

Segmentation of brain biomedical images to compute the volume of gliomas

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Abstract. The paper presents an algorithm of segmentation of brain imaging examination results - computed tomography (CT) and positron emission tomography (PET) - to identify, compute, and visualize the brain tumors. Computer software was developed in the MATLAB environment using active contour methods: Edge and Chan-Vese. A review of the current treatment plan for patients with diagnosed glioblastoma multiforme was included to emphasize the significance of the solved problem. The work presents executed steps in the algorithm with a detailed description of thresholding process. Visual results of tumors were performed and presented.

1 Problem statement

Gliomas account for 70% of all primary brain tumors [1]. The principal role in the group of primary central nervous system neoplasms is lead by glioblastoma multiforme (GBM), which is determined by the 4th (highest) histologic problem of WHO [2].

Despite technological progress made in the last decades, access to neurosurgery, radiotherapy, and the introduction of new chemotherapy, patients prognosis are not favorable. The average lifetime after the diagnosis is 12-15 months. Only 5% of patients live up to 3 years after the determination of the disease [3].

1.1 Treatment plan

The goal of surgical treatment is to increase and improve the quality of life of the patients. The traditional method of therapy includes the surgical resection of the tumor. In that case, after the craniotomy, lobectomy is possible with macroscopically complete excision of the tumor. For the remaining tumor distribution parts, the procedure is reduced to its removal within the limits of healthy tissue. Since the patient is left with a neurological deficiency after surgery, he or she may expect the effects of depriving a given fragment of the brain. For that reason, when postoperative complications undermine the benefits of the patient's lifetime, the deterioration in the quality of life due to neurological dysfunction, the procedure is not carried out.

Due to the problems mentioned above, doctors and scientists look for new methods of treatment. In the Nuclear Medicine Institute of the Medical University of Warsaw operating at the Independent Public Central Clinical Hospital in Warsaw, clinical trials are conducted

on the method of treatment of multiform gliomas. Its effectiveness is related to several factors, including analyzing software and determining the location, size, and volume of the tumor that determines the method of treatment.

2 Database of PET and CT images

Medical data used as the resource for image processing is the sequences of computed tomography (CT) and positron emission tomography (PET) images. The images were taken using a Siemens Biograph 64 PET-CT tomograph at the Department of Nuclear Medicine of the Medical University of Warsaw.

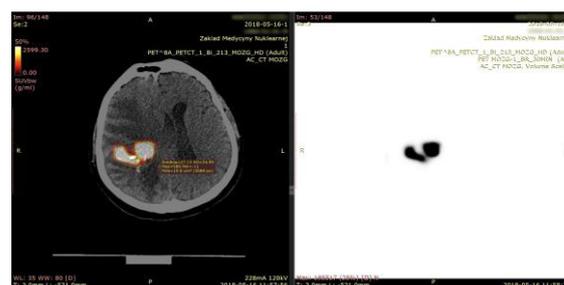


Fig. 1. The fusion of PET images with coupled CT images is one of the most accurate diagnostic methods allowing to localize pathological changes from 3 mm in size.

3 The algorithm

The algorithm was designed and implemented in MATLAB to support radiologists with their decision-making process. The main objective of the created software is the ability to localize, calculate the volume, and make a 3D visualization of the tumor. There are a couple of steps executed for single patients in the algorithm:

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1. Load patient medical tests results (PET and CT images).
2. Determine the global threshold based on a series of PET images.
3. Load the next pair of correlated PET and CT images.
4. Extract bone tissues from the CT image.
5. Scaling the PET images to 512x512.
6. Extract bone tissues from the PET images based on processed CT images.
7. If the identified area has more than 10px, then the active contour method starts on the PET images.
8. Calculate the total volume based on partial amounts.
9. Make a 3D tumor visualization.

3.1 Threshold

Thresholding crucially affects the final results of the designed algorithm: it follows the whole series of images and defines local thresholds for each model. Then, its most significant value creates a global threshold, determining whether there is a tumor in the analyzed area. If the pixel intensity in the image is higher than the defined threshold, then the value in the area is strengthened. The amount of the threshold is directly correlated with the Hounsfield scale, and hence to the representation of connective tissues in which the tumor does not appear. In DICOM images, the skull, i.e., the bone tissue, is brighter than the soft tissues.

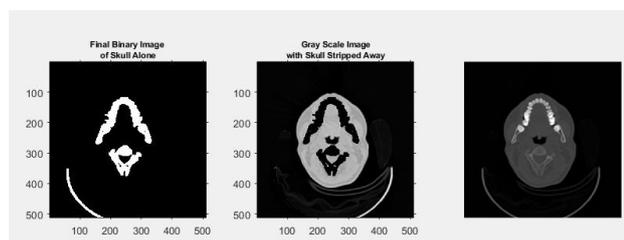


Fig. 2. The figure shows the process of removing bone structures from a CT image based on the calculated threshold. On the left side, there is a bone tissue found in the CT scan image presented. In the middle, the picture shows the image with merged tissue cut out, i.e., only soft tissues in which the existence of a tumor is possible. On the right side, there is shown an original unprocessed image.

3.2 Active contours methods

Tumor identification and determination of its edges and volume calculation follow image fusion. The active contour method was used for segmentation of the images. The active contour method - described in 1988 [4] was used to compute tumors volume. This method involves searching for boundaries between areas based on finding pixels that can belong to the edge of the object. The points are merged to the line and adjusted to the shape of the object, creating its boundaries. The general purpose of the active contour method is to minimize the contour energy, the value of which results from the image gradient, the distance between the individual points, or the curvature values. The active

contour assumes the continuity of the edges, even if they are, discontinuous.

4 The results

There were 2072 DICOM files used during the image processing process. The algorithm successfully identified tumors for all 21 patients. The best results were obtained for the Edge method when determining 20 maximum iterations, and for the Chan-Vese process for 100 iterations.

Table 1. The visualizations of identified tumours.

Lp.	Edge	Chan-Vese
1.		
2.		

5 Conclusions

The paper has presented an algorithm used for segmentation of biomedical images to compute gliomas volumes. Currently, the estimation of the tumor volume, and thus the amount of radiopharmaceutical administered to the postoperative box, is carried out manually by a radiologist using a program offering an only elliptical selection of the tumor area. It is a method exposed to error and lack of repeatability, which makes it difficult to consider its results as a reference. The created software gives reproducible results and thus can find practical applications in further work on medical imaging.

References

1. H. Ohgaki, P. Kleihues, *Acta Neuropathologica*, 2005, **109**, 93-108
2. M. Riemenschneider, G. Reifenberger, *International Journal of Molecular Sciences*, 2009, **10**, 184-212.
3. K. Okła, A. Wawruszak, S. Bliska, Glejaki — epidemiologia, klasyfikacja i etiologia, [in:] *Choroby nowotworowe: wybrane zagadnienia*, Fundacja na rzecz promocji nauki i rozwoju TYGIEL, red. M. Olszówka, K. Maciąg, Lubin, 2015, 7-18.
4. M. Kass, A. Witkin, D. Terzopoulos, *International Journal of Computer Vision*, 1988, **1**, 321-331.