Lyme detection with Deep Contrastive Learning

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Abstract

The bacteria Borrelia burgdorferi, which is spread to people by infected tick bites, can cause Lyme disease [5]. According to [3], one of the symptoms, which occurs in 70-80% of people, is Erythema Migrans (EM) rash. Early dectection of this rash is crucial to stop the development of the disease. While deep learning techniques can be used to make a contribution in this area, detecting Lyme disease in images has not received much attention from deep learning research. This project aims to make a contribution in this direction. It proposes a new approach, where high accuracy is achieved by using a Siamese architecture and by using only public dataset. Further, transfer learning problem was analyzed in the context of using a small Lyme dataset. Outperforming results (89% test accuracy) using low computation CNNs such as MobileNetV2 were achieved by the combination of these two approaches.

1. Introduction

In the Northern Hemisphere, Lyme disease is the most common illness transmitted by ticks. Particularly in territories of the United States and Western Europe. According to [4], one of the symptoms, which occurs in 70-80% of people, is Erythema Migrans (EM) rash. EM is a skin condition with an appearance as a "bull's eye" (see Figure 1) that must be diagnosed early to prevent serious health conditions, such as cancer or nervous system problems. This rash disappears within the first weeks and if it not detected in time, the worse symptoms can take months or even years to appear unnoticed. Therefore, an early detection of it is crucial but can be difficult because EM is not easily recognizable and differentiable from other skin conditions. It requires an expert to identify it.

The traditional clinician accuracy was found to be approximately 80% [13]. According to [10], deep learning approaches can be used in order to further improve this accuracy. Due to the limited dataset on Lyme disease publicly available, there are only a few papers addressing this issue. Their approach is to make use of data collected from private sources and perform transfer learning over generic datasets, such as ImageNet [7]. Moreover, there is only one publicly available annotated dataset for Lyme Disease that have been put together by web scrapping and annotated by competent doctors.

We strongly believe that this is an area of biomedical image analysis that has not been properly addressed by the research community and we would like to make a contribution in this field. We will detect early-stages of Lyme disease based on images using supervised-learning model with novel techniques on Convolutional Neural Networks.

Figure 1. Erythema Migrans rash. Image: [4].

2. Related Work

There have been few but consistent publications in the last decade on the field of detecting Lyme Disease based on images using supervised-learning techniques. Brief explanation on the previous work can be found below and the results on Table 1.

First publication found by Čuk et al., 2014 [18], the authors used private dataset, applied image segmentation and made use of several machine learning techniques together with neural networks.

Later, Burlina et al., 2018 [2] improved previous work making use of CNN models. Unfortunately, not just their data but also their paper is private, so there are no more insights that we could retrieve from this paper.

In the paper by Hossain et al., 2022 [10]. Most recent and comprehensive one, the authors prepared a dataset curated by expert dermatologists and trained over 23 architectures (such as ResNet, EfficientNet). Pre-training was

performed on ImageNet dataset [7] and on the skin lesions HAM10000 dataset [15]. For the finetuning of the architectures the authors used a private dataset, containing images collected from various hospitals.

A similar work is by [13], the authors performed transfer learning with ImageNet and fine-tuned six architectures using only the public Lyme disease rashes dataset [4] scrapped from the web and curated by a clinician.

Models	Accuracy
Čuk et al., 2014 [18]	69.23 to 80.42
Burlina et al., 2018 [2]	76.05±0.74
Hossain et al., 2022 [10]	84.42 ±1.36
Koduru and Zhang, 2021 [13]	91.95 (validation)

Table 1. Reported results of previous work.

3. Proposed approach

As mentioned in the previous section, Lyme disease detection using neural networks has been solved using private datasets. Our aim is to use only publicly available online datasets so that we can provide a benchmark for what is possible to achieve in this area. This is a difficult task to solve because of the limited dataset currently available [4]. In this paper are presented two different approaches for Lyme detection with deep learning.

3.1. First approach

The first method follows the same approach as previous works, performing transfer learning and finetuning, treating the problem as a two class classification: Lyme positive and Lyme negative. It is well known that deep learning can solve many tasks if we have enough data to train the models, otherwise the task itself is difficult to solve. Transfer learning offers a solution to this problem. It allows information from a network that has been trained on large datasets covering a variety of domains to be used in other tasks [17]. This is achieved by performing fine-tuning on a number of layers strictly for the specific task we want to solve [17]. This approach is extremely useful in our context, but one problem is encountered: the available pre-trained networks are trained on a completely different domain (natural images) than ours, with almost no overlap between classes. In addition, we have a small amount of data in our domain, which does not allow us to tune multiple layers to solve this task. Therefore, our problem is again difficult to solve. We believe that features captured from different skin diseases will significantly improve model performance.

Unlike previous work, we proposed to pre-train different architectures on more appropriate datasets that are similar to Lyme disease images. Based on our research, [8], [11]

and [15] are publicly available datasets with rich and diverse images of skin diseases. The motivation for this approach is that features captured from different skin diseases can significantly improve model performance. More on this is discussed in Section 5, where we consider whether the choice of dataset is crucial for this task.

In addition, we propose our own data augmentation to enrich our limited dataset and also to prevent the model from overfitting, being a well-known regularization technique [14]. We carefully considered research studies for biomedical imaging such as [1]. Our pipeline aimed to execute in the order mentioned: random flip, perspective skewing, 90 degree rotation, random brightness changes, random contrast and color changes. All of these are provided by Augmentor ([1]). In addition, we employ Torchvision to use fundamental transformations such as normalization and tensor transformation. The models trained in this paper are ResNet50 and MobileNetV2. The reason for choosing the former model is due to the mention of having a high performance in numerous research papers ([10], [2], [6], [16]). The latter was chosen to verify the results that can be obtained with a smaller network with fewer parameters compared to ResNet50. MobileNetV2 has also been tested in previous work [10], achieving lower performance compared to ResNet50.

3.2. Second approach

Our second architecture is a novel approach to Lyme disease detection. We propose to use Siamese networks, also known as twin networks, used to measure the similarity of features of a pair of images [12]. The proposed architecture is illustrated in Figure 2.
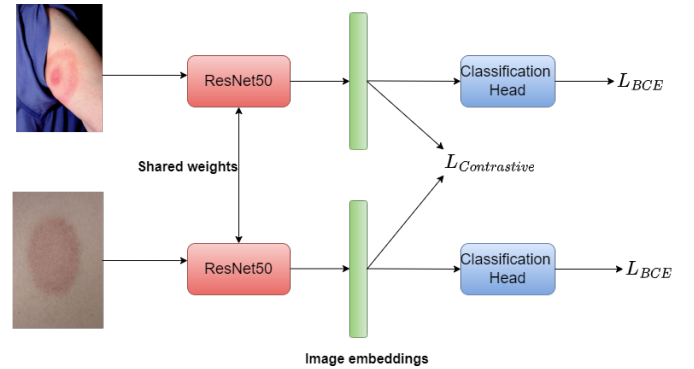

Figure 2. Proposed architecture for the Siamese network. It consists of two pre-trained networks with shared weights, to which classification heads are added to adapt the original architecture to a binary classification problem. Overall objective is to minimize the summation of all three losses.

The motivation for choosing this architecture is that it allows the use of a small amount of data. In addition, the

great benefit it brings is the feature similarity loss function. To improve the performance of the model, we employed the contrastive loss function that evaluates the distance between the features of the image pairs [9]. We first evaluate the mean squared error distance between the outputs of the networks. Following the architecture in Figure 2, the MSE loss function is:

$$MSE(X_1, X_2) = ||ResNet50(X_1) - ResNet50(X_2)||_2^2 \tag{1}$$

where X_1, X_2 are input images. Then, we compute the contrastive loss presented in the paper [9]:

$$Loss_{Contrastive} = \sum_{i=1}^{N}(1 - y_i)\frac{1}{2} \times MSE(X_1^i, X_2^i)^2$$
$$+ y_i\frac{1}{2} \times \max(0, m - MSE(X_1^i, X_2^i)) \tag{2}$$

where N is the number of image pairs, m represents a margin value and y_i is the label of the pair (X_1^i, X_2^i). According to [9], the margin defines a region in which loss from pairs coming from different classes can contribute. The authors mentioned that adding the margin has a crucial impact, otherwise minimizing the objective leads to a collapsed solution [9]. Further, to adapt the general architecture to our task, we evaluate the binary cross-entropy loss for both images in the given pair. The overall objective is therefore achieved. Our model is trained for the binary classification task and, at the same time, learns to maximize the variance between features of different classes and minimize it for those in the same class. The total loss function we minimize is:

$$L = Loss_{Contrastive} + L_{BCE}(X_1) + L_{BCE}(X_2) \tag{3}$$

4. Experiments

With regards to evaluation metrics, metrics that are suitable for binary image classification problem has been used. Hence the Accuracy metric has been chosen to evaluate our approach. This metric is well suited in our case due to the fact that we have balanced data.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{4}$$

Table 2. shows the results of the various experiments that were performed. The leftmost column shows the architecture that was used. Here "_SN" denotes the Siamese network implementation of the corresponding architecture. The second column indicates the dataset on which the model was pretrained. The third and fourth column denotes the results of the experiments with validation and test accuracy respectively.

Models	Pre-trained Dataset	Val. Accuracy	Test Accuracy
ResNet50	ImageNet	91.66	66.66
ResNet50	HAM10000	**93.05**	62.07
ResNet50	Dermnet	91.6	**67.35**
MobileNetV2	ImageNet	87.5	81.6
MobileNetV2	HAM10000	**90.27**	75.86
MobileNetV2	Dermnet	86.1	**85.0**
ResNet50_SN	ImageNet	100	86.20
ResNet50_SN	HAM10000	**100**	88.5
ResNet50_SN	Dermnet	99.3	**89.6**
MobileNetV2_SN	ImageNet	99.65	85.05
MobileNetV2_SN	HAM10000	**100**	**89.65**
MobileNetV2_SN	Dermnet	98.9	87.3

Table 2. Obtained results on Lyme dataset [4]

5. Analysis

In Table 2. it can be seen that the Siamese network implementation outperforms all other variants of the experiment. This shows that the inclusion of the Contrastive loss helps the network to learn the similarly correlated images of the lyme and non-lyme images. It is evident from the results that just using transfer learning is not sufficient for the problem in hand as it has a high degree of overfitting and a significant gap between the validation and testing accuracies. However, the Siamese network variants has a significant impact on the results potentially bridging the drawbacks of the simpler implementation. Our proposed approach reached a validation accuracy of 100 % and test accuracy of 89.6 % on the Resnet50 variant and 89.65 % on the MobilenetV2 variant. the reason for this behaviour is that due to the small nature of the dataset, MobilenetV2 being a lightweight model with fewer number of parameters adopts to it better than the Resnet50.
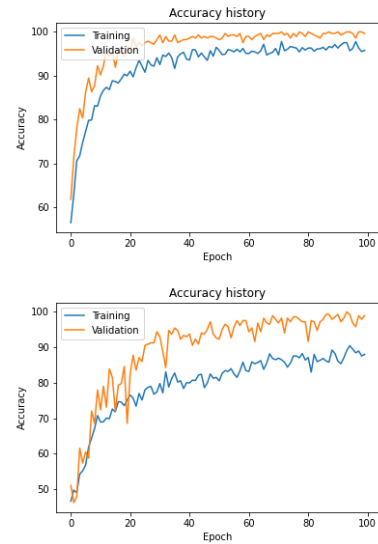

Figure 3. Accuracy MobileNetV2_SN vs ResNet50_SN.

From Figure 3. it is clear that our proposed approach does not suffer from overfitting compared to the naive implementation. Also the ResNet50 variant has a higher convergence rate than the MobilenetV2 variant owing to the higher number of parameters. In overall MobilenetV2 implementation is more suited to the problem than the Resnet50 variant. In terms of results when compared with the Literature Survey , our approach outperforms the methods by Čuk et. al [18], Burlina et.al [2] and Hossain et al [10]. Our validation accuracy also exceeded the one reported by Koduru et al [13]. Therefore, our method achieved state of the art results in Lyme detection.

6. Conclusions

A few things stood out from the experiments that helped our approach reach State Of the Art results of 89.65 % . The choice of the pre-trained dataset and selective and adequate augmentation had a big impact on the results. Thus this approach achieved SOTA results using only publicly available datasets.

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