

visually inappropriate results that gave lower JI comparing to the first method (0.2 to 0.65). The JI improved from 0.65 to 0.79 when the PVE correction was taken into account. **Conclusion:** The method based on intensity measurements was the most effective for the algorithm used in this study. PVE correction improves results of the segmentation, especially for small objects allowing to classify correctly small structures. **Acknowledgment:** Grant No. STRATEGMED2/267398/4/NCBR/2015. **References:** [1] Borys, D. et al., *EJNMMI*, Vol. 42, Sup. 1, p. S409–S410, 2015. [2] Borys, D. et al., *EJNMMI*, Vol. 43, Sup. 1, p. S496, 2016. [3] Pavan, M., Pellilo, M., *IEEE CVPR*, 2003

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Large bed overlap and short acquisition time or vice versa?

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Purpose: The reconstruction and data acquisition in 3D PET requires an overlap between each other following bed positions to compensate for low sensitivities in the field of view (FOV) edges when data are collected in a step-and-shoot acquisition mode. A small overlap between bed positions facilitates a larger throughput, i.e. larger scan length per unit time enabling full body scans in approximately 10 min. or shorter. Such scans hence enable fast whole body scans but at the cost of an uneven sensitivity profile across bed positions due to the triangular sensitivity profile of PET scanners along the scanner axis. In the current work the noise profile and quantitative accuracy were evaluated to determine the effect of bed overlap on image quality and to determine the optimal compromise between bed overlap and acquisition time per frame. **Methods:** A NEMA IQ phantom and a custom-made 55 cm long cylindrical tube with a diameter of 5.5 cm were scanned on a digital GE Discovery MI scanner with a 20 cm field of view. The phantoms were filled with a start activity of 5 kBq/cc of ^{18}F -FDG to mimic clinical relevant activity concentrations. Five series were acquired on the scanner with overlaps ranging from 15% to 50% in list mode acquisition. The acquired data were subsequently rebinned in frames ranging from 10 s. to 10 min. per bed position and reconstructed both with a standard 17/3 OSEM reconstruction with TOF and PSF applied and a Bayesian penalized likelihood reconstruction algorithm. Noise characteristics and quantitative accuracy were evaluated in 5 ROIs distributed in each slice of the phantoms as a function of slice position along the scanner axis. **Results:** Both the standard deviation of the voxel values, i.e. the noise, and the quantitative variation along the phantom length increased with smaller bed overlaps compared to larger overlaps. This was especially evident in short acquisition frames, i.e. time per bed position < 30 s. Little effect was observed on reconstruction method where both noise variation and quantitation accuracy were similar. **Conclusion:** The results suggest that large bed overlap and shorter acquisition time pr. bed position is advantageous compared to low bed overlap and longer acquisition time pr. bed position. The effect is especially evident in low count studies as for instance dosimetry scans with ^{124}I pri- or to ^{131}I therapy.

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Optimal quantitative SUV metrics over wide range of lesion sizes in advanced image reconstruction (TOF and PSF) for PET

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Aim: Tumor quantification using ^{18}F -FDG PET has significant impact on routine usage in treatment response assessment and for prognostication in cancer patient. Advanced image reconstruction techniques available in routine PET imaging lead to improved image quality and lesion detectability; yet their quantification accuracy remains a topic of debate. The aim of this study was to evaluate the accuracy of quantification metrics over these reconstruction methods, and to find the most accurate SUV quantification metric in a wide range of lesion sizes. **Material and Methods:** The NEMA-IEC body phantom was used, consisting of six standard spheres (10 to 37mm) and small lesions (2, 3,4,5,6 and 7 mm) with different contrasts (4:1,2:1) and background activities, acquired in 3D list-mode for 5 minutes-per-bed position. Images were reconstructed using 3D-OS-EM algorithm with and TOF and whit PSF-modeling. Quantification of each lesion VOI was performed using SUVmean, SUV42, SUV50, SUV70, SUVNestle, SUVmax, SUVpeak1cc and SUVpeak0.5cc. Subsequently, we determined Relative Errors (RE%) with respect to true SUV values for each metric. **Result:** In spheres larger than 13mm in diameter, SUVmax, SUVpeak0.5cc and SUVpeak1cc yielded significant overestimation (RE% of 44.8, 40.1 and 37.5 respectively). SUV50 was the only quantitative metric which had no statistically significant difference with respect to the true value in sphere (RE% of 11.77 to 0.44). In the 13 and 10 mm spheres, the best quantitative performance was obtained by SUVmax and SUVpeak0.5cc. Also, in spheres smaller than 10mm, all quantification metrics had significant underestimation and high relative error (-76.32 to -34.49). **Conclusion:** Our phantom study showed that optimal quantification of the ^{18}F -FDG tracer in PSF- and TOF-enabled reconstruction is size dependent. Even including PSF and TOF, quantification in spheres smaller than 10mm in diameter is underestimated. It is

important to also point out that incorporation of PSF and TOF in the reconstruction leads to overestimation in larger sphere for certain SUV metrics and as such, can lead to incorrect assessment of treatment response. Therefore, more caution should be exercised when using SUV metrics in the context of new PET reconstruction techniques.

E-PW119

A demonstration of the concept of numerical twins in esophageal cancer patients

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Purpose: The characterization of tumor heterogeneity using textural features in radiomic analyses of PET images has shown promise to predict patient response or survival. In this context, the goal of this study is to identify for each patient a radiomic numerical twin who has similar radiomic feature values to learn from the numerical twin's history and guide patient management. Here, we test this concept to predict treatment response.

Subjects & Methods: 107 patients with newly diagnosed esophageal cancer underwent pre-treatment 18F-FDG PET scan (data extracted from Ypsilantis et al, PLoS ONE 10(9):e0137036). All patients received a neoadjuvant chemotherapy and were later classified as non-responders (NR=69) or responders (R=38). In each patient, the primary lesion in the baseline scan was segmented using a threshold set to 40% of SUVmax. In each resulting volume of interest, 103 radiomic features were extracted including 85 textural or fractal features and 18 histogram indices. Each lesion was associated with a vector b of biomarkers. We computed the element-wise ratio between the vector $b(p)$ of one patient p and the vector $b(i)$ of each of the other 106 patients i ($i=1, P-1$). A patient N was identified as the radiomic numerical twin of patient p if the distance of $b(p)/b(N)$ to 1 was the lowest among the $P-1$ distances. Its response to treatment was then predicted as the one observed in patient N . We evaluated the ability of this approach to predict treatment response when using 2 or 3 biomarkers in b by calculating the Youden index in a leave-one-out validation. We compared the results with logistic regression and support vector machine (SVM) models.

Results: When including two biomarkers in b , the best performance using the numerical twin concept was obtained using Kurtosis and Energy with 87% NR lesions and 63.2% R lesions accurately classified (Youden=0.50). With three biomarkers (Kurtosis, Energy and Fractal Dimension mean), Youden index increased to 0.55. With 2 or 3 biomarkers, the logistic regression and SVM models always yielded Youden index less than 0.43. **Conclusion:** This concept of radiomic numerical twins is validated in esophageal cancer to predict treatment response. We found that lesions with similar radiomic profiles consisting of only 2 to 3 biomarkers had similar response to therapy. The identification of numerical twins could assist patient manage-

ment in the future, based on the disease evolution in the patients used to identify the numerical twin.