

Prostate Cancer Detection

Team members:

Anca Faur, ICA, anca.maria.faur@stud.ubbcluj.ro, 256

Nicu Coman, ICA, nicolae.coman@stud.ubbcluj.ro, 256

Catalin Galben, ICA, catalin.galben@stud.ubbcluj.ro, 256

The team is made up entirely by software developers that are currently studying applied computational intelligence during the master degree program. All of the skillsets are related to software development, so, the roles devised were not so separate of each other. In the end everyone had a hand in everything. It's more of a collective contribution rather than an individual one.

1. Introduction

As cancer is a serious matter that should not be overlooked, people can make use of technology in order to ease and speed up the process of detecting potential problematic areas within one's body. Such an example is the cancer of the prostate. Our team chose to tackle this particular problem via the use of an application which allows to quickly upload images representing prostate scans inside of an interface and obtain results that would suggest problematic areas within that scan as a result.

Since the data input to be processed consists of image type files, and the desired output is an edited version of the provided image, having an outline over a problematic area, it stands to reason that the necessary solution would be some sort of machine learning algorithm that parses the provided file, extracts information from within and provides an interpretation of said information. Normally, this step would be done by a doctor, that has knowledge in how to look at body scans and provide a useful outlook in them. The automation of the process can speed up

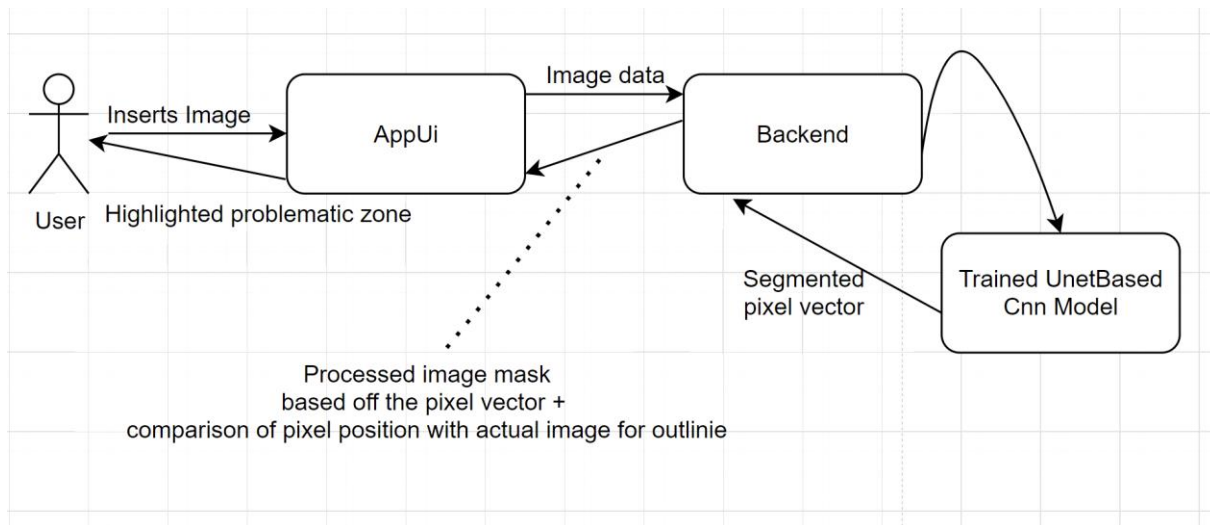
diagnosis of problems and severity, without the need of an actual person to be implicated. Details on the technical approach will be discussed later in the report.

2. Problem Description

Magnetic resonance imaging (or MRI) provides detailed anatomical images of the prostate and its zones, thus it can be said that it has a crucial role for diagnostic applications. Accurate prostate segmentation is very important for the task of image analysis that leads to cancer detection. Manual segmentation still is the most spread way to accurately segment prostate glands and regions. This being said, manual segmentation is quite a time-consuming task. Besides the time problem at hand, there are other inconvenience factors coming into play such as it is subjective and strongly depends on the level of experience. If the interobserver variation is high, the results will be poor reproducibility and inconsistency. Therefore, we can say that reliable automated segmentation of the prostate zones is highly desirable in daily clinical practice.

3. Graphic abstract

In Figure 0, one can observe the main flow of our application. The user provides an image and our system processes the image and outputs a secondary image in which the cancerous image pixels are marked. In the backend, the system uses a UNet Cnn model pre trained for such a segmentation task.



4. Related work

Other observed methods were based on multi-parametric MRI scans for segmentation of the prostate cancer. The most notable related work would be a 3D observation of the prostate cancerous status.

Hence in MRI images, the voxel intensities, and thus, the appearance characteristics of the prostate can greatly differ between different acquisition protocols, field strengths and scanners.

This leads to the desire to use a segmentation algorithm in order to deal with such issues. The dataset used was the open-source PROMISE12 challenge, which is including scans from different centers:

- Haukeland University Hospital, Norway
- Beth Israel Deaconess Medical Center, United States
- University College London, United Kingdom
- Radboud University Nijmegen Medical Centre, Netherlands

Some popular evaluated metrics used in related works [4] [5]:

- The Dice coefficient: Used in order to measure the similarity between output volumes

- Absolute relative volume difference: The percentage of absolute difference between the volumes (applicable in 3D cases)
- Average boundary distance: The average over the shortest distances between the boundary points of the volumes
- Hausdorff distance: the maximum of the shortest distances between boundary points of the volumes. In study, it is mentioned that 95% of the distance computation makes the metric less sensitive to outliers.

5. Input Data and Preprocessing

In order to obtain the AI segmentation model we have used the promise12 dataset[0] which consists of 50 training cases of traversal MR image of the prostate. The data is multi-center and obtained using different acquisition protocols so that the prostate differ in size and appearance. The test contains 20 cases that are used in evaluating our AI model.

At a pre-processing stage, we transform the data from MHD format to jpgs of resolution 128x128 with respect to the underlying frames. After this step, we have approximately 1000 labelled images in the training set that is used for the segmentation model.

6. Software Design and Implementation

We developed two main software assets. The first asset is a collection of scripts that are used for learning the AI algorithm that detects the cancerous region from prostate data. The second asset represents our interactive application that is web-based and provides the detection service to a user.

6.1. AI Learning Asset

6.1.1. Method Description and Architecture

Our AI asset builds a segmentation model starting from the UNet [1] architecture and following this tutorial [2]. UNet has a two path architecture. The first one is the contraction path, also known as the encoder and it is used to capture the overall context of the image. Basically, an encoder is nothing more than a stack of traditional convolutional and max pooling layers. The second path is a symmetric expanding path, also known as the decoder and it is used in order to be able to precisely localize areas, using transposed convolutions. In other words, the architecture described can be viewed as an end to end fully convolutional network. It only contains convolutional layers and does not contain any Dense layer due to potential compatibilities with image sizing that come with the use of the Dense layer.

The exact design is presented in the two following image taken from the UNet description paper. One of the key operations of this network is the convolution operation that uses hierarchical filters in order to identify higher level features, which is followed by the max pooling operation that reduces the data size in order to retain only the important features and reduce the weights' computation cost. As the input size is reduced, processed also called down-sampling, we might lose the where information that we require in the output image. In order to overcome this problem, we use the up sampling method called Transposed Convolution[3].

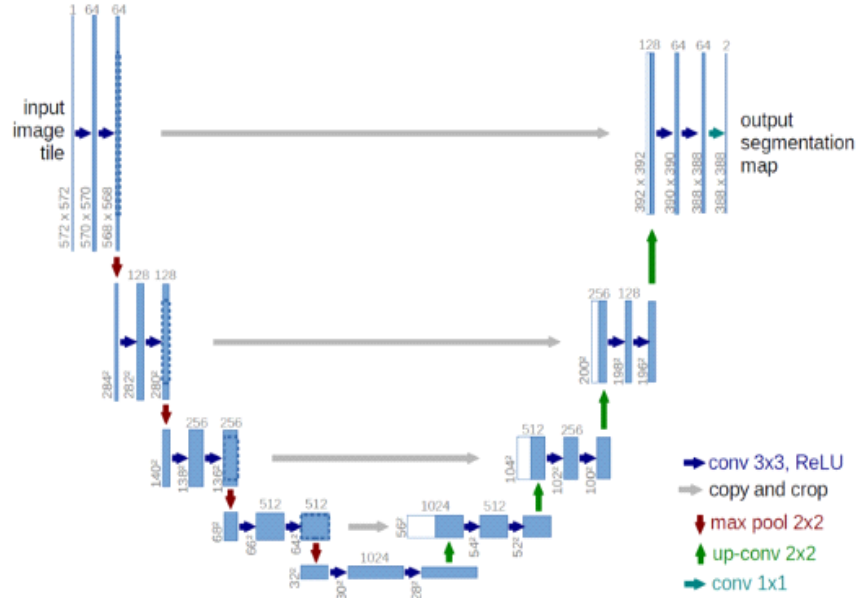


Fig. 1. U-net architecture (example for 32x32 pixels in the lowest resolution). Each blue box corresponds to a multi-channel feature map. The number of channels is denoted on top of the box. The x-y-size is provided at the lower left edge of the box. White boxes represent copied feature maps. The arrows denote the different operations.

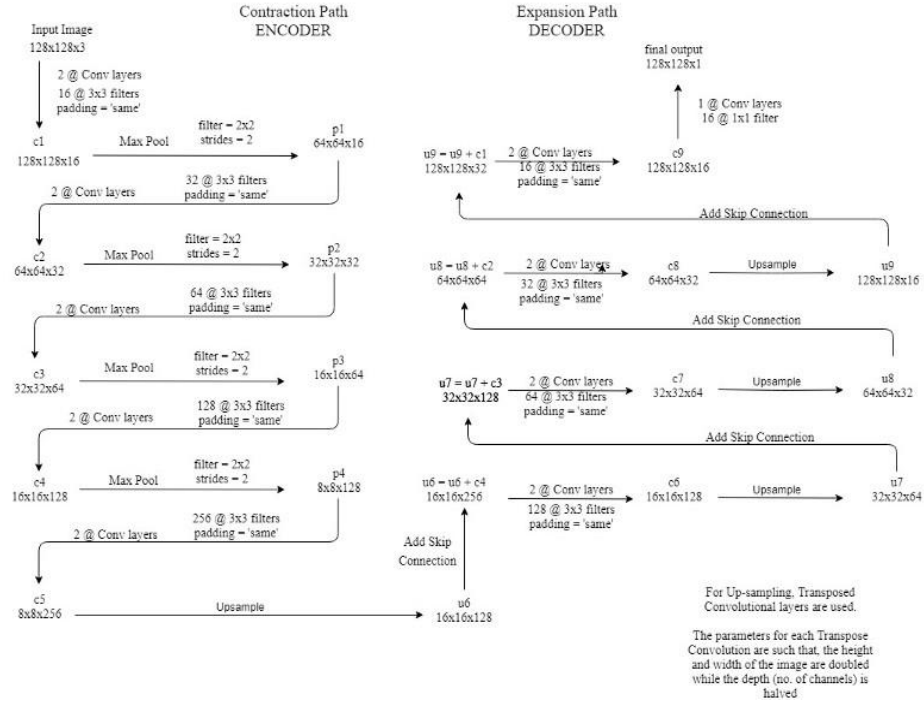


Fig 2

6.1.2. Training

We changed the size of the input to images of 128x128x3 in order to reduce the computation cost of the learning task. Also, we used the Adam Optimizer and binary cross entropy loss function in order to differentiate between the cancerous/non-cancerous image pixels. We decrease the learning rate if no improvement is obtained in validation after 5 consecutive epochs. In order to avoid performance issues, we added an early stopping for the model if validation is not improved in 10 consecutive epochs.

The training process is static and offline and the obtained model is exported in the user interactive asset.

6.2. User Interactive Asset

6.2.1. Architecture

Our interactive application uses the learned model and provides the service of detecting the cancerous region from a prostate image given by a user. This application has a client-server software architecture that allows the server, which theoretically has more computation power, to perform the computational expensive service for the client. Also, this architecture has increased security as the business secrets of the algorithm are maintained on the server side and cannot be accessed by the client.

The application is implemented in python, using the Django framework which is based on the MVC pattern (Model View Controller). This pattern is translated into Django as MTV (Model Template View) in which the model contains the business logic (AI model and input preprocessing steps), the template defines the user interaction and the view is the controller that provides the access to the service. This design results in a decoupled application that can be easily modified and managed. Moreover, the application saves the user's images on the server side. We thought that this would be useful for later training/testing the AI model on real data.

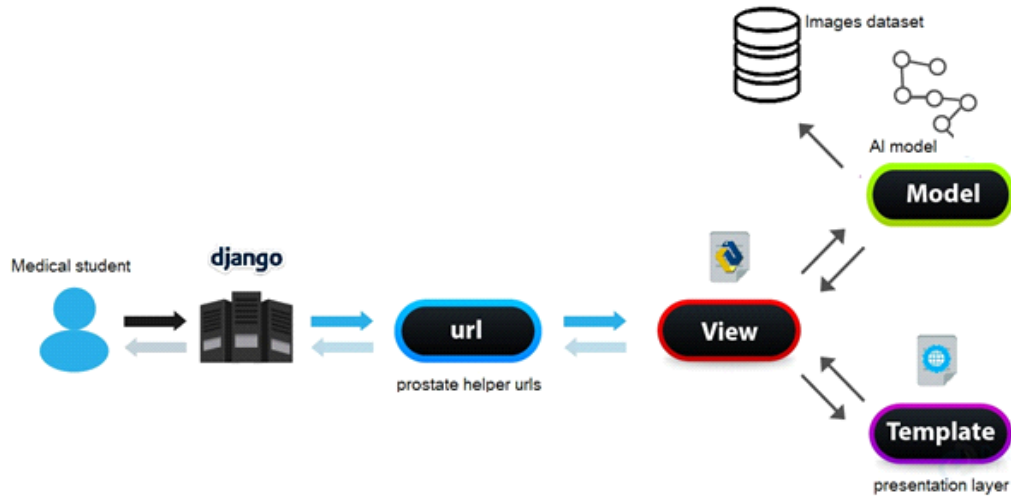


Fig 3

6.2.2. Deployment

Ideally, our server would run on a publicly available server and the user, using the browser of a regular PC connected to the Ethernet, would require our service by creating HTTP requests to the URLs of the server. However, for the purpose of this demo, we deploy the server on localhost, on the same PC as the client.

7. Technologies

7.1. Versioning tools

In order to facilitate team work, we have a common Github repository. Each develop used a local branch and merged with the master branch when the code was functional. Moreover, our history of commits is traced by GitHub and can provide a better understanding of the code using the commit messages.

7.2. Python Libraries

- Medical Document Preprocessing: SimpleITK
- Image processing: Skimage, Matplotlib
- For the AI model building and training: Tensorflow, Keras, Numpy, Pandas
- For the interactive application: Django

8. Evaluation

The evaluation of the obtained model has been computed on the validation set of images, which contains a total of 138 images. The evaluation metric used is the Jaccard similarity index. The Jaccard coefficient measures similarity between finite sample sets, thus, images are treated as sets of pixels, and is defined as the size of the intersection divided by the size of the union of the involved sets. A value of 0 indicates that the sets are disjoint and a value of 1 indicates that the sets are identical. This measure is also referred as intersection over union (IoU).

In order to compute the Jaccard similarity coefficient of two images, binarization of the images is required, so thresholding is needed before performing any computations. The area computation of intersection and union operations is straightforward, simply count the 1-valued pixels of the result images of union and intersection operations.


$$\text{IoU} = \frac{\text{Area of Overlap}}{\text{Area of Union}}$$


Fig 4

Out of the 138 given test images, 131 were successfully processed by the obtained model, yielding a correct segmentation result (either some lesion was detected, if the image truly represented an affected prostate or no lesion was detected in case of a healthy prostate). For 7 images, false segmentation results were obtained: 1 false negative and 6 false positives. As mentioned before, the quality of the segmentation procedure was addressed making use of the Jaccard similarity index. The similarity measure was computed only for images representing affected prostate, and an arithmetic mean has been computed over all results, obtaining a value of 0.767.

Some visual representations of the obtained results:

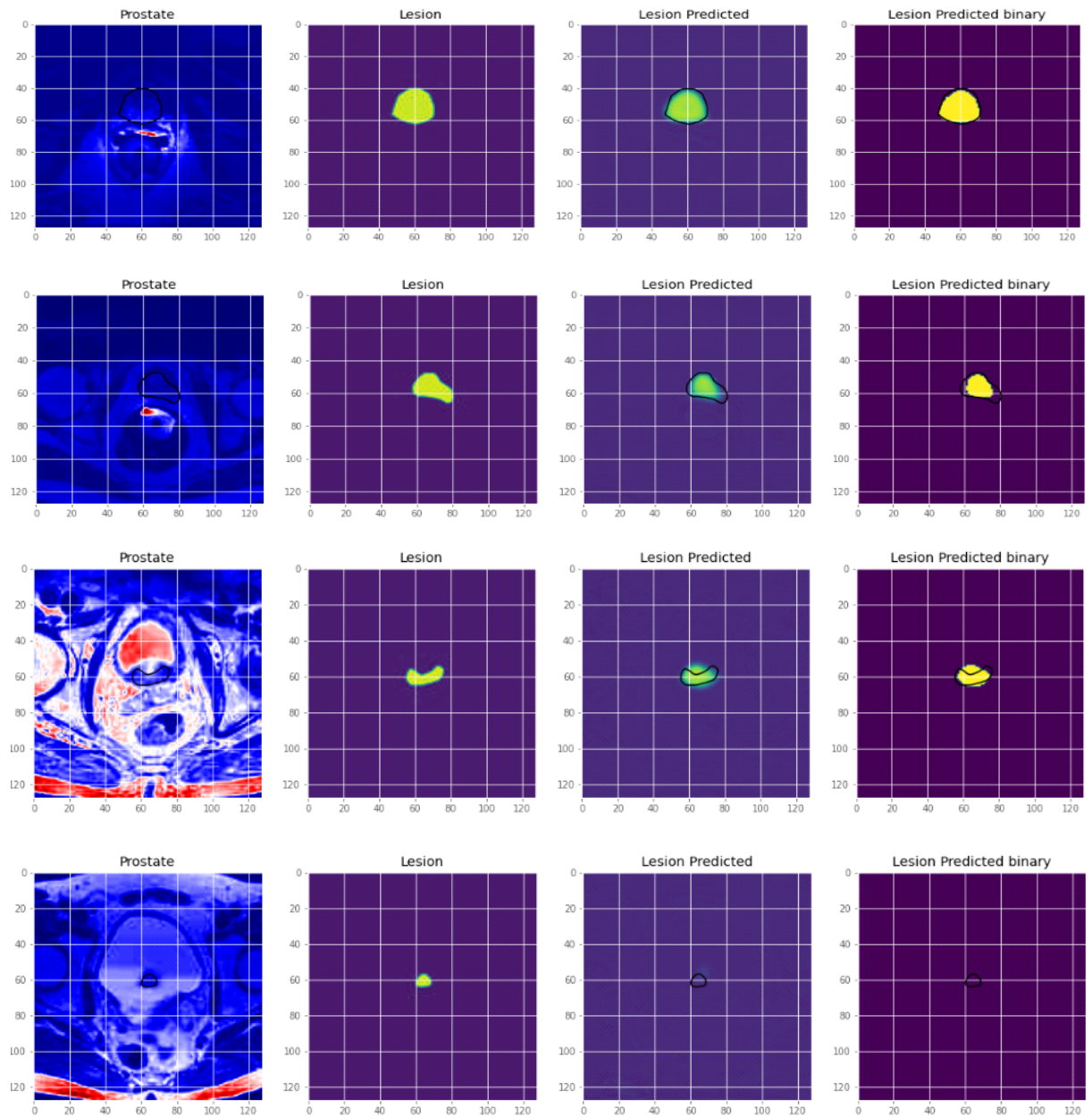


Fig 5

9. Philosophical Aspects

9.1. Social impact of your project & results

The project could be useful for a medical student or doctor in order to draw the attention on the certain regions of prostate images that are considered cancerous. Even if the exact pixels of the expected output mask are not perfectly identified, we notice that the algorithm succeeds in identifying the main region. If a region is identified, the doctor can better study the medical input or require further medical analysis. Also, as the system can be deployed on a publicly available server and its input are regular images, it can be considered easily available and easy to use.

9.2. Ethics in your ML-based projects

With respect to the data, the ML model was developed using a publicly available dataset ^{promise12} that can be used for education purposes. With respect to the underlying algorithm, it is based on UNet whose architecture is publicly available and again can be used for education purposes. With respect to the correctness of our results, we tried to evaluate our algorithm while following the best AI practices. For example, the splitting between the training, validation and testing sets and the computation of more evaluation metrics.

Our ML software saves the users' images on the server side so that they could be used later on for iterative training. This can be interpreted as a privacy issue and the user must accept that in order to use the service, he agrees that his data can be later on used to improve the algorithm.

10. Further improvements

We expect the segmentation learning task to have better results if we have a bigger and more preprocessed dataset. At the preprocessing step, we could filter the useful frames from the medical mhd input. If the service gets used, we would also have more real life medical images. These could be labeled manually and used for improving our algorithm using the process of iterative learning. Also, we should evaluate our algorithm against more metrics, such as Average boundary distance.

11. Conclusion

This project provides a helpful tool for segmenting cancerous regions from medical prostate images that can be used by a doctor/ medical student to facilitate the study of medical data. We consider that the segmentation algorithm has acceptable results and that our interactive application is simple to use and accessible. Also, we enjoyed learning about segmentation and the ML support for medical problems.

Bibliography

[0] Promise12 dataset

<https://promise12.grand-challenge.org/>

[1] Olaf Ronneberger and Philipp Fischer and Thomas Brox, U-Net: Convolutional Networks for Biomedical Image Segmentation, 2015 <https://arxiv.org/abs/1505.04597>

[2] UNet Segmentation Tutorial

<https://towardsdatascience.com/understanding-semantic-segmentation-with-unet-6be4f42d4b47>

[3] Vincent Dumoulin and Francesco Visin, A guide to convolution arithmetic for deep learning, 2018, 1603.07285, <https://arxiv.org/pdf/1603.07285.pdf>

[4] Milletari, Fausto, Navab, Nassir & Ahmadi, Seyed-Ahmad. (2016). V-Net: Fully Convolutional Neural Networks for Volumetric Medical Image Segmentation.

[5] Chandra, S.S., Dowling, J.A., Shen, K.K., Raniga, P., Pluim, J.P.W., Greer, P.B., Salvado, O., & Fripp, J., (2012). Patient specific prostate segmentation in 3-D magnetic resonance images. IEEE Trans. Med. Imaging 31, 19551964.