Self-supervised learning of mammograms with pathology aware

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Abstract

Screening mammography is recognized as an effective method to diagnose breast cancer (BC). However, for extremely dense breasts, there is a higher chance to induce misdiagnosing. To suppress misdiagnosis from radiologists in mammography reading, computer-aided diagnosis (CAD) based on imaging has been widely researched and applied. These CAD tools increasingly have deeper layers design aiming for better performance, but this may decrease robustness particularly in dense breast. Therefore, to benefit BC identification in the context of supervision from rare annotated datasets, we propose a self-supervised learning framework to normalize mammograms into pathology aware (PA) style, which is in line with the pathological local enhancement characteristic, and prove the value of PA mammogram for the downstream tasks. Experimental results on INBreast and CBIS-DDSM datasets suggest that our method can achieve better performance in both normal and dense breasts for classification and segmentation tasks.

Keywords: self-supervised learning, dense breast, pathology aware, CAD

1. Introduction

Screening mammography for dense breasts often suffers from detecting BC compared to exams of non-dense breasts. This is due to the poor visibility of tumors as they are embedded in dense tissues. Although previous traditional image enhancement methods achieved tumor enhancement and demonstrated better results on downstream tasks (like contrast limited adaptive histogram equalization (CLAHE))(Shivhare and Saxena, 2021), however, they do not fully show their potentials on the dense breast. Specifically, these methods usually enhanced image contrast globally, leading to no intensity difference between abnormal and normal tissue in mammograms. To alleviate such issues, we propose an end-to-end scheme to generate one mammogram with improving contrast of potential regions of interest (ROI) for cancers to their surroundings. Meanwhile, not only do we achieve a mammogram enhancement as PA, but also facilitate the downstream tasks including BC classification and segmentation tasks for both normal and dense breast.

2. Materials and Method

The proposed method in this work is validated on two public datasets: INbreast(Moreira et al., 2012) and CBIS-DDSM(Lee et al., 2017). The INbreast dataset is divided into 80% and 20% for training and test respectively. The CBIS-DDSM dataset is divided as its original database (85% for training and 15% for testing). We resized the mammograms to a standard size of 1024×512 fed into a UNet-like model in Figure 1A.



Figure 1: (A) Overview of the proposed Pathology Aware method. (B) Illustration of our PA model's outputs.

As Figure 1A shows, the goal of our method is to recover from a standard mammogram I to a high-contrast mammogram Y, which high-lighting the present abnormalities (thus constructing the PA mammogram). The difficulty lies in enlarging the intensity gap between abnormality and normality tissue in the context of non-annotated images. We are inspired by image dehazing(Chen et al., 2021), whose goal is to recover haze-free image from the low-contrast outdoor scenes. With the similar prior in mammograms (the intensity of abnormality tissue is generally with low-contrast), we decompose the stand mammogram as the following formula with defined pixel x:

$$I(x) = m(x)Y(x) + (1 - m(x)).$$
(1)

where I and Y are normalized to [0, 1], and m is a learning transmission map generated by one of the decoders in our model, which decays from the depth of intensity of input. By calculating Eq. 1, we can define the difference between I(x) and Y(x) as follows,

$$Sub(x) = I(x) - Y(x) = (m(x) - 1)(I(x) - 1)/m(x).$$
(2)

The brighter intensity in I(x), usually corresponding to abnormalities, the lower Sub(x) it achieves due to the term of I(x)-1. On the other hand, pixels in the normality region have lower intensity in I(x), which can achieve a higher value in Sub(x), resulting in enlarging the difference between the normality and the abnormality region. After generating m(x) and Y(x) by two decoders, the model can reconstruct image I'(x) based on Eq. 1. Meanwhile, we employ the L1 loss for constraining I'(x) with the input I(x).

3. Results

We compare the standard (baseline) and enhanced (CLAHE and proposed PA) mammograms in two downstream tasks: non-malignant(normal and benign) versus malignant classification based on ResNet-50 and tumor segmentation based on U-Net. Experimental results show that PA outperforms others, both in normal and dense breast. In specific, the AUC and Dice score by PA achieves 0.93 and 0.65 respectively from Table 1. Particularly, we also present the result on dense mammograms divided from the test set according to density ≥ 3 , which shows in the brackets of Table 1. This result demonstrates that the score of PA is still the best and not much different from the whole test set. These results suggest that models' robustness are enhanced by PA with promising potential. In addition, through the model's output visualization by Figure 1B, we can see the intensity changes before and after mammograms enhancement method. Subtraction can be seen more intuitively. For PA method, the intensity enhanced discriminatively between abnormal region and it's surroundings. Compared with CLAHE method, there is a consistent enhancement to global mammograms.

Table 1: Quantity results on INBreast(D1) and CBIS-DDSM(D2)

Method	AUC@D1	Dice@D1	AUC@D2	Dice@D2
Baseline	0.77(0.47)	0.54(0.31)	0.70(0.48)	0.58(0.40)
CLAHE	0.83(0.74)	0.63(0.60)	0.75(0.62)	0.73(0.69)
Proposed	0.93(0.86)	0.65(0.62)	0.78(0.67)	0.75(0.70)

4. Conclusion

In this study, we developed a self-supervised learning framework to generate PA style mammograms and evaluated the effect of our method on downstream tasks on two independent public breast datasets. The result proves PA method significantly improved the model's robustness especially in dense breast.

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