Patient-Specific Hybrid Whole-body PET Parametric Imaging From Speed Modulated Continuous Bed Motion Dynamic Data

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Abstract—**In our previous work a hybrid whole-body dynamic protocol was proposed, enabling full compartmental modelling, as well as whole-body (WB) Patlak analysis, in continuous bed motion (CBM) acquisition mode. While such an approach improves upon previous WB dynamic protocols, kinetic parameters are estimated with reduced precision and accuracy due to limited counting statistics. In this work we propose a new patient/pathology specific whole-body dynamic imaging protocol with the aim to maximize the counting statistics in the regions of interest and achieve optimum kinetic parameter accuracy and precision based on a personalized dynamic data acquisition. This is achieved by modulating the CBM bed speed within each pass depending on the FOV of primary interest as opposed to utilizing a constant speed for the entire FOV. Therefore in cases where the pathology is known and localized to a certain degree, such as in response to therapy or based on information from other modalities or clinical findings, the protocol can be modulated in such a way as to maximize the counting statistics and kinetic parameter accuracy and precision in a disease and patient specific way. Using dynamic WB simulations as well as initial clinical dynamic WB scans, we demonstrate the kinetic parameter estimation benefits and the clinical feasibility of the proposed protocol.**

I. INTRODUCTION

New protocols based on dynamic data acquisition and subsequent kinetic modelling are emerging as more robust and quantitative alternatives to previous static WB protocols [1]. Recently an updated protocol to dynamic WB imaging has been proposed [1,2]. The protocol involves an initial single-bed blood pool scan targeting both the pathology and blood pool (aorta or ventricles), followed by a series of temporally non-continuous WB passes at ever increasing time intervals. This allows the image derived input function to be estimated from the initial continuous scan and the following CBM passes. Furthermore it allows WB Patlak analysis to be performed using the CBM passes, as well as estimation of micro-parameters for the initial single bed FOV covering the pathology. However due to the axial FOV of a WB scan, leading to limited scan time of each slice, time frame counting statistics are even lower compared to a traditional single bed dynamic scan, exacerbating the already reduced accuracy and precision of the kinetic parameter estimates. To this end we propose and demonstrate the clinical feasibility of a new protocol which is based on patient specific, dynamic WB image acquisitions in order to optimize kinetic parameter accuracy and precision while preserving the same total pass and scan duration. The new protocol, like the previously proposed, is based on continuous bed motion acquisition, with the speed of the bed controlling the frame duration for each scanned slice. By varying the speed within each pass based on preselected FOVs within the total whole-body FOV, the frame duration and counting statistics can be maximized in a patient specific way in regions which are of high interest based on prior clinical findings, compared to regions which are of lesser interest. Therefore in cases where the pathology is known and localized to a certain degree (majority of clinical scans), such as in response to therapy or based on information from other modalities, the protocol can be modulated in such a way as to maximize the counting statistics and kinetic parameter accuracy and precision in a disease and patient specific way.

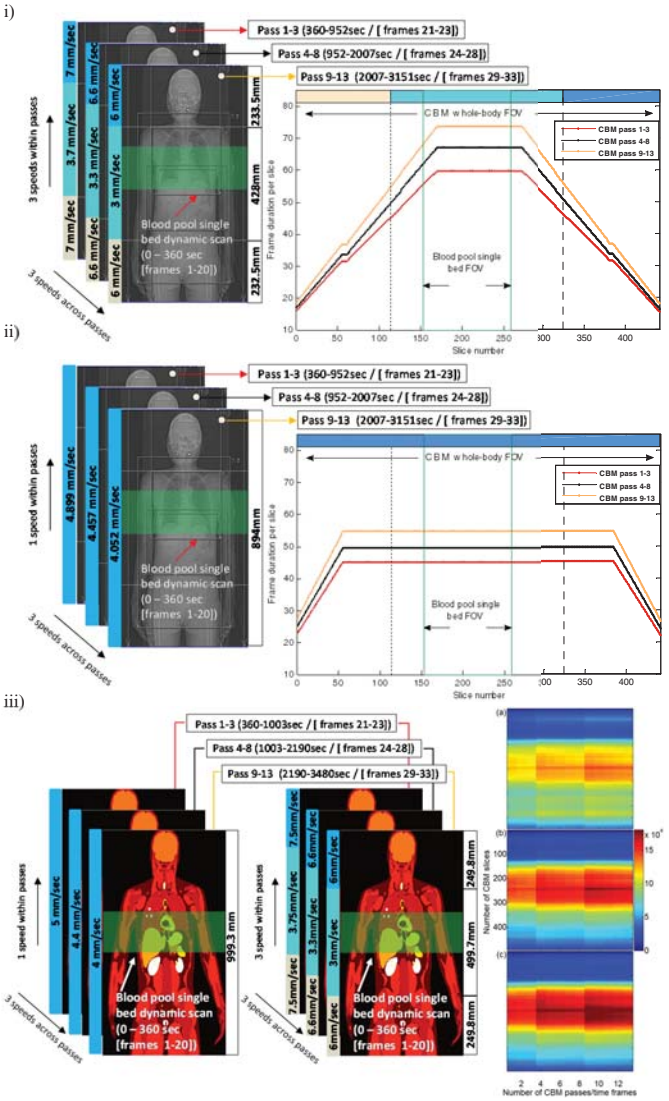

Fig.1 The newly-proposed patient-specific variable intra-pass speed protocol and previous (for comparison) scan time-equivalent constant intra-pass speed protocol in the clinical (i-ii) and simulated (iii) CBM dynamic datasets. In order to compare the 2 scan time-equivalent protocols, the proposed protocol was simulated both to the same total acquired counts (iii-b) and same injected activity (iii-c) to the previous protocol(iii-a). More counts are acquired in the middle region and less on the outer 2 regions on the new protocol due to the bed speed modulation (iii-b). This is due to the increased acquisition duration in the middle region where the pathology is localized. Also the increased tracer uptake of the organs in the middle region means that the total acquired counts are higher in the new protocol under same injected activity (iii-c).

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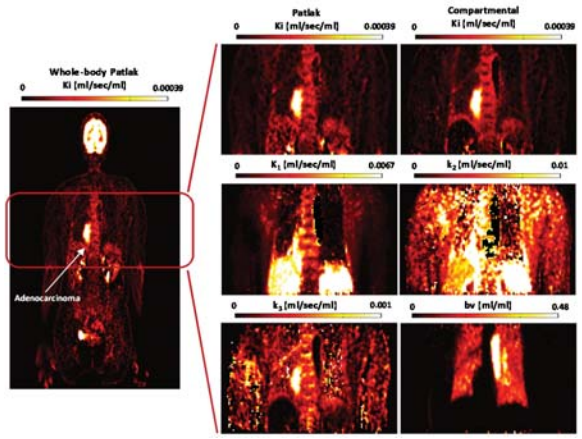

Fig. 2 Parametric images of Ki estimated with Patlak and full compartmental modelling, as well as K_1, k_2, k_3 and blood volume images.

II. METHODS

A clinical dataset was acquired on the mCT PET/CT to evaluate the clinical feasibility. Following a bolus injection of [^{18}F]FDG (~250MBq), the protocol involved an initial single-bed 6-min scan over the suspected disease and blood pool (descending aorta and heart ventricles) followed by 13 WB passes/frames in CBM mode. Three sub-regions were identified on the topogram and within the total scanned axial FOV, with each region having a different intra-pass CBM speed and with the middle region (containing almost the entire torso, therefore also the FOV of the initial single bed scan) having half the speed compared to the outer 2 regions. Furthermore, three progressively slower bed speeds were selected across passes for each of the 3 sub-regions in order to generate time frames of progressively longer duration similar to single-bed dynamic imaging. List-mode data from the single-bed 6-min scan were split into 20 frames, while CBM data framing varied for each slice due to differential CBM pass bed speed. Apart from clinical data, 2 dynamic WB protocols were simulated (XCAT) based on the newly, as well as previously proposed protocols for comparison, using an in-house CBM kinetic modelling simulator. The 1st protocol simulated 3 bed speeds across passes but with a constant intra-pass speed similar to our previous protocol [2]. The 2nd newly proposed protocol used 3 bed speeds across passes as well as 3 intra-pass bed speeds for 3 preselected sub-regions, with the middle region having half the speed of the outer regions, similar to the clinical protocol. The speed of each sub-region within each pass was calculated so as the total time for each pass to be identical between the 2 protocols, therefore also constituting in no change on the overall scan time. Three noise levels where considered with 20 noisy realizations each. The 2 WB dynamic protocols were evaluated both at the same total acquired counts (different simulated injected activities) but also at the same simulated injected activity (different total acquired counts). The clinical and simulation protocols are depicted in Fig.1 and for both, Patlak analysis was performed in the entire WB image, while full compartmental modelling using a 2-tissue model (4 parameters) and the GLLS method, was performed in the FOV covering the initial single-bed scan.

III. RESULTS - CONCLUSION

Kinetic analysis of the clinical dataset using the patient specific protocol is shown in Fig.2. Apart from WB Patlak analysis, micro-parameters were also estimated in the FOV of the initial single-bed blood pool scan. Qualitative comparison of Ki shows slightly more defined physiology and higher tumor-to-background ratio using full kinetic modelling. However comparison to evaluate benefits compared to the previous protocol is not feasible. Such a comparison though is feasible on the simulated data. WB Patlak Ki analysis shows improved bias and variance in the middle region of interest using the optimized protocol and increased bias and variance in the outer regions which are of lesser interest. Interestingly though comparing Ki both from Patlak and full kinetic modelling it appears that the increased counts in the CBM part of the scan, stemming from the proposed patient-specific protocol, has clearly improved Patlak Ki bias and variance, but Ki from full kinetic modelling shows only modest to no bias and variance improvement. This can be explained by the fact that the initial single bed dynamic scan which is used only for full compartmental analysis, doesn't change between the 2 protocols. Therefore improvements using compartmental modelling are only limited to parameters depending on the later CBM part of the scan which does change, such as k_3, leading to modest changes overall to Ki bias and variance.

By modulating the bed speed, disease and patient specific protocols can be used in the clinic enabling truly personalised PET parametric imaging for optimum parameter estimation with no additional effort/scan time to previous WB protocols.

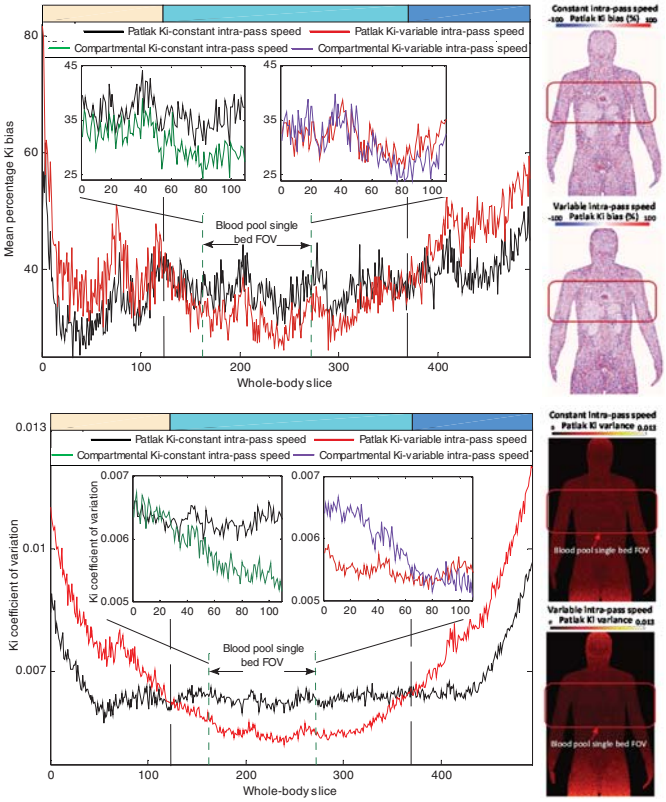

Fig.3 Graphs of Ki absolute bias and normalized variance using Patlak (whole-body) and both Patlak and full comparmental modelling (initial single bed blood pool FOV) using the patient specific variable intra-pass CBM speed and previous scan-time equivalent constant intra-pass CBM speed protocol.

IV. REFERENCES

[1] N. A. Karakatsanis et al, *Phys Med Biol,*(58), 7391-418,2013.
[2] F Kotasidis et al, *MIC IEEE & NSS, M02-1,* 2016.