Can We Predict Histological Images Using Mammograms?

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Abstract

Along with the improvement in medical image analysis, exploring deep learning based approaches in the context of mammography and histology image processing has also become more realistic. We propose a computer based breast cancer modelling approach: “the Mammography–Histology–Linking–Model”, which develops a mapping of features between mammographic abnormalities and their histopathological representation. Potential clinical contribution of this model is that it avoids the needs for further biopsy if the abnormality is deemed benign by estimating and generating histological images.

Keywords: Mammography, Generative Adversarial Network, DenseNet, Detection, Segmentation, Classification

1. Introduction

Breast cancer has a high incidence among women worldwide. The assessment process for breast screening follows a triple assessment model: appropriate imaging (i.e. mammography as a primary imaging modality for finding early changes in breast tissue) plus clinical assessment and, where appropriate, needle biopsy (i.e. H&E 2 stained histology). Mammography and H&E histological images of breast tissue are the two commonly used imaging modalities. Among women who undergo mammographic screening, about 10% are recalled for additional evaluation. Among these, 8 to 10% will have suspicious abnormal findings, which warrant undergoing breast biopsy. However, the impact of unnecessary biopsy and the downstream diagnostic burden includes increased anxiety, morbidity and stress for the women concerned and increased health care costs. The development of a specific discrimination model that could indicate benign abnormalities would reduce this burden. Recent development in biomedical image analysis using deep learning based neural networks have motivated research to enhance the performance of Computer Aided Diagnosis (CAD) systems (Hamidinekoo et al., 2018a). We propose a computer based breast cancer modelling approach: “the Mammography–Histology–Linking–Model”, which develops a mapping of features between mammographic abnormalities and their histopathological representation.

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2. Proposed Methodology

2.1. Dataset

Three multi-centred, publicly available mammographic databases were used to build the mammographic CAD model. These datasets included: (1) the wide-ranging annotated Breast Cancer Digital Repository (BCDR) (Lopez et al., 2012), which contained digitised film (F03) and full field digital mammographic images (D01) from women in northern Portugal; (2) a sub-set of the Digital Database for Screening Mammography (DDSM) (Heath et al., 2001), that was provided by the University of South Florida and contained mammographic images with mass abnormalities; (3) the Inbreast (Moreira et al., 2012) repository, acquired in Portugal, which provided full field digital mammographic images. A combination of these data repositories was referred to as “Set-1”. Set-1 was used to train a mammographic CAD model to classify mass lesions in mammographic images as benign or malignant.

From histological point of view, the Bio-imaging’15 dataset (Araújo et al., 2017) was selected, which contained breast histology images from four classes: normal, benign, in situ carcinoma and invasive carcinoma. This dataset was composed of high-resolution digitised H&E stained images from the Bioimaging 2015 breast histology classification challenge. The labels (4 classes) were provided by two pathologists. A subset of this dataset (referred to as “Set-2”) along with Set-1, were utilised to train the M-H-GAN model (shown in Figure 1) in order to generate artificially histology samples.

After building the Mammography–Histology–Linking–Model, the model performance was evaluated using an unseen test dataset collected between 2016-17, from the Norfolk and Norwich University Hospital, UK. This dataset consisted of full field digital mammograms accompanied with the respective histology whole slide images and the meta-data. It also included detailed explanation of an expert radiologist and a histopathologist for the collected dataset (referred to as “Set-3”).

2.2. Model Architecture

To develop this model, from a mammographic point of view, a supervised deep convolutional neural network was trained. Based on a comparative study (Hamidinekoo et al., 2018b), among the well-known deep convolutional neural networks, DenseNet (Huang et al., 2017) was found as an appropriate model for mass classification due to its key characteristic to bypass signals from preceding layers to subsequent layers. For this model, DenseNet’s growth rate was set to 4 to construct an architecture with 4 dense-blocks and 3 transition layers. In this model (referred to as CADi), the final Softmax classifier made a binary decision based on the created features. The final deep abstracts were extracted and introduced as deep features in a vectorised manner to the subsequent M-H-GAN model (see Figure 1). The objective of training for the CADi was to minimise the difference error between the network prediction and the expected output (benign (0) vs. malignant (1)). During training this network, transfer learning with the ImageNet dataset was conducted, whilst the network was fine-tuned using Set-1.

In order to translate each deeply extracted feature from the CADi to a histological representation, we used a specifically designed Generative Adversarial Network (M-H-GAN),
inspired by (Goodfellow et al., 2014; Isola et al., 2017). The M-H-GAN model was fed with the deeply extracted feature from the CADi. Applying a specific condition on the input images, a conditional generative model was trained to generate histology samples. In the architecture of the proposed model, a fully convolutional based structure and a convolutional PatchGAN classifier were used as the generator and the discriminator, respectively. The generator was trained to generate histology images from deep abstracts representing mammographic mass lesions. The generated images were expected to be similar to the histology images of the real observed images from the Set-2 histology samples. Figure 1 shows the model schematically, which was used during the training phase. The developed Mammography–Histology–Linking–Model, which was built on publicly available datasets, was applied to Set-3 (unseen testing samples). Figure 1 shows the final model, to which test samples were fed.
References


