MR-based attenuation correction for MR-PET studies with continuous-valued attenuation coefficients for bone through a conversion from R2* to CT Hounsfield units

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Target Audience: MR scientists interested in pursuing simultaneous MR-PET applications, especially those that require accurate quantitation of data.

Purpose: Photon attenuation in positron emission tomography (PET) results in a loss of signal that, if left uncorrected, can adversely affect the quantitative accuracy of PET studies. The primary challenge in developing an MR-based attenuation correction method arises from the differences in the source of MR signal (proton density, tissue relaxation) and the underlying cause of photon attenuation (electron density). This poses a problem in bone tissue because bone exhibits a high level of attenuation but low signal when using conventional MR techniques. Ultra-short TE (UTE) sequences have been proposed for directly imaging the skull without the need for population information. In most UTE-based methods, a segmentation is usually employed to classify non-background voxels into bone, air, soft tissue and/or fat. Since there is no known relationship between MR signal and electron density, each tissue type is then assigned a single linear attenuation coefficient (LAC). However, bone tissue exhibits a large range of LACs, rendering the assignment of a single LAC to all voxels problematic. **We hypothesize that the decay parameter R2* is associated with CT Hounsfield units (CT-HU) in bone and could help accurately estimate bone LACs.** The goal of this study is to derive a relationship between R2* and CT-HU and to use this relationship in an MR-based method for accurate attenuation correction in MR-PET neurological studies.

Methods: MR-PET and CT datasets were retrospectively obtained from 98 patients using an IRB-approved protocol and with informed consent. Estimates of R2* were computed using images from both echoes of an ultra-short echo time (UTE) sequence as previously described[1]. Next, regression analysis was performed between corresponding R2* and CT-HU for each patient using data only from voxels identified as bone by both CT[2] and R2* [1]. Due to noise in the R2* maps, a voxel-by-voxel comparison between R2* and CT was avoided. Instead, a spatially-matched binning approach was followed. For each patient, the R2* (and corresponding CT-HU) values of bone voxels were numerically sorted and divided into 100 equally-sized bins. The mean of each R2* and CT bin was then computed and plotted only for the first 98 bins due to increased effects of noise in the last two. Regression analysis was performed in a "leave-one-out" scheme, generating a conversion model for each patient using data from the remaining subjects. A bone/air separation technique was also developed in order to accurately identify bone voxels for conversion to CT values. A threshold of 550 s^{-1} was used to identify bone from the R2* image[1] while the reciprocal of the UTE_1 image (iUTE) was thresholded (cut-off = 0.06) to identify air. The remaining tissue was further divided into fat and water using thresholds of the weighted images from a two-point Dixon sequence[3]. Dice coefficients were computed against CT-based segmentation to assess segmentation accuracy. Attenuation maps were generated by assigning the following LACs to each tissue class[3,4]: fat=0.092 cm^{-1}, soft tissue=0.1 cm^{-1} [4], air=0 cm^{-1}, bone=varies. For bone voxels, the R2* values were first converted to CT-HU values using the derived equations and then translated to PET LACs using a piece-wise linear scaling method[5]. This piece-wise scaling was also applied to all voxels in the CT image to obtain the gold standard CT-scaled map. Six patients were excluded from the segmentation and PET reconstruction analysis due to imaging failures with the PET or Dixon scans. Raw PET data for the remaining 92 patients was reconstructed separately with both of the above attenuation maps as well as a vendor-provided UTE map[6] (with classifications for bone, air, and soft-tissue) using the vendor-provided reconstruction software package (E7tools, Siemens Medical). Percent-error maps were generated for the results with respect to the gold standard. The mean absolute percent-error (MAPE) in whole-brain was computed to measure the magnitude, and the difference between 95th percentile and 5th percentile (W95-5) was computed to measure the range of the errors.

Results: Representative regression results (**Fig 1**) showed a strong (r^2 = 0.95) sigmoid relationship between mean bin R2* and CT values. Mean Dice coefficients across patients for the proposed method were 0.75 for bone and 0.60 for air, while the vendor-provided UTE method exhibited values of 0.60 for bone and 0.52 for air. Representative segmentation results for one patient (**Fig 2**) show good overlap for both bone and air compared to CT when using the proposed method. The MAPEs (± SD) across patients in whole-brain for the proposed method and the vendor-provided UTE method were 2.55% (±0.86) and 12.25 (±2.09), respectively ($p < 0.01$). The W95-5 (± SD) across patients in whole-brain for the proposed method and the vendor UTE method were 9.89% (±4.22) and 20.93% (±9.77), respectively ($p < 0.01$). The proposed method produced drastically reduced percent-errors compared to the vendor-provided UTE method across the whole brain as demonstrated in **Fig 3**.

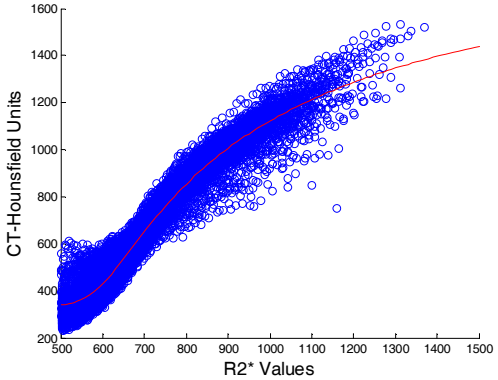

Figure 1: A representative scatter plot of the mean R2* and CT-HU values (blue) shows a sigmoid relationship. A 5-parameter sigmoid model was used for the fit (red).

Discussion: To the best of our knowledge, **the proposed method is the first MR-based attenuation correction method to directly associate MR R2* relaxation with CT-HU in bone tissue**, providing continuous-valued attenuation coefficients for bone using only patient-specific information. Of note, atlas-based methods also provide continuous-valued LACs but rely on variants of averaging over population data. In addition, a novel bone/air separation method is presented that helps improve attenuation correction by properly identifying bone voxels. The proposed method has been shown to be highly accurate, producing a < 3% error in whole-brain compared to a >10% error with the vendor-provided UTE method which was derived using the same UTE data. Furthermore, this method has been automated and does not require any tweaking of the parameters (including thresholds) across patients. Finally, the required UTE images can be acquired quickly (~ 1.5 min), and the attenuation maps can be computed rapidly (< 15 sec).

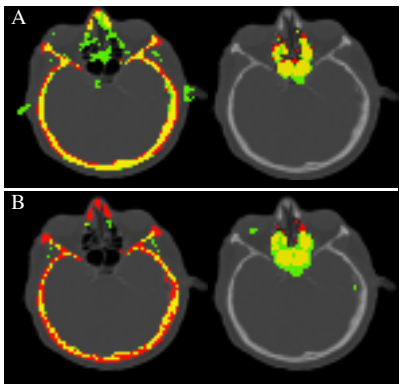

Figure 2: Representative overlap images for bone (left) and air (right) between CT & proposed method (A), CT & vendor method (B) are shown with the true positives (yellow), false positives (green), false negatives (red).

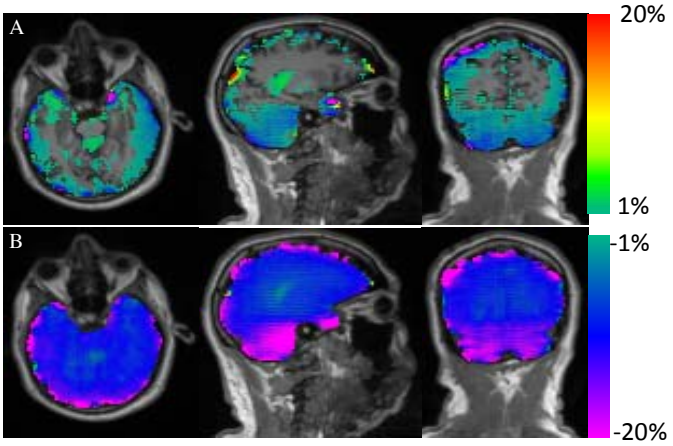

Figure 3: Representative percent-error maps of PET reconstructions using the proposed method (A) and vendor method (B) overlaid on T1-MR images are shown here. Errors less than ±1% and larger than ±20% were suppressed.

References:

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