Context-aware Self-supervised Learning for Medical Images Using Graph Neural Network

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Abstract

Although self-supervised learning enables us to bootstrap the training by exploiting unlabeled data, the generic self-supervised methods for natural images do not sufficiently incorporate the context. For medical images, a desirable method should be sensitive enough to detect deviation from normal-appearing tissue of each anatomical region; here, anatomy is the context. We introduce a novel approach with two levels of self-supervised representation learning objectives: one on the regional anatomical level and another on the patient-level. We use graph neural networks to incorporate the relationship between different anatomical regions. The structure of the graph is informed by anatomical correspondences between each patient and an anatomical atlas. In addition, the graph representation has the advantage of handling any arbitrarily sized image in full resolution. Experiments on large-scale Computer Tomography (CT) datasets of lung images show that our approach compares favorably to baseline methods that do not account for the context. We use the learned embedding for staging lung tissue abnormalities related to COVID-19.

1 Introduction

Self-supervised learning has emerged as a powerful way of utilizing unlabelled data and achieved state-of-the-art performance in the computer vision [1, 2, 3]. For medical imaging analysis, a large-scale annotated dataset is rarely available, especially for emerging diseases, such as COVID-19. However, there are lots of unlabeled data available. Thus, self-supervised pre-training presents an appealing solution in this domain. There are some existing works that focus on self-supervised methods for learning image-level representations [4, 5, 6]. Despite their success, current methods suffer from two challenges: (1) These methods do not account for anatomical context. For example, the learned representation is invariant with respect to body landmarks, which are highly informative for clinicians. (2) Current methods rely on fix-sized input. The dimensions of raw volumetric medical images can vary across scans due to the differences in subjects’ bodies, machine types, and operation protocols. The typical approach for pre-processing natural images is to either resize the image or crop it to the same dimensions because the convolutional neural network (CNN) can only handle fixed dimensional input. However, both approaches can be problematic for medical images. Taking chest CT for example, reshaping voxels in a CT image may cause distortion to the lung [7], and cropping images may introduce undesired artifacts, such as discounting the lung volume.

To address the challenges discussed above, we propose a novel method for context-aware unsupervised representation learning on volumetric medical images. First, in order to incorporate context information, we represent a 3D image as a graph of patches centered at landmarks defined by an anatomical atlas. The graph structure is informed by anatomical correspondences between the subject’s image and the atlas image using registration. Second, to handle different sized images, we

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propose a hierarchical model that learns anatomy-specific representations at the patch level and learns subject-specific representations at the graph level. On the patch level, we use a conditional encoder to integrate the local region’s texture and the anatomical location. On the graph level, we use a graph convolutional network (GCN) to incorporate the relationship between different anatomical regions. The schematic is shown in Fig. 1.

Figure 1: Schematic diagram of the proposed method. We represent every image as a graph of patches. The context is imposed by anatomical correspondences among patients via registration and graph-based hierarchical model used to incorporate the relationship between different anatomical regions. We use a conditional encoder $E(\cdot, \cdot)$ to learn patch-level textural features and use graph convolutional network $G(\cdot, \cdot)$ to learn graph-level representation through contrastive learning objectives.

2 Method

Constructing Anatomy-aware Graph of Patients Our method views images of every patient $X_i$ as a set of nodes $\{x_j^i\}_j^N$, where nodes correspond to image patches covering the lung region of a patient. To define a standard set of anatomical regions, we divide the atlas image into a set of $N$ equally spaced 3D patches with some overlap. We register a patient’s image to the anatomical atlas by minimizing the following objective function: $Sim(\phi_i(X_i), X_{Atlas}) + Reg(\phi_i)$, where $Sim$ is a similarity metric, $\phi_i(\cdot)$ is the fitted subject-specific transformation, $Reg(\phi_i)$ is a regularization term to ensure the transformation is smooth enough. We use $\{p_j^i\}_j^N$ to denote the center coordinates of the patches in the Atlas coordinate system. After solving this optimization for each patient, we can use the inverse of this transformation to map $\{p_j^i\}_j^N$ to each subject (i.e., $\{\phi_i^{-1}(p_j^i)\}$). We use well-established image registration software ANTs [8] to ensure the inverse transformation exists. To incorporate the relationship between different anatomical regions, we represent an image as a graph, whose adjacent matrix $A_i$ is determined by the Euclidean distance between patches’ centers and a threshold hyperparameter that controls the density of graph.

Learning Patch-level Representation We adopt a conditional encoder $E(\cdot, \cdot)$ that takes both patch $x_j^i$ and its location index $j$ as input. It is composed with a CNN feature extractor $C(\cdot)$ and a MLP head $f_i(\cdot)$, thus we have the encoded patch-level feature: $h_j^i = E(x_j^i, j) = f_i(C(x_j^i) \parallel p_j^i)$, where $\parallel$ denotes concatenation. We adopt the InfoNCE loss [9] to train the conditional encoder, obtain a positive sample pair by generating two randomly augmented views from the same query patch $x_j^i$, and obtain a negative sample by augmenting the patch $x_j^i$ at the same anatomical region $j$ from a random subject $v$.

Learning Graph-level Representation We adopt the Graph Convolutional Network (GCN) [10] to summarize the patch-level representation into the graph-level representation. Specifically, the GCN model $G(\cdot, \cdot)$ takes patch-level representation $H_i = \text{concat}(\{h_j^i\}_j^N)$ and adjacency matrix $A_i$ as inputs, and propagates information across the graph to update node-level features $H_i'$. We then obtain subject-level representation by global average pooling all nodes in the graph followed by a MLP head $f_g: S_i = f_g(\text{Pool}(H_i'))$. We adopt the InfoNCE loss to train the GCN on the graph level, obtain a
positive pair by taking two views of the same image $X_i$ under random augmentation at the patch level, and obtain a negative sample by randomly sample a different image $X_j$.

**Overall Model** The model is trained in an end-to-end fashion by integrating the two InfoNCE losses obtained from patch level and graph level: $\mathcal{L} = \mathcal{L}_i(E) + \mathcal{L}_g(\hat{G})$.

### 3 Experiments

**COPDGene Dataset** We evaluate the proposed method on the COPDGene dataset [11], a multi-center observational study designed to identify the underlying genetic factors of the Chronic Obstructive Pulmonary Disease (COPD). We use a large set of 3D CT images of 9,180 subjects from the COPDGene dataset and perform self-supervised pre-training with our method. We then freeze the extracted subject-level features and use them to train linear models to predict various clinically relevant phenotypes (See Supplementary Material for more details). We report the mean $R^2$ scores for regression tasks and the mean accuracies for classification tasks in five-fold cross-validation.

We compare the performance of our method against: (1) supervised approaches, including Subject2Vec [7], Slice-based CNN [12] and (2) unsupervised approaches, including Models Genesis [13], MedicalNet [14], MoCo (3D implementation) [3], Divergence-based feature extractor [15], K-means algorithm applied to image features extracted from local lung regions [15], and Low Attenuation Area (LAA), which is a clinical descriptor.

Table 1 shows that our proposed model outperforms unsupervised baselines in all metrics except for Future AE. While MoCo is also a contrastive learning based method, we believe that our proposed method achieves better performance for two reasons: (1) Our method incorporates anatomical context. (2) Since MoCo can only accept fixed-size input, we resize all volumetric images into $256 \times 256 \times 256$. In this way, lung shapes may be distorted in the CT images, and fine-details are lost due to downsampling. In comparison, our model supports images with arbitrary sizes in full resolution by design. Our method also outperforms supervised methods, including Subject2Vec and 2D CNN, in terms of CLE, Para-septal, AE History, Future AE, and mMRC; for the rest clinical variables, the performance gap of our method is smaller than other unsupervised methods. We believe that the improvement is mainly from the richer context information incorporated by our method. Subject2Vec uses an unordered set-based representation, which does not account for spatial locations of the patches. 2D CNN only uses 2D slices and does not leverage 3D structure.

**MosMed dataset** We use 3D CT scans of 1,110 subjects from the MosMed dataset [15] provided by municipal hospitals in Moscow, Russia. We first perform self-supervised pre-training with our method on the MosMed dataset. Then we freeze the extracted patient-level features and train a logistic regression classifier to predict the severity of lung tissue abnormalities related to COVID-19, a five-grade categorical variable based on the CT findings and other clinical measures. We compare the proposed method with benchmark unsupervised methods, including MedicalNet, ModelsGenesis, MoCo, and one supervised 3D CNN model. We use the mean test accuracy in five-fold cross-validation as the metric for quantifying prediction performance. Table 2 shows that our proposed model outperforms both the unsupervised and supervised baselines. The

| Method          | Supervised | logFEV1pp | logFEV1/FVC | GOLD | CLE | Para-septal | AE History | Future AE | mMRC |
|-----------------|------------|-----------|-------------|------|-----|-----------|-----------|----------|------|
| LAA-950         | ✓          | 0.44 ± 0.02 | 0.60 ± 0.01 | 55.8 | 32.9 | 33.3 | 73.8 | 73.8 | 41.6 |
| K-Means         | ✓          | 0.55 ± 0.03 | 0.69 ± 0.02 | 57.3 | -   | -   | -   | -   | -   |
| Divergence-based | ✓          | 0.58 ± 0.03 | 0.70 ± 0.02 | 58.9 | -   | -   | -   | -   | -   |
| MedicalNet      | ✓          | 0.47 ± 0.10 | 0.59 ± 0.06 | 57.0 ± 1.1 | 40.3 ± 1.9 | 53.1 ± 0.7 | 78.7 ± 1.3 | 81.4 ± 1.7 | 47.9 ± 1.2 |
| ModelsGenesis   | ✓          | 0.58 ± 0.01 | 0.64 ± 0.01 | 59.5 ± 2.3 | 41.8 ± 1.4 | 52.7 ± 0.5 | 77.8 ± 0.8 | 76.7 ± 1.2 | 46.0 ± 1.2 |
| MoCo            | ✓          | 0.40 ± 0.02 | 0.43 ± 0.02 | 52.7 ± 1.1 | 36.5 ± 0.7 | 52.9 ± 1.4 | 78.6 ± 0.9 | 82.0 ± 1.2 | 46.4 ± 1.7 |
| 2D CNN          | ✓          | 0.53 ± 0.03 | 0.74 ± 0.01 | 65.4 | 40.6 | 52.8 | 76.9 | 68.3 | 43.6 |
| Subject2Vec     | ✓          | 0.62 ± 0.01 | 0.70 ± 0.01 | 63.2 ± 1.1 | 50.4 ± 1.3 | 56.2 ± 1.1 | 78.8 ± 1.3 | 81.1 ± 1.0 | 51.0 ± 1.0 |

- ✓ indicates not reported.

| Method          | Supervised | % Accuracy |
|-----------------|------------|------------|
| MedicalNet      | ✓          | 62.1       |
| ModelsGenesis   | ✓          | 62.0       |
| MoCo            | ✓          | 62.1       |
| 3D CNN          | ✓          | 61.2       |
| Ours            | ✓          | 65.3       |
supervised 3D CNN model performed worse than the other unsupervised methods, suggesting that it might not converge well or become overfitted since the size of the training set is limited.

4 Conclusion

We introduce a novel method for context-aware unsupervised representation learning for medical images. Experiments on multiple datasets demonstrate that our method is effective and generalizable.

Broader Impact

Our research advances self-supervised representation learning for medical images by exploiting anatomical context embedded in them. For potential practical benefits, our method enables knowledge transformation from existing datasets to detecting emerging diseases, such as COVID-19. In addition, our method doesn’t require hand-crafted label, so it avoids selection bias in the setting of supervised learning with limited data. To the best of our knowledge, we are not aware of any impact of our work that has negative ethical and societal consequences.

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