Interaction between Common MRI Acquisition Defects and Image Post Processing Output: Brain Boundary Shift Integral

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Background: Measuring rates of brain atrophy from serial MR studies has emerged as a promising way to assess disease progression in neurodegenerative disorders, particularly Alzheimer's disease (AD). In the most widely studied approach, termed the boundary shift integral (BSI), two MRI volumes are spatially registered and volume change between the two scans is computed from intensity differences at the brain-CSF interface (1). The BSI has been used as an outcome metric in a number of major natural history and therapeutic intervention studies. In practice, one or both of the MRI studies entered into a BSI calculation often deviate from the ideal in some way, for example head motion. The objective of this study was to evaluate how common scan non-idealities affect the output of the BSI algorithm.

Methods: We simulated three types of image non-idealities: errors in MR protocol consistency between serial scans, head motion, and noise. Each of 6 normal volunteers underwent a 3D SPGR scan: 24cm FOV, TR= 23ms, TE=6ms, 256 x 192 matrix, 124 partitions, with a 25 degree flip angle (FA), which we refer to as the "base" scan. The subject was withdrawn from the scanner, repositioned, and an identical scan was repeated, which we refer to as the "match" scan. This was followed by scans which were identical except the FA was changed to 5 degrees and then 12 degrees respectively (Fig 1). The "match" scan was then modified by adding 5 levels of motion blurring (2)(Fig 2) and then 5 levels of noise (Fig 3). Twelve BSI values were computed in each subject: base-to-match; base-to-5 and 12 degree FA; base – to- 5 levels of motion blurring in increasing severity; and, base –to- 5 levels of noise in increasing severity (3).

Results: In theory the BSI volume difference between each pair of images should be zero. Deviation from zero represents corruption of the BSI measurement by some non-ideality in the second scan in the pair. Mean and SD BSI values across the 6 volunteers are presented in 3 tables. The base-match value in the first column of Table 1 provides a reference measure of BSI test retest precision. Table 1 also illustrates that as image contrast in the second image deviates from that of the base scan, the BSI result deviates progressively more from the expected value of zero. Tables 2 and 3 illustrate that as the severity of motion and noise (respectively) in the second scan increases, the calculated BSI values deviate from zero.

Discussion: MR is increasingly viewed as an attractive way to measure useful phenotypic properties in therapeutic and natural history studies. This is particularly true in AD where no in vivo biomarker exists. However, in practice image non idealities do occur. This study illustrates the magnitude of the error that can result from commonly encountered deviations from ideal image quality.

Table 1 - FA	Base - Match	5 deg. FA	12 deg. FA
Mean BSI	-0.02 (0.43)	-48.08 (3.0)	1.7 9 (0.8)

Table 2 - Motion	Level 1	Level 2	Level 3	Level 4	Level 5
Mean BSI	0.54 (1.06)	-6.28 (16.99)	-0.08 (0.56)	-0.50 (1.80)	-1.18 (2.03)

Table 3 - Noise	Level 1	Level 2	Level 3	Level 4	Level 5
Mean BSI	0.17 (0.38)	0.12 (0.36)	-0.93 (0.32)	-4.44 (1.20)	-7.96 (2.10)

Figure 1 - FA

25 deg. FA   5 deg. FA   12 deg. FA

Figure 2 - Motion

Level 1   Level 2   Level 3

Figure 3 - Noise

Level 1   Level 2   Level 3

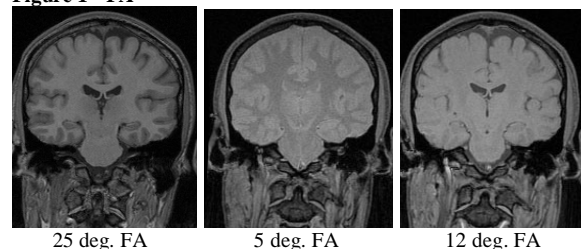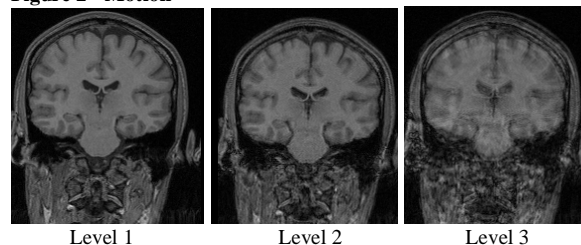**References:** (1) Freeborough P, Fox N.,IEEE Trans Med. Imaging 1997; 16:623-629. (2) Ehman RL, Felmlee JP. Radiology 1989; 173:225-263. (3) Gunther JL, JMRI 2003, 18:16-24.