BREAST ULTRASOUND COMPUTER-AIDED DIAGNOSIS USING STRUCTURE-AWARE TRIPLET PATH NETWORKS

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ABSTRACT

Breast ultrasound (BUS) is an effective imaging modality for breast cancer diagnosis. The structural characteristics of breast lesions play an important role in computer-aided diagnostic methods for breast cancer due to its non-invasiveness, safety, and affordability [1]. Extensive research has been conducted on computer-aided diagnosis (CAD) for breast ultrasound in order to assist radiologists and improve diagnostic accuracy [2]. Deep learning has gained wide application in CAD [3]. It has the ability to automatically learn discriminative features from raw data [4]. However, training deep networks from scratch for breast cancer ultrasound CAD is challenging due to the requirement for a large amount of labeled training data. There are popular approaches based on the unsupervised feature learning, which leverages unsupervised learning tasks like image reconstruction to extract high-level features. Cheng et al.[5] employed an unsupervised autoencoder method to extract high-level features for image reconstruction, followed by supervised fine-tuning of the classifier using labeled training samples for classification. However, existing unsupervised learning methods have limitations: (1) Unsupervised autoencoders may not generate suitable features for classification tasks as they capture features based on data characteristics without considering labels, making classification challenging. (2) Differentiating benign and malignant lesions using a single autoencoder structure for image reconstruction is difficult due to small structural differences, necessitating separate systems for each. (3) The image intensity-based $\ell_2$-norm cost function is ineffective in capturing lesion structure attributes. The $\ell_2$-norm has poor correlation with image quality as perceived by human observers[6] since it fails to consider the shape or contour attributes of breast lesions, which play crucial roles in breast diagnosis.

To address the challenges of limited training datasets and enhance the utilization of prior domain knowledge, this study proposes a novel approach called Structure-Aware Triplet Path Networks (SATPN) (as depicted in Fig. 1). The network combines clinical knowledge of lesion features (BI-RADS features[7]) with the triplet path network and the Structural Similarity Index Measure (SSIM) for accurate lesion classification in breast ultrasound images. In this approach, breast images are transformed into BI-RADS-oriented feature maps (BFMs) using the distance-transformation coupled Gaussian filter. BFMs not only preserve the original information of breast cancer ultrasound images but also enhance the structural features of lesions, including shape, lesion boundary, undulation, and angle features. Subsequently, the

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Index Terms— Breast cancer, ultrasound, computer-aided diagnosis, deep learning, semi-supervised learning

1. INTRODUCTION

Breast ultrasound (BUS) is a widely used early imaging diagnostic method for breast cancer due to its non-invasiveness, safety, and affordability [1]. Existing research has been conducted on computer-aided diagnosis (CAD) for breast ultrasound in order to assist radiologists and improve diagnostic
BFMs serve as inputs to SATPN, which performs multi-task learning by integrating two unsupervised image feature extraction pipelines based on Stacked Convolutional Autoencoders (SCAE) and a supervised lesion classification pipeline tailored for diagnosis. This integrated multi-path network allows SCAE (using SSIM as a cost function) to independently extract image features for benign and malignant lesions while being constrained by lesion classification, achieved by leveraging SCAE encoder features and convolutional networks. In other words, SATPN learns lower-level features through unsupervised reconstruction networks and utilizes supervised classification to guide the learning of lower-level features, which is advantageous for the classification task. Finally, lesions are classified through weighted voting using reconstruction errors and label prediction errors.

2. METHODS

In a previous paper [8], BFMs were proposed to explicitly use orientation, echo patterns, and a posteriori features in a deep learning approach. The original breast images were converted to BFMs in the following manner:

\[
BFMs = I \cdot e^{-\frac{D_{B}(x)^{2}}{\sigma^{2}}} \tag{1}
\]

The SCAE follows the unsupervised encoder-decoder paradigm [9]. Standard SCAE is trained to learn representative features for image reconstruction. In the final stage, parameters are fine-tuned using supervised learning, which may have limited impact on the classification task. More importantly, it does not consider the structural properties of breast lesions that play a crucial role in breast diagnosis.

The image reconstruction pipeline is similar to the standard SCAE structure, consisting of an encoder and a decoder, as shown in Fig. 1. The encoder maps the input \( x \) to a hidden feature representation \( h \). Then, the decoder maps the hidden \( h \) to the output \( \hat{x} \). \( \hat{x} \) is the expected approximate reconstruction of the input \( x \). SCAE model is trained to minimize the reconstruction error as much as possible.

In this paper, two image reconstruction pipelines are established, one for benign lesion images and the other for malignant lesion images. The design of the benign pipeline aims to reconstruct benign images well but struggles to reconstruct malignant images. Therefore, the objective function for the benign pipeline is as follows:

\[
\min_{\theta_{B}} J_{B} = \frac{1}{N_{B}} \sum_{i=1}^{N_{B}} \text{loss}_{r}(x_{B}^{(i)}, \hat{x}_{B}^{(i)}) - \frac{\alpha}{N_{j}} \sum_{j=1}^{N_{j}} \text{loss}_{r}(x_{M}^{(j)}, \hat{x}_{M}^{(j)}) + \gamma \cdot R(\theta_{B}) \tag{2}
\]

The malignant pipeline, on the contrary, has the opposite effect: it can reconstruct malignant images well but struggles to reconstruct benign images. Therefore, the objective function for the malignant pipeline is as follows:

\[
\min_{\theta_{M}} J_{M} = \frac{1}{N_{M}} \sum_{j=1}^{N_{M}} \text{loss}_{r}(x_{M}^{(j)}, \hat{x}_{M}^{(j)}) - \frac{\alpha}{N_{i}} \sum_{i=1}^{N_{i}} \text{loss}_{r}(x_{B}^{(i)}, \hat{x}_{B}^{(i)}) + \gamma \cdot R(\theta_{M}) \tag{3}
\]

Where \( x_{B}^{(i)} \) and \( x_{M}^{(j)} \) represent benign and malignant samples, respectively. \( \hat{x}_{B}^{(i)} \) and \( \hat{x}_{M}^{(j)} \) represent the reconstructions of \( x_{B}^{(i)} \) and \( x_{M}^{(j)} \) in the benign pipeline, while \( \hat{x}_{M}^{(j)} \) and \( \hat{x}_{BM}^{(i)} \) represent the reconstructions of \( x_{M}^{(j)} \) and \( x_{B}^{(i)} \) in the malignant pipeline. Additionally, \( \theta_{B} = [W_{en}, b_{en}; W_{Bde}, b_{Bde}] \) and \( \theta_{M} = [W_{en}, b_{en}; W_{Mde}, b_{Mde}] \) are the weights used in the loss function for regularization purposes. The reconstruction loss function utilizes the SSIM [10]:

\[
\text{loss}_{r}(x, \hat{x}) = 1 - \text{SSIM}(x, \hat{x})
\]

The loss function is regularized by \( R(\theta_{B}) = \|W_{en}\|_{F}^{2} + \|W_{Bde}\|_{F}^{2} \) and \( R(\theta_{M}) = \|W_{en}\|_{F}^{2} + \|W_{Mde}\|_{F}^{2} \).

The parameters \( \{\alpha, \gamma\} \in [0, 1] \) balance the term each.

The lesion classification task is implemented by the encoder network and the softmax classifier, as shown in Fig. 1. \( \hat{y} \in \mathbb{R}^{K} \) represents the output of the classifier, ranging from 0 to 1. The objective function for classification is given by:

\[
\min_{\theta_{c}} J(\theta_{c}) = \frac{1}{N} \sum_{n=1}^{N} \text{loss}_{c}(\hat{y}^{(n)}, \hat{y}^{(n)}) + \gamma \cdot R(\theta_{c}) \tag{4}
\]

The variable \( \theta_{c} = [W_{cn}, b_{cn}; \beta] \) is learned or adjusted through the training dataset. Typically, the network uses cross-entropy as the loss function during training. However, to incorporate clustering characteristics into the training results, a clustering penalty term needs to be added to the loss function. Therefore, the loss function \( \text{loss}_{c}(\cdot) \) is given by:

\[
\text{loss}_{c}(y, \hat{y}) = -\sum_{k=1}^{K} \delta(y(k) = 1) \cdot \log(\hat{y}(k)) + \mu \|x - c_{y}\|^{2} \tag{5}
\]

In the given formulation, \( \delta(\cdot) \) is the indicator function, and \( c_{y} \) represents the training samples and centers (i.e., mean values) for each category. If the value is 1 if \( y(k) = 1 \) and \( K \)}
is the number of classes. The loss function consists of two terms: the first term is the standard softmax cross-entropy loss, which helps to separate samples belonging to different classes by maximizing the distances between class representations. The second term is the clustering penalty term, which encourages the feature representations of training samples to be as close as possible to the centers of their respective classes ($c_i$). This term helps to minimize the distances between samples within the same class. In this case, since there are two classes, $K = 2$. Therefore, the loss function aims to both increase the separation between different classes and decrease the distance within the same class.

The objective function of SATPN, combining both image reconstruction pipelines and the classification pipeline, can be represented as follows:

$$\min_{\theta} \lambda \cdot (J_B + J_M) + (1 - \lambda) \cdot J_C$$

(6)

The balancing of classification and reconstruction tasks is achieved using $\theta = [\theta_B, \theta_M, \theta_C]$ and $\lambda \in [0, 1]$ in the feature learning process. The encoding parameters, denoted as $W_{en}$, are shared among the three tasks, while the decoding parameters are only involved in the reconstruction task. The objective function can be realized through alternating learning [11].

In testing phase, $x$ is classified by combining the reconstruction error and the label prediction error:

$$\hat{y} = \min_{0,1} \left\{ -\ln (P_{CB} \cdot P_{rB}), -\ln (P_{CM} \cdot P_{rM}) \right\}$$

(7)

Where $P_{CB}$ and $P_{CM}$ are the category probability estimates from the classification pipeline, $\hat{x}_B$ and $\hat{x}_M$ are the outputs of the two reconstruction pipelines, $P_{rB} = \text{SSIM}(x, \hat{x}_B) / (\text{SSIM}(x, \hat{x}_B) + \text{SSIM}(x, \hat{x}_M))$ and $P_{rM} = \text{SSIM}(x, \hat{x}_M) / (\text{SSIM}(x, \hat{x}_B) + \text{SSIM}(x, \hat{x}_M))$.

In this paper, the classification pipeline consists of four convolutional layers: 8 (Conv1), 16 (Conv2), 32 (Conv3), and 64 (Conv4). Each Conv layer has a filter size of $3 \times 3$, followed by a max pooling layer of size $2 \times 2$. There are also three fully connected layers as shown in Fig. 1. The output layer has two neurons with a softmax function. ReLU activation is used in all hidden layers. The two reconstruction pipelines each have an encoder and a decoder. The encoder is shared with the classification pipeline and consists of four convolutional layers (Conv1, Conv2, Conv3, and Conv4) and two fully connected layers. The decoder has the opposite configuration of the encoder, including two fully connected layers, four pairs of convolution and upsampling layers, and a convolutional output layer with a linear activation function.

3. EXPERIMENTS AND RESULTS

3.1. Experimental Setups

UDIAT dataset: The publicly available dataset used in this study is a B-mode US image dataset of breast cancer [12]. For this research, 128 images were selected and cropped to 512×512 pixels with the lesion at the center. Among these images, there are 45 malignant lesions and 83 benign lesions.

UTSW dataset: The in-house clinical dataset is a B-mode US breast image dataset [8]. In this study, we selected 258 images, including 178 benign lesions and 80 malignant lesions. The images were resampled to a resolution same as UDIAT dataset. We used a marker-controlled watershed segmentation [13] to create the tumor boundary.

To evaluate the performance and generalization ability of the SATPN, three schemes were designed to assess the SATPN within and across two datasets: (1) Classification on the single dataset: for each dataset, 80% of randomly selected samples from both benign and malignant lesions were used as the training set, while the remaining 20% were used as the test set. (2) Classification across two Datasets: The combined training set consisted of 80% of samples from UDIAT and 80% of samples from the UTSW dataset, while the remaining samples from each dataset were used as two separate test sets. The training data was randomly divided into 90% for training and 10% for validation by random assignment. In the experiments, the pixel grayscale values were normalized to the range of [0, 1]. In this paper, ACC, AUC, SEN, SPE, PPV, NPV, and MCC represent seven performance metrics [14].

3.2. Classification Results on Single Dataset

Table 1 present the classification results of the six methods on the UDIAT and UTSW datasets, respectively. Firstly, the paper compares the methods using different inputs (SCAE and BFM-SCAE, SSDL and BFM-SSDL, TPN and SATPN). It is found that the BFM-based methods outperform the methods based on the original images in terms of the seven performance metrics. This indicates that the BFM-based methods utilize the structural information in the BI-RADS-oriented feature maps to enhance the diagnostic accuracy. With the guidance of BMFs, the DL-based methods can focus on the breast lesion features specified by clinical requirements. Next, the paper compares different networks with the same input. The proposed TPN and SATPN outperform SCAE and SSDL, suggesting that they learn more effective features for lesion classification. SATPN utilizes BI-RADS-oriented feature maps that contain structural information. Additionally, SATPN integrates a multi-pathway semi-supervised network that independently extracts image features for benign and malignant lesions, thereby improving classification accuracy. By incorporating these design elements, SATPN achieves superior performance compared to other methods in the study.

3.3. Model Validation across Dataset

Table 2 and Table 3 summarize the classification results across datasets. Despite the different characteristics of the two datasets collected from different manufacturers’ devices, the results obtained by all methods are similar to those shown
Table 1. Classification results (mean ± std %) for different methods when training and testing on UDIAT and UTSW dataset, respectively.

| Ref. | Dataset (benign / malignant) | Availability | Features / Classifier | Performance (%) |
|------|-----------------------------|--------------|-----------------------|-----------------|
| Single et al. | 86 / 90 | Private | Manual feature / BPNN | 95.96 / 93.14 / 95.98 |
| Han et al. | 42/43/101 | Private | GoogleNet | 91.25 / 86.03 / 86.15 |
| Zampi et al. | 125 / 37 | Private | Boltzmann machine | 95.40 / 86.80 / 87.10 |
| Zampi et al. | 187 / 25 | Private | SDAE | 92.40 / 86.90 / 87.10 |
| Zhang et al. | 104 / 100 | Private | CNN | 92.60 / 86.70 / 87.90 |
| Antunes et al. | 1975 / 415 | Public | Manual feature / VGG | 90.00 / 90.10 / 90.20 |
| Prasad et al. | 71 / 50 | Private (GraVIE) | Manual feature / SVM | 95.83 / 96.00 / 97.10 |
| Byra et al. | 86 / 51 | Public (DIABUD) | VGG19 / FLDA | 84.00 / 85.31 / 85.40 |
| Zhang et al. | 178 / 10 | Private | BFM / SSDL | 94.23 / 82.92 / 88.61 |
| Ours | 83 / 45 | Public (UDIAT) | SATPN | 96.71 / 91.88 / 98.96 |
| Ours | 178 / 10 | Private | SATPN | 91.03 / 67.22 / 99.87 |

Table 2. Classification results (mean ± std %) for different methods when training on a combined UDIAT and UTSW dataset and testing on UDIAT dataset.

| Ref. | Dataset (benign / malignant) | Availability | Features / Classifier | Performance (%) |
|------|-----------------------------|--------------|-----------------------|-----------------|
| Single et al. | 86 / 90 | Private | Manual feature / BPNN | 95.96 / 93.14 / 95.98 |
| Han et al. | 42/43/101 | Private | GoogleNet | 91.25 / 86.03 / 86.15 |
| Zampi et al. | 125 / 37 | Private | Boltzmann machine | 95.40 / 86.80 / 87.10 |
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| Byra et al. | 86 / 51 | Public (DIABUD) | VGG19 / FLDA | 84.00 / 85.31 / 85.40 |
| Zhang et al. | 178 / 10 | Private | BFM / SSDL | 94.23 / 82.92 / 88.61 |
| Ours | 83 / 45 | Public (UDIAT) | SATPN | 96.71 / 91.88 / 98.96 |
| Ours | 178 / 10 | Private | SATPN | 91.03 / 67.22 / 99.87 |

Table 3. Classification results (mean ± std %) for different methods when training on a combined UDIAT and UTSW dataset and testing on UTSW dataset.

| Ref. | Dataset (benign / malignant) | Availability | Features / Classifier | Performance (%) |
|------|-----------------------------|--------------|-----------------------|-----------------|
| Single et al. | 86 / 90 | Private | Manual feature / BPNN | 95.96 / 93.14 / 95.98 |
| Han et al. | 42/43/101 | Private | GoogleNet | 91.25 / 86.03 / 86.15 |
| Zampi et al. | 125 / 37 | Private | Boltzmann machine | 95.40 / 86.80 / 87.10 |
| Zampi et al. | 187 / 25 | Private | SDAE | 92.40 / 86.90 / 87.10 |
| Zhang et al. | 104 / 100 | Private | CNN | 92.60 / 86.70 / 87.90 |
| Antunes et al. | 1975 / 415 | Public | Manual feature / VGG | 90.00 / 90.10 / 90.20 |
| Prasad et al. | 71 / 50 | Private (GraVIE) | Manual feature / SVM | 95.83 / 96.00 / 97.10 |
| Byra et al. | 86 / 51 | Public (DIABUD) | VGG19 / FLDA | 84.00 / 85.31 / 85.40 |
| Zhang et al. | 178 / 10 | Private | BFM / SSDL | 94.23 / 82.92 / 88.61 |
| Ours | 83 / 45 | Public (UDIAT) | SATPN | 96.71 / 91.88 / 98.96 |
| Ours | 178 / 10 | Private | SATPN | 91.03 / 67.22 / 99.87 |

3.4. Effect of the Number of Training Samples

As shown in Fig. 2, this paper investigates the impact of different numbers of training samples on the proposed method (SATPN) on two datasets. BFM-SACB and BFM-SDSL are used as baseline methods. The training sample sets are composed of randomly selected samples at different percentages (ranging from 50% to 90%) per class, while the remaining samples form the test set. As shown in Fig. 2, the performance of all test classifiers generally improves with an increase in the number of training samples. For both datasets, SATPN achieves satisfactory results when trained with 80% of the samples. Overall, the proposed SATPN outperforms other methods in each case of different training sample sizes and provides state-of-the-art results with limited training sample sizes, further confirming the feasibility of integrating structural information into breast cancer ultrasound CAD.

4. DISCUSSION AND CONCLUSIONS

This paper proposes a novel SATPN method that leverages structural information for accurate lesion classification in breast ultrasound images. SATPN integrates clinical knowledge of lesion features and a triple-pathway network that independently extracts image features of benign and malignant lesions under the constraint of lesion classification task. The effectiveness of SATPN is validated on two breast ultrasound image datasets, demonstrating high diagnostic accuracy.

Table 4. The performance summary of breast ultrasound CAD system.

| Ref. | Dataset (benign / malignant) | Availability | Features / Classifier | Performance (%) |
|------|-----------------------------|--------------|-----------------------|-----------------|
| Single et al. | 86 / 90 | Private | Manual feature / BPNN | 95.96 / 93.14 / 95.98 |
| Han et al. | 42/43/101 | Private | GoogleNet | 91.25 / 86.03 / 86.15 |
| Zampi et al. | 125 / 37 | Private | Boltzmann machine | 95.40 / 86.80 / 87.10 |
| Zampi et al. | 187 / 25 | Private | SDAE | 92.40 / 86.90 / 87.10 |
| Zhang et al. | 104 / 100 | Private | CNN | 92.60 / 86.70 / 87.90 |
| Antunes et al. | 1975 / 415 | Public | Manual feature / VGG | 90.00 / 90.10 / 90.20 |
| Prasad et al. | 71 / 50 | Private (GraVIE) | Manual feature / SVM | 95.83 / 96.00 / 97.10 |
| Byra et al. | 86 / 51 | Public (DIABUD) | VGG19 / FLDA | 84.00 / 85.31 / 85.40 |
| Zhang et al. | 178 / 10 | Private | BFM / SSDL | 94.23 / 82.92 / 88.61 |
| Ours | 83 / 45 | Public (UDIAT) | SATPN | 96.71 / 91.88 / 98.96 |
| Ours | 178 / 10 | Private | SATPN | 91.03 / 67.22 / 99.87 |
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