Tumour Segmentation and Volume estimation from PET Lymphoma Data Using a Pre-trained U-Net Model and Probability Contour Framework

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Accurate tumour delineation is critical for utilizing total metabolic tumour volume (TMTV) as a reproducible prognostic biomarker in lymphoma PET imaging [1]. This study focuses on achieving robust tumour segmentation specifically from PET data [1] by applying a pre-trained U-Net model [2] and a kernel-smoothed probability contour framework [3]. Additionally, ongoing segmentation experiments on various other PET datasets are underway to validate and generalize this approach further

Tumour segmentation was conducted using a pre-trained U-Net model, initially developed on the AutoPET II PET challenge dataset [4]. The model achieved a Dice similarity coefficient of 0.65 on the new lymphoma PET benchmark dataset [1]. To enhance interpretability and reliability, a kernel-smoothed probability contour framework was applied as a post-processing step, generating voxel-wise uncertainty information for each segmented subvolume without compromising Dice accuracy.

The U-Net model segmented lymphoma tumours from the international TMTV benchmark dataset [1] with a Dice score of 0.65. Applying SUV thresholding and a probability contour framework improved performance to 0.85 (SUV = 4). Both SUV thresholds and contour percentiles showed strong correlation with gold standard volumes ($R^2 \approx 0.75$), while the contour framework additionally quantified uncertainty, highlighting regions of high and low confidence. This combined approach provides a robust and interpretable solution for PET-based lymphoma tumour delineation, offering clinicians explainable AI visualizations through the integration of SUV thresholds with probability contours.

Integrating a pre-trained U-Net model with a kernel-smoothed probability contour approach enables standardized and reproducible tumour segmentation from PET data in lymphoma. The provision of uncertainty metrics significantly enhances the segmentation's reliability, supporting the potential of TMTV as a robust clinical biomarker. Future research leveraging this PET-focused framework will continue to explore and validate its clinical utility across additional PET lymphoma datasets.

References:

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