BCT Boost Segmentation with U-net in TensorFlow

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Abstract. In this paper we present a new segmentation method meant for boost area that remains after removing the tumour using BCT (breast conserving therapy). The selected area is a region on which radiation treatment will later be made. Consequently, an inaccurate designation of this region can result in a treatment missing its target or focusing on healthy breast tissue that otherwise could be spared. Needless to say that exact indication of boost area is an extremely important aspect of the entire medical procedure, where a better definition can lead to optimizing of the coverage of the target volume and, in result, can save normal breast tissue. Precise definition of this area has a potential to both improve the local control of the disease and to ensure better cosmetic outcome for the patient. In our approach we use U-net along with Keras and TensorFlow systems to tailor a precise solution for the indication of the boost area. During the training process we utilize a set of CT images, where each of them came with a contour assigned by an expert. We wanted to achieve a segmentation result as close to given contour as possible. With a rather small initial data set we used data augmentation techniques to increase the number of training examples, while the final outcomes were evaluated according to their similarity to the ones produced by experts, by calculating the mean square error and the structural similarity index (SSIM).

Key words: breast cancer, breast conserving therapy, image segmentation, U-net, Keras, Tensor-Flow

1. Introduction

Breast cancer is a type of tumour that develops in breast region when cells located there rapidly divide. In result, those rapidly dividing cells can grow out of control, finally forming large, abnormal masses. It can be characterized as anomalous swelling of a part of the body or growth of tissue, where there is no local inflammation. Tumours can be roughly divided into two main types: benign and malignant. First type of cancer occurs, when its cells spread only to areas surrounding tumour, while second type means that cells travelled by lymph nodes to different organs, spreading through either body and producing metastasis. Breast tumour can be seen with X-ray and can be felt during standard test as a lump, that is irregular in shape. Such lumps will be fixed to the tissue in the breast and can have firm or solid filing because of that. Depending from the specific case, they can be painful or painless, also tumours can start from different parts

of breast. Usually breast cancer will start in the ducts (ductal cancers), while some of them will start in the glands (lobular cancer).

Recent years have shown advancements both in image diagnostics as well as available treatments. At this time prevention is discussed besides potential medication and surgery. Because the actual disease is better understood, there were considerable changes in treatment methodologies. Such shift allowed multidisciplinary approach to the problem itself, changing its understanding and finding more efficient methods for both diagnosing breast cancer as well as ways to introduce improvements during different stages of treatment [1].

One of the core problems that influence final stages of the breast conserving therapy is denoting boost area that remains after removing recognized tumour for further radiation treatment. When boost area is not correctly marked it can result in actual treatment missing its target (completely or partially), while healthy tissue, that otherwise could be spared will be targeted. Even when entire boost area is covered by the procedure, from cosmetic point of view it is best to limit its overlay with healthy cells, saving as much of the breast as possible. Because of above reasons more precise and efficient method for denoting boost area from CT images was necessary.

When it comes to different visual recognition tasks, especially in recent years, deep convolutional neural networks have performed considerably well (see [5,6]). Since for the convolutional neural network (or CNN) usually large amount of data is required before it will render acceptable results, application to medical images was rather limited. In case of such applications sample sizes are usually rather small (like in our case, when we have 246 samples total), while acquisition methods are lenghty and complicated. Another problem is that while typically CNN would be applied to classification task, in medical images usually additional data, such as localization is needed, therefore requiring for any proposed algorithm to assign class value to each pixel in input image.

One of recent solutions called U-net is focusing on medical image segmentation for determining location of single cells in given samples [2]. Proposed network uses two paths: contracting and expansive. Contracting paths consists of repeated application of two 3 by 3 unpadded convolutions, each followed by a rectified linear unit (ReLU) and a 2 by 2 max pooling operation with stride 2 for downstamping. For the expansive path each step includes upsampling feature map, next followed with 2 by 2 up-convolution (halving number of feature channels), concatenation with corresponding cropped feature map and finally two 3 by 3 convolutions, each of them followed by ReLU. In that approach both small initial sample size as well as other problems concerning medical image processing are considered, and we use proposed U-net network as a base for out further research when it comes to our case of post-surgery boost area segmentation for breast cancer. For outline of U-net network structure see Fig. 1

Due to its large success we decided to use U-net as a base of our solution and adjust it to boost area segmentation problem. In our approach we use CT images, that were
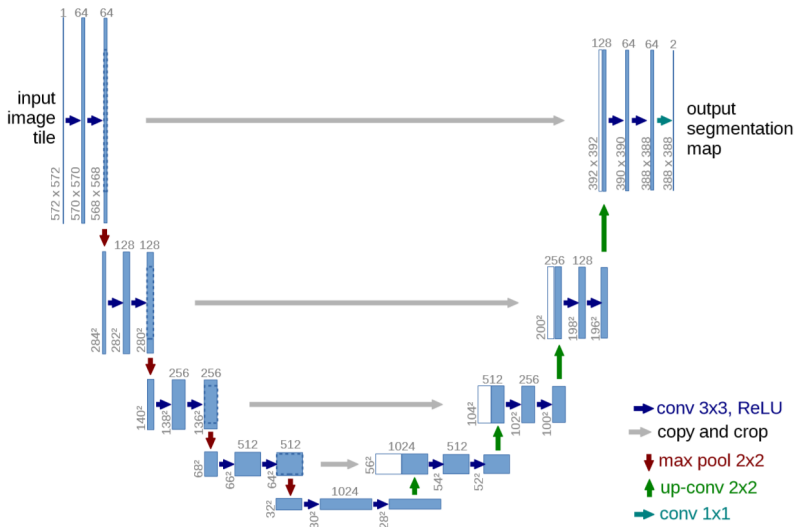
Fig. 1: U-net network architecture example for 32x32 pixels in lowest resolution [2].

originally saved in DICOM format. Each sample contained numerous slices along with expert outlines denoting boost area for those examples (see Fig. 2 for example slice along with GT expert outline and Fig. 3 for more specific indication of boost area). For those slices segmentation process was performed, in which we tried to achieve region selection as close to area pointed out by the expert as possible. We use Keras U-net network along with TensorFlow as a base for our methodology and adjust them to this specific problem using data augmentation methodologies for increasing total number of instances for the training process (to further increase accuracy of final segmentation algorithm). Please refer to [8] for Keras library documentation and [9] for TensorFlow.

2. Network architecture

Image segmentation for medical purposes can be tiresome and time consuming process, especially when high precision is necessary, like it is the case with boost area denotation. Usually for such application general machine learning algorithms and convolutional neural networks specifically would be prepared. Main issue occurring in this type of problems is small number of available samples, hence network learning from scratch cannot be used, simply because it would not achieve acceptable precision. Another problem lies with the fact, that while CNN is quite good for classification problems it requires some adjustments for area denotation, some of which were addressed in [2]. In one of previous
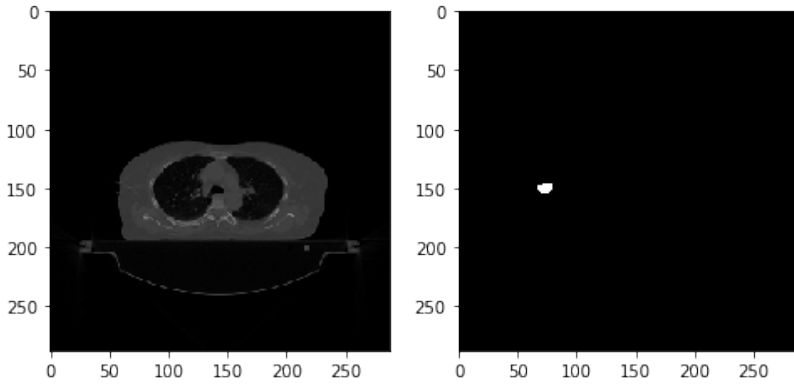
Fig. 2: Example of a single CT image (left), with expert outline of boost area (right).
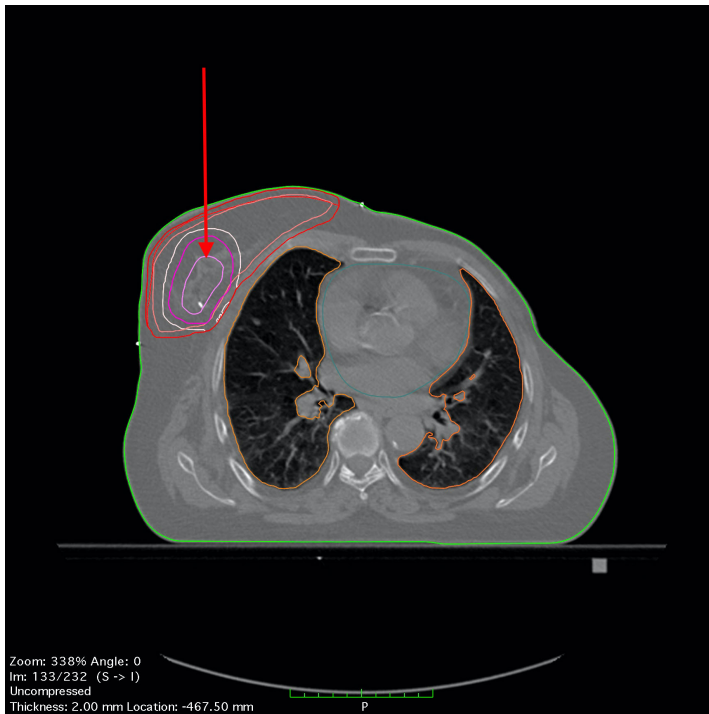

Fig. 3: Identification of area that needs to be outlined relatively to entire CT image.

works [7]CNN was used for drill wear recognition. Similarly as in this case, very small number of samples were available for training (only 242 examples for three recognized classes). Presented approach showed, that using pretrained model and adjusting it to different problem by exchanging classification layers is a very promising approach. We chose similar solution, basing our algorithm on Keras version of U-net algorithm.

Since our images have size 288 by 288 pixels, we needed to adjust network structure to accommodate that. To better fit entire solution to boost area segmentation problem, we removed last 3 layers of Keras U-net network, and retrained them using available samples. Full network structure is described in Table. 1.

3. Training

Solution presented in this paper is based on Keras version of U-net network, that was adjusted to accommodate different image size (288x288 in our case), and had last [??] layers retrained to better fit our segmentation problem. Initial set of data contained 246 samples. We used 216 of them for the training process, 24 for validation and remaining 6 samples were denoted as test data.

Such small dataset is a common occurrence in case of medical images, therefore instead of trying to get more original images, we used data augmentation to artificially increase number of samples we could use. By performing operations such as scaling, rotation or simple translations we could efficiently increase number of available images, without the need to perform lengthy operations required for obtaining original images. Such approach reduces time required for preparations, while still significantly increasing obtained accuracy (augmented samples will not differ greatly from original images, while still increasing overall neural network accuracy). Example images after performing simple image operations are presented at Fig. 4.

4. Experiments

After preparing and augmenting initial data set, we used obtained images to train Keras U-net. All experiments presented in this paper were done on Ubuntu operating system (version 18.04.3 LTS), with 2x AMD Ryzen Threadripper 2990WX 32-Core Processor, 128GM of Ram, and two graphic cards Nvidia TITAN RTX. We chose Python [10] as our programming language (version 3.7.4) since due to its specifics as well as availability of extensive libraries it was most comprehensive approach for combining different solutions, including Keras library (version 2.3.1) and TensorFlow (verision 2.0.0).

Evaluation was performed for all 6 samples of test data. Obtained segregation results are presented at Fig. 5. To further evaluate final regions selected by prepared solution, we calculate mean squared error according to equation 1:

Tab. 1: Structure of BCT boost segmentation network.

| Layer (type)	Output shape	Param #	Connected to
input_8 (InputLayer)	(None, 288, 288, 1)	0	
conv2d_64 (Conv2D)	(None, 288, 288, 8)	80	input_8[0][0]
max_pooling2d_22 (MaxPooling2D)	(None, 144, 144, 8)	0	conv2d_64[0][0]
conv2d_65 (Conv2D)	(None, 144, 144, 16)	1168	max_pooling2d_22[0][0]
max_pooling2d_23 (MaxPooling2D)	(None, 72, 72, 16)	0	conv2d_65[0][0]
conv2d_66 (Conv2D)	(None, 72, 72, 32)	4640	max_pooling2d_23[0][0]
max_pooling2d_24 (MaxPooling2D)	(None, 36, 36, 32)	0	conv2d_66[0][0]
conv2d_67 (Conv2D)	(None, 36, 36, 32)	1056	max_pooling2d_24[0][0]
up_sampling2d_22 (UpSampling2D)	(None, 72, 72, 32)	0	conv2d_67[0][0]
concatenate_22 (Concatenate)	(None, 72, 72, 64)	0	up_sampling2d_22[0][0], conv2d_66[0][0]
conv2d_68 (Conv2D)	(None, 72, 72, 32)	8224	concatenate_22[0][0]
up_sampling2d_23 (UpSampling2D)	(None, 144, 144, 32)	0	conv2d_68[0][0]
concatenate_23 (Concatenate)	(None, 144, 144, 48)	0	up_sampling2d_23[0][0], conv2d_65[0][0]
conv2d_69 (Conv2D)	(None, 144, 144, 24)	4632	concatenate_23[0][0]
up_sampling2d_24 (UpSampling2D)	(None, 288, 288, 24)	0	conv2d_69[0][0]
concatenate_24 (Concatenate)	(None, 288, 288, 32)	0	up_sampling2d_24[0][0], conv2d_64[0][0]
conv2d_70 (Conv2D)	(None, 288, 288, 16)	2064	concatenate_24[0][0]
conv2d_71 (Conv2D)	(None, 288, 288, 64)	1088	conv2d_70[0][0]
dropout_8 (Dropout)	(None, 288, 288, 64)	0	conv2d_71[0][0]
conv2d_72 (Conv2D)	(None, 288, 288, 1)	65	dropout_8[0][0]
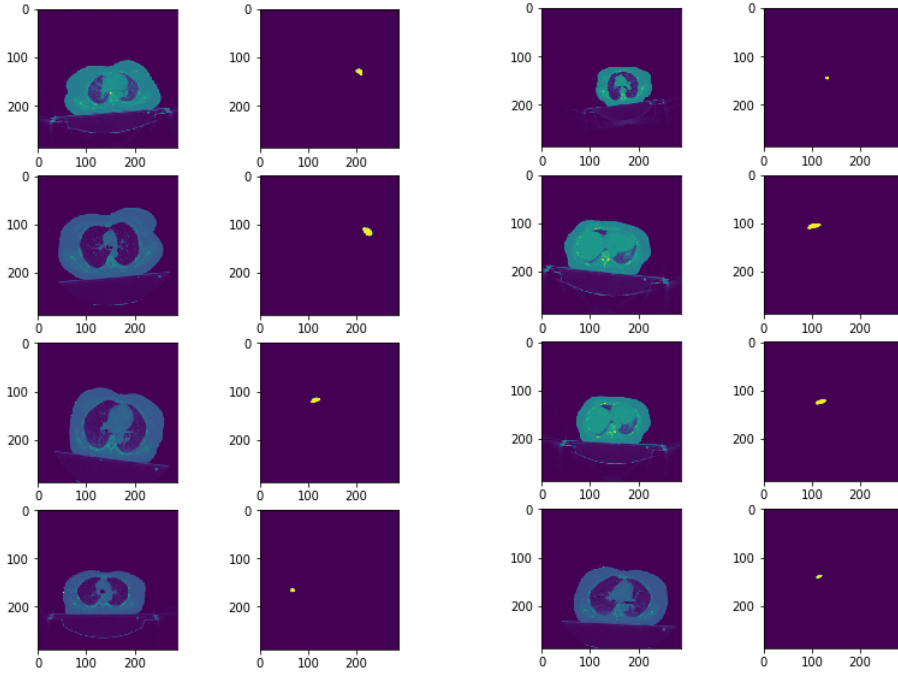
Fig. 4: Examples of images obtained after performing simple image transformations (i.e. rotation, scaling, translation), along with denoted boost area.

$$MSE = \frac{1}{mn} \sum_{i=0}^{m-1} \sum_{j=0}^{n-1} [I(i,j) - K(i,j)]^2 \tag{1}$$

Second used parameter is SSIM (Structural Similarity Index) [4] in the form of equation 2.

$$SSIM(x,y) = \frac{(2\mu_x\mu_y + c_1)(2\sigma_{xy} + c_2)}{(\mu_x^2 + \mu_y^2 + c_1)(\sigma_x^2 + \sigma_y^2 + c_2)} \tag{2}$$

Using SSIM is not a standard solution, but we decided, that in case of comparing two selected regions determining exactly how similar our solution is to the target outline will be an important factor. SSIM index values range from -1 to 1, where first value denotes completely different elements, without common parts, while second value denotes perfect similarity. Results obtained for each of test samples are presented in Table. 2.
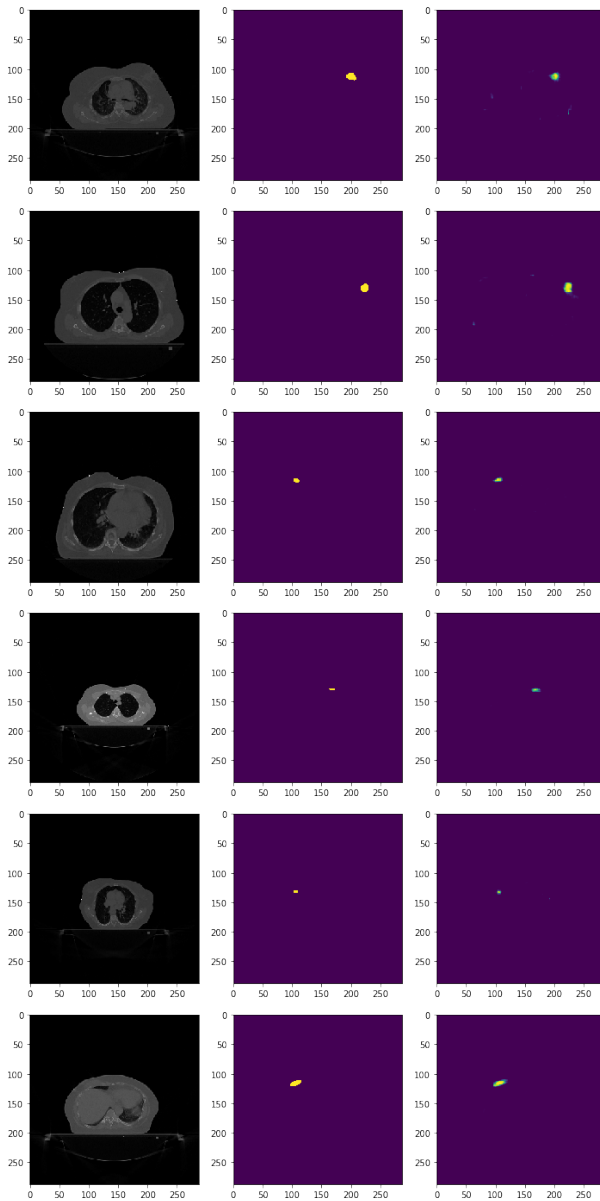
Fig. 5: Example segregation results: original image (left), GT denoted by expert (middle) and result obtained with our solution (right).

Tab. 2: Mean square error (MSE) and structural similarity index (SSIM) obtained for all test samples by our boost area segmentation method.

Sample number	MSE	SSIM
1	0.0003858	0.9975356
2	0.0008077	0.9965344
3	0.0004701	0.9964890
4	0.0004581	0.9971912
5	0.0003375	0.9982249
6	0.0004581	0.9980749

5. Conclusion

In this paper we present machine learning approach to segmentation problem of boost area in breast conserving therapy, which is a result of performed surgery. Since outline obtained during that process will later be used to determine region for radiation treatment, precise and exact definition is crucial for limiting exposure of healthy tissue and minimizing risk of missing the target. Our solution uses U-net network available in Keras library, modified and adjusted to specified problem, and is able to accurately denote specified region. We used relatively small number of initial samples, while entire set used for network training was artificially expanded using simple image operations.

We evaluated our results using MSE (mean square error) and SSIM (structural similarity index) as main parameters, apart from visual confirmation of final outline quality. For given set of test examples (6 samples in total) we were able to achieve satisfactory results. All of samples achieved similarity index above 0.99 (with lowest similarity index equal 0.9964890 for sample number 3), while calculated errors remained at relatively low level (highest obtained error equalled 0.0008077 for sample number 2). Visually all obtained results were very close to the GT prepared by expert.

Overall presented solution has great potential and requires further study. Our approach still needs to be evaluated on larger set of test images. It also might require additional methods for more complex cases (i.e. when more than one area will need to be outlined). Despite that current version of presented solution was able to generate precise outlines of boost areas in given set of CT images, and can be used during medical procedures as an support tool for the expert.

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