Dynamic Multi-Bed FDG PET Imaging: Feasibility and Optimization

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\textbf{Abstract—}Multi-Bed FDG PET/CT as applied to oncologic imaging is currently widely and routinely used for assessment of localized and metastatic disease involvement. In the past, based on conventional (single-bed) dynamic PET imaging, standard tracer kinetic modeling techniques have been developed to estimate the FDG uptake rate $K_t$. However, routine clinical multi-bed FDG PET imaging commonly involves a single time frame per bed, i.e., static imaging, and the standardized uptake value (SUV), a surrogate of metabolic activity, is employed to estimate the uptake rate $K_t$. The accuracy depends on two conditions: (i) in the voxel or region of interest, contribution of non-phosphorylated FDG is negligible relative to phosphorylated FDG, and (ii) time integral of plasma FDG concentration is proportional to injected dose divided by lean body mass, which can fail in clinical FDG PET imaging and pose problems in differentiating malignant from benign tumors. The objective of the proposed work is to facilitate, for the first time, a transition from static to dynamic multi-bed FDG PET/CT imaging in clinically feasible times where, given the challenge of sparse temporal sampling at each bed, novel dynamic acquisition schemes should be employed to yield quantitative whole-body imaging of FDG uptake. Thus, a set of novel dynamic multi-bed PET image acquisition schemes have been modeled, using Monte Carlo simulations, to quantitatively evaluate the clinical feasibility of the method and optimize the number of passes per bed and the total study duration. It has been determined that a data acquisition scheme consisting of 6 whole-body passes and constant time frames of 45sec produces parametric images with the optimal noise vs. bias performance. Finally, clinical whole-body patient data have been acquired dynamically and results demonstrate the potential of the proposed method in enhancing treatment response monitoring capabilities of clinical PET studies.

\section{I. INTRODUCTION}

The management of a wide variety of serious life-risking diseases including lung, lymphoma, head and neck, melanoma and colorectal cancer has been considerably enhanced due to the powerful modality of PET/CT using the radiotracers FDG (fluoro-deoxy-glucose) [1]–[3], a marker of glucose metabolism. Nowadays, routine FDG PET/CT imaging involves scanning the patient over multiple bed positions to achieve whole-body imaging, which is especially important for evaluation of metastatic cancer. However, whole-body PET/CT is currently involving static data acquisition, i.e., employs only a single temporal frame per bed position to measure the FDG concentration; thus, the scanner passes over each bed position once (single-pass) [4]–[7]. The standardized uptake value or SUV, a semi-quantitative surrogate of metabolic activity, is used for this purpose.

SUV can be considered as a simple estimate of the FDG uptake rate constant $K_t$, but the accuracy in the estimation depends on two conditions: (i) in the voxel or region of interest, contribution of non-phosphorylated FDG is negligible relative to phosphorylated FDG, and (ii) time integral of plasma FDG concentration is proportional to injected dose divided by body weight, lean body mass or body surface area, which can induce inaccuracies in clinical FDG PET imaging and potentially pose problems in quantifying follow-up PET studies [2]. Alternatively, in the research setting, dynamic single-bed FDG PET imaging has been performed to quantitatively measure the rate $K_t$ over different time frames for a given bed position [8]–[10].

We are proposing a novel shift of the two previous data acquisition schemes into the dynamic multi-bed domain, where the benefits of both multi-bed acquisition and truly quantitative imaging can potentially be combined. PET dynamic whole-body acquisition involves the scanner performing sequential whole-body acquisitions over time. Therefore, each bed position is scanned at multiple passes (multi-pass) but not continuously in time, as in the case of single bed dynamic acquisition. The series of PET measurements collected for each bed position over time are later employed for the derivation of a number of parameters quantifying physiological or biochemical processes, such as the rate of glucose metabolism. Furthermore, the estimation of these parameters across all bed positions, at the voxel level, can lead to parametric whole-body PET imaging, which allows for truly quantitative analysis of serial PET images of the same subject, obtained on different occasions (e.g. prior to and following treatment). This is particularly crucial in the whole-body domain, where the time progress of a large variety of metastatic cancer diseases, as spread across multiple bed positions, is determined over large periods of treatment. Thus, multi-bed dynamic imaging can allow for truly quantitative whole-body PET imaging and, therefore, potentially enhance treatment response monitoring capabilities.

The objective of this study is to facilitate, for the first time, a transition from conventional static SUV towards dynamic
multi-bed FDG PET/CT imaging by demonstrating clinical feasibility as well as by optimizing the associated data acquisition protocol, given the challenge of sparse temporal sampling (non-continuous kinetic data) at each bed position.

II. METHODS AND MATERIALS

In the proposed work a set of novel dynamic multi-bed PET acquisition schemes is designed by carefully selecting different number of passes per bed position and total study durations and, also, by ensuring that a clinically acceptable total time of 50min post injection is not exceeded. Subsequently, a series of Monte Carlo (MC) simulations is performed to model the selected data acquisition schemes and generate PET projection data, which are later reconstructed to produce a set of dynamic PET images. Afterwards, Patlak graphical analysis method is applied to estimate the $K_i$ parameter on a voxel basis and derive the parametric images. Furthermore, the $K_i$ images are analyzed in terms of noise and bias performance in order to quantitatively evaluate the clinical feasibility of the examined acquisition protocols and optimize the number of passes per bed position as well as the total study duration. Moreover, patient clinical data are acquired, based on the optimal acquisition scheme determined above, to validate our simulated results. Finally, the clinical whole-body $K_i$ images are compared with respective SUV images obtained 60min post injection.

A. Estimation of FDG uptake rate constant $K_i$ using kinetic modeling

The SUV metric employed in static imaging is defined as:

$$
SUV = \frac{C(t)}{Dose/LBM}
$$

where, $C(t)$ is the FDG concentration, decay corrected with respect to the tracer injection time, $Dose$ is the amount of injected activity and $LBM$ is the lean body mass. Due to the simplicity of its calculation, SUV is widely used in conventional static (single-pass) whole body clinical FDG studies. However, in reality, the SUV measure: (i) cannot differentiate between non-metabolized and metabolized FDG concentrations, and (ii) does not take into account the plasma FDG dynamics [1], [8], [11]–[13].

As a result, the SUV can be considered a semi-quantitative surrogate of the metabolic rate in certain cases in clinical FDG PET imaging [14]–[16]. For instance, if a patient is undergoing chemo- or hormone-therapy, and has impaired renal function, the clearance of plasma FDG could be significantly reduced and, therefore, the total amount of FDG in blood plasma available for absorption could be larger than what would be predicted from the injected dose and lean body mass alone (Eq.1). In such a case, SUV will overestimate the metabolic rate of glucose in tumor [16]–[19]. Thus, the therapy response may not be accurately reflected by the change in SUV. Consequently, assessments of treatment response, based solely on SUV as obtained in static PET imaging, can potentially be erroneous and, therefore, lead to mistakes in treatment planning, for certain cases.

$$
\frac{C(t)}{C_p(t)} = K_i \int_0^t \frac{C_p(\tau)}{C_p(t)} d\tau + V, \quad t \geq t^* \tag{2}
$$

The parameter $K_i$ is the slope of linear regression and represents the tracer uptake rate constant in the tissue. $K_i$ is considered a macro-parameter as it can be expressed in terms of the kinetic micro-parameters $K_1$, $k_2$, $k_3$ and $k_4$ of the 2-compartment tracer kinetic model as follows:

$$
K_i = \frac{K_1 k_3}{k_2 + k_3}, \quad k_4 = 0, \quad t \geq t^* \tag{3}
$$

If $V_p$ is the effective plasma volume in the tissue region, such that $V_p C_p$ is the exchangeable amount of tracer in the blood, $f$ is the fraction of the amount of tracer in the reversible compartment $C_1(t)$ that goes back into the blood and leaves the system and $V_e$ is the steady-state volume of the reversible compartment $C_1(t)$, then the intercept of the regression, $V$, is expressed by eq. (4) [20], [23]:

$$
V = fV_e + V_p, \quad t \geq t^* \tag{4}
$$

The tracer concentration in the tissue, $C(t)$, as measured by PET, is given by eq. 5:

$$
C(t) = (1 - V_p) C_1(t) + C_2(t) + V_p C_p(t) \tag{5}
$$

The Patlak plot is a fast graphical analysis method, which can be employed to estimate the $K_i$ and $V$ parameters on a voxel basis and, thus, produce a powerful image of glucose metabolism uptake rates and blood volume fraction across all bed positions. By comparing equations (1) and (2), it is concluded that $K_i$ measures the metabolic rate of tracer concentration normalized with respect to the time-course of
tracer concentration in the plasma, while SUV-based metrics does not take the plasma FDG dynamics into account.

Micro-parameter $k_4$ of the kinetic model is assumed to be equal to zero when deriving Patlak equation (2). It has been shown that if it is erroneously assumed that $k_4 = 0$, while in reality $k_4 \neq 0$, then $k_4$ and, therefore, $K_4$, are underestimated from eq. (2) and (3) [24]. For certain organs and tracers, such as the FDG in normal liver, high levels of glucose-6-phosphatase produce much higher values of $k_4$ in normal tissues than in tumors. Consequently, uncorrected Patlak graphical analysis underestimates $K_4$ in normal liver resulting in enhancement of the contrast between tumor and background in the parametric $K_4$ images. [24].

The time activity curves used as an input to MC simulations are derived from actual FDG kinetic micro-parameter and effective plasma blood volume values reported in literature (Table I.) [25]-[33].

<table>
<thead>
<tr>
<th>TABLE I</th>
</tr>
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<tbody>
<tr>
<td><strong>FDG KINETIC MICRO-PARAMETERS</strong></td>
</tr>
<tr>
<td>Regions</td>
</tr>
<tr>
<td>Normal Liver</td>
</tr>
<tr>
<td>Liver Tumor</td>
</tr>
<tr>
<td>Normal Lung</td>
</tr>
<tr>
<td>Lung Tumor</td>
</tr>
<tr>
<td>Myocardium</td>
</tr>
</tbody>
</table>

Fig. 2(a) depicts the noise-free samples and the fitted curves for the modeled input function $C_p(t)$ and TACs of the regions of Table I. These, later, are used as an input to MC simulations. Moreover, the respective Patlak points, as derived from the modeled samples, and the Patlak curves for each region, after performing linear regression, are plotted in Fig 2(b). This process is repeated below for the noisy PET measurements, as generated by MC simulations.

**B. Design of dynamic multi-bed acquisition scheme**

The transition from single-bed to multi-bed PET kinetic modeling techniques poses new significant challenges for the data acquisition including the limited total scan duration and the non-continuous sampling of the imaged subject at each bed position. In this study we are examining a set of novel acquisition schemes that can efficiently address these challenges while satisfying restrictions imposed by scanner specifications and clinical routine protocols regarding total study time. Dynamic PET multi-bed acquisition has been realized in this study by defining two separate time phases. During the first phase, a 6-min dynamic acquisition is performed over the heart bed position, immediately after the injection of FDG tracer to the subject, in order to derive the time-course of the FDG activity concentration at the blood plasma, or input function. First, 12 frames of 10sec each are acquired, followed by 12 frames of 20sec each. The GE Discovery RX LYSO PET/CT scanner, located at Johns Hopkins PET center, has been utilized for this study.

Subsequently, in the second phase a series of conventional whole-body acquisitions, each consisting of 7 bed positions, are repeated sequentially over time. Each repeated whole-body acquisition is noted as a pass. The time frames acquired for each bed position are equal over all bed positions and passes. The scan direction of all passes is the same (cranio-caudal direction). As a result, each bed position is scanned for the same number of passes, non-continuously and with equal sampling frequency.

In the case of single-bed dynamic acquisition, the counts of all slices of a bed at each time frame $i$ are assigned the same time point $t_i^{mid}$, which is the average of the start time $t_i^{start}$ and end time $t_i^{end}$ of the particular frame. However, in the whole-body acquisition protocol the adjacent beds are overlapping and, therefore, 11 slices from each side of the intermediate beds, out of the total 47 slices contained in each bed, as well as 11 slices from the edge beds are scanned twice at each pass. In these slices, a portion of the counts were acquired at current time frame $i$ corresponding to the current bed, while the remaining portion at time frame $i+1$, which refers to the next bed. Therefore, an intermediate time point $t_{i+1/2}^{mid}$ is assigned to all counts of these slices for each pass, as derived by eq. (6):

$$ t_{i+1/2}^{mid} = \frac{t_{i}^{mid} + t_{i+1}^{mid}}{2} $$

where $t_{i}^{mid} = (t_{i}^{start} + t_{i}^{end})/2$ and $t_{i+1}^{mid} = (t_{i+1}^{start} + t_{i+1}^{end})/2$ are the average (middle) time points of frames $i$ and $i+1$.

Currently we are proposing acquisition schemes that can be performed during the first 50min post injection, followed by a conventional SUV scan 60min post injection. Our quantitative criteria to optimize the data acquisition protocol is the noise vs. bias performance of the derived parametric $K_4$ images, as the number of OSEM iterations of the original PET dynamic images increases. Our optimization strategy consists of two steps:
Initially, we utilize all available clinical time between initial injection and final SUV scan, which is usually not less than 50 min. Therefore, we determine the optimal acquisition scheme, assuming availability of a 50 min total study time, by attempting different number of passes and different time frames per bed. We start by examining only 2 passes per bed and time frames of 165 sec each. In order to limit the total study time to 50 min, as the number of passes increases, the duration of the time frames is reduced. The scheme that produces the best parametric images, in terms of noise vs. bias performance, is considered the optimal.

Subsequently, we select the optimal protocol derived above and consider for the second step its associated global time frame length as a constant. Then we repeat the acquisition by omitting the last frame every time until we reach the case of only 2 passes per bed, which is the minimum acceptable number of passes required for Patlak parameter estimation method. Our purpose is to determine how the gradual subtraction of the last pass from all bed positions and, therefore, the reduction of the total study time, affects the noise vs. bias performance of the parametric images in an attempt to demonstrate that shorter total acquisition times are possible without significant degradation of the quality of $K_i$ images.

The acquisition schemes selected along with the range of optimization parameter values examined are listed in Table II. The protocols have been assigned names in the format NPx_TFy, where x and y stand for number of passes per bed, or NP, and time frame length in sec, or TF, respectively. The first 4 columns describe the specifications of the protocols evaluated during the first phase of the optimization process, while the last 4 columns are referring to the set of protocols compared in the second phase. Also the total study time TT for each protocol is presented.

<table>
<thead>
<tr>
<th>Protocol</th>
<th>NP</th>
<th>TF(s)</th>
<th>TT(m)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NP5_TF31</td>
<td>8</td>
<td>31</td>
<td>48</td>
</tr>
<tr>
<td>NP7_TF38</td>
<td>7</td>
<td>38</td>
<td>48</td>
</tr>
<tr>
<td>NP6_TF45</td>
<td>6</td>
<td>45</td>
<td>48</td>
</tr>
<tr>
<td>NP5_TF58</td>
<td>5</td>
<td>58</td>
<td>48</td>
</tr>
<tr>
<td>NP4_TF57</td>
<td>4</td>
<td>57</td>
<td>48</td>
</tr>
<tr>
<td>NP3_TF106</td>
<td>3</td>
<td>106</td>
<td>48</td>
</tr>
<tr>
<td>NP2_TF165</td>
<td>2</td>
<td>165</td>
<td>48</td>
</tr>
</tbody>
</table>

TABLE II

ACQUISITION SCHEMES FOR DYNAMIC MULTI-BED PET

C. Production of simulated data

We employed Geant4 Application for Tomography Emission (GATE), a well-validated MC simulation package, to model the GE Discovery RX LYSO PET/CT scanner. We chose GATE, among many other competing candidates, because both its ability to simulate time-dependent phenomena as well as its accurate description of all physics processes underlying emission tomography, inherited by Geant4 package, makes it an ideal solution for our proposed study [34]. Furthermore, the realistic XCAT human torso phantom was utilized to model the attenuation as well as the time-dependent activity maps for specific tissues and tumors commonly examined in oncology whole-body PET studies [35]. Fig. 3 depicts characteristic examples of whole-body activity and attenuation XCAT maps. Both GATE and XCAT are state-of-the-art software packages capable of producing, when combined, realistic simulated PET data.

After the completion of the MC simulations, the generated list mode PET data are binned into 3D sinograms, according to the time frame sequence specified by each proposed acquisition scheme and, later, reconstructed using OS-MAP-OSL algorithm, which is a 3D OSEM One-Step-Late MAP reconstruction algorithm. It is implemented in STIR2.1, an open-source software toolkit customized for emission tomography image reconstruction [36]. All dynamic PET frames are reconstructed using 21 subsets and for all number of iterations ranging between 1 and 15. Furthermore, the simulated data are corrected for normalization, scatter, randoms and attenuation and the correction factors are incorporated into the sensitivity image of the OSEM algorithm.

Subsequently, the input function $C_p(t)$ is measured from ROIs drawn in the left ventricle (LV) blood pool region of the initial 24 dynamic cardiac frames at the first 6 min and the subsequent frames over the heart. Alternatively the input function $C_p(t)$ can be derived by arterial blood sampling at time points corresponding to the acquisition frames. Then, $C_p(t)$ data are combined with the PET measurements $C(t)$ for each voxel at each bed, according to Patlak eq. 2. In this particular simulation study we assume arterial blood sampling and, therefore, the true noise-free input function data are used in the Patlak equation, instead of the ROI-based measurements. Thus, if we express eq. (2) in the form $y = K_i x + V$, a data point $(x, y)$ can be plotted for each frame, as defined in eq. (7):

$$
(x, y) = \left( \int_0^t \frac{C_p(t)}{C_p(t)} \, d\tau \right) \, C(t) \left( t \geq t^* \right)
$$

Then simple linear regression is employed only to Patlak points where $t \geq t^*$ to estimate $K_i$ and $V$ parameters of interest. The proposed kinetic parameter estimation algorithm across all bed positions is performing at the voxel level, resulting in whole-body parametric images.

D. Quantitative optimization criteria

The determination of the optimal acquisition protocol is based on the quantitative criteria of the normalized mean square error (NMSE) and the normalized standard deviation (NSD), which are utilized to quantitate the bias and the
noise in the derived parametric \( K_i \) image from each protocol. Initially, a set of ROIs are drawn in the parametric images, based on the true activity maps, and the NMSE and NSD values are calculated for each ROI. Then, using the size of each ROI as a weight, the weighted average of NMSE and NSD value over all ROIs is calculated, as a metric of the overall bias and noise of the parametric images.

The NMSE is calculated for each ROI according to eq. 8:

\[
\text{NMSE} = \frac{1}{R} \sum_{r=1}^{R} \left( \frac{|\hat{f}^r - \hat{\mu}|}{\mu} \right)
\]

(8)

where \( \hat{f}^r = \frac{1}{n} \sum_{i=1}^{n} f_i^r \) and \( \hat{\mu} = \frac{1}{n} \sum_{i=1}^{n} \mu_i f_i^r \) denote the \( i^{th} \) voxel value from \( r^{th} \) noise realization and \( \mu \) denote the reference true activity value; \( n \) is the number of voxels in the ROI and \( R \) is the number of noise realizations. Thus, first a normalized bias is calculated over all voxels of an ROI for each noise realization. Then, all bias values are averaged over the different noise realizations to determine a single NMSE value. By first adapting a spatial calculation of the bias over an ROI and, subsequently, averaging over different noise realizations, we believe to alleviate the negative effect to the bias calculation, induced by the relatively high noise that characterizes the individual voxels of a parametric image.

Similarly, for the calculation of the NSD, first the spatial standard deviation over the ROI was calculated, followed by an averaging over the different noise realizations employed, as defined in eq. 9:

\[
\text{NSD} = \frac{1}{R} \sum_{r=1}^{R} \sqrt{\frac{1}{n-1} \sum_{i=1}^{n} (f_i^r - \hat{f}^r)^2} / \hat{f}^r
\]

(9)

These quantitative calculations are repeated for parametric images derived from all examined protocols and for different number of OSEM iterations of the original dynamic PET images. Finally, the NSD is plotted against NMSE for all parametric images of each protocol, i.e. for all iterations. Thus, a single noise vs. bias curve is generated for each protocol. Finally, the curves from different protocols are plotted together for comparative evaluation. The protocol which produces parametric images with curves closer to the origin of the axes is considered as the optimal acquisition scheme in this study.

III. RESULTS

True (noise-free) images and simulated frames acquired with protocol NP6_TF45 are presented in Fig. 4. In the 1st row, they are displayed from left to right the true activity map of the last dynamic frame, the true parametric \( K_i \) image derived derived by performing Patlak fitting on the noise-free activity maps and a 3min frame simulated 60min post injection to approximate an SUV image. In the (2nd and 3rd row, they are displayed, from left to right, the last 6 dynamic frames acquired with GATE simulations and reconstructed with OS-MAP-OSL algorithm (21 subsets, 5 iterations).

The parametric \( K_i \) images produced by various acquisition schemes simulated in this study are presented in Fig. 5. In Fig 5(a), from left to right and row by row, they are displayed the parametric \( K_i \) images produced by schemes with constant total study time of 50min post injection and variable number of passes starting from 8 and decreasing to 2. The bed time frames increase proportionally as the number of passes decreases in order to keep the total time of the study lower than 50min. The specific values of time frames are presented in Table II. Similarly, in Fig 5(b), from left to right and row by row, they are displayed the parametric \( K_i \) images produced by schemes with constant 45sec bed time frames and variable number of passes starting from 6 and decreasing to 2. The total study time decreases as the number of passes decreases according to Table II.

Furthermore, in Fig. 6 the (a) overall and (b) ROI-based noise vs. bias curves are plotted together for the parametric images produced by the protocols with a constant total study time of 50min. Similarly, Fig. 7 presents the (a) overall and (b) ROI-based noise vs. bias curves for the parametric images corresponding to protocols with constant time frames of 45sec and variable number of passes ranging from 2 to 6.

For the first time a clinical dynamic whole-body study in FDG PET/CT has been performed in order to demonstrate clinical feasibility of the proposed acquisition schemes and validate the results of the current optimization study. The clinical study was conducted at Johns Hopkins PET center, it involved a patient with lung tumor, and the optimal protocol NP6_TF45 was applied. The first two rows of Fig. 8 display the last 6 dynamic frames of patient data. The 3rd row of Fig. 8 presents from left to right the SUV conventional PET image, acquired 60min post injection, the produced parametric \( K_i \) image after utilizing all 6 last dynamic frames and the parametric image after omitting the last 2 frames.

IV. CONCLUSIONS & DISCUSSION

The comparative quantitative evaluation of the simulated parametric \( K_i \) images in Fig. 6 shows that the optimal acquisition scheme, when all 50min of available time span are utilized, is NP6_TF45 and involves 6 passes over all beds,
Fig. 5. Parametric $K_t$ images produced by acquisition schemes of (a) From left to right, row by row: constant 30min total scan time and variable number of passes starting from 8 and decreasing to 2. (b) From left to right, row by row: constant 45sec bed time frames and variable number of passes starting from 6 and decreasing to 2.

Fig. 6. (a) Overall and (b) ROI-based noise vs. bias plots for for parametric $K_t$ images acquired according to protocols with a constant 30min total scan time post injection and variable number of passes and time frames.

Fig. 7. (a) Overall and (b) ROI-based noise vs. bias plots for parametric $K_t$ images acquired according to protocols with a constant time frame of 45sec and various number of passes ranging from 2 to 6.

Fig. 8. The first 3 (1st row) and last 3 (2nd row) dynamic frames acquired with NP6_TF45 protocol. 3rd row, from left to right: The SUV image, the $K_t$ image derived from all 6 last frames and the $K_t$ image after omitting the last 2 frames.

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while each bed frame lasts for 45sec. On the other hand, it is observed that the quality of parametric images is deteriorated when employing a protocol with more than 6 passes per bed, for which the time frames are shorter than 45sec to keep the total study time below 50min. However, the discrepancies in noise and bias in all cases with total study time of 50min are not dramatic and therefore qualitatively it is difficult to observe their effect in the parametric images of Fig. 5(a).

Moreover, Fig. 7 demonstrates the effect of gradual subtraction of the last frames to the noise and bias of the parametric images for the optimal case of 6 passes per bed. The deterioration of bias is tolerable even if we omit the last 2 frames and reduce the total study duration to 33min. This is confirmed by the qualitative evaluation of the parametric images of Fig 5(b). However, the noise in all parametric k' images is significantly high for all studied protocols, as observed in Fig 6(b) and confirmed by the noise vs bias plots of Fig. 6 and 7.

Our first clinical demonstration of dynamic whole-body FDG PET imaging, as illustrated in Fig. 8, shows the clinical feasibility of the proposed method and suggests enhanced tumor-to-background contrast of the resulting parametric images with respect to conventional SUV images. Currently, the present work is aiming to initiate a shift of whole-body PET imaging to a novel dynamic domain, potentially allowing for quantitative whole-body assessment of patient response to treatments over short and long time periods.

Therefore, for future plans we are planning to implement advanced techniques for the measurement of the input function by utilizing more data from multiple bed positions, which are now available. Furthermore, we are going to expand our parameter estimation methods to the direct 4D domain and apply spatial constraints to efficiently address the challenges of temporal sparse sampling per bed and high noise per voxel in parametric images.

REFERENCES


