

An automated pipeline for tumor detection followed by segmentation in PET imaging of diffuse large B-cell lymphoma

Quantitative Radiomolecular Imaging & Therapy

(Qurit.ca)

S. Ahamed^{1,2}, B. Yin¹, J. H. O³, N. Dubljevic¹, I. Bloise⁴, L. H. Sehn⁴, K. J. Savage⁴, P. Martineau⁴, D. Wilson⁴, I. Shiri⁵, H. Zaidi^{5,6}, C. F. Uribe^{4,7}, A. Rahmim^{1,2,7}, F. Yousefirizi²

¹ Department of Physics and Astronomy, University of British Columbia, Vancouver, BC, Canada ² Department of Integrative Oncology, BC Cancer Research Institute, Vancouver, BC, Canada ³ Seoul St. Mary's Hospital, College of Medicine, The Catholic University of Korea, Seoul, Republic of Korea ⁴ BC Cancer, Vancouver, BC, Canada

⁵ Division of Nuclear Medicine and Molecular Imaging, Geneva University Hospital, Geneva, Switzerland

⁶ Geneva University Neurocenter, Geneva University, Geneva, Switzerland

⁷ Department of Radiology, University of British Columbia, Vancouver, BC, Canada

BACKGROUND

- ☐ Accurate detection and segmentation of diffuse large B-cell lymphoma (DLBCL) tumors in PET images is important for total metabolic tumor volume (TMTV) calculation [1].
- ☐ Manual segmentation by physicians is a time-consuming task; supervised Al segmentation methods may require a large amount of accurately annotated data by physicians [2].
- Determining crude regions of interest (ROIs) around the suspicious region, (weak annotations), would save physicians' significant time and will help them delineate more cases efficiently.

OBJECTIVES

- 1) Implementing a fast and accurate tumor detection routine for the PET images of DLBCL patients using the deep learning-based object detection framework named **You Only Look Once (YOLO)** [3].
- 2) Implementing two hybrid, automated segmentation techniques namely fixed 50% thresholding & active contours [4] and hybrid K-nearest neighbors [5] to segment the tumors inside the YOLO predicted ROIs around the detected tumors.

METHODS

1. Detection on whole body PET images

Pretraining the detection network: YOLOv3 network with randomly initialized weights and biases was pretrained on 44665 axial slices of PET images of 157 patients with non-small cell lung cancer (NSCLC), obtaining a tumor detection accuracy of 69% and mean average precision (mAP) of 0.56.

METHODS

Fine-tuning on DLBCL data: We fine-tuned this pretrained network using PET images from 51 DLBCL patients (16818 axial slices), obtaining a tumor detection accuracy of 70%, mAP of 0.57, and average centroid localization error of 7 mm.

2. Segmentation inside the predicted ROIs

- 50% thresholding (T) + Active contour (AC): This segmentation technique obtained an average Dice score of 0.73, an average Jaccard score of 0.57, and an average Hausdorff distance of 1.68 on the DLBCL test dataset.
- Hybrid K-Nearest Neighbor (KNN): This segmentation technique obtained an average Dice score of 0.77, an average Jaccard score of 0.65, and an average Hausdorff distance of 1.70 on the DLBCL test dataset.

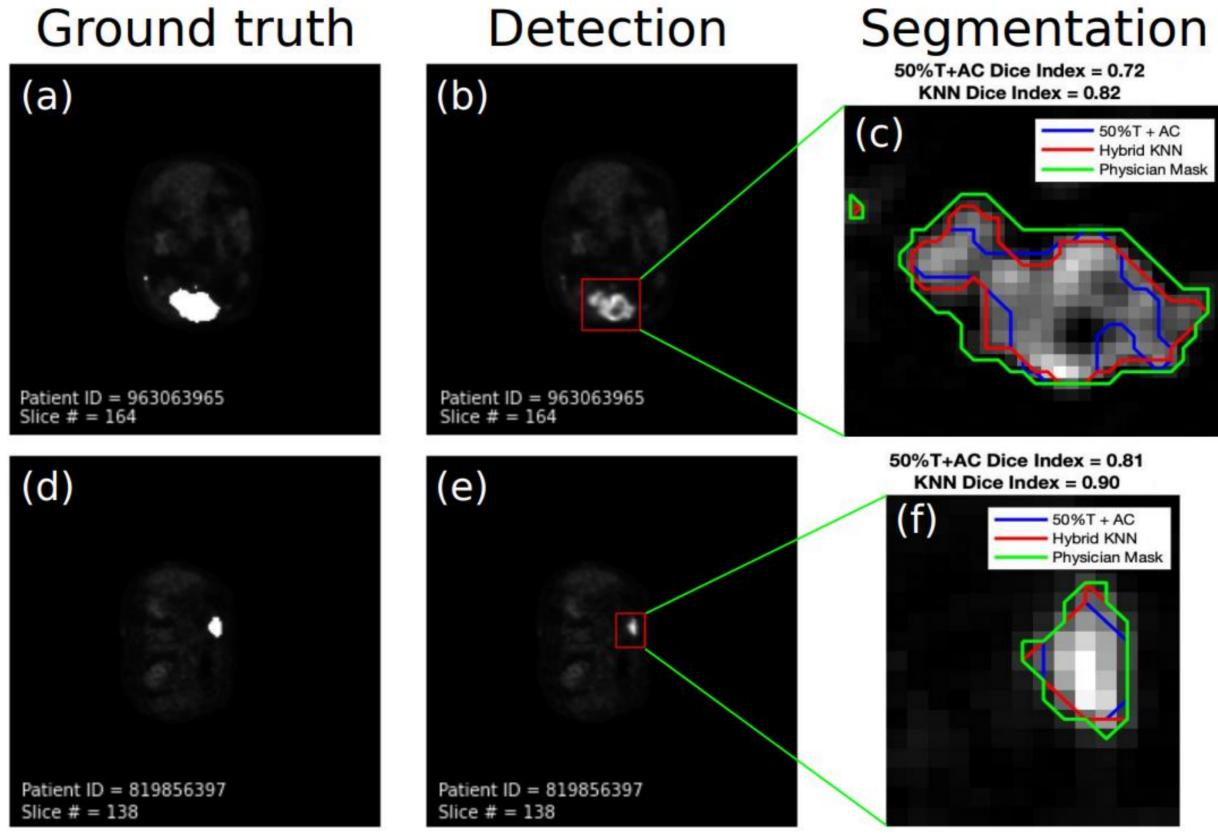


Figure 1: Detection + segmentation pipeline. (a) and (d) show two axial slices of the DLBCL PET scan, with the tumors delineated by an expert (shown as white patches). (b) and (e) show the YOLOv3 predicted ROIs (red) around the detected tumors. (c) and (f) show the segmentation contours inside the predicted ROIs, predicted via 50% T + AC, and hybrid KNN.

RESULTS AND CONCLUSION

- Detection before segmentation reduces the dependence of supervised segmentation methods on delineations, thereby improving overall network performance.
- Our two-step detection + segmentation method is more efficient than the segmentation of whole-body PET images. The whole-body image is used only in the detection part while the segmentation is performed only inside the extracted ROIs around the tumors.

Task	Model	Test Data	Scores		
			Detection accuracy	Mean average precision	Localization error
Detection	YOLOv3 (random initialization)	NSCLC	69%	0.56	-
Detection	YOLOv3 (pretrained on NSCLC)	DLBCL	70%	0.57	7 mm
			Dice score	Jaccard score	Hausdorff distance
Segmentation	50% thresholding (T) + active contour (AC)	DLBCL	0.73	0.57	1.68
Segmentation	Hybrid K-Nearest Neighbors (KNN)	DLBCL	0.77	0.65	1.70

Table 1: A summary of results of our automated tumor detection and segmentation pipeline.

REFERENCES

- 1. L. Vercellino et al., "High total metabolic tumor volume at baseline predicts survival independent of response to therapy," Blood, vol. 135, no. 16, 2020.
- 2. Willemink, M.J., et al., Preparing Medical Imaging Data for Machine Learning. Radiology, 2020.
- 3. Redmon, J. and A. Farhadi, "YOLOv3: An Incremental Improvement", in arXiv e-prints2018, arXiv:1804.02767.
- 4. Zhuang, M., R.A. Dierckx, and H. Zaidi, "Generic and robust method for automatic segmentation of PET images using an active contour model", Med Phys, 2016.
- 5. Jóźwik, A., "A learning scheme for a fuzzy k-NN rule". Pattern Recognition Letters, 1983.