University of Claude Bernard Lyon 1

Polytech Lyon

Multimodal MRI-PET Imaging: Estimation of Image-Derived Arterial Input Function in Brain PET Imaging Application to Modeling PET Dynamics of Glucose Metabolism in Patients with Impaired Consciousness

By Sepand Ali Madad Soltani

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Supervised by Inés Mérida and Nicolas Costes

Academic Advisor: Kevin Tse Ve Koon

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Abstract

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Contents

Introduction

1.1 Positron Emission Tomography

Positron Emission Tomography (PET) is a functional imaging technique widely used in clinical and research settings to monitor physiological processes. In PET, a biologically active molecule is labeled with a positron-emitting radioisotope, known as radiotracer (e.g. $[^{11}C]$ or $[^{18}F]$), and introduced into the body. As the radiotracer accumulates in target tissues, its radioactive decay produces positrons, which interact with electrons to emit pairs of gamma photons in nearly opposite directions. These photons are detected by the PET scanner, and through image reconstruction algorithms, a three-dimensional representation of tracer distribution is generated. This imaging modality allows for the investigation of metabolic changes, receptor binding, and other biochemical processes, providing invaluable information in oncology, neurology, cardiology, and other fields.

Unlike static PET imaging that captures a snapshot of radiotracer distribution, dynamic PET involves acquiring a series of images over a period of time immediately following tracer administration. This temporal information is crucial for understanding the kinetics of radiotracer uptake and clearance. The resulting time-activity curves (TACs) represent the change in tracer concentration within a region of interest over time. TAC modeling employs mathematical and statistical methods to describe these curves and extract quantitative parameters that reflect underlying physiological processes. Such kinetic modeling is essential for distinguishing between different tissue characteristics, assessing drug-receptor interactions, and improving the accuracy of diagnostic and prognostic evaluations.

1.2 Need for Input Function in PET

1.3 Image Derived Input Function

Materials and Methods

2.1 Dataset Description

We utilized a dataset of 56 comatose patients, aged between X and Y years, in which dynamic PET imaging was conducted 90 minutes using 18FDG as the tra with arterial blood sampling and TOF-MRA images acquired during the same session.

2.2 Carotid Segmentation

Since vessels appear as hypersignal in TOF-MRA, a high-intensity thresholding technique was employed. First, a threshold value was computed by selecting all nonzero intensity values outside the brain mask and determining a high quantile of these intensities. Only voxels exceeding this threshold and located outside the brain mask were retained. Next, a region-growing step was applied to refine the initial selection, ensuring that continuous vascular structures were captured as the final carotid mask.

In addition to arteries, venous structures and lesions may also appear as hypersignal and might be selected by the algorithm. To exclude them, a cuboid mask was defined in a reference image covering the neck area, where the carotids are most likely to appear. This mask was first registered and then applied to the uncorrected carotid mask.

2.3 IDIF Estimation

2.3.1 Geometric Transfer Matrix

Direct quantification with the IDIF extracted from the MRI mask of the carotids is impractical due to the strong Partial Volume Effects (PVE) in PET images. This however can be corrected by the use of the Geometric Transfer Matrix (GTM) method. This method considers the observered TAC to be the linear combination of the true real value and the other effecting regions. Here we define two regions, the carotids and the background mask which was generated by dilating the carotid mask by 5 pixels and subtracting the voxels corresponding to the carotid mask.

$$\underbrace{\begin{bmatrix} T_c \\ T_{bg} \end{bmatrix}}_{\text{Observered}} = \underbrace{\begin{bmatrix} \omega_{c\to c} & \omega_{bg\to c} \\ \omega_{c\to bg} & \omega_{bg\to bg} \end{bmatrix}}_{\text{Geometric Transfer Matrix}} \cdot \underbrace{\begin{bmatrix} T_{IF} \\ T_{bg} \end{bmatrix}}_{\text{Unknown}}, \tag{2.1}$$

where $\omega_{n\to m}$ is the spill coefficient of region n onto region m, which is obtained by convolving the binary mask of region n with the system's point spread function and integrating the resulting intensity over region m, normalized by the total signal in region m. where

$$\omega_{n\to m} = \frac{\displaystyle\int_{\Omega_m} \big(h * \chi_n\big)(\mathbf{r})\, d\mathbf{r}}{\displaystyle\int_{\Omega_m} \big(h * \chi_m\big)(\mathbf{r})\, d\mathbf{r}}, \tag{2.2}$$

with χ_n and χ_m denoting the binary masks of regions n and m, respectively, h the system's point spread function, and Ω_m the spatial domain of region m.

T_c and T_{bg} are respectively the observered carotid and background TACs and C_{IF} and C_{bg} are the real unknown TACs of the carotid (the input function) and the background tissue.

By inversing the GTM, this system of equations can be easily solved. However, the GTM being a low rank matrix makes the inversion sensitive to noise and biased on small regions such as carotids.

2.3.2 Bayesian Geometric Transfer Matrix

To overcome challenges posed to GTM method, we utilized a Bayesian framework that jointly estimates the input function and tissue kinetics. For each subject, C_{IF} is modeled as a linear combination of a population mean and its principal components. These components are derived by performing principal component analysis (PCA) on a set of AIFs collected from the population. Specifically, for each subject, a subset of 10 random subjects is selected from the dataset—excluding the subject under study—to construct the PCA model.

$$C_{IF}(t) = \mu(t) + \theta_1 v_1(t) + \theta_2 v_2(t) + \theta_3 v_3(t), \tag{2.3}$$

where $\mu(t)$ is the population mean AIF, $v_i(t)$ are the principal components obtained from PCA, and θ_i are the subject-specific weighting coefficients.

The background TAC is then generated by convolving this modeled input function with an impulse response function defined by a two-tissue compartment model [1].

$$C_{bg}(t) = C_{IF}(t) \circledast f(t; K_1, k_2, k_3), \tag{2.4}$$

where K_1, k_2, and k_3 are kinetic parameters of the two-tissue compartment model denoted by f.

Parameter estimation is performed using a Metropolis-within-Gibbs Markov Chain Monte Carlo (MCMC) sampler, which explores the posterior distribution of both the kinetic parameters and the PCA coefficients. In the Bayesian framework, all model parameters are collected into the vector Θ. The posterior distribution of Θ given the observed data $\mathcal{D}$ is expressed as

$$p(\Theta \mid \mathcal{D}) \propto p(\mathcal{D} \mid \Theta)\pi(\Theta), \tag{2.5}$$

where $p(\mathcal{D} \mid \Theta)$ is the likelihood function and $\pi(\Theta)$ is the prior distribution over the parameters Θ. The maximum a posteriori (MAP) estimate of Θ is given by:

$$\hat{\Theta} = \arg\max_{\Theta} \left\{ \ln p(\mathcal{D} \mid \Theta) + \ln \pi(\Theta) \right\}. \tag{2.6}$$

This Bayesian formulation naturally incorporates prior knowledge and accounts for uncertainties in both the input function and tissue kinetics, resulting in robust parameter estimates.

2.4 FDG Quantification

To accurately measure the performance the performance of the estimated IDIF, absolute quantification must be performed

2.5 Evaluation and Assessment

Implementation

Results

4.1 Segmentation

4.2 Quantification

Discussion

Conclusion

References

[1] Camille Jouvie. “Estimation of the input function in dynamic positron emission tomography applied to fluorodeoxyglucose; Estimation de la fonction d’entree en tomographie par emission de positons dynamique: application au fluorodesoxyglucose”. In: (2013).