Estimating PET partial volume full-width-half-maximum directly from human data

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Introduction and Motivation

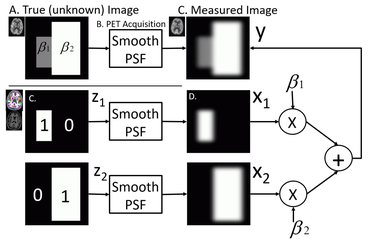
- PET suffers from partial volume effects (PVEs)
- PVEs …
  - Are a type of blurring of the image
  - Can cause reduced apparent uptake in some ROIs ("spill out")
  - Can cause increased apparent uptake in some ROIs ("spill in")
  - Can interact with brain atrophy to cause false positives and false negatives
  - Can cause inter-site/-scanner variability
- Methods exist to correct for PVEs (partial volume correction, PVC), eg
  - Geometric Transfer Matrix (GTM, [1])
  - Muller-Garnter (MG, [2])
  - Region-based Voxelwise (RBV, [3])
- These methods require a measure of the point spread function (PSF)
- PSF usually obtained from a point source
  - Hard to do
  - Not always available
  - Does not take into account influence of reconstruction technique and other factors
- PVC cannot be applied without a measure of the PSF!
- This poster describes a technique called Adaptive GTM (AGTM) to estimate the PSF directly from human PET and MRI data.
  - The PSF is determined using the GTM
  - Once the PSF is known, can be used by other PVC methods
- All software available from PETsurfer ([4,5])
  - surfer.nmr.mgh.harvard.edu/fswiki/PetSurfer)
  - Works hand-in-glove with FreeSurfer

Methods

- The GTM is a linear model with ROI uptake values as the unknown (see Figure 1).
- The GTM is solved assuming a certain PSF.
- The AGTM works by adjusting the PSF to minimize the GTM residual variance (see Figure 2).
- Anatomical MRIs are analyzed in FreeSurfer to generate whole head segmentation.
- MRI and PET are rigidly registered
- The PSF is model as a space-invaraint isotropic Gaussian parameterized by three FWHMs, one for each dimension (X, Y, Z).
  - Other models are possible

Data

- Harvard Aging Brain Study (HABS).
  - 99 subjects, Siemens HR+, 18F-FDG, aged 66-87
- Alzheimer's Disease Neuroimaging Initiative (ADNI)
  - 5 scanners, 10 subjects from each, FDG
- CIMBI SB ligand for $5HT_4$
  - HRRT and Advance, 5 subjects scanned on both,
  - BP_{ND} computed with MRTM2
  - Analyzed with:
    - No PVC (NoPVC)
    - Nominal PVC (NomPVC)
      - HRRT: FWM= 4mm
      - Advance: FWHM= 6mm
    - AGTM
- Simulation using Software for Tomographic Image Reconstruction (STIR). Figure 3.
  - Based on the HABS99 subjects using HR+ scanner with 24 OSEM iterations
  - Allows assessing of accuracy of uptake estimates against ground truth
  - Gaussian noise injection allows an alternate method of computing the FWHM by computing the correlation between adjacent voxels [6].



(1) $y = x_1\beta_1 + x_2\beta_2 = X\beta$ (forward equation)
(2) $\hat{\beta} = (X^T X)^{-1} X^T y$ (ROI means)
(3) $\hat{y} = X\,\hat{\beta}$ (signal estimate)
(4) $r = y - \hat{y}$ (residual error)
(5) $\sigma^2 = r^T r / DOF$ (residual variance)

Figure 1. Derivation of GTM model. (A). True distribution of activity in two distinct ROIs with unknown uptake β_1 and β_2. The acquisition process (B) applies some kind of smoothing PSF to arrive at the blurred acquired image (C). The GTM model requires a segmentation; a binary image is created from each segment (D), which is then smoothed (E), weighted by the uptake (β_1 and β_2), then summed together. This process is represented by a linear equation (1). The unknown βs can then be solved by inverting the model (eq 2). The residual variance is a measure of the fit and will include errors due to mis-specified PSF. X depends on both the ROI segmentation and the PSF. AGTM works by adjusting the PSF to minimize the residual variance.

Results

- Figure 4 shows that the AGTM-measured uptake was very close to the gold standard in the simulated data. Over all ROIs and subjects, the recovery coefficient (RC) was 1.02 for the AGTM and 0.68 when not performing PVC.
- The AGTM-computed FWHM (averaged across all simulated subjects) was 4.4mm, 3.9mm, and 4.1mm for XYZ respectively
- The correlated computed FWHM was 4.0mm, 3.7mm, 4.0mm which compares very well with the AGTM
- Table 1 shows the mean FWHM values for both real and simulated subjects. The values are reasonable for the given scanner.
- AGTM performs well on both OSEM and FBP reconstructions as well as on Siemens, GE, and Philips scanners.
- Intersubject variability of the estimated FWHM is relatively small (on the order of 10%). See Table 1
- AGTM resulted in much less inter-scanner variability, especially in cortex (Figure 5 and Table 2)

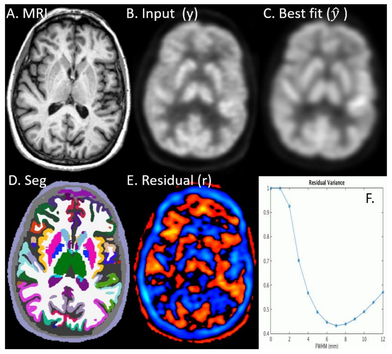


Figure 2. GTM on real data. (A) Anatomical MRI. (B) Input PET image (y, 18F-FDG, HABS). (C) Best fit image (eq. 3), (D) Segmentation of MRI into the ROIs used for the GTM. (E) Map of residual error (eq 4). (F) Plot of residual variance (eq. 5) against PSF FWHM; there is a clear minimum at about 7mm FWHM. AGTM finds this minimum.

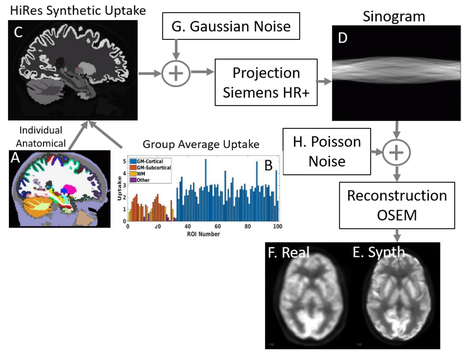


Figure 3. Simulation scheme. (A) Anatomical MRI segmented by FS. (B) ROI averages of 18F-FDG from real HABS99. (C) Synthetic high-res image made by merging (A) and (B). (D) Sinogram after projection. (E) Simulated PET image with PVEs. (F) True PET image. The simulation has the ability to inject Gaussian noise (G) into the hi-res image and Poisson noise (H) into the sinogram. Projection and Reconstruction use STIR.

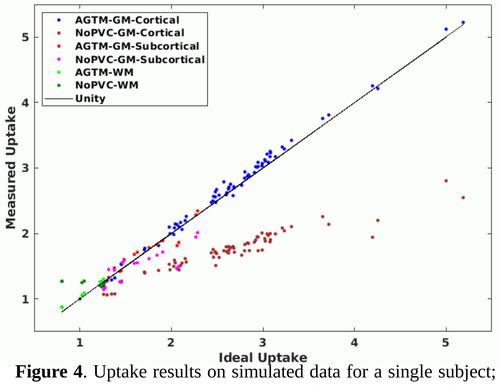


Figure 4. Uptake results on simulated data for a single subject; each dot is an ROI. AGTM is very close to the ideal for all ROIs but does especially better than NoPVC in cortex. Over all ROIs and subjects, the recovery coefficient (RC) was 1.02 for the AGTM and 0.68 when not performing PVC. This shows that AGTM does a good job accurately removing PVEs.

Site	Man	Scanner	Recon	xFWHM	yFWHM	zFWHM
HABS-Sim	Si	HR+	OSEM	4.4 (0.12)	3.9 (0.09)	4.1 (0.04)
HABS-Real	Si	HR+	OSEM	8.9 (0.44)	8.0 (0.42)	6.4 (0.39)
ADNI-128	Si	HR+	OSEM	6.9 (0.47)	6.4 (0.46)	5.7 (0.42)
ADNI-005	GE	DiscoveryST	FBP	8.0 (0.52)	7.8 (0.80)	6.7 (0.53)
ADNI-127	Ph	GeminiTF	OSEM	6.7 (0.24)	7.9 (0.58)	8.6 (0.54)
ADNI-033	GE	Advance	FBP	8.0 (0.31)	9.0 (0.38)	7.4 (0.26)
ADNI-114	Si	HRRT	OSEM	6.6 (0.44)	6.8 (0.51)	6.2 (0.49)
NRU-Adv	GE	Advance	OSEM	8.6 (0.10)	8.8 (0.37)	8.6 (0.30)
NRU-HRRT	Si	HRRT	OSEM	5.7 (0.22)	4.4 (0.21)	3.8 (0.13)

Table 1. AGTM FWHM (mm) estimates for various scanners, real and simulated. The value in parentheses is the standard deviation across subject. Si=Siemens, GE=GE, Ph=Philips. OSEM=ordered subsets expectation maximization, FBP=filtered back projection.

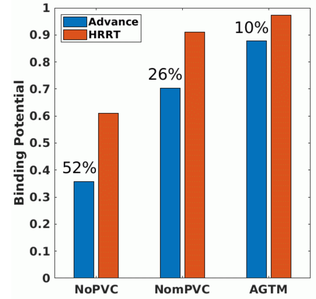


Figure 5. $5HT_4$ binding potential in a single subject in the lateral occipital region across both scanners and three PVC methods. AGTM results in a substantial reduction in inter-scanner variability. NomPVC is the GTM with nominal FWHM for each scanner.

Method	SubCtx	Ctx
NoPVC	33%	53%
NomPVC	22%	35%
AGTM	20%	30%

Table 2. Average percent difference between the BPND of the two scanners averaged over subject and ROI. As in Figure 5, the AGTM results in substantial reduction in inter-scanner variability, even when compared with GTM with the nominal FWHM; the effect is especially prominent in cortex.

Conclusions

- This poster introduces the Adaptive Geometric Transfer Matrix (AGTM) algorithm to estimate the point spread function (PSF) directly from human PET and MR data.
- AGTM works by minimizing the residual error in the AGTM with respect to the PSF.
- Realistic simulations show uptake is recovered to within a few percent
- Simulations also showed that the FWHM estimated by AGTM were extremely close to another method for computing the FWHM based on spatial correlation of noise injected at the input image phase.
- Application of AGTM to real FDG data across multiple scanners and subjects showed the method gave reasonable FWHM and that it was very robust.
- In a kinetic modeling study, AGTM was shown to greatly reduce the inter-scanner variability relative to not using PVC or using PVC with nominal FWHM.
- The PSF obtained by AGTM can be used in other PVC algorithms.

References

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