Detecting Thoracic Diseases via Representation Learning with Adaptive Sampling[☆]

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Abstract

The recently released chest X-ray dataset, ChestX-ray14, has attracted more and more attention on automatic detection of thoracic diseases. In this work, we use deep learning techniques to develop a multi-class classifier. Given a chest X-ray image as input, the classifier outputs a vector of probability values, of which each component corresponds to the probability of having one specific thoracic disease. The merit of our proposed solution is based on several major observations of the ChestX-ray14 data. First, the diversity in ChestX-ray14 is much smaller than that in other natural image datasets such as ImageNet due to very similar global outlines of chest X-ray images. Second, ChestX-ray14 is much more imbalanced than the datasets considered in most existing studies. The size of the largest class is 87.57 times larger than that of the smallest class. Third, from the application perspective, the task is not really cost-sensitive to misclassifications, thus it is difficult to manually fix weights for different misclassifications. To deal with these difficulties, we propose an adaptive sampling method that monitors the performance of the model during training and automatically increase the weight of relatively poorly performed classes. Extensive experiments demonstrate that our proposed method outperforms the state-of-the-art algorithms.

Keywords: Thoracic disease detection, Deep learning, Imbalanced learning, Adaptive sampling

1. Introduction

Thoracic diseases refer to a large collection of diseases located in the thoracic cavity. Despite of various rare cases, certain thoracic diseases, such as pneumonia, pneumothorax, edema, etc., are very common in clinical practice. For example, it has been reported that pneumonia is the single largest cause of death in children worldwide, accounting for approximately 20% of childhood deaths [43]. Chest X-ray is one of the most commonly used imaging tools to detect thoracic diseases in clinical practice due to its wide availability and cost-effectiveness. Still, it requires sufficient knowledge and experience to accurately interpret an X-ray image. Indeed, the process of *X-ray interpretation* involves complex decision-making with various uncertainties, thus even the most experienced physicians/radiologists may have disagreement in the interpretation of the same X-ray image [3, 9].

Since the number of experienced professionals is always limited, artificial intelligence (AI) techniques become practically important, attracting lots of attention [8, 36, 45]. For example, unsupervised (spectral) learning has been widely used in

various image processing tasks [29, 48, 50, 51]. Recently, many *deep learning* techniques have been developed [31] and successfully applied in various medical image analysis tasks [22]. Such success of deep learning mainly comes from the advances of big data techniques, which reduce the cost of collecting and storing huge amount of training data, as well as the advances of computer hardware such as GPUs, which enhance the machines with greater computing power.

With data and computing power, deep learning offers not only an end-to-end solution, directly from image inputs to diagnoses, but also a systematic way to learn the *representations* of data. Indeed, *representation learning* (a.k.a. feature learning) is important because the success of machine learning largely depends on data representations [2, 49]. Conventionally, data representations of medical images are designed via interdisciplinary collaborations between medical professionals and AI researchers. Such handcrafted data representations certainly capture some important features for accurate diagnoses (see, e.g., [27]); nonetheless, due to the uncertain nature of the clinical interpretation process, it remains open whether the representations are good enough for machine learning approaches. Considering this, representation learning provides an alternative to automatically discover a good representation of data, which may lead to an expert-level accuracy in diagnoses [22].

In this paper, we aim at accurate detection of common thoracic diseases via representation learning using the recent ChestX-ray14 dataset [41], which is a hospital-level dataset

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containing 112,120 frontal-view chest X-ray images of 30,805 unique patients. There are 14 common pathological keywords (i.e., labels) involved in the dataset, and each image is attached with either some (one or more) of the 14 labels or a single label of ‘No Finding’. Since the release of ChestX-ray14, several deep learning solutions have been proposed to detect thoracic diseases. Wang et al. [41] built a unified framework upon several deep models pre-trained with ImageNet [6]. Yao et al. [44] proposed a multi-class classifier, based on the long short-term memory (LSTM) architecture [13], considering the interrelationships between the 14 labels. Rajpurkar et al. [32] proposed CheXNet, which is essentially a 121-layer DenseNet [14]. Mao et al. [23] built a deep generative model based on several pre-trained encoders. Wang et al. [42] developed a text-image embedding network, TieNet, based on an argument that not only the X-ray images but also the text reports are useful.

To the best of our knowledge, all the state-of-the-art solutions overlook the fact that *the ChestX-ray14 dataset is highly imbalanced*. For example, there are 19,871 (17.72%) samples labeled with ‘Infiltration’ but merely 227 (0.20%) labeled with ‘Hernia’. It is well known that such a skewed class distribution may have a major impact on the practical performance of classifiers [11]. Existing solutions to imbalanced learning mainly involve data sampling techniques and cost-sensitive approaches. For example, Jeatrakul et al. [17] used a complementary neural network, consisting of a pair of feed-forward back-propagation neural networks, to implement under-sampling; Khan et al. [20] introduced cost-sensitive considerations into the loss functions, where the class-sensitive costs are learned from data during the training process; Ren et al. [33] proposed a meta-learning approach to reweight the training examples. Unfortunately, all of these solutions were designed to perform general-purpose classifications and none of them is tailored for the detection of thoracic diseases with the ChestX-ray14 dataset. Our task challenges the existing imbalanced learning solutions since:

- The *diversity* in ChestX-ray14 is much smaller than that in other natural image datasets such as ImageNet, a basic data resource of many deep learning solutions. This is because the frontal-view chest X-ray images tend to have highly similar global outlines, only with small (yet very important) differences in local areas.
- ChestX-ray14 is much more imbalanced than the datasets considered in most existing studies (e.g., those in [20]). The imbalance ratio of ChestX-ray14 generally leads to very large weights on minority classes since the weights should, in principle, be inversely proportional to the sizes of classes. It is well known that large weights tend to make the learning process unstable, even divergent [16].
- From the application perspective, the task is not really cost-sensitive to misclassifications. In fact, any misclassification of the thoracic diseases should be considered equally unfortunate. Thus, hardly any prior knowledge is available if one wants to modify the loss functions or design the reweighting schemes.

In this work, we tackle the imbalanced learning problem

via *adaptive sampling*. The basic idea is that we dynamically change the weights of different classes in the training process. Specifically, we monitor the performance of the model during each training iterations. Whenever the model has a relatively poor performance on a class, that class will be emphasized more during the next training iteration. Our main contributions are the following. First, we build a DenseNet-based deep structure as the model for multi-class classification. Second, we propose an adaptive data augmentation technique to handle the data imbalance problem. Last but not least, we experimentally compare our proposed method with the state-of-the-art solutions on the ChestX-ray14 dataset. The results confirm the advantage of our proposed method.

The rest of this paper is organized as follows. Section 2 reviews some studies related to our research. Section 3 shows the basic statistics, especially the high skewness, of ChestX-ray14 and presents a formal problem formulation. Section 4 explains our proposed method in detail. Section 5 compares our proposed method with the existing solutions. Finally, Section 6 concludes the paper.

2. Related Work

Computer-aided diagnosis (a.k.a computer-aided detection, CAD) has long been an active research and application direction, of which the most recent advances are usually recognized as *medical AI* solutions. In addition to those studies mentioned in Section 1, the following lines of research are related to our work in general.

2.1. Signal Processing for CAD

Parveen and Sathik [30] employed wavelet and Fourier transform techniques to extract features from chest X-ray images, based on which a fuzzy *c*-means clustering was used to detect pneumonia. Ellington et al. [7] carried out a computerized lung sound analysis for paediatric pneumonia diagnosis. Morillo et al. [26] used short-term Fourier transform analysis to extract features from the recorded respiratory sounds. Then, after the dimensionality reduction using principal component analysis (PCA), they trained a probabilistic neural network (PNN) to detect pneumonia in patients with chronic obstructive pulmonary disease (COPD). These line of work typically relies on signal-level features, thus the focus is very different from ours.

2.2. Conventional Machine Learning for CAD

During the past decades, there have been several comparative studies of conventional machine learning methods. Cooper et al. [5] compared eight statistical and machine learning methods, including neural networks, Bayesian classification, etc., on their performance in predicting mortality of patients with pneumonia. Chapman et al. [4] compared the performance of expert-crafted rules, a Bayesian network, and a decision tree in detecting bacterial pneumonia based on the chest X-ray reports. Sousa et al. [39] showed that support vector machines (SVMs) outperformed naïve Bayes and *k*-nearest neighbor classifiers in

the detection of childhood pneumonia using chest X-ray images. Naydenova et al. [27, 28] considered applying different feature selection techniques, including LASSO [34], sparse linear discriminant analysis (sLDA) [25], etc., on dozens of clinical characteristics. The selected features were then used to train machine learning models, such as SVMs and random forests, to detect childhood pneumonia. In addition, Jun et al. [18] trained an SVM to detect lung diseases based on the texture and shape features of high-resolution computed tomography (CT) images.

2.3. Deep Learning for CAD

In recent years, deep learning has been widely adopted in CAD. Most of them also adopt *transfer learning* techniques to handle the data sparsity problem. Ausawalaithong et al. [1] employed a 121-layer DenseNet for lung cancer prediction, where they considered transfer learning between the ChestX-ray14, JSRT [37] and ImageNet datasets. Kermany et al. [19] transferred a convolutional neural network (CNN) model pre-trained from ImageNet for the screening of patients with common treatable blinding retinal diseases. Then, they showed the generality of their method by transferring the model for the detection of pediatric pneumonia using chest X-ray images. Haloi, Rajalakshmi, and Walia [10] proposed a confidence-aware deep learning system to distinguish between pneumonia and tuberculosis. Transfer learning techniques were used to make full use of several different datasets. Zech et al. [46] considered the transfer performance of the CNN models between X-ray images obtained from different hospitals. They found that the CNN models tended to achieve better internal than external performance. Recently, Saraiva et al. [35] used a two-phase method to implement pneumonia category classification. First, a fully convolutional network (FCN) model is used to segment the images into regions. Then, a deep CNN model is used to classify the target lung regions. It is argued that the automatically extracted features outperform the manually chosen ones. For state-of-the-art advances of deep learning for medical image analysis, interested readers are further referred to recent surveys by Litjens et al. [22] and Mazurowski et al. [24].

3. Data and Problem Formulation

The ChestX-ray14 dataset [41] contains 112,120 frontal-view chest X-ray images of 30,805 unique patients aged from 1 to 95³, in which 63,340 (56.49%) are males and 48,780 (43.51%) are females. There are in total 15 different labels in the dataset (14 common pathological keywords plus ‘No Finding’). Figure 1 shows the distribution of classes in the ChestX-ray14 dataset. Note that the percentage values do not sum up to 1 because one image may be labeled with multiple classes. As can be seen, the ChestX-ray14 dataset is very imbalanced. Over 53.83% of the images are without any class label (i.e., labeled ‘No Finding’). Major classes such as ‘Infiltration’ have sizes up to 87.54 times larger than that of minor classes such as ‘Hernia’. In fact, the average and standard deviation of the

Figure 1: The imbalanced class distribution in ChestX-ray14.

percentage values of different class labels are 8.42% and 0.134, respectively.

Problem formulation. Given ChestX-ray14 as the training dataset, our task is to train a classifier $\mathcal{M}$, such that for each input image X , $\mathcal{M}(X)$ returns a 14-dimensional vector, $\mathbf{p}^T$, each element of which represents the probability of X being labeled with the corresponding disease. Note that if each component $p_k \approx 0$, the image X belongs to the 15th class of ‘No Finding’. We aim at developing a good classifier $\mathcal{C}$ in the sense that it can produce more accurate predictions.

4. Our Method

4.1. Network structure

As is mentioned in Section 1, the diversity of the input X-ray images are small since they tend to have similar global outlines with small local differences. Thus, to capture the details in the X-ray images, we employ multi-layer networks. Specifically, we use DenseNet-121, in which the input features, including the original images, have more connections with higher layers and objective functions, which could make the identification of tiny pathology possible. The architecture of DenseNet-121 is illustrated in Figure 2.

As we can see, the main structure of the network is 4 consecutive dense blocks connected by 3 transition layers.

ℓ -layer dense blocks. An ℓ -layer dense block consists of ℓ dense layers. The j -th dense layer can be seen as a nonlinear function H_j ($j = 1, 2, \dots, \ell$), converting the input features $\mathbf{x}_0, \mathbf{x}_1, \dots, \mathbf{x}_{j-1}$ into an output feature $\mathbf{x}_j$. Specifically, the function H_j is implemented as the consecutive execution of the sequence BN-ReLU-Conv(1×1)-BN-ReLU-Conv(3×3). Here, BN stands for batch normalization [16]. There are 4 dense blocks with 6, 12, 24, 16 layers, respectively, used in the network architecture.

Transition layers. The 4 dense blocks are connected by 3 transition layers. Each transition layer consists of a BN-ReLU-Conv(1×1) sequence followed by an average pooling layer.

³16 age values are found abnormal (≥ 148) and are thus ignored.

Figure 2: Deep network architecture.

First layers. Before the first dense block, the very first layers of the network are a sequence of Conv(7 × 7)-BN-ReLU followed by a max pooling layer.

Last layers. After the last dense block, a BN layer and a linear layer are used to produce the final scores (i.e., probabilities) p^T .

4.2. The Training Process

Given the deep network model $\mathcal{M}$ as shown in Figure 2, the training process is presented as Algorithm 1. As can be seen, Algorithm 1 takes the inputs of the deep model $\mathcal{M}$, the training dataset $D^{\text{tr}} = \bigcup_{k=1}^K D_k^{\text{tr}}$, and the validation dataset $D^{\text{val}} = \bigcup_{k=1}^K D_k^{\text{val}}$, where K is the total number of classes. D_k^{tr} and D_k^{val} are the training and validation dataset of the k -th class, respectively. Each data sample is of the form $(X, \mathbf{y}^T)$, where X is the image and $\mathbf{y}^T \in \{0, 1\}^K$ indicates the set of labels. The k -th component of $\mathbf{y}^T$, y_k , takes value 1 if X belongs to the k -th class and 0 otherwise. Note that $D_i^{\text{tr}} \cap D_j^{\text{tr}} \neq \emptyset$ is possible even if $i \neq j$ since a data item x may have multiple class labels.

The training process consists of a total number of T iterations. Our key idea of handling data imbalance is to bias towards those classes with relatively poor performance. To that end, we propose an adaptive data augmentation (i.e., oversampling) technique. Specifically, for the k -th class we set up an *augmentation ratio* $\delta_k \geq 1$, which is initially 1 (Line 1), to control how the training data of the k -th class, D_k^{tr} , is augmented. In each iteration, we first augment D_k^{tr} to make it δ_k times larger by randomly duplicating its data samples (Lines 3-4). Then, we shuffle the augmented dataset $D^{\text{tr}} = \bigcup_{k=1}^K D_k^{\text{tr}}$ (Line 5) and split D^{tr} into equally-sized batches to facilitate model training

Algorithm 1 Adaptive Training

Input: Deep model $\mathcal{M}$; Num. of classes K ; Training dataset $D^{\text{tr}} = \bigcup_{k=1}^K D_k^{\text{tr}}$; Validation dataset $D^{\text{val}} = \bigcup_{k=1}^K D_k^{\text{val}}$; Max. augmentation ratio $\Delta > 1$; Learning rate η ; Batch size b ; Num. of iterations T

Output: The well-trained deep model $\mathcal{M}$

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1: Initialize the augmentation vector  $\delta \leftarrow \mathbf{1}_K$ 
2: for  $t \leftarrow 1$  to  $T$  do
3:   for  $k \leftarrow 1$  to  $K$  do
4:     Augment  $D_k^{\text{tr}}$  with augmentation ratio  $\delta_k$ 
5:   Shuffle the augmented training set  $D^{\text{tr}} \leftarrow \bigcup_{k=1}^K D_k^{\text{tr}}$ 
6:    $S \leftarrow \lceil \frac{1}{b} \cdot |D^{\text{tr}}| \rceil$ 
7:   Equally divide  $D^{\text{tr}}$  into  $S$  batches  $B_1, B_2, \dots, B_S$ 
8:   for  $s \leftarrow 1$  to  $S$  do
9:     Train  $\mathcal{M}$  by SGD with  $B_s$  and learning rate  $\eta$ 
10:  for  $k \leftarrow 1$  to  $K$  do  $e_k \leftarrow$  Evaluate  $\mathcal{M}$  on  $D_k^{\text{val}}$ 
11:  for  $k \leftarrow 1$  to  $K$  do
12:     $\pi_k \leftarrow$  Ranking position of  $e_k$  in  $\{e_1, e_2, \dots, e_K\}$ 
13:    Update  $\delta_k \leftarrow \frac{\pi_k - 1}{K - 1} \cdot (\Delta - 1) + 1$ 
return  $\mathcal{M}$ 

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(Lines 6-7). Each batch is then fed into the model $\mathcal{M}$ where a stochastic gradient descent (SGD) algorithm is employed to tune the model $\mathcal{M}$ (Line 9). SGD is a standard and widely-used technique to solve optimization problems [47]. During the SGD process, the *loss* of generating a probabilistic prediction

$\mathbf{p}^\top$ for a single training sample $(X, \mathbf{y}^\top)$ is

$$L(X, \mathbf{y}^\top; \mathbf{p}^\top) = \sum_{k=1}^K (-y_k \log p_k - (1 - y_k) \log(1 - p_k)),$$

which is known as the *unweighted binary cross entropy loss*. Note that we use an unweighted loss since any misclassification is equally unfortunate in our application. The tuned model $\mathcal{M}$ is then validated using the validation dataset D_k^{val} . The performance of $\mathcal{M}$ on the k -th validation dataset, e_k , can thus be evaluated (Line 10). After that, we set π_k , taking values from $1, 2, \dots, K$, to be the ranking position of e_k in the descending order of $\{e_1, e_2, \dots, e_K\}$ (Line 12). For example, if $e_1 = 0.86$, $e_2 = 0.62$ and $e_3 = 0.9$, then $\pi_1 = 2$, $\pi_2 = 3$ and $\pi_3 = 1$ since $e_3 > e_1 > e_2$. If the k -th class has a large π_k value, it means that the performance on the k -th class is relatively unsatisfactory. Therefore intuitively, we want to further focus on the training on the k -th class. This is implemented by updating the augmentation ratio δ_k by a factor of π_k (Line 13). In particular, we update δ_k as

$$\delta_k = \frac{\pi_k - 1}{K - 1} \cdot (\Delta - 1) + 1,$$

where the parameter $\Delta > 1$ is the maximum possible augmentation ratio. Indeed, since π_k takes values from $1, 2, \dots, K$, we see that $1 \leq \delta_k \leq \Delta$. In this way, the relatively poorly performed classes will have a relatively larger augmentation during the next training iteration (Lines 3-4).

5. Experiments

To evaluate our proposed method, we conduct a set of experiments on the ChestX-ray14 dataset. We implemented our method using PyTorch. Table 1 shows the parameters used in our implementation. Basically, for each parameter used in Algorithm 1 (i.e., the learning rate (η), the maximum augmentation ratio Δ , the batch size b , and the total number of iterations T), we first determine a wide range of candidates and then choose the best parameter setting that achieves the best practical performance.

Table 1: Parameters

Parameters	Range of values
Learning rate η	0.1, 0.01, 0.001
Max. augmentation ratio Δ	2, 4, 8, 16
Batch size b	32, 64, 128, 256
Total num. of iterations T	5, 10, 15, 20, 25, 30

We compared our method with the following three competitors:

1. **SVM**. This is the conventional SVM classifier using the *histogram of oriented gradients* (HOG) features. HOG counts the occurrences of gradient orientation in localized areas of an image. HOG features have been widely and successfully used in many object detection tasks.

2. **LSTM**. This method is proposed by Yao et al. [44] which uses an LSTM architecture as the basic classification model.
3. **DCNN**. This method is proposed by Wang et al. [41]. This method uses a unified deep convolutional neural network (DCNN) framework which includes ImageNet pre-trained AlexNet [21], GoogleNet [40], VGGNet [38] and ResNet [12] as components.

We used exactly the same experiment setting with those of [44] and [41]. Note that comparing to DCNN, our model require no pre-training.

For each of the $K = 14$ disease classes, we use the the *Area Under the Curve* (AUC) value to measure the performance, which is a widely used performance measure for imbalanced learning [15]. Specifically, AUC measures the area under the *receiver operating characteristic* (ROC) curve, of which the x-axis and the y-axis are the false positive rate and the true positive rate, respectively. The ROC curve depicts relative trade-offs between true positives and false positives. An AUC value is within the range of 0.5 to 1, which can be interpreted as the probability of a randomly chosen positive instance being scored higher by the model than a randomly chosen negative instance. Hence, a higher AUC value indicates a better classifier.

Mathematically, given a classifier $\mathcal{M}$ and a test dataset D^{test} , for each $X_i \in D^{\text{test}}$, $\mathbf{p}_i^\top = \mathcal{M}(X_i)$ is the K -dimensional vector of probabilistic prediction. Then, AUC of the k -th class is calculated as

$$\text{AUC}(\mathcal{M}, k) = \frac{\sum_{i=1}^{N_k^+} \sum_{j=1}^{N_k^-} \mathbb{I}(p_{i,k} > p_{j,k})}{N_k^+ N_k^-},$$

where N_k^+ and N_k^- are the number of positive and negative samples in the k -th class and $\mathbb{I}(\cdot)$ is the indicator function.

Table 2: AUC Values

Pathology	SVM	LSTM	DCNN	Ours
Atelectasis	0.523	0.772	0.716	0.814
Cardiomegaly	0.514	0.904	0.807	0.899
Effusion	0.537	0.859	0.784	0.873
Infiltration	0.535	0.695	0.609	0.701
Mass	0.517	0.792	0.706	0.840
Nodule	0.513	0.717	0.671	0.775
Pneumonia	0.506	0.713	0.633	0.662
Pneumothorax	0.519	0.841	0.806	0.865
Consolidation	0.540	0.788	0.708	0.789
Edema	0.575	0.882	0.835	0.874
Emphysema	0.526	0.829	0.815	0.924
Fibrosis	0.513	0.767	0.769	0.809
PT	0.520	0.765	0.708	0.772
Hernia	0.595	0.914	0.767	0.923
Average	0.53	0.80	0.74	0.82
Std. Dev.	0.025	0.071	0.070	0.079

Table 2 shows the AUC values of SVM, LSTM, DCNN, and our proposed DenseNet-based adaptive sampling method,

in which the performance values of LSTM and DCNN are reported in [32]. As can be seen, our proposed method achieves the best AUC performance in 11 out of the 14 cases. Even in the rest 3 cases of cardiomegaly, pneumonia, and edema, the performance of our method is very close to the best performance. The results demonstrate the effectiveness of our proposed method.

6. Conclusion

A recently released chest X-ray dataset, ChestX-ray14, has attracted more and more attention on automatic detection of thoracic diseases. In this work, we aimed at building an effective multi-class classifier for automatic diagnosis of thoracic diseases. Our design was based on important observations of the ChestX-ray14 data. First, the diversity in ChestX-ray14 is very small. Second, ChestX-ray14 is very imbalanced. Third, from the application perspective, the task is not really cost-sensitive to misclassifications. Based on such observations, we proposed an adaptive sampling method that can monitor the performance of the model during the training process and automatically increase the weight of relatively poorly performed classes. Extensive experiments showed that our method may outperform the state-of-the-art solutions by a large margin.

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