# Deep learning for detection and diagnosis of prostate cancer from bpMRI and PSA: Guerbet's contribution to the PI-CAI 2022 Grand Challenge

Noëlie Debs*, Alexandre Routier*, Clément Abi-Nader, Arnaud Marcoux, François Nicolas, Alexandre Bône, and Marc-Michel Rohé

Guerbet Research, Villepinte, France
noelie.debs@guerbet.com, alexandre.routier@guerbet.com

**Abstract.** In this paper, we present an overview of our proposed method at the PI-CAI 2022 Grand Challenge, which aims to validate Artificial Intelligence (AI) algorithms for automated 3D detection and diagnosis of clinically significant prostate cancer (csPCa) in bi-parametric MRI (bpMRI). Our method consists of 4 main sequential steps: (1) first, a nnU-Net was trained to segment the prostate gland, (2) then a second nnU-Net was trained only on the positive cases (*i.e.* cases with cancer) to perform a voxel-level segmentation of cancer lesions, (3) then a Retina U-Net was trained on both positive and negative cases to perform an anchor based detection of cancer lesions. Only Retina lesions that spatially matched nnU-Net lesions were retained. Lastly (4), final ensembling method was applied on each lesion candidate: the final probability of cancer for a given lesion was defined as a linear combination of the probability returned by the nnU-Net, the probability returned by the Retina U-Net and a Prostate-Specific Antigen (PSA) density (reported on a scale between 0 and 1). All models were trained using 5-folds cross-validation. Our proposed method obtained an AUC-ROC of 0.889 and Average Precision (AP) of 0.615 on the hidden test set of 1000 patients, and was ranked second during the open development phase of the challenge.

**Keywords:** deep learning · prostate cancer· computer-aided detection · bi-parametric MRI · PSA density

## 1 Introduction

Prostate cancer is the second most common cancer in men [1]. Bi-parametric MRI is now emerging as the most promising technique for the diagnosis and management of prostate cancer. Many studies has shown that the analysis of different MRI sequences can allow to considerably improve the detection, localization and evaluation of tumor aggressiveness. Nevertheless, the visual interpretation of multiple MRI sequences is not easy, and there is a high inter-reader

* These authors contributed equally to this work

diagnosis variability [2], especially when the images contradict each other. In these conditions, a strong interest has been shown in AI computer-aided detection tools, in order to help the radiologist in his decision.

The PI-CAI challenge is a Grand Challenge aiming to benchmark modern prostate-AI solutions and evaluate their clinical viability for the detection and diagnosis of clinically significant prostate cancer (csPCa).

## 2 Material and Methods

We describe in this section the pipeline chosen for the challenge. This pipeline is decomposed in 4 steps: for each step, the corresponding model was trained using 5-fold cross-validation.

### 2.1 nnU-Net for prostate gland segmentation

A baseline nnU-Net [3] was trained to segment the prostate gland, using the 1500 cases training data from PI-CAI dataset. The network took as input 3 modalities (T2w, ADC, DWI), and the ground truth was AI-derived prostate masks.

The training parameters were chosen by the nnU-Net heuristic. Among others, the chosen loss was a combination of Cross-Entropy (CE) and dice.

### 2.2 nnU-Net for lesion segmentation

Our objective was to create a network that tends to over-segment cancer lesions. To do so, we considered a subset of the PI-CAI dataset consisting of cases with lesions only, to which we added the 83 positive cases from Prostate158 dataset [4]. We considered 3 modalities (T2w, ADC, DWI) as inputs, and the ground truth was lesion masks annotated by experts if available, otherwise masks from AI algorithm.

Based on the prostate segmentation algorithm trained in 2.1 we cropped the images along the xy-axes, thus allowing the network to focus on the prostate while accelerating the training speed of the segmentation algorithm. Finally, we relied on a modified version of the nnU-Net segmenting both the prostate gland and lesions, in which we used a different loss function depending on the segmented structure. We used the common combination of Dice and CE to segment the prostate gland, and a combination of Tversky loss [5] and CE to segment the lesions and push the network to over-segment them. The $\beta$ parameter of the Tversky loss was arbitrarily set to 0.7. The nnU-Net was trained in 5-fold cross-validation and the best model of each fold was retained. In inference mode an ensemble prediction of these 5 models is used to provide a lesion map of vowel-wise softmax outputs.

### 2.3 Retina U-Net for lesion detection

A Retina U-Net [6] was trained to detect cancer lesion. The model was first pretrained on the public large-scale object detection COCO [7], to initialize the weights. Then the model was trained on medical images, using the 1500 cases training data from PI-CAI dataset and 158 cases from the public medical dataset Prostate158 [4]. The network took as input 3 modalities (T2w, ADC, DWI), and the ground truth was lesion masks annotated by experts if available, otherwise masks from AI algorithm.

Since the training dataset was imbalanced ($\sim$ 25% of training data correspond to positive cases), we ensured that for each training batch, half of cases was randomly picked among positive cases, and the other half was randomly picked among negative cases. We also used a focal loss function in order to focus learning on hard misclassified examples. Also, a wide range of spatial and contrast data augmentation techniques were applied. Finally, we ensured that anchor sizes were adapted to ground truth lesion sizes.

The Retina algorithm returned bounding box outputs around suspicious regions of the image. Only bounding boxes that matched spatially both output nnU-Net lesions and prostate gland mask, with a minimum IoU of 0.1 for each, were retained as output of the Retina U-Net model.

### 2.4 Final ensembling

Final detection maps were created by combining the results of all pipeline components, as well as complementary biological information. The spatial localization of lesions was entirely determined by the lesion segmentation method detailed in Section 2.2. The corresponding probabilities were computed by ensembling: (i) the average softmax score from the lesion segmentation method, (ii) the detection score from the lesion detection method detailed in Section 2.3, and (iii) the Prostate-Specific Antigen (PSA) measurement normalized by the total volume of the gland as measured by the prostate segmentation method detailed in Section 2.1. Ensembling weights were learned using a logistic regression approach.

## 3 Results

On cross-validation dataset, nnU-Net performing prostate gland segmentation showed a mean overall 3D patient level dice of 0.98. Our final ensembled model achieved a mean overall AUC-ROC of 0.854 and AP of 0.489 on validation set. On the hidden testing dataset of 1000 patients, the same proposed model achieved an AUC-ROC of 0.889 and AP of 0.615 on the hidden test set of 1000 patients.

## 4 Conclusion

We proposed an ensemble method to predict csPCa for the PI-CAI challenge. This approach has several advantages: 1) the segmentation of the prostate gland

allows to better focus the segmentation and detection networks around the area of interest, 2) the output detection map does not depend on a single network, but corresponds to the combination of a semantic network, an anchor-based network, and clinical information using PSA density. One limitation of the study is that in case of missing PSA information, we performed imputation with the mean value from PI-CAI dataset. However, this should have a limited impact since PSAd had a weak contribution in logistic regression coefficients.

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