0.23	Pul
Dataset:side	1.56	152.6	35.716	2.16E- 11	*	0.048	Pul
Dataset	1.65	161.51	523.075	7.27E- 66	*	0.74	СМ
side	1	98	277.192	2.52E- 30	*	0.127	СМ
Dataset:side	2.09	205.2	80.828	1.95E- 27	*	0.101	СМ
Dataset	1.62	159.22	641.411	5.30E- 71	*	0.758	MD-Pf
side	1	98	37.576	1.85E- 08	*	0.036	MD-Pf
Dataset:side	1.58	155.05	147.22	5.01E- 32	*	0.202	MD-Pf