Extending BrainWeb for Evaluating Methods of Brain Volume Change: Simulation of Central and Peripheral Brain Atrophy

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Objectives: (1) To develop simulated MRIs (sMRI) with controlled volume differences that allow evaluation of volume *change* measurement methods in whole brain (WB), gray matter (GM), and white matter (WM), (2) apply commonly-used brain volume change estimation methods from FSL, SPM, FreeSurfer, and our in-house tensor-based morphometry technique (Pairwise Jacobian Integration method, PJI) on the new data, and (3) compare the accuracy of these methods in measuring percent volume changes (PVC) in WB (PVC_{WB}), GM (PVC_{GM}), and WM (PVC_{WM}).

Methods: We used the framework of BrainWeb[1] where a realistic MRI was simulated from 11 tissue probability maps and from an MRI simulator, which incorporated discrete-level Bloch equations[2]. We simulated central atrophy (CA) and peripheral atrophy (PA) by deforming the lateral ventricles and cortical GM, respectively. CA is simulated using a previously described method[3]: 1) the lateral ventricles were automatically segmented on artifact-free sMRI using a patch-based method[4], 2) ventricular CSF probability maps were dilated to simulate enlarging ventricles, 3) other probability maps were proportionally decreased to simulate brain tissue loss (mostly in WM), 4) using the new probability maps, new MRI images were simulated using the simulator (mrisim, MINC toolkit). To simulate PA, we 1) created cortical surface objects using FreeSurfer[5], 2) calculated surface normal vectors for each vertex on the pial surface, 3) mapped the vectors back to the image, which represented the deformation field, 4) smoothed the deformation field to be realistic, 5) deformed all the 11 probability maps, and 6) generated sMRIs. For both CA and PA, we varied the degree of dilation or deformation to simulate progressively atrophying brain MRIs.

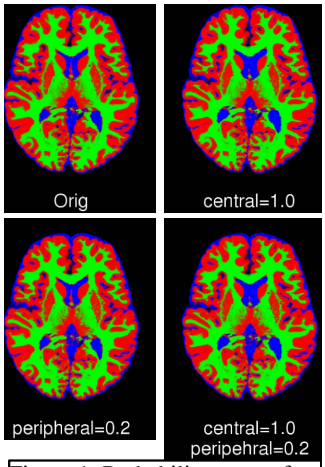

Figure 1: Probability maps after simulation after simulation of atrophy showing the original map on upper left corner, from left to right, progressive CA, and downward, greater PA.

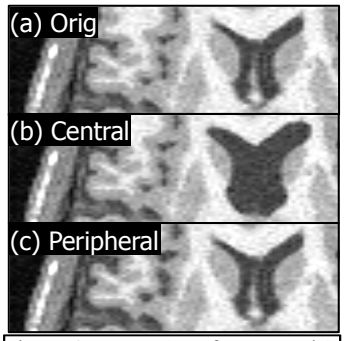

Figure 2: Examples of sMRIs with central & peripheral atrophy.

Therefore, the procedure was repeated for 6 levels of CA, 3 levels of PA, and 4 levels of combined atrophy for 20 brain phantoms for total of 280 sMRIs (including the original); examples of GM, WM and CSF probability maps with selected levels of atrophy are shown in Fig 1. It is important to note that we modified the probability maps and not the images directly, which allowed accurate calculation of tissue volumes from the probability maps. We applied SIENAX and SIENA/FSL[6], Segment/SPM[7], FreeSurfer[5], and PJI[8] on 280 sMRIs and calculated PVC_{WB}, PVC_{GM}, and PVC_{WM}. From the probability maps, $PVC_{[WB,GM,WM]}$ were also calculated as the gold standard PVC. We computed Pearson correlation coefficient (r), slope, and intercept, and performed paired t-tests on mean absolute difference (MAD) between measured and gold-standard PVC.

Results: The simulated probability maps are shown in **Figure 1**, sMRI with simulated atrophy is shown in **Figure 2** for the original (a), largest CA (b) and PA (c) cases. The enlarged ventricle is visible in (b) and subtle sulcal expansion in (c). The evaluation of accuracy from SPM, FSL, FS, and PJI is shown in Table 1. For the combined atrophy, all methods had correlations greater than 0.9, and the highest correlation in each tissue was with PJI. The overall MAD was significantly smaller for PJI than all other methods except FreeSurfer in GM and WB.

Table 1	SPM			SIENAX			SIENA	FreeSurfer			PJI		
	GM	WM	WB	GM	WM	WB	WB	GM	WM	WB	GM	WM	WB
Central atrophy													
Slope	0.13	1.19	0.97	0.70	0.99	0.92	1.51	0.83	1.09	1.02	0.82	1.01	0.95
r	0.15	0.95	0.88	0.74	0.98	0.93	0.99	0.66	0.94	0.96	0.93	0.99	0.99
MAD	0.90	0.52	0.27	0.36	0.22	0.20	0.52	0.36	0.49	0.16	0.32	0.22	0.14
Peripheral atrophy													
Slope	0.87	1.22	1.00	0.87	0.58	0.81	1.06	1.04	0.83	1.01	0.81	0.68	0.82
r	0.99	0.73	0.99	0.98	0.56	0.96	0.99	0.99	0.83	0.99	0.99	0.90	0.99
MAD	0.36	0.57	0.31	0.37	0.44	0.39	0.22	0.33	0.27	0.22	0.41	0.26	0.27
Combined atrophy													
Slope	0.91	1.11	1.02	0.90	0.97	0.89	1.27	1.03	1.09	1.02	0.92	0.96	0.93
r	0.90	0.94	0.96	0.96	0.97	0.96	0.97	0.95	0.98	0.98	0.99	0.99	0.99
MAD	0.72	0.73	0.21	0.43	0.25	0.32	0.45	0.36	0.34	0.18	0.31	0.14	0.14

Conclusion & Discussion: Interestingly, SIENA overestimated central atrophy by 27% in combined atrophy. This has been seen in a previous study that found 20% overestimation compared to BSI [9]. Overall, PJI performed better than the other methods and exhibited high correlations. We will take advantage of the sMRI framework to vary noise levels, inhomogeneity artifacts, image resolution, and contrast levels, and will further validate various techniques. The sMRIs will be available to the research community after publication to allow evaluation of other methods of volume *change* and will be on the BrainWeb website (www.bic.mni.mcgill.ca/brainweb).

References: [1] Collins et al. IEEE TMI 1998. [2] Kwan et al IEEE TMI 1999. [3] Nakamura et al. 2014 ISMRM. [4] Coupe et al 2011 NeuroImage. [5] Fischl et al. 1999 NeuroImage. [6] Smith et al 2004 NeuroImage, [7] Ashburner et al 2005 NeuroImage. [8] Nakamura 2014 NeuroImage: Clinical. [9] Smith et al 2007 NeuroImage.