MR-based PET Attenuation Correction – Method and Validation

M. Hofmann[1,2,3], F. Steinke[2], V. Scheel[1], G.C. Charpiat[2], J.M. Brady[3], B. Schölkopf[2], B.J. Pichler[1]
[1]Laboratory for Preclinical Imaging and Imaging Technology, Clinic of Radiology, University of Tübingen, Germany
[2]Max Planck Institute for Biological Cybernetics, Tübingen, Germany
[3]Wolfson Medical Vision Laboratory, University of Oxford, United Kingdom

I. Introduction

In combined PET/MR, the high soft tissue contrast of Magnetic Resonance Imaging (MRI) and the functional information of Positron Emission Tomography (PET) are combined in one machine. Although this combination still poses many technological challenges, recent progress [1] indicates that it is only a matter of time before PET/MR machines enter the market. On the software side, attenuation correction, which accounts for radiation attenuation properties of the tissue, is mandatory for obtaining PET images that are sufficiently accurate for quantification. Usually the attenuation map is obtained from a transmission scan, which uses a rotating source. In the case of a PET/MR, there is insufficient space for the rotating source and the attenuation map needs to be determined in another way. Ideally, one would want to calculate it from the MR image. This is inherently difficult: The intensities in the MR image are proportional to the proton density; however, the PET attenuation value is not directly related to the proton density. For example bone compacta and air both do not contribute a MR signal whereas their attenuation values are maximally distinct. Thus, standard intensity based segmentation is bound to fail. In order to determine the attenuation value for a position we have to include additional knowledge. We show how such knowledge can be extracted from local image patches and the registration with an atlas.

Attenuation correction directly influences the standard uptake values (SUV) and can therefore directly impact diagnostic decisions derived from the images. This means that any attenuation correction method needs to be validated carefully. We will introduce a method for quantifying the impact of errors in the attenuation map on the reconstructed PET image.

II. Methods

One straightforward approach to determine the attenuation map from a given MR scan is by atlas registration: We assume that we have an atlas comprising a complete MR image and the corresponding attenuation map. For future subjects, a non-rigid registration algorithm automatically computes a deformation field that aligns the MR atlas with the patient's MR image. Applying the same deformation to the atlas attenuation map then yields the desired result.

Instead of working only with one atlas image pair we have built an atlas database using MR (T1SE) and CT images from 16 patients. (From the CT image the PET attenuation map can be determined via a scaling function. Currently, we use formula and parameters from [2]). The alignment between the individual MR-CT pairs was performed using B-Splines deformable registration, as described separately in [3]. Our atlas is built from images from subjects of different ages and genders and we assume that it incorporates intersubject variance.

Given a patient MR image, we can now compute a registration of all atlas images to the patient MR. For 16 atlas image pairs this also yields 16 CT images matched to the patient MR. Whereas it would be possible simply to average over these transformed CT images, this would lose the information of how well the individual transformed atlas images locally match the patient image. To make use of this knowledge in the prediction of the final CT image, we suggest using kernel ridge regression. Inputs for the regression function are the local image patch and its position, using a combined radial basis function kernel.

Our method does not require a locally high precision of the atlas-patient registration method. Using the spatial normalisation function of SPM5, with standard settings, enabled registration of all atlas images within approximately 15 minutes. The kernel ridge regression is computationally more expensive but could be optimised to similar times on standard hardware.

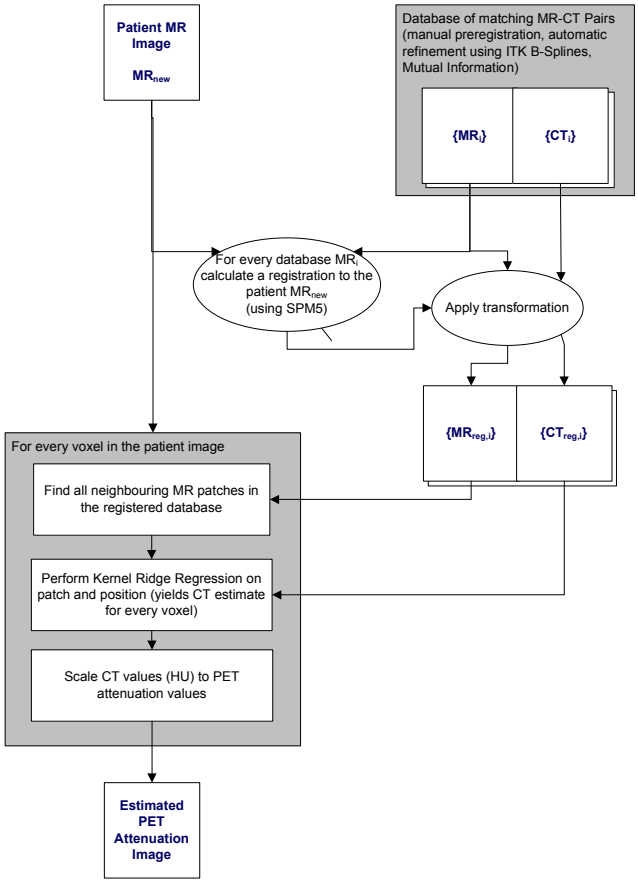

Fig. 1: Flowchart of the steps used for predicting the attenuation map.

For the quantitative evaluation of our estimated attenuation maps we follow [4] and compare activity in volumes of interest (VOI) for: a) the ground truth CT-attenuation corrected (CTAC) PET and b) the MR-based attenuation corrected (MRAC) PET. The VOIs were defined using an atlas of 116 labelled brain structures. Our approach allows a very thorough evaluation; it requires however that PET, MR and CT images from the same patient are available.

III. Results

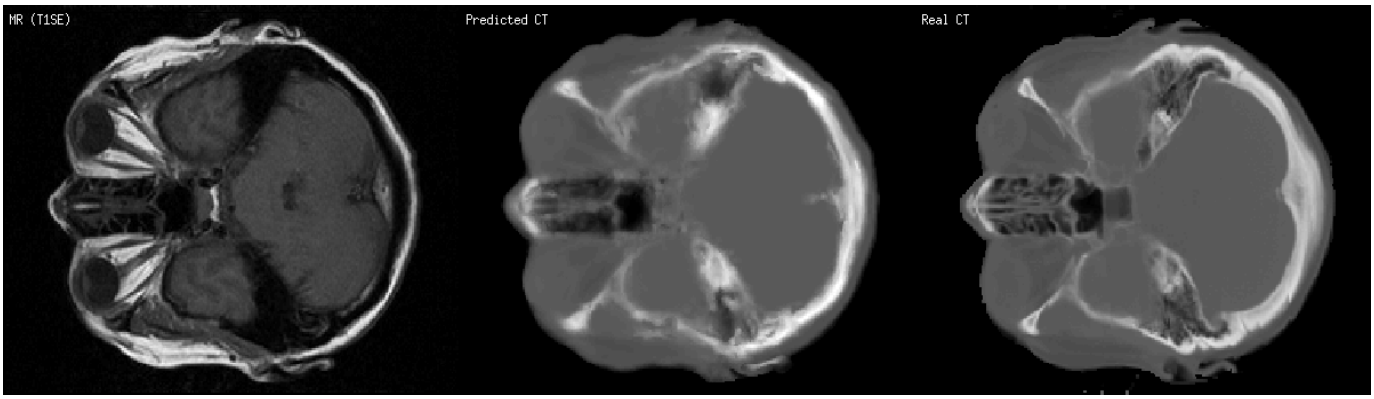

Fig. 2: Left: The patient MR image. Middle: The "Pseudo-CT" as predicted using our method. Right: The real CT image.

Using leave one out cross validation (LOOCV), the average per voxel error in the predicted CT images was 100.7 HU. As can be seen in Fig. 2 even in regions where bone and air (both of which are black in the MR) are mixed, our method manages to distinguish bone, air and soft tissue with high accuracy. In contrast to other algorithms that have previously presented for MR-based determination of the attenuation map [5] our method predicts attenuation values on a continuous scale instead of just a small number of tissue classes. This has the advantage that different bone densities can be considered.

For the quantitative evaluation 116 VOIs were segmented in the patient MR images and the activity in the corresponding regions both in the "ground truth" CT-attenuation corrected PET image and in the PET image that was attenuation corrected using our attenuation map estimated from the MR.

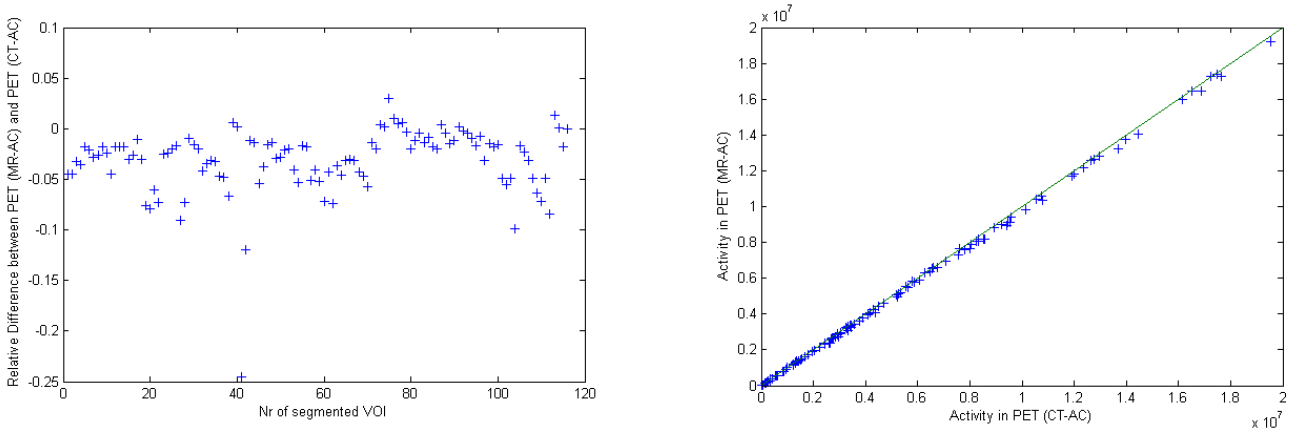

Fig. 3: Left: Relative differences between activity concentrations in the PET image obtained using MR-based AC in comparison to CT-based AC. Right: Scatter plot, with the ideal diagonal in green.

The relative differences between PET (MR-AC) and PET (CT-AC) typically lie in a range of +/- 7%. It is worth noting that with our approach, in contrast to the approach and results presented in [5], across subjects we observe no significant systematic bias towards under- or overestimation of activity.

IV. Conclusion and Next Steps

We have presented a novel method for atlas-based prediction of attenuation images given the MR image. On a database of 16 MR-CT pairs we have shown that our method reliably allows predicting the CT image. On an additional dataset of MR-CT-PET triplets we have quantitatively validated that our approach allows PET quantification with an error that is smaller than what would be clinically significant.
It should be mentioned that our approach is not limited to brain imaging but instead we assume that it is particularly strong for whole body attenuation correction. We do not yet have sufficient data to prove this.
Our method is general in that it does not rely on a specific MR sequence. As long as MR-CT pairs are available for the atlas database our method could be used for CT image prediction. In particular our approach could be combined with novel MR sequences that yield a signal even from dense bone structure. This might further improve the accuracy in bone/air delineation.

References

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