Abstract—Computer-aided diagnosis plays a salient role in more accessible and accurate cardiopulmonary diseases classification and localization on chest radiography. Millions of people get affected and die due to these diseases without an accurate and timely diagnosis. Recently proposed contrastive learning heavily relies on data augmentation, especially positive data augmentation. However, generating clinically-accurate data augmentations for medical images is extremely difficult because the common data augmentation methods in computer vision, such as sharp, blur, and crop operations, can severely alter the clinical settings of medical images. In this paper, we proposed a novel and simple data augmentation method based on patient metadata and supervised knowledge to create clinically accurate positive and negative augmentations for chest X-rays. We introduce an end-to-end framework, SCALP, which extends the self-supervised contrastive approach to a supervised setting. Specifically, SCALP pulls together chest X-rays from the same patient (positive keys) and pushes apart chest X-rays from different patients (negative keys). In addition, it uses ResNet-50 along with the triplet-attention mechanism to identify cardiopulmonary diseases, and Grad-CAM++ to highlight the abnormal regions. Our extensive experiments demonstrate that SCALP outperforms existing baselines with significant margins in both classification and localization tasks. Specifically, the average classification AUCs improve from 82.8% (SOTA using DenseNet-121) to 83.9% (SCALP using ResNet-50), while the localization results improve on average by 3.7% over different IoU thresholds.

Index Terms—Thoracic Disorder, Contrastive Learning, Chest-Xray, Classification, Bounding Box

I. INTRODUCTION

Chest X-rays (CXR) are one of the most common imaging tools used to examine cardiopulmonary diseases. Currently, CXRs diagnosis primarily relies on professional knowledge and meticulous observations of expert radiologists. Automated systems for medical image classification face several challenges. First, it heavily depends on manually-annotated training data which requires highly specialized radiologists to do manual annotation. Radiologists are already overloaded with their diagnosis duties and their hourly charge is costly. Second, common data augmentation methods in computer vision [1], [2] such as crop, mask, blur, and color jitter can significantly alter medical images and generate inaccurate clinical images. Third, unlike images in the general domain, there is subtle variability across medical images. In addition, a significant amount of the variance is localized in small regions.

Thus, there is an unmet need for deep learning models to capture the subtle differences across diseases by attending to discriminative features present in these localized regions.

Recently, contrastive learning frameworks which heavily rely on data augmentation techniques [1]–[3] have become promising due to their ability to capture fine-grained discriminative features in the latent space. This paper proposes a novel and simple data augmentation method based on patient metadata and supervised knowledge such as disease labels to create clinically accurate positive samples for chest X-rays. The supervised classification loss helps SCALP create decision boundaries across different diseases while the patient-based contrastive loss helps SCALP learn discriminative features across different patients. Compared to other baselines [4], [5], SCALP uses simpler ResNet-50 architecture and performs significantly better. SCALP uses GradCAM++ [6] to generate activation maps that indicate the spatial location of the cardiopulmonary diseases. The highlights of our contribution are:

- Our augmentation technique for contrastive learning utilizes both patient metadata and supervised disease labels to generate clinically accurate positive and negative keys. Positive keys are generated by taking two chest radiographs of the same patient P while negative keys are generated using radiographs from patients other than P and having the same disease as P.
- A novel unified framework to simultaneously improve cardiopulmonary diseases classification and localization. We go beyond the conventional two-staged training (pre-training and fine-tuning) involved in contrastive learning. We demonstrate that single-staged end-to-end supervised contrastive learning can improve existing baselines significantly.
- We propose an innovative rectangular Bounding Box generation algorithm using pixel-thresholding and dynamic programming.

II. RELATED WORK

A. Medical Image Diagnosis

In the past decade, machine learning and deep learning have played a vital role in analyzing medical data, primarily medical imaging data. Recognition of anomalies and their localization has been a prevalent task for image analysis. Recent surveys
A. Image Model

As shown in Figure 1 we use the residual neural network (ResNet-50) architecture considering its manageable training with limited GPU resources and popularity in numerous image classification and object detection challenges. Inspired by Triplet attention [20], we incorporated the lightweight attention module in our ResNet-50 architecture to use cross-dimension interaction between the spatial dimensions and channel dimension for better localization. Image input with shape $h \times w \times c$ produces a feature tensor with shape $h' \times w' \times c'$, where $h, w, c$ are the height, width, and the number of channels of the input image, respectively while $h' = h/32, w' = w/32, c' = 2048$. Our framework is composed of two parallel modules: the supervised classification module and the contrastive learning module. Both modules share the same ResNet-50 encoder, i.e., the same set of parameters for encoding the chest X-ray image inputs.

1) Supervised Classification Module:: This module is responsible for learning the high-dimensional decision boundaries across different cardiopulmonary diseases. The encoded input chest X-ray images pass through a global average pooling layer to generate a 2048-dimensional feature vector. The feature vector is fed to a non-linear MLP layer to generate the probability distribution over 8 cardiopulmonary diseases. We calculate $L_{Cross-Entropy}$ by summing loss from each class.

2) Contrastive Learning Module:: In addition to the inter-class variance of abnormalities in chest X-rays (i.e., feature differences between different diseases which are captured by classification loss), chest X-rays also have a high intra-class variance (i.e., differences in the X-rays of different patients having the same disease). To capture these intra-class variances, we introduce a supervised contrastive learning module to learn discriminative intra-class features. Our Supervised Patient Metadata based Augmentation module (Section III-C) generates two augmented views $<x_p', x_p'^\prime>$ for each image in the batch. After being encoded by a shared encoder $f(\cdot)$, both views are fed to the global average pooling layer to generate feature embedding $f(x_p')$ and $f(x_p'^\prime)$. These feature embeddings are then transformed through the non-linear projection head similar to $g(\cdot)$ to generate $g(f(x_p'))$ and $g(f(x_p'^\prime))$. $L_{Contrastive}$ loss is calculated by maximizing the agreement between $g(f(x_p'))$ and $g(f(x_p'^\prime))$.

B. Triplet Attention

To augment the quality of the localization by exploiting attention from the cross-dimension interaction in feature tensors, we integrate the Triplet Attention [20] into our architecture. Cross-Dimension Interaction involves computing attention weights for each dimension in tensor against every other dimension to capture the spatial and channel attention. In simple terms, spatial attention tells where the channel to focus on, while the channel attention tells what channel to focus on. With a minimal overload of few learnable parameters, the triplet attention mechanism successfully captures the interaction between the spatial and channel dimension of the.
input tensor. Following [20], the input tensor with dimension $H \times W \times C$ in SCALP uses a branching mechanism to capture dependencies between $(C, H)$, $(C, W)$, and $(H, W)$.

### C. Supervised Patient-Metadata Based Augmentation

Recently proposed Supervised Contrastive Learning [19] provides an innovative way to leverage label information for generating positive and negative keys effectively. In our case, we have acutely used patient metadata and label information simultaneously to generate positive and negative keys for the SCALP contrastive learning module. The motivation behind introducing contrastive learning in SCALP is to capture intra-class discriminative features between patients diagnosed with the same disease. Figure [2] provides an overview of our novel technique.

1) Positive Sampling: Data augmentation in medical imaging is sensitive to augmentation techniques such as random crop, Gaussian blur, and color jitter proposed in prior self-supervised learning [1]–[3]. For medical images, such operations may either change the disease label or are not meaningful for grayscale X-ray images. Since our goal is to incorporate discriminative features between two different patients to SCALP, we randomly select two chest X-ray studies having the same disease label of a patient $P$ using patient metadata. The first study is called query, and the second is called a positive key. We use the contrastive loss to maximize agreement between them in latent space.

2) Negative Sampling: As shown in Figure [2], we select $k$ negative keys for each patient $P$ in our input batch. Negative keys are selected randomly from the pool of chest X-ray studies from patients except $P$, having the same diagnosis as query. This helps SCALP to distinguish the subtle differences between patients who are diagnosed with the same disease. Contrastive loss tries to push these negative keys away from query during training.

### D. Loss Function

SCALP is trained using the linear combination of supervised classification and contrastive loss. For the supervised classification, we use binary cross-entropy loss. For contrastive learning, we use the extended version of NT-Xent loss [1].

1) Supervised classification Loss: Our disease classification is a multi-class classification problem where we have 8 disease types. Multiple diseases can often be identified in one chest X-ray image and diseases are not mutually exclusive. We, therefore, define 8 binary classifiers for each class/disease type. Since all images in our dataset have 8 labels, the loss function for class $k$ can be expressed as minimizing the binary cross-entry as:

$$L_k = -y_k \cdot \log(p(k|I)) - (1 - y_k) \cdot \log(1 - p(k|I))$$ (1)

where $y_k$ is the ground-truth label of the $k$-th class, and $I$ is the input image. To enable end-to-end training across all the classes, we sum up the class-wise loss to calculate total supervised loss as:

$$L_{Cross-Entropy} = \sum_{n=1}^{batch-size} \sum_{k=1}^{8} l^n_k$$ (2)

2) Contrastive Loss: Our contrastive loss extends the normalized temperature scaled cross-entropy loss (NT-Xent). Using our patient-based sampling, we randomly select a batch of N chest X-ray images belonging to N patients. We derive the contrastive loss on the pairs of augmented examples from the batch. Let $I'_{PD}$ be an image in batch belonging to patient $P$ with disease $D$, $\text{sim}(x, y)$ denotes similarity between $x$ and $y$, and $f(.)$ denotes ResNet-50 encoder, $g(.)$ denotes the projection head. The loss function $l(I'_{PD})$ for a positive pair of example $<I'_{PD}, I''_{PD}>$ is defined as:

$$l(I'_{PD}) = -\log \frac{e^{\text{sim}(g(f(I'_{PD})), g(f(I''_{PD})))}/\tau}}{\sum_k W[p \neq P, d=D] e^{\text{sim}(g(f(I'_{PD})), g(f(I''_{PD})))}/\tau}}$$ (3)

where $W[p \neq P, d=D]$ is an indicator function evaluating to 1 iff $p \neq P$ and $d = D$, $\tau$ is the temperature parameter. The final contrastive loss is calculated as the sum over all instances in batch:

$$L_{Contrastive} = \sum_{k=1}^{batch-size} l(I'_{PD})$$ (4)

Eventually, we treat SCALP learning as the optimization of both contrastive and supervised cross-entropy loss together. Total loss for SCALP is defined as:

$$L_{Total} = \lambda \times L_{Cross-Entropy} + (1 - \lambda) \times L_{Contrastive}$$ (5)

### E. Bounding Box Generation Algorithm

We propose an innovative and time-efficient approach $O(n^2)$ to generate regular-shaped rectangular bounding boxes on chest X-rays indicating the approximate spatial location of the predicted cardiopulmonary disease. As shown in Figure [3], we feed the k-th layer of our image encoder (ResNet-50) to
TABLE I

COMPARISON WITH THE BASELINE MODELS FOR AUC OF EACH CLASS AND AVERAGE AUC. FOR EACH COLUMN, RED VALUES DENOTE THE BEST RESULTS. NOTE THAT THE BEST BASELINE WITH MEAN AUC 0.828 USES THE DENSENET-121 ARCHITECTURE, WHILE OUR MODEL IS TRAINED USING A COMPARATIVELY SIMPLE AND LIGHT-WEIGHT RESNET-50 ARCHITECTURE.

| Method        | Atelectasis | Cardiomegaly | Effusion | Infiltration | Mass | Nodule | Pneumonia | Pneumothorax | Mean       |
|---------------|-------------|--------------|----------|--------------|------|--------|-----------|--------------|------------|
| Wang et. al.  | 0.72        | 0.81         | 0.78     | 0.61         | 0.71 | 0.67   | 0.63      | 0.81         | 0.718      |
| Wang et. al.  | 0.73        | 0.84         | 0.79     | 0.67         | 0.73 | 0.69   | 0.72      | 0.85         | 0.753      |
| Yao et. al.   | 0.77        | 0.90         | 0.86     | 0.70         | 0.79 | 0.72   | 0.71      | 0.84         | 0.786      |
| Raj. et. al.  | 0.82        | 0.91         | 0.88     | 0.72         | 0.86 | 0.78   | 0.76      | 0.89         | 0.828      |
| Kum. et. al.  | 0.76        | 0.91         | 0.86     | 0.69         | 0.75 | 0.67   | 0.72      | 0.86         | 0.778      |
| Liu et. al.   | 0.79        | 0.87         | 0.88     | 0.69         | 0.81 | 0.73   | 0.75      | 0.89         | 0.801      |
| Seyed et. al. | 0.81        | 0.92         | 0.87     | 0.72         | 0.83 | 0.78   | 0.76      | 0.88         | 0.821      |
| Our model     | 0.79        | 0.92         | 0.79     | 0.89         | 0.88 | 0.87   | 0.77      | 0.81         | 0.839      |
| (std)         | ±0.01       | ±0.00        | ±0.01    | ±0.01        | ±0.02| ±0.00 | ±0.01     | ±0.02        |            |

**Algorithm 1: Bounding Box Generation Algorithm**

1. **Input:** k-th layer attention map/heatmap from ResNet-50
2. **Output:** coordinates (x1, y1, x2, y2) of the bounding box
3. Scale heatmap intensities to [0, 255] and create a mask matrix with the same dimension as the heatmap.
4. If \( \text{pixel} > 180 \) then
5. \( \text{mask}[\text{pixel}] = 1 \)
6. else
7. \( \text{mask}[\text{pixel}] = 0 \)
8. Using dynamic programming [25], generate k maximum area rectangles as candidate BB.
9. Expand candidate rectangles uniformly across the edge till newly added ratio (0s count, 1s count) > 1
10. Select the rectangle with the maximum average pixel intensity mapped in the heatmap and return its coordinates.

**C. Disease Identification**

SCALP classification is a multi-label classification problem. It assigns one or more labels among 8 cardiopulmonary diseases. We conduct a 3-fold cross-validation (Table II). We compare SCALP with reference models, which have published state-of-the-art performance of disease classification on the NIH dataset. We have used Area under the Receiver Operating Characteristics (AUC) to estimate the performance of our model in Table II. Our results also present the 3-fold cross-validation to show the robustness of our model. Compared to other baselines, SCALP achieves a mean AUROC score of 0.839 using ResNet-50 across the 8 different classes, which is 0.011 higher than the SOTA (uses DenseNet-121) on disease classification.

To understand the importance of contrastive module for disease classification, we trained SCALP with and without the contrastive loss and evaluated performance on the test set of NIH data. Table III presents the significant drop of > 9% AUC when we exclude the contrastive module from the SCALP pipeline. This demonstrates the importance of our innovative association of contrastive modules with the...
TABLE II
DISEASE LOCALIZATION UNDER VARYING IOU ON THE NIH CHEST X-RAY DATASET. NOTE THAT SINCE OUR MODEL DOESN’T USE ANY GROUND TRUTH BOUNDING BOX INFORMATION, TO FAIRLY EVALUATE THE PERFORMANCE OF OUR MODEL, WE ONLY CONSIDER THE PREVIOUS METHODS’ RESULTS WITH THE SAME SETTINGS AS SCALP.

| T(IoU) | Model     | Atelectasis | Cardiomegaly | Effusion | Infiltration | Mass | Nodule | Pneumonia | Pneumothorax | Mean   |
|--------|-----------|-------------|--------------|----------|--------------|------|--------|-----------|--------------|--------|
| 0.1    | Baseline  | 0.69        | 0.94         | 0.66     | 0.71         | 0.40 | 0.14   | 0.63      | 0.38         | 0.569  |
|        | Our Model | 0.62        | 0.97         | 0.64     | 0.81         | 0.51 | 0.12   | 0.8       | 0.29         | 0.595  |
| 0.2    | Baseline  | 0.47        | 0.68         | 0.45     | 0.48         | 0.26 | 0.05   | 0.35      | 0.23         | 0.371  |
|        | Our Model | 0.42        | 0.92         | 0.42     | 0.6          | 0.25 | 0.04   | 0.56      | 0.18         | 0.434  |
| 0.3    | Baseline  | 0.24        | 0.46         | 0.30     | 0.28         | 0.15 | 0.04   | 0.17      | 0.13         | 0.221  |
|        | Our Model | 0.29        | 0.78         | 0.23     | 0.37         | 0.13 | 0.01   | 0.4       | 0.05         | 0.283  |
| 0.4    | Baseline  | 0.09        | 0.28         | 0.20     | 0.12         | 0.07 | 0.01   | 0.08      | 0.07         | 0.115  |
|        | Our Model | 0.18        | 0.55         | 0.12     | 0.19         | 0.09 | 0.01   | 0.25      | 0.02         | 0.176  |
| 0.5    | Baseline  | 0.05        | 0.18         | 0.11     | 0.07         | 0.01 | 0.01   | 0.03      | 0.03         | 0.061  |
|        | Our Model | 0.07        | 0.33         | 0.04     | 0.10         | 0.04 | 0.0    | 0.14      | 0.10         | 0.102  |
| 0.6    | Baseline  | 0.02        | 0.08         | 0.05     | 0.02         | 0.00 | 0.01   | 0.02      | 0.03         | 0.029  |
|        | Our Model | 0.02        | 0.14         | 0.02     | 0.04         | 0.03 | 0.0    | 0.07      | 0.00         | 0.040  |
| 0.7    | Baseline  | 0.01        | 0.03         | 0.02     | 0.00         | 0.00 | 0.00   | 0.01      | 0.02         | 0.011  |
|        | Our Model | 0.01        | 0.04         | 0.01     | 0.03         | 0.01 | 0.0    | 0.02      | 0.00         | 0.015  |

TABLE III
AUC COMPARISON OF SCALP WITH AND WITHOUT CONTRASTIVE LEARNING MODULE.

| AUC   | 0.766 | 0.794 | 0.822 | **0.839** | 0.818 | 0.785 |
|-------|-------|-------|-------|-----------|-------|-------|

TABLE IV
AUC COMPARISON OF SCALP FOR VARYING λ IN EQUATION 7. A HIGHER VALUE OF λ IMPLIES LOWER WEIGHT TO THE CONTRASTIVE LOSS. SCALP ACHIEVES THE BEST PERFORMANCE WHEN 80% WEIGHT IS GIVEN TO CLASSIFICATION LOSS AND 20% WEIGHT IS GIVEN TO CONTRASTIVE LOSS.

| λ     | 0.99  | 0.90  | 0.85  | 0.80  | 0.75  | 0.70  |
|-------|-------|-------|-------|-------|-------|-------|
| AUC   | 0.766 | 0.794 | **0.839** | 0.818 | 0.785 |

classification pipeline. Our experiments in Table IV prove our hypothesis that both contrastive and cross-entropy loss is important. In a calculated ratio, they help SCALP learn both disease-level and patient-level discriminative visual features.

D. Disease Localization

The NIH dataset has 880 images labeled by radiologists with the bounding box information. We have used this dataset to evaluate the performance of SCALP for disease localization. Many prior works [12], [13] have used a fraction of ground truth (GT) bounding boxes for training and evaluated their system on the remaining. To ensure a robust evaluation, we do not use any GT for training, and Table II presents our evaluation results on all 880 images. For localization, we evaluated our detected regular rectangular regions against the annotated ground truth (GT) bounding boxes, using intersection over union ratio (IoU). The localization is defined as correct only if IoU > T(IoU). We evaluate SCALP for different thresholds ranging from \{0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7\} as shown in Table II. A higher IoU threshold is preferred for disease localization because clinical usage requires high accuracy. Note that SCALP mean performance for 8 diseases is significantly better than the baseline under all IoU thresholds. When the IoU is set to 0.1, SCALP outperforms the baseline in terms of Cardiomegaly, Infiltration, Mass, and Pneumonia. Note that our innovative bounding box generation algorithm successfully eliminates dispersed attention, and identifies regions where maximum attention is concentrated. For example, in "Effusion", the generated heatmap has dispersed attention on both sides of the lungs. However, attention intensity is concentrated in the left side of the lung. Our algorithm is able to generate a bounding box on the left side of the lung and have a high overlap with the ground-truth. Similarly, for "Infiltration" and "Nodule", many undesirable patches of attention have been eliminated which is helpful in improving the IoU evaluation of SCALP. The attention maps generated by SCALP are sharp and focused compared to our reference baseline [9]. Overall, our results show that the predicted disease localizations have significant alignment with the ground truth and can serve as interpretable cues for the disease classification.

V. Conclusion

In this work, we propose a simple and effective end-to-end framework SCALP using supervised contrastive learning to identify cardiopulmonary diseases in chest X-ray. We go beyond two-stage training (pre-training and fine-tuning), and demonstrate that an end-to-end supervised contrastive training using two images from the same patient as a positive pair, can significantly outperform SOTA on disease classification. SCALP can jointly model disease identification and
Batch Size
SCALP AUC
0.78
0.80
0.82
0.84
25 50 75 100 125

Prior works [1], [2] have verified that contrastive learning benefits from a larger batch size. SCALP shows a similar trend with increasing batch size.

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