



Active Organs Segmentation in Metastatic Breast Cancer Images combining Superpixels and Deep Learning Methods

Constance Fourcade, Gianmarco Santini, Ludovic Ferrer, Caroline Rousseau, Mathilde Colombié, Mario Campone, Mathieu Rubeaux, Diana Mateus

► To cite this version:

Constance Fourcade, Gianmarco Santini, Ludovic Ferrer, Caroline Rousseau, Mathilde Colombié, et al.. Active Organs Segmentation in Metastatic Breast Cancer Images combining Superpixels and Deep Learning Methods. NTHS - Nuclear Technology for Health Symposium, Feb 2020, Nantes, France. hal-02565107

HAL Id: hal-02565107

<https://hal.science/hal-02565107>

Submitted on 15 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

4th Nuclear Technologies for Health Symposium
February 13-14, 2020
Nantes, France

Abstract submission form

Abstract review session

1 ☒

2 ☐

3 ☐

4 ☐

Active Organs Segmentation in Metastatic Breast Cancer Images combining Superpixels and Deep Learning Methods

Constance Fourcade^{1,2}, Gianmarco Santini² PhD, Ludovic Ferrer^{3,4} PhD, Caroline Rousseau^{3,4} MD PhD, Mathilde Colombié⁴ MD, Mario Campone^{3,4} MD PhD, Mathieu Rubeaux² PhD and Diana Mateus¹ PhD

¹ LS2N, Centrale Nantes, Nantes, France

² Keosys, Saint Herblain, France

³ University of Nantes, CRCINA, INSERM UMR1232, CNRS-ERL6001, Nantes, France

⁴ ICO Gauducheau Cancer Center, Saint Herblain, France

Email: constance.fourcade@ls2n.fr

Acknowledgments. This work is partially financed through "Programme opérationnel régional FEDER-FSE Pays de la Loire 2014-2020" noPL0015129 (EPICURE) and by the SIRIC ILIAD Nantes-Angers-INCA-DGOS-Inserm 12558 grant.

Hypothesis

In the clinical follow-up of metastatic breast cancer patients, semi-automatic measurements are performed on ¹⁸FDG PET/CT images to monitor the evolution of the main metastatic sites. Apart from being time-consuming and prone to subjective approximations, semi-automatic tools cannot make the difference between cancerous regions and active organs, presenting a high ¹⁸FDG uptake.

In this work, we develop and compare fully automatic deep learning-based methods segmenting the main active organs (brain, heart, bladder), from full-body PET images.

Methods

We combine deep learning-based approaches with superpixels segmentation methods. In particular, we integrate a superpixel SLIC segmentation at different depths of a convolutional neural network, i.e. as input and within the optimization process. Superpixels reduce the resolution of the images, keeping sharp the boundaries of the larger target organs while the lesions, mostly smaller, are blurred. Results are compared with a deep learning segmentation network alone.

The methods are cross-validated on full-body PET images of 36 patients from the ongoing EPICURE_{seinmeta} study. The similarity between the manually defined ground truth masks of the organs and the results is evaluated with the Dice score. Moreover, these methods being preliminary to tumor segmentation, the precision of the networks is defined by monitoring the number of segmented voxels labelled as "active organ", but belonging to a lesion.

Results

Although the methods present similar high Dice scores (0.96 ± 0.006), the ones using superpixels present a higher precision (on average 6, 16 and 27 selected voxels belonging to a tumor, for the CNN integrating superpixels in input, in optimization and not using them, respectively).

Conclusion

Combining deep learning with superpixels allows to segment organs presenting a high ^{18}F FDG uptake on PET images without selecting cancerous lesions. This improves the precision of the semi-automatic tools monitoring the evolution of breast cancer metastasis.