# Morphological brain images acquired with a tilting MRI scanner: feasibility and quality evaluations

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| **Poster No.:** | C-1387 |
| **Congress:** | ECR 2018 |
| **Type:** | Scientific Exhibit |
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| **Keywords:** | Anatomy, Neuroradiology brain, MR, Segmentation, Education and training |
| **DOI:** | 10.1594/ecr2018/C-1387 |

## Aims and objectives

Conventional Magnetic Resonance Imaging (MRI) scanners allow patients to be imaged only in the supine position. Conversely, tilting MRI scanners allow to examine a subject also in the sitting position, for Weight-Bearing (WB) MRI studies. However, the last types of scanners have a lower magnetic field (typically between 0.2 T and 0.4 T), with a consequent lower signal-to-noise ratio (SNR) [1].

For what concerns brain neuroimaging, a tilting MRI scanner might be used as a non-invasive tool for investigating the postural effect on syndromes such as intracranial hypotension and Arnold-Chiari. Verifying the brain morphological image quality obtained with tilting scanners is a preliminary necessary step for its clinical application.

For this reason, morphological 3D T1 brain images acquired with a tilting 0.25 T and a 1.5 T MRI scanner were compared in this study. The quality of the former was compared to the latter through the evaluation of contrasts between different tissues, Signal to Noise Ratio (SNR) and tissue segmentation performance.

## Methods and materials

*Subject population:*

Two subjects (age 38 - subject 1 - and age 49 - subject 2 -, males) underwent head MRI on a tilting 0.25 T system (GScan Brio, Esaote, Italy) and on a 1.5 T scanner (Magnetom Avanto, Siemens, Germany).

*Data acquisition:*

An isotropic (resolution $1 \times 1 \times 1\,mm^3$) high-resolution T1-weighted 3D image, using a magnetization-prepared rapid acquisition with gradient echo (MPRAGE) sequence, was acquired on both scanners in the supine position. The sequence parameters for 0.25 T were the following: TR=12 ms, TE=6 ms, 200 axial slices, in-plane matrix size= $256 \times 256$. The sequence parameters for 1.5 T were the following: TR=1900 ms, TE=3.37 ms, TI=1100 ms, 176 axial slices, in-plane matrix size= $192 \times 256$.

For the 49 years old subject, the same sequence was also acquired during WB on the 0.25 T system and twice, after repositioning, on the 1.5 T scanner.

The *Speed Up* technique, based on the mathematical theory of compressed sensing [2], was used to optimize acquisition time and SNR on the 0.25 T system.

*Data analysis:*

In order to compare the quality of the 3D T1 images obtained from the different scanners and between supine and WB positions, we evaluated: 1) the volumes of different segmented tissues; 2) the images obtained from the same subjects with the different scanners (or positions), coregistering them to the 1.5 T images; 3) the SNR of the whole brain; 4) the contrast of the different tissues.

All the MRI data were processed with FMRIB's Software Library (FSL, http://www.fmrib.ox.ac.uk/fsl).

The non-brain tissue was removed from the MPRAGE images, using the Brain Extraction Toolbox (BET) [3]. Then, each subject's MPRAGE image was segmented into gray matter (GM), peripheral GM (pGM), white matter (WM), and ventricular cerebrospinal fluid (vCSF) with SIENAX [4]. In addition, right/left thalamus, caudate, putamen, pallidum, hippocampus, amygdala, and nucleus accumbens were segmented using FIRST [5] on the betted data.

The volumes of the GM, pGM, WM, vCSF, and subcortical GM (SGM) structures were computed. Brain volume was estimated as the sum of WM and GM volumes.

The rigid transformation for coregistering the 0.25 T 3D T1 on the 1.5 T MPRAGE was estimated and applied to the GM mask for a visual comparison of the GM segmentations obtained with the different scanners.

The SNR was computed for the whole brain from the following equation, as suggested in our previous work [6]:

$$SNR=0.655*S/N$$

Where:

- N is the noise, estimated for each raw image as the standard deviation of the signal intensity extracted from six areas, carefully drawn in the background (air) outside the brain.

- S is the mean signal in the brain. The brain mask was obtained as the sum of the eroded GM and WM masks. The GM and WM tissues were eroded in order to increase the confidence of extracting the signal from the brain tissue.

The contrasts between the different couples of tissues (GM, WM, vCSF) were computed using the following equation:

$$Contrast(A_{vs}B)=(A-B)/(A+B)$$

where A and B are the couple of tissue of interest. The contrasts between WM and GM; WM and CSF; GM and CSF were evaluated and compared between the two scanners.

For each subject, the volumes, SNR and Contrasts obtained with the two scanners, were compared computing the difference of the corresponding values, normalized by their average.

The scan-rescan repeatability was estimated at 1.5 T, computing the difference of corresponding volumes, normalized by their average. These values were used as reference when evaluating the differences between scanners.

## Results

The 3D T1 images obtained for the two subjects with the two scanners in the supine position are reported in Figure 1. The 3D T1 images of Subject 2 in the supine and sitting position at 0.25 T are shown in Figure 2.

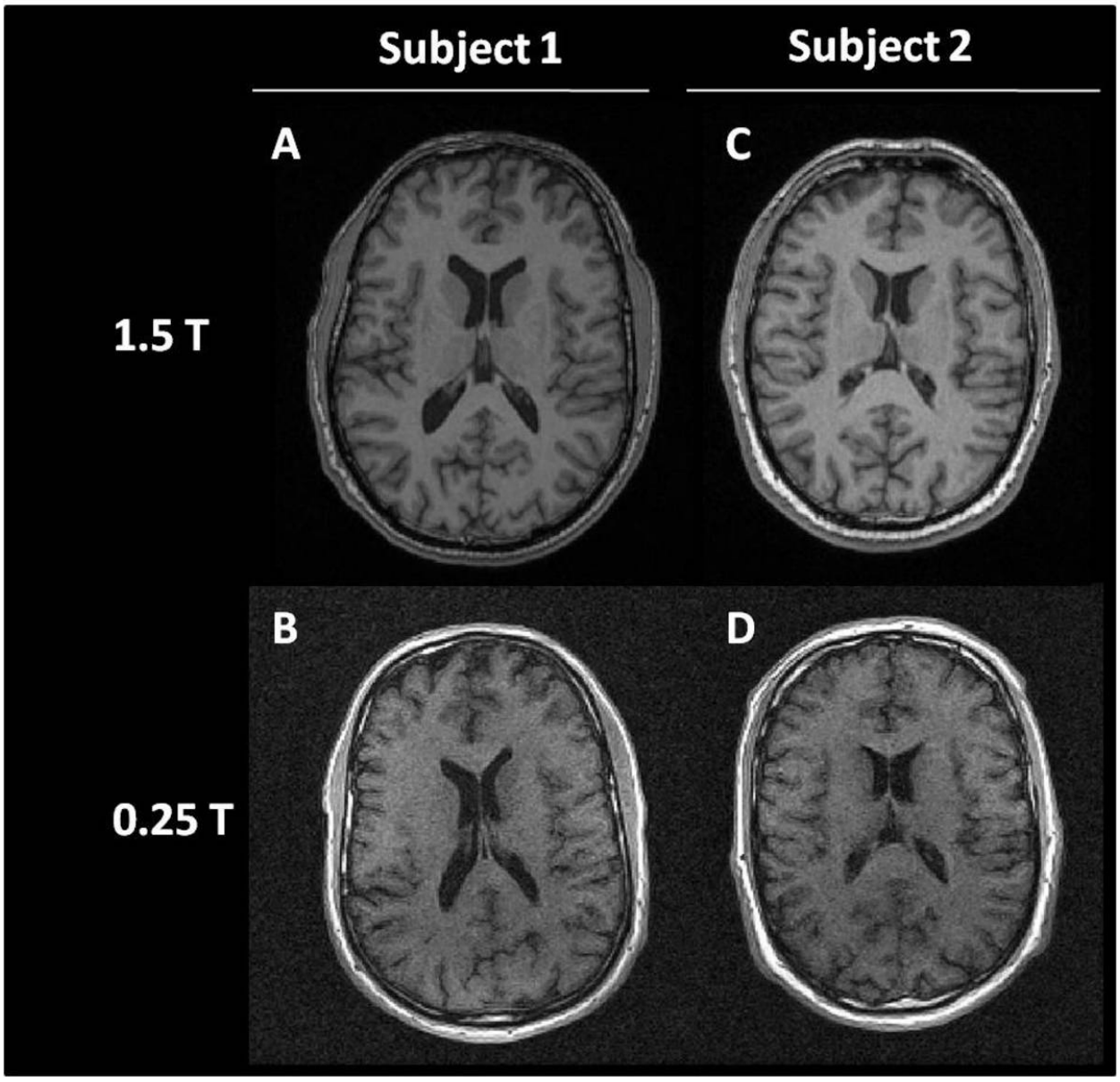


**Fig. 1**: 3DT1 of the two subjects, acquired with the two scanners and in different positions. Subject 1 (A and B) and Subject 2 (C and D) at 1.5 T (A, C) and at 0.25 T (B, D). Corresponding axial exemplificative slices were chosen for a proper comparison.
***References:*** Fondazione Don Carlo Gnocchi ONLUS, Milan, Italy

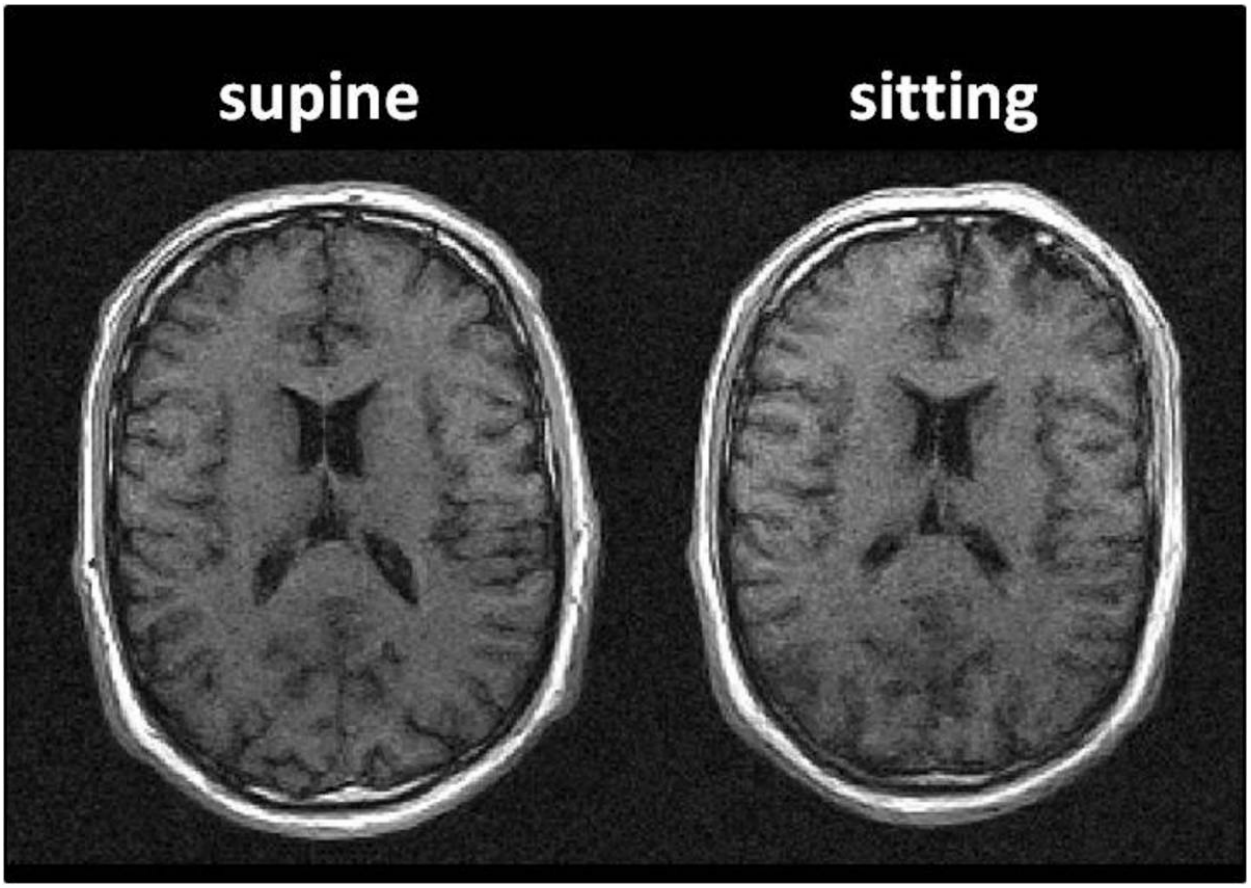


**Fig. 2**: Comparison of 3DT1 of Subject 2, acquired at 0.25 T while he was sitting and supine. Corresponding axial exemplificative slices were chosen for a proper comparison.

***References:*** Fondazione Don Carlo Gnocchi ONLUS, Milan, Italy

*Tissue segmentation and volumes*

The performance of the GM segmentation obtained with the two scanners is shown in Figure 3, where the GM obtained at 0.25 T was coregistered and superimposed to the GM obtained at 1.5 T.

The differences between the corresponding volumes obtained at 1.5 T vs 0.25 T, normalized by their average, are shown in the 2$^{nd}$ and 3$^{rd}$ columns of Table 1 (one for each subject), where positive values mean that the tissue of interest is overestimated at 0.25 T compared to 1.5 T.

The differences between supine and sitting position at 0.25 T, normalized by their average, are reported in the 4$^{th}$ column of Table 1. Positive values mean higher values in the supine vs sitting position.

The repeatability obtained at 1.5 T is reported in the 5$^{th}$ column of Table 1. Positive values mean higher values for the first acquisition, compared to the second one.

Table 1. Comparisons between scanners, positions, and runs. The difference of corresponding tissue volumes, normalized by their average, is reported. Legend: GM=grey matter; pGM=peripheral GM; SGM=subcortical GM; WM=white matter; vCSF=ventricular cerebrospinal fluid; Brain=brain =GM+WM.

| Tissue | Subject 1:<br><br>1.5 vs 0.25 T | Subject 2:<br><br>1.5 vs 0.25 T | Subject 2:<br><br>Supine vs WB | Subject2:<br><br>scan 1 vs scan 2 |
|---|---|---|---|---|
| GM | 5.67% | -1.21% | -3.10% | 0.96% |
| pGM | 10.33% | 2.35% | 1.09% | 0.35% |
| SGM | 3.60% | 0.73% | 0.06% | 2.68% |
| WM | -1.35% | -3.02% | -4.77% | -1.51% |
| vCSF | 0.08% | -9.35% | -4.67% | 0.12% |
| Brain | 2.33% | -2.08% | -3.90% | -0.22% |

*SNR*

The SNR obtained with the two scanners in the whole brain was: 9.22 and 54.39 for the Subject 1 at 0.25 T and 1.5 T respectively; 9.90 and 10.29 for the Subject 2 at 0.25 T in the supine and sitting positions respectively, and 48.86 and 54.59 for the two different acquisitions of Subject 2 at 1.5 T.

*Contrasts*

The differences of the contrasts obtained at 1.5 T vs 0.25 T, normalized by their average, are reported in Table 2 for the two subjects. All the values are positive, which means higher SNR at 1.5 T.

Table 2. Differences between 1.5 T and 0.25 T contrasts, normalized by their average.

| | Subject 1<br><br>1.5 vs 0.25 T | Subject 2<br><br>1.5 vs 0.25 T |
|---|---|---|
| WMvsGM | 1.55% | 4.81% |
| WMvsCSF | 10.17% | 3.80% |
| GMvsCSF | 14.64% | 4.02% |

# Conclusion

Cortical and subcortical GM volumes were underestimated (range 0.1-10.3%) and WM volume was overestimated (range 1.3-4.8%) by 0.25 T compared to 1.5 T, likely because parts of the cortical GM were misclassified as WM (as shown in Figure 3).

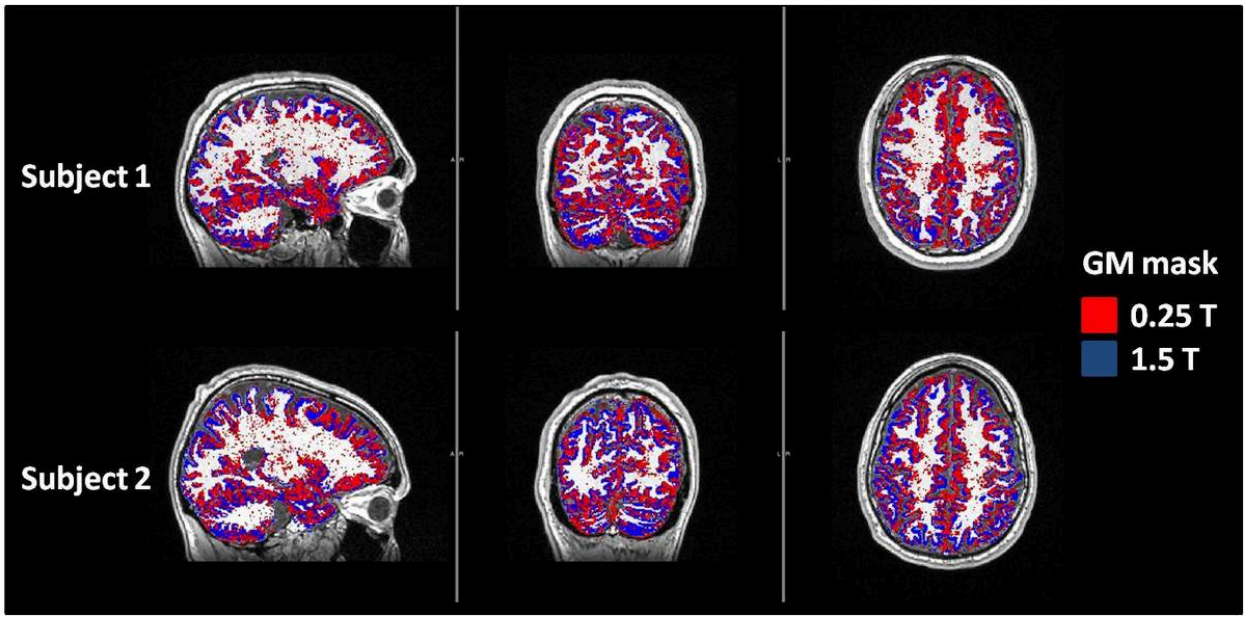


**Fig. 3**: Grey matter (GM) segmentation results at 1.5 T and 0.25 T. The GM masks obtained from 0.25 T (red) and 1.5 T (blue) are superimposed to the MPRAGE. The 0.25 T GM mask (red) is superimposed to the 1.5 T GM mask (blue), in order to highlight the regional differences. The 0.25 T 3D T1 was coregistered to the 1.5 T one, for Subject 1 (upper panel) and Subject 2 (lower panel).
***References:*** Fondazione Don Carlo Gnocchi ONLUS, Milan, Italy

The differences of tissue volumes computed using different scanners and positions, although higher than the repeatability at 1.5 T, were in line with the repeatability reported in a specific study using a 3 T scanner [7].

Since SNR is directly dependent on magnetic field strength [1], we expected that the ratio between the SNR at 0.25 T and 1.5 T was 0.25/1.5=0.17.

Brain SNR of the 0.25 T *vs* 1.5 T images was equal or higher than expected (range of the normalized ratios: 0.17 to 0.21), probably thanks to the *Speed Up* technique.

The tissues were well contrasted also in the 0.25 T acquisitions, although some cortical regions were critical because their gray-level at 0.25 T was similar to the WM one, or to the surrounding CSF (Figure 1). The Contrast of the different tissues was always higher at 1.5 T compared to the one obtained at 0.25 T, as expected. However, the differences between scanners in terms of tissue volumes (2$^{nd}$ and 3$^{rd}$ columns of Table 1: range 0.08-10.33%) were lower compared to the contrast differences between scanners (Table 2: range 1.55-14.64%).

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