Purpose: The aim of this study was to investigate the accuracy of volume and activity estimates derived from single photon emission computed tomography (SPECT) images using methods practical for clinical use in dose calculations for targeted radionuclide therapy.

Methods: Five patients with suspected neuroendocrine tumours were injected with ~900 MBq of Tc-99m-Tektrotyd and a SPECT/CT scan was acquired. A phantom experiment was performed to establish an adaptive threshold curve, allowing for the optimal choice of segmentation threshold based on the source-to-background ratio of activity. The SPECT images were reconstructed using a standard clinical reconstruction with attenuation correction (AC). Additionally, an advanced reconstruction method was applied that included AC, resolution recovery and scatter correction. Source regions were segmented in the SPECT images using three different thresholds: 1) 40%, as commonly used in the literature, 2) the adaptive threshold for true volume estimation (ThV), and 3) the adaptive threshold for true activity determination (ThA).

Results: Using the fixed 40% threshold, organ volume estimates from the clinical reconstruction exceeded the advanced reconstruction estimates by 32.4% +/- 23.9% on average. When ThV was applied this difference in volume estimation improved to -2.5% +/- 9.1%. Visual inspection of the SPECT derived organ contours drawn on the CT slices confirmed that ThV organ segmentation corresponded to the true organ boundaries. Activity in regions segmented using ThA was on average 23% greater than activity inside the same regions delineated using ThV, highlighting the importance of using ThA to recover activity blurred out of the region's true volume in the SPECT images.

Conclusions: Adaptive thresholding can be used to accurately obtain source region volume and activity estimates from clinical reconstructions. This provides a clinically feasible alternative to obtaining these estimates from images reconstructed using time consuming, advanced methods or from manually delineating regions slice by slice on CT.