Investigation of Motion Induced Errors in Scatter Correction for the HRRT Brain Scanner

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Patient motion during PET scans introduces errors in the attenuation correction and image blurring leading to false changes in regional radioactivity concentrations. However, the potential effect that motion has on simulation-based scatter correction is not fully appreciated. Specifically for tracers with high uptake close to the edge of head (e.g. scalp and nose) as observed with [^{11}C]Verapamil, mismatches between transmission and emission data can lead to significant quantification errors and image artefacts due to over scatter correction. These errors are linked with unusually high values in the scatter scaling factors (SSF) returned during the single scatter simulation process implemented in the HRRT image reconstruction. Reconstruction of μ-map with TXTV (an alternative μ-map reconstruction using non-linear filtering rather than brain segmentation and scatter correction of the transmission data) was found to improve the scatter simulation results for [^{11}C]Verapamil and [^{18}F]FDG. The errors from patient motion were characterised and quantified through simulations by applying realistic transformations to the attenuation map (μ-map). This generated inconsistencies between the emission and transmission data, and introduced large over-corrections of scatter similar to some cases observed with [^{11}C]Verapamil. Automated Image Registration (AIR) based motion correction was also implemented, and found to remove the artifact and recover quantification in dynamic studies after aligning all the PET images to a common reference space.

I. Introduction

The High Resolution Research Tomograph (HRRT) is a dedicated brain scanner with a spatial resolution of 2-3 mm. With such high spatial resolution even small amounts of motion during PET scanning become a substantial source resolution degradation. Most dynamic brain PET studies require scanning for more than an hour during which time translations in the range of 5-20 mm and rotations 1 to 4 degrees are observed even when using head restraints.

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[^{11}C]Verapamil is a substrate to efflux pumps, such as P-glycoprotein, resulting in low brain uptake with relatively high concentrations of the tracer in the scalp and nose. In 2 out of 42 such scans performed to date at our institute, a substantial artifact was observed in the PET images, as shown in Figure 1. Initial investigations suggested that the artifact was caused by over-correction for scattered coincidences, due to a small misalignment of the transmission and the emission data.

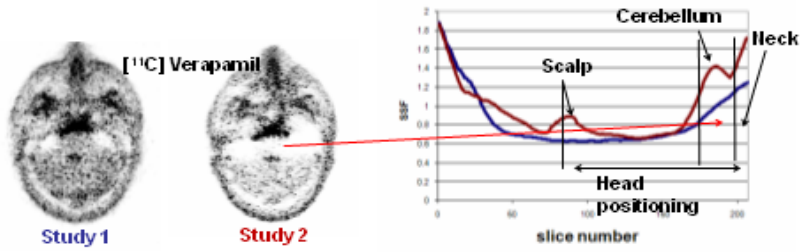


Figure 1. **Left**: Summed images (60 min) of [11C]Verapamil in the same subject. In study 1 (EM-TX match) no artifact is present. In study 2 (EM-TX mismatch) an artifact is visible in the lower areas of the brain. **Right**: Scatter Scaling Factor (SSF) returned by the scatter simulation program. Flat profile over all axial planes for study 1. Two peaks, one corresponding to the cerebellum region where the artifact is present and one to the top of the scalp, are detected for study 2.

Scatter Correction Simulation

Single Scatter Simulation (SSS) [1] is used for scatter correction in image reconstruction of HRRT data. SSS can be divided into two steps. In the first step, scatter is estimated from emission data using the trues sinogram (corrected for randoms and normalized) and the attenuation sinogram map (μ-map).

As this scatter simulation makes a number of approximations (use of trues sinogram which includes scatter events, no multiple scatter events, and no out of field of view scatter), scatter is over-estimated and a second scatter scaling down step is necessary. This scaling assumes that non-random coincidences on LORs with attenuation correction values lower than a threshold of 1.03 are composed purely of scatter. The calculation of these Scatter Scaling Factors (SSF) is performed in sinogram space. For each axial plane a SSF is applied to the scatter correction in order to equalize the total number of counts in the scatter correction with the total number of non-random coincidences in the acquired projection data, as evaluated over those sinogram bins with a low attenuation correction factor (i.e. fitting to scatter tails).

The SSFs for an axial plane is calculated as the ratio of measured trues's (which include the unknown distribution of

scatter) divided by the simulated scatter counts returned by the first step in the SSS outside the object (attenuation values lower than the threshold). This calculation is performed for all the projection views in the axial plane.

Scatter correction errors can arise when motion occurs between the transmission scan and emission scan. Specifically, true events can be located in the LORs just outside of the object, resulting in an overcorrection of scatter as a consequence of the scaling step and a negative bias in the image. An example of over scatter correction when the scatter profiles are calculated is shown in Figure 2. Smaller subject motions may lead to significant errors in the PET images that are less clearly visible. If the SSF increases are large, clear image artifacts are visible as shown in Figure 1.

Attenuation Map Reconstruction

Initially the transmission data was reconstructed with HRRT reconstruction algorithm MAP-TR [2]. Since the new transmission reconstruction TXTV [3] became available we reconstructed a few set of data of [^{11}C]Verapamil using the new transmission reconstruction to assess potential differences between images reconstructed with each transmission map.

Higher values in the calculation of SSF are found when attenuation data reconstructed with MAP-TR are used in comparison with those from the newer TXTV, as reported previously by other authors [4]. This is due to poor soft tissue characterization of this reconstruction method in comparison with the TXTV. It was found that when MAP-TR is used, activity that would be within soft tissue was located outside the object and when used in the calculation of the SSFs returned larger values than those obtained using TXTV (Figure 3).

Motion Simulation and Correction

In order to better understand and quantify the effect of movement scatter correction of [^{11}C]Verapamil images, motion simulations were conducted. An imaged based motion correction was implemented and used to remove the artifact and to align all the reconstructed frames to a reference frame for kinetic analysis. This imaged based motion correction was modified to use both the AIR software [5] adapted for the HRRT from the user community and automatic registration from the Vinci software [6].

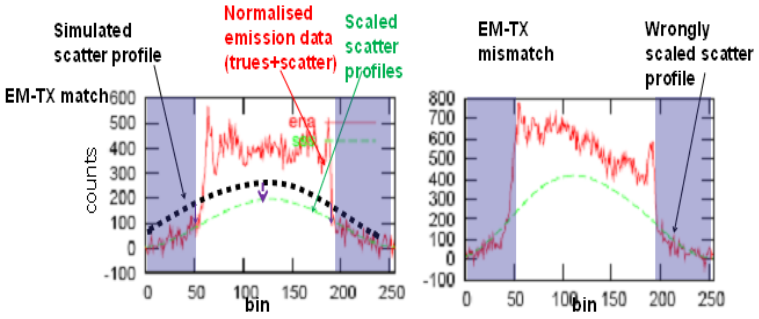


Figure 2. Profiles of coincidences for a plane in radial direction. **Left**: representation of the correct calculation of Scatter Scaling Factors (EM-TX match). The black dashed curve represents the calculated Scatter Profile in step 1 of the SSS and the green line the corrected Scaled Scatter Profile when the scatter scaling factor is applied. The Scattered profile is aligned or fits the tail of the emission data (red curve) outside the object (blue shaded area). **Right**: Example showing wrongly scaled scattered profile due to mismatch between Emission and Transmission scan. This wrongly fitted profile will result in a negative bias in the image reconstruction as the scatter correction is overestimated.

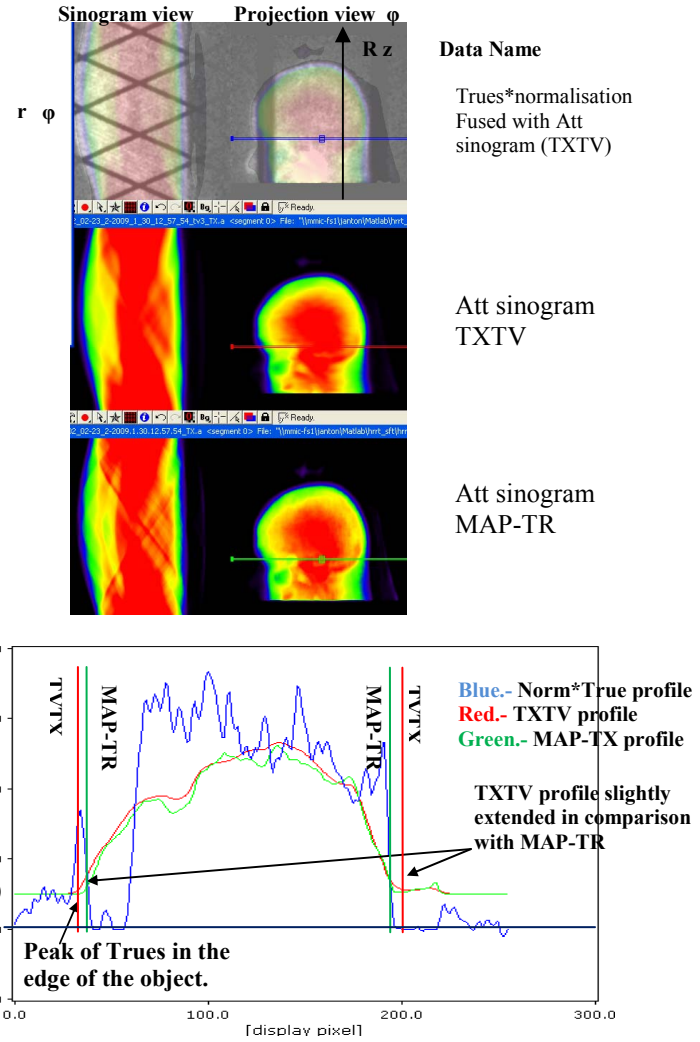


Figure 3. **Top**: Sinogram views for a normalised trues (true + scatter) sinogram for a 60 min frame of a [^{11}C]Verapamil scan fused with the TXTV attenuation sinogram, attenuation sinograms reconstructed with attenuation image reconstructed with TXTV and MAP-TR. **Bottom**: Profile taken from each sinogram in the projection view. The profiles show the extended edges of the TXTV profile in comparison with MAP-TR. A greater proportion of true events in the edge of the object will be allocated outside the object when MAP-TR is used, leading to higher values in the calculation of SSFs when MAP-TR is used in comparison with TXTV.

II. METHODS

Comparison between TXTV and MAP-TR scaling factors

HRRT PET data were reconstructed with the new transmission reconstruction TXTV and compared with the previous MAP-TR to assess potential differences in the SSFs returned and the impact on the final image. The HRRT images were reconstructed using ultra-fast OSEM reconstruction [7]. Assessment of the resulting SSFs using region of interests (ROI) in different brain areas was done for a subject injected with [^{11}C]Verapamil and another subject injected with[^{18}F]FDG in order to compare the effects of scatter correction for a tracer that has less uptake in the nose and scalp than [^{11}C]Verapamil.

The subject used for the [^{18}F]FDG study was scanned for 65 minutes following injection of approximately 370 MBq of [^{18}F]FDG. Transmission scan was performed before the emission scan using a rotating ^{137}Cs point source. The last 40 minutes of the emission data were reconstructed as a summation image. Four sets of reconstructions were performed for the [^{18}F]FDG study: using a μ-map reconstructed with the MAP-TR or TXTV algorithm for attenuation correction; and using a μ-map generated using the MAP-TR or TXTV algorithm for scatter correction. .

Uptake values of [^{18}F]FDG in different brain regions were extracted using atlas-based ROIs in all images reconstructed.

Motion Simulation

The subject used for the motion simulation and for comparison of reconstruction with different μ-maps using [^{11}C]Verapamil underwent paired PET scans for 60 min following injection of 531 and 516 MBq of [^{11}C]Verapamil. A post-emission transmission scan was performed at the end of each scan. The emission and transmission mismatch from the second scan (with image artifact shown in Figure 1) was applied to the first scan (no image artifact) in an attempt to reproduce the artifact. In order to quantify the increases in the scatter scaling factors and the negative bias in the PET image, stepwise motion was simulated by re-slicing μ-map reconstructed with new transmission reconstruction TXTV and compared with the previous MAP-TR.

The motion simulated was the tilting down of the head together with some small translations. This movement was chosen to mimic the relaxation of the patient during the scan and is commonly observed in other scans. To simulate the rotation of the head down the scanner small rotation steps of 0º (match EM-TX),1º,1.5º,2º,3º,4º were performed (simulations 1 to 6) using an automatic application with Vinci software. Along with the rotation, translation movements were also added for more realistic movement (mainly translations of 1 to 3 mm in the axial direction out of the scanner as the movement increased).

The analysis was performed on the summated image of all the acquired emission data. For each resliced μ-map a new image reconstruction was performed using the same emission data but with new scatter and attenuation sinograms. For each step in motion simulation the SSF for segment 0 were plotted. Atlas-based regions of interest were applied to the brain images in order to quantify the impact of each motion on the PET images.

Motion correction

Imaged based motion correction for a set of dynamic brain PET data using AIR and automatic application of Vinci software was implemented to run with minimal input from the user using batch files. The process to reconstruct a full dynamic with motion correction can be summarized as:

1. Select a Reference frame with good statistics (EM_Ref) and where the patient remained still. Reconstruct the emission scan for this reference frame using OSEM3D (no scatter and no attenuated corrected) using PSF modelling in the reconstruction. Apply Gaussian Filter to the image (6mm FWHM) → $EM(NC)^{REF}$.
2. Automatic registration of μ-map to reference frame. We used an automatic application from Vinci software (co-registration of images based on a multi-modality algorithm) → $\mu\text{-map}_{ref}$
3. Reconstruction of non-corrected frames using OSEM3D_PSF with no scatter and attenuation correction as in step 1→$EM(NC)_{1..N}$
4. Rigid body registration (either with Vinci or AIR) of Reference Frame with EM images of step 3. We obtain $AIR_{1..N}$ files with transformation details for each frame or if Vinci is used a $XML_{1..N}$ files with the translations and rotations calculated in the registration step.
5. Create μ-map for each frame with $\mu\text{-map}_{ref}$ from (2) with inverse transformers from (4) → $\mu\text{-map}_{1..N}$
6. Reconstruct all frames with corresponding $\mu\text{-map}_{1..N}$ from (5) (i.e. scatter and attenuation correction for each frame) → $EM_{1..N}$
7. Register all reconstructed frames from (6) using transformation from (4) to have all frames in same reference Space → $(EM_{1..N})^{ref}$.

III. RESULTS

Comparison between TXTV and MAP-TR scaling factors

μ-maps reconstructed via TXTV were found to lead to lower SSFs than via MAP-TR. For the [^{11}C]Verapamil study even when emission and transmission data were aligned, SSFs for planes near the lower part of the brain were >15 % higher in the case of MAP-TR as compared to TXTV (Figure 4). These differences, along with the differences in the attenuation correction, can lead to a 20 % lower intensity in the PET images when using MAP-TR for the lower areas of the brain such as the cerebellum (Table 1). For a region in the frontal lobe (the Inferior Frontal Gyrus) the negative bias between images reconstructed MAP-TR and TXTV was lower than in the cerebellum but still substantial (10%).

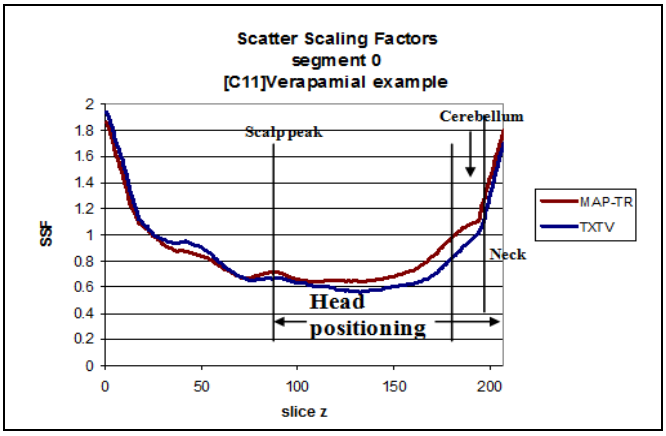


Figure 4 Scatter Scaling factors for [^{11}C]Verapmail study using MAP-TR and TXTV. Differences between the two SSFs returned are visible for most of the axial planes where the head would be in the FOV. The higher differences correspond to the lower areas of the brain (high values in the axial plane z).

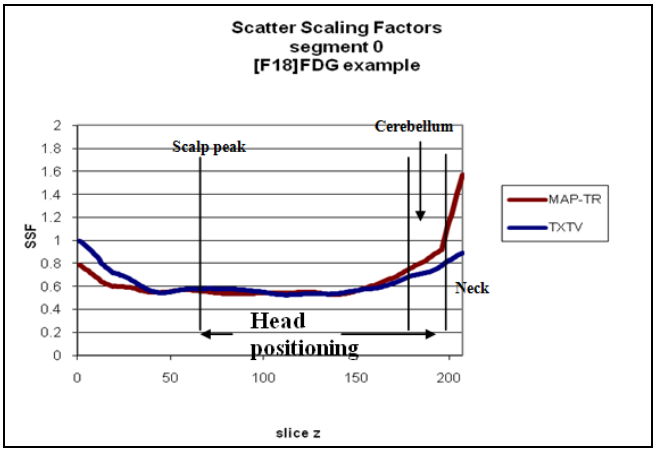


Figure 5 Scatter Scaling factors for [^{18}F]FDG study using MAP-TR and TXTV. Differences between the two SSFs returned are visible in the areas that correspond to the lower areas of the brain (high value in the axial plane z). As the axial plane decreases towards to upper areas of the head, the differences between SSFs become minimal.

A similar analysis was performed for the [^{18}F]FDG study. For this tracer differences in the SSF returned by the Scatter Simulation program were also observed as shown in Figure 5. However, the differences in the SSF were lower than those found with [^{11}C]Verapamil. Unlike the case of [^{11}C]Verapamil the SSF differences were minimal in the axial planes that corresponded to the upper regions of the head. The differences in [^{18}F]FDG uptake in the cerebellum in images that were processed with different MAP-TR were 7 % lower than uptake calculated when TXTV μ-maps were used (Table 1). For the Frontal lobe region (the Inferior Frontal Gyrus) the uptake differences were negligible, up to 1% or less, if the μ-map was processed with MAP-TR.

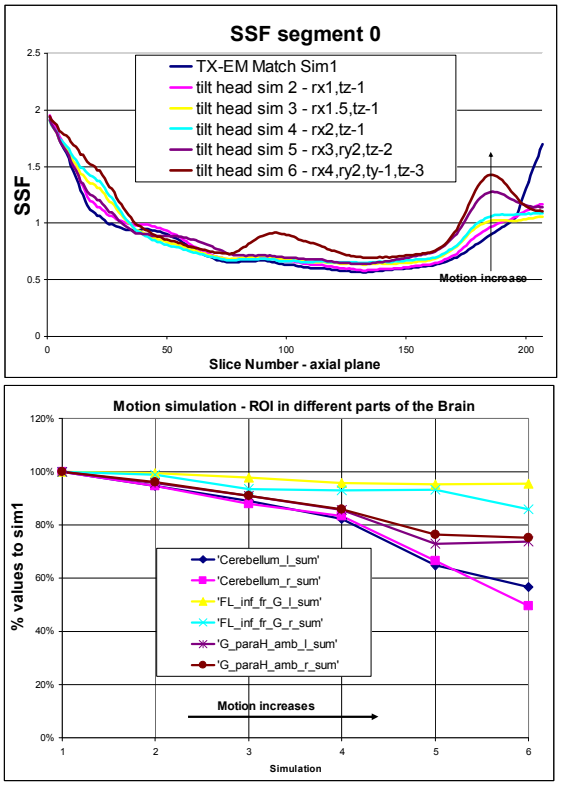
The analysis of the [^{18}F]FDG study was extended to reconstructions using mixed (MAP-TR and TXTV) μ-maps for attenuation and scatter corrections. The results show that when the MAP-TR μ-map is used separately for attenuation and scatter corrections, there is a negative bias of 3-4% within the cerebellum (Table 1) compared to using TXTV for both corrections. Hence scatter correction induced errors from using μ-map MAP-TR are present but to a lesser extent with other more common tracers such [^{18}F]FDG.

Tracer	μ-map for Attenuation correction	μ-map for Scatter correction	Cerebellum R/L	Frontal Lobe Inferior Frontal Gyrus R/L
[^{11}C]Verapamil	TXTV	TXTV	1.6 / 1.6 KBq/ml	1.7/1.8 KBq/ml
	Map-TR	Map-TR	-19/-21 %	-10/-11 %
[^{18}F]FDG	TXTV	TXTV	24.8 / 25.5 kBq/ml	33.5 / 32.5 kBq/ml
	Map-TR	Map-TR	-7/-6 %	-1/-1 %
	TXTV	Map-TR	-4/-3 %	-1/0 %
	Map-TR	TXTV	-3/-3 %	-1/-1 %

Table1: Differences between uptake values of images reconstructed with MAP-TR and TXTV for the Cerebellum and for the Frontal lobe. The reference values were taken from the image reconstructed with μ-map TXTV for attenuation and scatter corrections. Uptake values for [^{11}C]Verapamil and [^{18}F]FDG are shown in red.

Motion Simulation

The simulation showed that as the misalignments increases between emission and transmission, the SSF values returned by the scatter simulation program increased. The quantitative analysis of the resulting images, shown in Figure 6, found a decrease in the uptake values for the areas of the brain studied. The uptake values relative to simulation 1 decrease across the brain (frontal and temporal lobes) but more so in cerebellum where a decrease of 5% is estimated for a small translations of 1 mm and a 1º rotation around the x-axis (rx), 10% for a rx of 1.5º and 17% for a rx of 2º. For larger rotations and translations the artefact gradually appears with motion in the planes corresponding to increased SSF values. The final artefact is similar to the one found in Figure 1, and was produced by a similar degree of EM-TX mismatch.



EM-TX mismatch increases

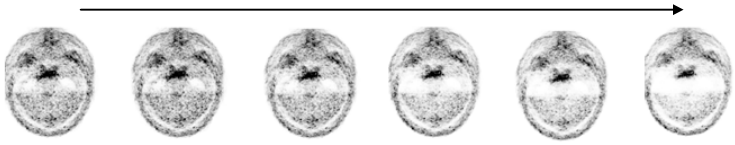


Figure 6. **Top**: The first simulation was performed when emission and transmission data were matching, showing flat response of SSF. As mismatch increases the SSF increases, especially in the higher axial planes which correspond to the lower areas of the brain of the patient. The uptake values (middle graph) are relative to simulation 1 (EM-TX match). The ROI in the brain studies were Cerebellum, Frontal Gyrus and Para hippocampus for the left and right size of the brain. **Middle**: In cerebellum areas drops in values of 5% for 1º rotation in the x plane and small translations of 1 mm, 10% for a 1.5º rx and 1 tz mm, 17% 2º rx 1 tz mm. **Bottom**: Images for each simulation show the induced artifact in those planes where there is an increase in SSF. The µ-map used for these reconstructions were processed with TXTV.

Motion correction

Major improvements between initial reconstruction and AIR corrected reconstruction were found in the image quality and quantification parameters for the two studies with a clear artifact, an example of which is shown in Figure 7. The reference frame for [^{11}C]Verapamil was chosen to be the first 5 min of emission scan. The initial short frames of this dynamic study of durations 5 sec and 10 sec (11 frames in total) were considered to be in the reference frame to avoid co-registration of poor statistics images which could lead to errors in the process. In the case of [^{11}C]Verapamil using a reference of the first 5 minutes contained features of the earlier stages of the tracer and the later stages of the biodistribution which produced satisfactory registration between reference frame and the rest of the dynamic study. We also found that using PSF modelling option in the reconstruction of the non-corrected for attenuation and scatter emission frames (Step 1 and Step 3 in the imaged based motion correction strategy) produced better results for using both AIR and Vinci.

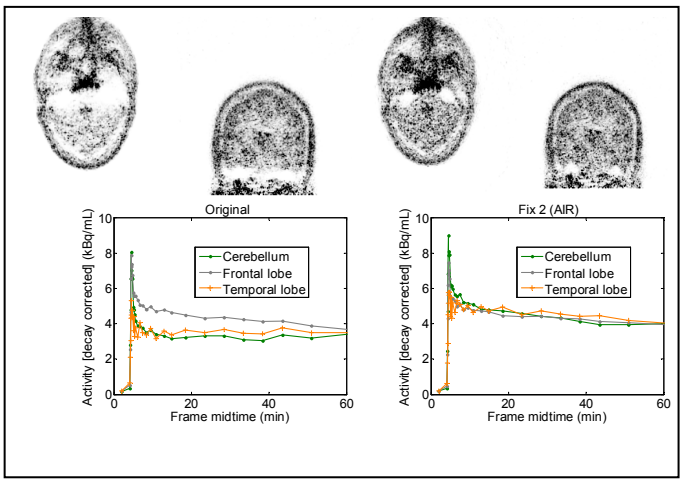


Figure 7. Summed Image reconstructed with (right) and without AIR correction showing major improvements in its image quality and disappearance of the artifact (left). Expected TAC uniformity in three different ROI's in areas of the brain selected are shown in the corrected set of data when AIR correction is used.

V. Discussion

TXTV provides better soft tissue characterization and smoother edges compared with MAP-TR and produces more accurate µ-maps than MAP-TR, as reported by other authors. Even in the case of little or no motion, we observed that errors can occur when using µ-maps reconstructed with MAP-TR for scatter correction, and hence recommend the use of TXTV.

In the SSF calculation step, radioactivity located in soft tissue boundaries and nose might be allocated outside the head where it is assumed to be scatter. This error is more likely to happen when using MAP-TR than with TXTV. This error was shown to lead to erroneously high SSF values, even for the transmission-emission matching situation. These errors are bigger for tracers with high uptake close to the edge of the head such as [^{11}C]Verapamil but are also present with other tracers such as [^{18}F]FDG.

In addition, motion can introduce significant errors in scatter correction by creating a mismatch between the transmission and emission data which is more noticeable for tracers such as [^{11}C]Verapamil which combines low brain uptake with high uptake in the nose and in the scalp. Using simulated motion on real artifact-free images we were able to replicate and quantify artifacts observed in other scans.

An image based motion correction strategy was implemented using AIR and Vinci to revert the transmission-emission mismatches created by motion, The artifact was successfully removed and quantification recovered in dynamic studies after applying the image based motion correction, providing a greater robustness against the scatter correction errors discussed herein.

Since the SSFs calculated in the scatter simulation are accessible to the user, motion QC can be performed by checking the SSF profile for unusual high values. After imaged based motion correction (using AIR or Vinci), the SSF

profile no longer displayed unusual high values or peaks as those appearing in the motion simulation .

A new option has recently become available in the new scatter correction software for HRRT (HRRT version 1.2), where the user can specify an additional margin (in pixels) from the attenuation edges to make scatter scaling less sensitive to emission-transmission mismatches. However, this option leaves fewer data on which to perform fitting of the scatter tails.

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