

Reliability of MR sequences used for attenuation correction in PET/MR

Mathias Lukas¹, Anne Kluge², Jorge Cabello¹, Christine Preibisch^{2,3}, and Stephan Nekolla¹

¹Department of Nuclear Medicine, Klinikum rechts der Isar, TU München, Munich, Germany, ²Department of Neuroradiology, Klinikum rechts der Isar, TU München, Munich, Germany, ³Department of Neurology, Klinikum rechts der Isar, TU München, Munich, Germany

Introduction: In contrast to PET/CT systems, PET/MR does not provide information about electron density that essentially is needed for quantitative emission tomography. Several concepts have been proposed to solve this issue by generating synthetic attenuation maps [1-4]. All of them depend on reliable identification of air, bone and soft tissue structures in MR images. The accuracy of such methods is influenced by signal (SNR) and contrast-to-noise ratio (CNR), thus it is crucial to maintain it constant. Apart from imaging parameters the image quality depends on a wide range of physical factors like temperature, subject geometry, acquisition hardware, shimming, etc. of which some may vary over time. Sequences based on ultrashort echo times (UTE) for instance, are filling k-space already during gradient ramping. Thus, it is strongly affected by hardware instability during gradient ramping and by eddy currents [5]. Also routine maintenance calibrations are supposed to affect SNR and CNR. In this work, the quality of MR data currently used for attenuation correction (AC) in PET (UTE, DIXON, MPRAGE) was observed under changing clinical conditions within one day, one week and over 3 months to investigate the reliability and robustness for in-house established MR based AC methods.

Material und Methods: All measurements were done at a clinical 3 T, Biograph mMR (Siemens AG Medical Solutions) equipped with a 16-channel head/neck coil. The scan protocol comprised MPRAGE (voxel size 1.3 mm³, TR/TE/TI = 2300/2.98/900 ms, $\alpha = 9^\circ$), UTE (voxel size 1.56 mm³, TR/TE₁/TE₂ = 3.98/0.07/2.46 ms, $\alpha = 10^\circ$) and DIXON (2.34 x 2.34 x 2.73 mm³, TR/TE_{IN}/TE_{OP} = 3.6/2.46/1.23 ms, $\alpha = 10^\circ$). For SNR calculation each sequence ran twice. The same volunteer was scanned for 4 days every morning after scanner start-up and every evening immediately after the last clinical patient. Subsequently the test series was continued once per week for further 12 weeks ($n_{\text{total}} = 20$). System and room temperature as well as the volunteer's body temperature were documented. For each time point all data were coregistered to MPRAGE data and the cerebrospinal fluid (CSF), grey matter (GM) and white matter (WM) segments were obtained from MPRAGE's magnitude images using SPM8 (rev4252, University College London). The segmentation of bone, cavital air and background was done using the UTE-AC map generated by the scanner. For each segment the mean weighted by segment probability and the standard deviation (SD) were extracted. SNR and CNR were calculated as described in NEMA recommendation [6]. The datasets were analyzed descriptively using SPSS (v21, IBM Corporation). The dependence of means and SD from time of day was analyzed by *Mann-Whitney U test*. The means and SD and their central tendency over the week and months were tested with *Kruskal-Wallis one-way analysis of variance by ranks test*.

Results: The room and volunteer's body temperature varied with $21.3 \pm 0.4^\circ\text{C}$ and $37.1 \pm 0.4^\circ\text{C}$, respectively. The scanner's cooling system temperature changed from 21°C up to 32°C after special scans (e.g. DWI, EPI). The repositioning accuracy over all 20 scans was $x/y/z = \pm 2.1/\pm 2.3/\pm 12.3$ mm and tilt $x/y/z = \pm 1.8/\pm 4.6/\pm 3.0^\circ$. Figure 1 A show SNR and CNR for GM, WM and bone. SNR and CNR remained remarkably constant for all MR sequences. The standard deviations within each segment over all measurements were less than 3% for high signal (e.g. WM, GM) and less than 5% for low signal tissues (e.g. bone). That also resulted in highly invariant tissue contrasts. There were no statistically significant correlations of SNR and CNR, neither for body, room or cooling temperature nor for time, head position and tilt (equal distribution, significance $\alpha > 0.9$). Results of pixel-wise analysis are shown in Figure 1 B, where the SDs are overall very low. Deviations up to 20% exclusively occur in low signal regions. The resulting attenuation maps (Figure 1 B, 3rd column) of UTE and MPRAGE show negligible deviations and the UTE sequence with its radial readout was found to be much less prone to motion artefacts than MPRAGE, where swallowing reflexes often provoked motion artefacts in facial and neck regions. However, analyzing the reliability does not allow for prediction of accuracy of the attenuation correction itself but for the reproducibility of underlying image quality.

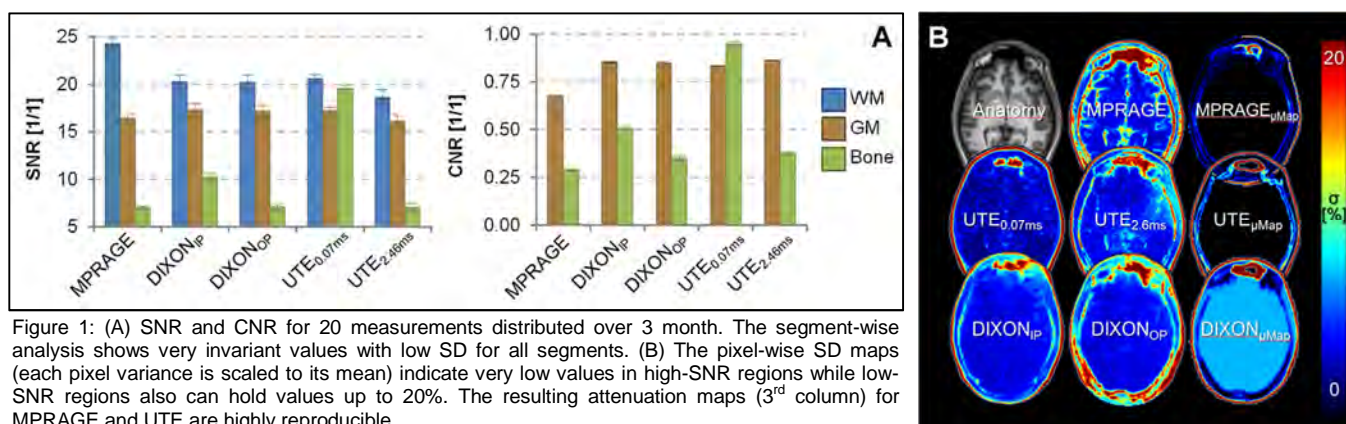


Figure 1: (A) SNR and CNR for 20 measurements distributed over 3 month. The segment-wise analysis shows very invariant values with low SD for all segments. (B) The pixel-wise SD maps (each pixel variance is scaled to its mean) indicate very low values in high-SNR regions while low-SNR regions also can hold values up to 20%. The resulting attenuation maps (3rd column) for MPRAGE and UTE are highly reproducible.

Conclusion: In this study a volunteer was scanned 20 times over an extended period of 3 month. It was found, that SNR and CNR for WM, GM, CSF and bone were highly invariant and independent of head position, tilt, body temperature and time, even after maintenance calibrations. In context of reliability all sequences can be used unhesitatingly to generate attenuation maps with high reproducibility. However, temporal stability does not predict accuracy with respect to attenuation correction. While MPRAGE delivered the highest and DIXON the lowest spatial resolution, UTE provides the most information about bone and lung tissue which are the crucial tissues needed to be corrected for attenuation and scatter.

References: [1] Wagenknecht G. et al. Magn Reson Mater Phy 2013; 26:99–113; [2] Poynton C.B. et al. Am J Nucl Med Mol Imaging 2014; 4(2):160–171; [3] Hofmann M. et al. J Nucl Med 2008; 49:1875–1883; [4] Schreiber E. et al. Med Phys 2010; 37:2101–2109; [5] Keereman, V. et al. J Nucl Med. 2010; 51:812–818; [6] NEMA Standards Publication MS 1-2008