IMPLEMENTATION METHOD OF THE PI-CAI CHALLENGE (SWANGEESE TEAM)

TECHNICAL REPORT

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ABSTRACT

This article summarizes the methods our team used in the PICAI 2022 Challenge. The PICAI2022 Challenge is a competition to train the network to predict prostate cancer regions using 1295 labeled and 205 unlabeled MRI data. Our team only uses two-dimensional neural networks, including an ITUNet[2] converted to 2D operations and a classification network EfficientNet-b5[1]. Although the method is very simple, we achieved the highest AUROC score of 0.918 on validation set of open development phase, and got the AP score of 0.649.

Keywords Prostate cancer detection · ITUNet · EfficientNet

1 Introduction

Prostate cancer (PCa) is one of the most common cancers in men. One million men are diagnosed and 300000 people die of clinically significant PCa (csPCa) every year in the world. Multi parameter magnetic resonance imaging (mpMRI) plays an increasingly important role in the early diagnosis of prostate cancer. However, prostate cancer could exhibit a broad range of clinical behavior and highly heterogeneous morphology in MRI. Therefore, low inter-reader agreement (<50%), sub-optimal interpretation and overdiagnosis may occur in assessments. At present, using artificial intelligence technology to complete the analysis and processing of clinical medical images has been proved feasible by a large number of studies, while using deep learning networks to complete high-precision prediction of tumors by learning the feature information in the data can solve the challenges arising from the above problems.

This paper will use the deep learning network to complete the detection of prostate cancer. Different from the general methods for medical images, the text will convert all 3D images into 2D slices, and use the 2D slice data to train our method. In the prediction part, we will restore the prediction results of 2D slices back to the 3D form, and give the final prediction probability.

2 Methods

2.1 Preprocessing

We used axial T2W scan, axial DWI scan and axial ADC scan as three mode medical images to train all deep learning networks. We used the preprocessing tools provided by A. Saha et al[3]. to preprocess all the data. The preprocessing of experimental data includes the resampling operation and center clipping of all prostate MRI images. According to the spatial spacing information of all prostate MRI images, during the resampling process, the spatial spacing of all images is re unified to (3.0, 0.5, 0.5), so that the spatial physical meaning of adjacent voxels of all images can be consistent. It is observed that all tumor regions are roughly located in the center of the image, so the center clipping operation is performed for all images. After the spatial distribution of all tumor regions is calculated, the image size is fixed to (24, 384, 384) by center clipping for all images.

2.2 Network

We used a segmentation network and a classification network to complete the prediction of prostate cancer.

For the semantic segmentation network, based on the previous work of our team, we selected the network structure that we think has the best segmentation performance: ITUNet. ITUNet was originally a network structure designed for organ segmentation tasks of clinical medical images. Because of its good performance in organ segmentation tasks, especially its excellent segmentation accuracy for small and variable organs, we believe that it can also complete the task of tumor segmentation. We changed the original 3D network into a 2D network. The specific operation is to convert the original 3D convolution layer and pooling layer into the corresponding 2D structure, without making any other unnecessary modifications. For the training process, we use pixel level FocalLoss[4] as the loss function.

For the classification network, we selected EfficientNet-b5. EfficientNet-b5 is a network structure discovered by Tan M et al[1]. and has been verified to be effective on multiple tasks. We use the truth tag of the data to generate image level tags. For images containing cancer areas, we mark them as Category 1, otherwise they are marked as Category 0. We used cross entropy loss during training.

2.3 Training Method

Since there are 205 unlabeled data in the available data set, it is necessary to generate pseudo labels for these 205 data to expand the number of data available for training. We first trained a segmentation network using the images of 220 patients diagnosed with prostate cancer in the data set. The segmentation network used ITUNet, and the training process used 5 folds cross validation. This training process is fast due to the small amount of data, and it only takes about two days on the single GPU A100 to complete the training. Then, we use the weights obtained from the training to predict the unlabeled data, and only reserve the maximum two prediction regions with the largest connectivity region for each prediction case.

Then, we use labeled data and pseudo labeled data to complete semi supervised training of classification network and segmentation network. The weight obtained by semi supervised learning is used as the final prediction weight.

2.4 Postprocessing

For the prediction probability map generated by semantic segmentation, we still use the processing method provided by A. Saha et al[3] to generate the prediction region for prostate cancer. For the prediction of case level, we combine the prediction probabilities of the segmentation network and classification network. For the segmentation network, we take the prediction probability of region with the highest prediction probability as the prediction probability of the segmentation network for the case level prediction. For the classification network, we take the average confidence of the highest seven prediction probabilities as the prediction probability of the case. Finally, We will average the prediction probability of the segmentation network and classification network as the final result of case level prediction.

3 Results

3.1 Evaluation Metrics

We used AUROC(Area Under Receiver Operating Characteristic) to evaluate the prediction accuracy of our method at the case level, and AP(Average Precision) to evaluate the prediction accuracy of our method at the lesion level. The final performance evaluation uses the average of the two.

$$Score = (AP + AUROC)/2 \tag{1}$$

3.2 Experiment Result

We compared our method with the baseline method and recorded it in Table 1 and Table 2. The comparison methods are nnU-Net[5], U-Net[6] and nnDetection[7].

Table 1: Submission results on Validation and Tuning Leaderboard

Method	AUROC	AP	Ranking Score
nnU-Net	0.818	0.610	0.714
U-Net	0.829	0.633	0.731
nnDetection	0.885	0.582	0.734
Ours	0.918	0.649	0.784

The data set of Validation and Tuning Leaderboard contains 100 undisclosed test cases. Our method obtained an AUROC score of 0.918 and an AP score of 0.649 on the validation set, both of which were better than other baseline methods compared.

Table 2: Submission results on Testing Leaderboard

Dataset	AUROC	AP	Ranking Score
nnU-Net	0.865	0.576	0.721
U-Net	0.848	0.576	0.712
nnDetection	0.874	0.546	0.710
Ours	0.886	0.593	0.740

The data set of Testing Leaderboard contains 1000 undisclosed test cases, which is more illustrative because it contains more test data. Our method obtained 0.886 AUROC scores and 0.593 AP scores on the test set, both of which were also higher than the other three baseline methods compared.

4 Conclusion

Faced with the problem of prostate cancer detection, this paper only used some simple 2D deep learning networks to achieve patient-level prediction and lesion-level prediction of prostate cancer in MRI, and achieved good prediction results.

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