

# Towards Multi-modality Fusion and Prototype-based Feature Refinement for Clinically Significant Prostate Cancer Classification in Transrectal Ultrasound

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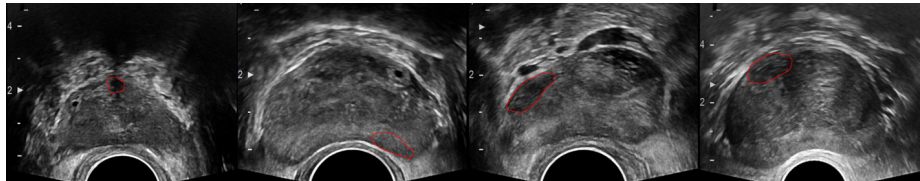
**Abstract.** Prostate cancer is a highly prevalent cancer and ranks as the second leading cause of cancer-related deaths in men globally. Recently, the utilization of multi-modality transrectal ultrasound (TRUS) has gained significant traction as a valuable technique for guiding prostate biopsies. In this study, we present a novel learning framework for clinically significant prostate cancer (csPCa) classification by using multi-modality TRUS. The proposed framework employs two separate 3D ResNet-50 to extract distinctive features from B-mode and shear wave elastography (SWE). Additionally, an attention module is incorporated to effectively refine B-mode features and aggregate the extracted features from both modalities. Furthermore, we utilize few shot segmentation task to enhance the capacity of the classification encoder. Due to the limited availability of csPCa masks, a prototype correction module is employed to extract representative prototypes of csPCa. The performance of the framework is assessed on a large-scale dataset consisting of 512 TRUS videos with biopsy-proved prostate cancer. The results demonstrate the strong capability in accurately identifying csPCa, achieving an area under the curve (AUC) of 0.86. Moreover, the framework generates visual class activation mapping (CAM), which can serve as valuable assistance for localizing csPCa. These CAM images may offer valuable guidance during TRUS-guided targeted biopsies, enhancing the efficacy of the biopsy procedure. *The code is available at <https://github.com/2313595986/SmileCode>.*

**Keywords:** Clinically significant prostate cancer · Transrectal ultrasound · Shear wave elastography · Multi-modality fusion · Few-shot learning.

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**Fig. 1.** Visualization of csPCa masks (red) on the specific frames from 4 TRUS videos.

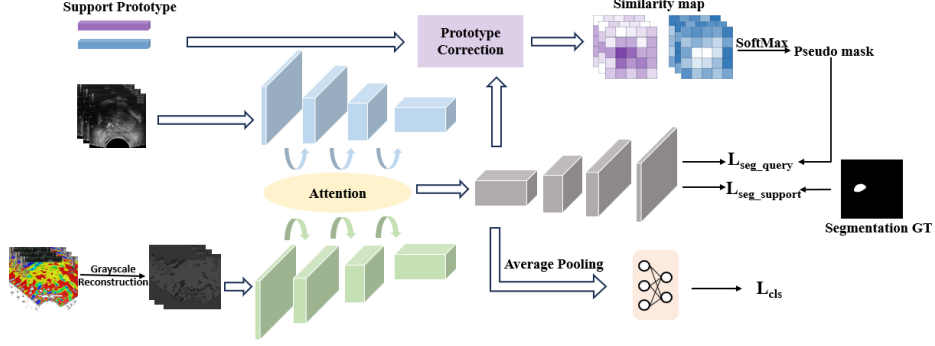
## 1 Introduction

Prostate cancer (PCa) is one of the most prevalent malignancies among men [16]. Prostate biopsy is the most reliable method for PCa diagnosis. Based on the microscopic appearance of prostate tissue, the results can be divided into benign prostatic hyperplasia (BPH), clinically significant PCa (csPCa) and clinically insignificant PCa (cisPCa) [13]. Since csPCa generally exhibits a worse prognosis and requires timely treatment, identifying csPCa patients helps improve the survival rate.

According to the current guidelines, any suspected PCa patients should have a multiparametric magnetic resonance imaging (mp-MRI) before biopsy [2]. Prostate mp-MRI is capable of depicting localization and morphology of PCa, thereby facilitating the implementation of the biopsy. However, the widespread implementation of prostate mp-MRI is restricted due to complex operations and high cost. Transrectal ultrasound (TRUS) serves as a commonly used modality for the guidance of prostate biopsies [6], yet the low contrast TRUS poses challenges for clinicians to identify PCa regions (see Fig. 1). It inevitably results in more unnecessary biopsies, with a higher risk of complications such as rectal bleeding [12]. Hence, it is crucial to develop effective strategies for csPCa detection in TRUS.

Previous study [1] indicated that regions assigned a Gleason score of 7 exhibited statistically higher Young’s modulus compared to regions with a Gleason score of 6. Building upon this finding, Wildeboer *et al.* [19] developed a random forest classifier analyzing B-mode, shear wave elastography (SWE) and contrast-enhanced ultrasound, reached area under curves (AUC) of 0.75 for PCa. Liang *et al.* [10] utilized a radiomics model that incorporated B-mode and SWE to classify the PCa and achieved an AUC of 0.85. Notably, the above two methods required the biopsy pathology as reference to draw all region of interests (ROIs). Recently, deep learning method has been applied to analyze TRUS videos for identifying csPCa. Sun *et al.* [17] proposed a prostate mask guided hierarchical framework to identify csPCa, and achieved an AUC of 0.85 in the external validation set.

In this study, we propose a multi-modality TRUS video classification network for the accurate identification of csPCa patients. Inspired by the multi-task learning strategy, a limited number of segmentation masks of csPCa are reconstructed based on biopsy pathology (see Fig. 1) and employed to train an



**Fig. 2.** Schematic overview of our method for identification of csPCa. Segmentation serves as an auxiliary task for enhancing classification performance.

auxiliary task for enhancing the encoder of classification network. Experiments on a large-scale multi-modality TRUS video dataset demonstrate the efficacy of our method. Our contributions can be summarized as follows:

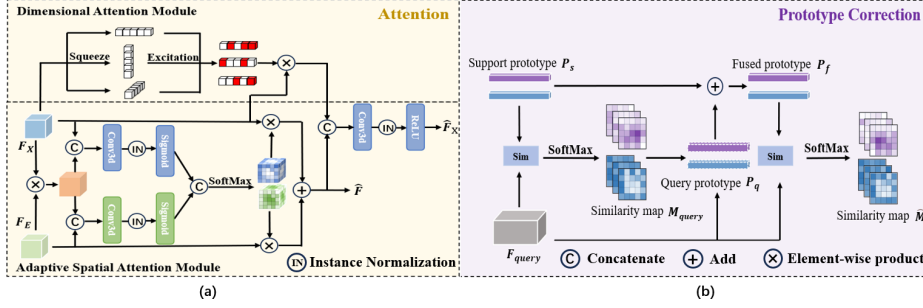
- To our knowledge, this is the first deep learning based framework for the classification of csPCa in multi-modality TRUS videos. More important, the framework generates visual class activation mapping (CAM) images, which may offer valuable guidance for TRUS-guided targeted biopsies.
- To better leverage the multi-modality information, we propose an attention module to optimize B-mode features, and fuse the features of B-mode and SWE.
- We add segmentation task as an auxiliary task to enhance the classification encoder, and employ a prototype correction module to address the issue of limited csPCa segmentation masks.

## 2 Method

The proposed framework is illustrated in Fig. 2. Two 3D ResNet-50 [7] are employed to extract features from B-mode and SWE respectively and perform the classification task. We employ a dimensional attention module to refine the extracted features from B-mode and adopt an adaptive spatial attention module to fuse the features from two modalities (Fig. 3 left). Furthermore, we add a 3D U-Net decoder [4] with skip-connection to perform the segmentation task. The segmentation task serves as an auxiliary task to enhance the encoder. Given the limited availability of csPCa masks, we train the segmentation network in a few-shot paradigm (Fig. 3 right).

### 2.1 Dimensional Attention Module

To enforce the network’s attention towards the csPCa regions, we introduce a dimensional attention module [20], as shown in the left of Fig. 3. It utilizes



**Fig. 3.** Architectures of the attention module and the prototype correction module.

dimension-wise attention to re-weight the features and fuses the re-weighted features afterwards. Specifically,  $F_X \in \mathbb{R}^{H \times W \times T \times C}$  can be viewed as  $H$  feature cubes along the first dimension and same for other dimensions, where  $F_X$  denotes B-mode features,  $H$ ,  $W$ ,  $T$  indicate the dimension sizes, and  $C$  is the channel number. For each feature cube, we first apply average pooling along the three different dimensions then obtain three vectors  $F^H \in \mathbb{R}^H$ ,  $F^W \in \mathbb{R}^W$  and  $F^T \in \mathbb{R}^T$ . Subsequently, squeeze-and-excitation [8] is employed to compute the attention scores:

$$s_D = \sigma(FC(F^D)), D \in \{H, W, T\}, \quad (1)$$

where  $FC$  is fully connected layer and  $\sigma$  is sigmoid operation. Then we re-weight  $F_X$  by the attention scores and fuse them together.

## 2.2 Adaptive Spatial Attention Module

Abnormal hypoechogenicity in B-mode [14] and abnormal stiff regions in SWE [1] can be considered as an indicator of csPCa. Motivated by recent advancements in attention mechanisms for feature aggregation [9, 18], we introduce an adaptive spatial attention module to aggregate features from two modalities in pixel-level.

As shown in Fig. 3 (a), we first compute the element-wise product of the features  $F_X$  (B-mode) and  $F_E$  (SWE). Then the computed features are concatenated with the modality-specific features and passed through the convolutional blocks (Conv3d, instance norm, sigmoid) to provide modality-specific attention weights. These attention weights from two modalities are then normalized by the softmax operation. Subsequently, we multiply the attention weights with the corresponding modality feature maps to generate the fused feature maps  $\hat{F}$ . As depicted in Fig. 2,  $\hat{F}$  are subsequently integrated back into the SWE branches. For the B-mode branches,  $\hat{F}$  are concatenated with the output of the dimensional attention module, and then passed through the convolutional block (Conv3d, instance norm, ReLU) to generate  $\hat{F}_X$  before integration.

### 2.3 Few Shot Segmentation for csPCa

Considering the interplay between the tumor classification and segmentation tasks [3, 22], we add the segmentation task as an auxiliary task to assist the classification network to extract more discriminative features. Due to the limited availability of csPCa masks, we also introduce a prototype correction module to extract representative prototypes of csPCa.

As shown in Fig. 2, we add a 3D U-Net decoder with skip-connection to perform the segmentation task. Specifically, we denote the csPCa set with segmentation masks as support set  $(X_{support}, Y_{support})$  and the csPCa set without masks as query set  $X_{query}$ . For the non-csPCa set, we denote it as  $X_{neg}$ .

For the classification task, the loss function is defined as:

$$\mathcal{L}_{cls} = -Y_{cls} \log(\hat{y}_{cls}) - (1 - Y_{cls}) \log(1 - \hat{y}_{cls}), \quad (2)$$

where  $\hat{y}_{cls}$  is the classification prediction of the network and  $Y_{cls}$  represents the classification label.

For the support set in the segmentation task, we minimize the cross entropy loss:

$$\mathcal{L}_{seg\_support} = -Y_{support} \log(\hat{y}_{seg}) - (1 - Y_{support}) \log(1 - \hat{y}_{seg}), \quad (3)$$

where  $\hat{y}_{seg}$  denotes the predicted probability map for  $X_{support}$ . Since the non-csPCa set does not contain csPCa regions, we employ zero supervision for its segmentation:

$$\mathcal{L}_{seg\_neg} = -\log(1 - \hat{y}_{seg}). \quad (4)$$

For the query set, we adopt the few shot segmentation paradigm [5, 11] to generate pseudo label and use them to supervise the network training. Concretely, we perform mask average pooling (MAP) operation within the csPCa mask  $Y_{support}$  and compute support prototype  $P_s$  from the features of  $X_{support}$ :

$$\begin{aligned} P_s &= \frac{1}{K} \sum_{k=1}^K \text{MAP}(f_\theta(X_{support}^k), Y_{support}^k) \\ &= \frac{1}{K} \sum_{k=1}^K \frac{\sum F_{support}^k \cdot Y_{support}^k}{\sum Y_{support}^k}, \end{aligned} \quad (5)$$

where  $K$  denotes the number of  $X_{support}$ ,  $f_\theta$  denotes the encoder and  $F_{support}$  are the extracted support features. Then we generate the cosine similarity maps between extracted query features  $F_{query}$  and support prototype  $P_s$ :

$$M_{query} = \text{softmax}(\text{sim}(F_{query}, P_s)), \quad (6)$$

where  $\text{sim}(\cdot, \cdot)$  is the cosine similarity function, and  $F_{query} = f_\theta(X_{query})$ .

However, the support prototype  $P_s$  are biased to represent the csPCa class due to the limited number of csPCa masks. We introduce a prototype correction module (PCM) to refine the support prototype without introducing extra

training parameters. As shown in Fig. 3 (b), we generate the query prototype based on the similarity maps  $M_{query}$  and the query features  $F_{query}$ , and then fuse them with the support prototype  $P_s$  to obtain the fused prototype  $P_f$ :

$$P_f = \frac{1}{2}(\text{MAP}(F_{query}, M_{query}) + P_s). \quad (7)$$

Finally, we rank the similarity and select the top 100 points as pseudo label, with half chosen from the foreground similarity map and the other half from the background similarity map. Then we minimize the cross entropy at pixel-level:

$$\mathcal{L}_{seg\_query} = -\frac{1}{|\mathcal{P}|} \sum_{\mathbf{j}_p \in \mathcal{P}} \log(\hat{Y}_{seg}(\mathbf{j}_p)) - \frac{1}{|\mathcal{N}|} \sum_{\mathbf{j}_n \in \mathcal{N}} \log(1 - \hat{Y}_{seg}(\mathbf{j}_n)), \quad (8)$$

where  $\mathcal{P}$  denotes the set of points sampled as foreground,  $\mathcal{N}$  denotes the set of points sampled as background.

In summary, we employ the sum of the classification loss and the segmentation loss to train the network:

$$\mathcal{L} = \mathcal{L}_{cls} + \mathcal{L}_{seg\_support} + \alpha \cdot \mathcal{L}_{seg\_query} + \beta \cdot \mathcal{L}_{seg\_neg}, \quad (9)$$

where  $\alpha$  and  $\beta$  are weighting coefficients.

### 3 Experiments

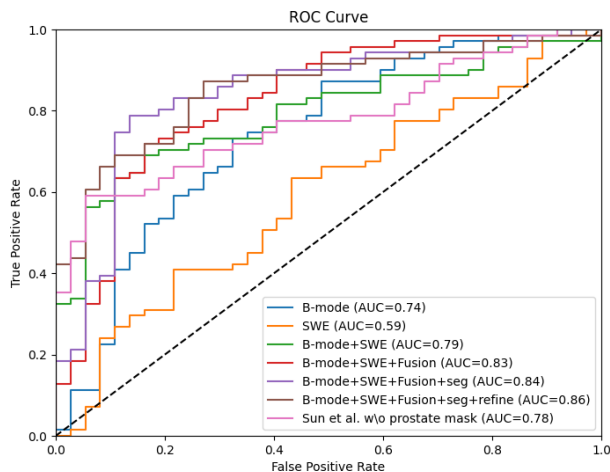
**Dataset.** We performed experiments on an in-house multi-modality TRUS video dataset collected from the Cancer Center of Sun Yat-Sen University. This study included a cohort of 512 patients who underwent B-mode ultrasound, SWE, and prostate biopsy procedures. Among them, 346 patients were diagnosed with csPCa, while 166 presented with non-csPCa (BPH or cisPCa). We randomly employed 404 scans (275 with csPCa) for training, and 108 scans (71 with csPCa) for testing. The TRUS videos were resized to  $200 \times 144 \times 144$  for reducing computational cost. The intensities of B-mode within each video were normalized to  $[0, 1]$ . The SWE images were underwent grayscale reconstruction according to [21].

The segmentation annotation of csPCa is very difficult to obtain. Firstly, pathologists examined specimens under a microscope and identified the spatial location of the csPCa on TRUS. Subsequently, ultrasound radiologists used it as a reference to annotate the locations of cancerous lesions. Segmentation masks of csPCa in 4 scans were manually annotated by ultrasound radiologists using ITK-SNAP. These 4 labeled samples in training set were used as support set  $(X_{support}, Y_{support})$ , and 271 unlabeled positive samples were query set  $X_{query}$ .

**Implementation Details.** The method was implemented on PyTorch, using an NVIDIA RTX8000 GPU with 48G memory. The network was optimized by a stochastic gradient descent optimizer for 200 epochs, with an initial learning

**Table 1.** Comparison of different methods (best results are highlighted in bold).

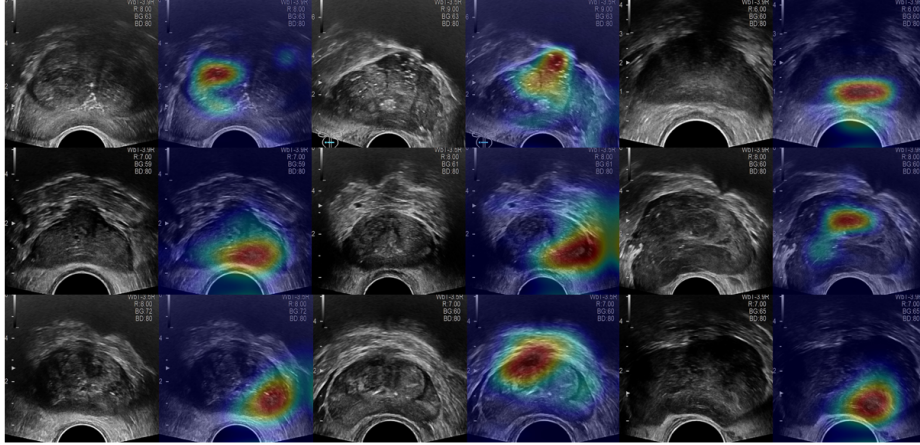
| B-mode                                   | SWE | Attention | Multi-task | PCM | AUC         | F1          | Acc         | Sen         | Spe         |
|------------------------------------------|-----|-----------|------------|-----|-------------|-------------|-------------|-------------|-------------|
| ✓                                        |     |           |            |     | 0.74        | 0.81        | 0.68        | <b>0.99</b> | 0.08        |
|                                          | ✓   |           |            |     | 0.59        | 0.80        | 0.68        | 0.97        | 0.11        |
| ✓                                        | ✓   |           |            |     | 0.79        | 0.81        | 0.71        | 0.87        | 0.41        |
| ✓                                        | ✓   | ✓         |            |     | 0.83        | 0.86        | 0.79        | 0.93        | 0.51        |
| ✓                                        | ✓   | ✓         | ✓          |     | 0.84        | 0.86        | 0.81        | 0.87        | 0.68        |
| ✓                                        | ✓   | ✓         | ✓          | ✓   | <b>0.86</b> | <b>0.87</b> | <b>0.81</b> | 0.86        | <b>0.73</b> |
| Sun <i>et al.</i> [17] w/o prostate mask |     |           |            |     | 0.78        | 0.80        | 0.69        | 0.55        | 0.95        |

**Fig. 4.** Comparison of ROC curves for different methods on the testing set.

rate of 0.0001. The ploy learning policy was used,  $(1 - \text{epoch}/200)^{0.9}$ . To address the class imbalance issue, the batch size was set to 2, with each batch consisting of a csPCa and a non-csPCa. For the loss function,  $\alpha$  and  $\beta$  were set to 0.001 and 0.1, respectively.

**Quantitative and Qualitative Results.** To evaluate the classification performance of our framework, we employed five evaluation metrics: area under the ROC curve (AUC), F1-score (F1), accuracy (Acc), sensitivity (Sen), and specificity (Spe). Higher scores of these metrics show better performance.

To evaluate the impact of each component in our method, we conducted ablation analyses on single modality, where we used only B-mode or SWE information. Additionally, we performed ablation experiments to assess the influence of the attention module, auxiliary task, and prototype correction module. These ablation studies allowed us to determine the contribution of each component in improving the classification outcomes. Quantitative results are listed in Table 1 and the ROC curves are depicted in Fig. 4. Our method achieved an AUC



**Fig. 5.** Nine examples illustrating TRUS frames and their corresponding CAM generated by our network. The ultrasound radiologists verified that the model’s predictions of suspicious tumor regions were in agreement with the spatial locations provided by the pathologists.

of 0.86, F1-score of 0.87, accuracy of 0.81, sensitivity of 0.86 and specificity of 0.73, demonstrating its strong performance in csPCa classification. It can be observed that concatenating the two modalities (B-mode and SWE) resulted in a notable improvement in AUC compared to using either modality individually. This proves the importance of leveraging the complementary information provided by multiple modalities to improve the classification. Moreover, the addition of the fusion module improved the accuracy of the model, and the addition of the segmentation task and the PCM has largely improved the specificity of the model. We also compared our method with the most relevant work by [17]. Our method outperformed [17]’s AUC by 0.08 when its prostate segmentation module was excluded. Even without adding the csPCa segmentation task, our method outperformed [17] by 0.05 in terms of AUC.

To identify the frames and specific locations within TRUS videos that played a significant role in network’s prediction of csPCa, we utilized gradient-weighted class activation mapping [15]. This approach allowed us to generate heat maps, visualizing the regions of interest and their contribution to the prediction, as shown in Fig. 5. Ultrasound radiologists confirmed that the suspicious tumor regions predicted by the model were consistent with the spatial location offered by pathologists. This finding suggests the potential feasibility of TRUS-guided targeted biopsy, by leveraging the CAM images generated using our method.

## 4 Conclusion

We introduce a multi-task learning framework for the recognition of csPCa in multi-modality TRUS. The primary attribute is to fully exploit B-Mode and

SWE image information through the attention module and use few shot segmentation to help the encoder learn more representative features. Experimental results demonstrate our proposed framework is effective in classifying and positioning csPCa. This may provide useful information to assist doctors conducting TRUS-guided targeted biopsy. Future work is to validate our proposed method on a large external dataset to evaluate its accuracy and generalization performance.

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**Disclosure of Interests.** The authors have no competing interests to declare that are relevant to the content of this article.

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