large volume difference (>10%) objects. 22 patients’ (10 men, 12 women, mean age: 60 years) low-dose CT images (120 KeV, 50-100 mA, slice thickness: 2.5 mm) were evaluated.

Results: The automatically detected lung segments according to Boyden’s nomenclature were the following (small volume difference in percentage of all cases): RU1 (72.7), RU2 (77.2), RU3 (90.9), RM4-5 (95.5), RL6 (72.7), RL7 (50), RL8 (59.1), RL9 (90.9), RL10 (90), LU1-2 (86.4), LU3 (81.8), LU4-5 (77.3), LL6 (90.9), LL7-8 (72.7), LL9 (100), LL10 (100). In some cases adjacent segments were segmented as mixed region (PSF). Images were segmented using MIM (MIM Software, USA) with 20%,25%,30%,40%,50% fixed threshold (FT) and MIM’s gradient-based algorithm (PET Edge+). Total metabolic tumour volume (TMTV) and total lesion glycolysis (TLG) was determined for each tumour. Results: For images unlisted for 1min bed duration, TMTV percent bias using 25% FT was -7.6% (3mL), -14.5% (21mL), and 2.3% (71mL). TMTV percent bias using gradient method was -3.5% (3mL), -32.5% (21mL), and -24.0% (71mL). TLG percent bias using the 25% FT had a percent bias of -18.3% for the 3mL lesion and 6.6% for the 71mL lesion. TLG percent bias with gradient method was -17.3% for the 3mL lesion and -11.6% for the 71mL lesion.

Conclusion: Our results suggest that 25% FT is best for TMTV quantification of PMBCL tumours, which is consistent with previously performed simulations [1]. Care should be taken with the gradient algorithm as it failed to accurately delineate tumour boundaries for some cases. References: [1] Fedirgo et al, Proc. JNM, 2021

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**EPS-215**


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Aim/Introduction: [18F]FDG PET is frequently used to stage Non-Hodgkin’s lymphoma and evaluate treatment response. However, the disease varies within the population and each patient responds differently to treatment, making disease management particularly challenging. There is evidence that quantitative imaging metrics, such as total metabolic tumour volume (TMTV) can enhance the prognostic value of PET and its ability to guide treatment decisions. There is significant motivation to implement automated segmentation of TMTV, as manual segmentation is time-consuming and not feasible within a clinical setting. In this study, we evaluate fixed threshold (FT) and gradient-based segmentation algorithms using Negative-Cast Modelling for Oncology (NCMO). This work is applied to primary mediastinal B-cell lymphoma (PMBCL), although these methods can be easily translated to other forms of lymphoma and cancer.

Materials and Methods: Negative-Cast Modelling for Oncology (NCMO) was used to cast tumour models using segmented lesions from 5 PMBCL patients (2.7mL to 76mL). [18F]FDG concentration was based on an analysis of 22 lesions from 13 PMBCL patients. Tumour models were inserted into the Probe-IQ phantom (without background activity) and imaged using the GE MI PET/CT scanner (2x10min bed positions), to determine the radioactivity ground truth. Next, the Probe-IQ liver and background was injected with [18F] FDG to achieve target concentrations determined from the patient analysis (11.0kBq/mL and 3.7kBq/mL, respectively). 2x30min bed positions were acquired in list-mode. Images were reconstructed using OSEM (4 iterations, 8 subsets) with time-of-flight (ToF) and point-spread function modelling (PSF). Images were segmented using MIM (MIM Software, USA) with 20%,25%,30%,40%,50% fixed threshold (FT) and MIM’s gradient-based algorithm (PET Edge+). Total metabolic tumour volume (TMTV) and total lesion glycolysis (TLG) was determined for each tumour. Results: For images unlisted for 1min bed duration, TMTV percent bias using 25% FT was -7.6% (3mL), -14.5% (21mL), and 2.3% (71mL). TMTV percent bias using gradient method was -3.5% (3mL), -32.5% (21mL), and -24.0% (71mL). TLG percent bias using the 25% FT had a percent bias of -18.3% for the 3mL lesion and 6.6% for the 71mL lesion. TLG percent bias with gradient method was -17.3% for the 3mL lesion and -11.6% for the 71mL lesion.

Conclusion: Our new, fully automated method for lung segment identification was developed. Based on the evaluation the proposed segmentation method can facilitate and speed up the localization of the lung segments using low-dose CT images. References: none

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**EPS-216**

**Comparison of atlas-based and manual segmentation versus simple ROI placement for quantification of liver and spleen metabolism in FDG-PET/CT**

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Aim/Introduction: 18F-FDG PET is routinely used to assess response following cancer treatment. FDG uptake in tissues not directly involved in disease can provide additional information on response and side-effects, but its clinical utility is largely unassessed due to the impracticality of manually segmenting entire organs. As a step towards a time-efficient whole-body metabolic survey, we applied an atlas-based segmentation method and compared the accuracy of the extracted PET SUV metrics against those from manually segmented organs and volumes of interest (VOI) placed on the PET/CT images which are routinely used in clinic.

Materials and Methods: Manual segmentations of the liver and spleen were performed on the PET and CT component of 50 PET/CT scans. Manual PET segmentations were used as the reference standard, with manual CT segmentations used to train the atlas using the ‘leave one out’ method. The atlas was trained on CT data to assess if algorithms trained on CT can be directly applied to PET and generate accurate SUV metrics. Clinically realistic PET measurements (e.g. as applied