Detecting Manual Alterations in Biological Image Data Using Contrastive Learning and Pairwise Image Comparison

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Abstract

In this paper, we address the problem of detecting manipulations in biological images. Ensuring the integrity of biological image data is essential for reliable scientific research. The study focuses on developing a model for pairwise image comparison using contrastive learning, demonstrating high pairwise comparison metrics to detect manual modifications or more subtle alterations. The proposed method outperforms state-of-the-art models, including CLIP and Barlow Twins, in the task of biological image comparison on fMRI scans and cell datasets. This work contributes to automated fraud detection and data validation in biological research.

Keywords: Machine Learning, Pairwise Image Comparison, Self-Supervised Learning, Fine-Tuning, Automated Fraud Detection, Detecting Data Alterations

1 Introduction

Our work aims to develop a machine learning solution for the problem of reusing existing biological and medical snapshots to demonstrate results in newly published biological articles. Fake images negatively impact on medicine by providing false or fabricated results and undermining the credibility of new scientific work in these fields. Existing state-of-the-art self-supervised learning approaches demonstrate remarkable results in pairwise image comparison tasks (`SimCLR` [1], `CLIP` [2], Barlow Twins [3]). However, their performance significantly worsens when applied to complex biological data. It requires developing model that is more sensitive to subtle changes in the image content while remaining resistant to various manual alterations, such as color jittering, flipping, rotation, noise application, and random affine transformations. At present, the problem of matching biological and medical images remains unsolved due to the complexity of distinguishing snapshots of similar objects, where differences can only be identified by experts in the field.

We propose a solution, based on `Barlow Twins` [3], trained and fine-tuned specifically for complex biological scans. The model belongs to the family of self-supervised learning (SSL) methods, which have been proven to be competitive with supervised representations ([1], [2], [3], [4], [5]). By leveraging a pretrained model, it does not require large snapshot datasets to achieve state-of-the-art accuracy on the `Haxby fMRI`, `CIL Epithelial Cell`, `CIL Lymphocyte Cell` datasets. This

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solution can be widely used by biological articles proofreaders to verify the authenticity of provided images and detect borrowings from known datasets.

2 Problem

Given dataset $\mathcal{D}$, consisting of N biological snapshots:

$$\mathcal{D} = \{d_i \in [0, 256)^{l \times l \times 3}, i \in [0, N)\}$$

where d_i is the RGB-decoded image, l – the length of an image side.

For simplicity, we will refer to a pair of images with the same content before alterations as a *similar* pair; otherwise, it will be called *dissimilar*. Our goal is to build a model $\mathcal{M}$ using self-supervised contrastive learning (SSCL), which should be able to distinguish dissimilar pairs of images and identify similar ones.

Let x and y be two images ($x, y \in [0, 256)^{l \times l \times 3}$). The model consists of two main parts:

$$\mathcal{M}(x, y) = h(f_\theta(x), f_\theta(y)))$$

where f_θ is an encoder with a trainable parameter set θ, and h is the linear classifier:

$$f_\theta(x) = v_x \in \mathbb{R}^d$$

$$h(v_x, v_y) = s \in \{0, 1\}$$

Value $s = 1$ corresponds to similar pairs, $s = 0$ represents dissimilar pairs.

To train the encoder, let us define the loss function $\mathcal{L}$:

$$\mathcal{L}(v_x, v_y, I(x, y)) \in [0, +\infty)$$

where v_x and v_y are the embeddings of images x and y, respectively, and $I(x, y)$ is defined as follows:

$$I(x, y) = \begin{cases} 1, \text{if } x \text{ and } y \text{ are similar,} \\ 0, \text{otherwise} \end{cases}$$

The model's accuracy will be evaluated by counting the number of correctly classified similar pairs and incorrectly classified ones, producing a single accuracy value to compare with other state-of-the-art models.

3 Computational Experiment

In this section, we conduct an experiment to train the projector of the `Barlow Twins` model on a blood cells dataset. Our goal is to determine if the model, with its state-of-the-art pretrained encoder, can be successfully adapted to our problem.

The model's encoder is the pretrained `ResNet50` from the original article [3]. The dataset consists of 320 images of lymphocyte cells, split into a training set of 256 images and a validation set of 64 scans. The projector is composed of three groups of layers; each group contains a linear layer, batch normalization, and a ReLU activation function. The input dimensions for the groups are 2048, 1024, and 1024, respectively.

The loss function is identical to that described in the original article. For optimization, we use the `Adam` optimizer with the following learning rate schedule:

$$q_k = \frac{1}{2} \cdot (1 + \cos(\pi \cdot \frac{k}{K}))$$

$$\gamma_k = \gamma_{start} \cdot q_k + \gamma_{end} \cdot (1 - q_k)$$

where k is the epoch number, K is the total number of epochs, $\gamma_{start} = 5 \cdot 10^{-3}$, $\gamma_{end} = 5 \cdot 10^{-4}$.

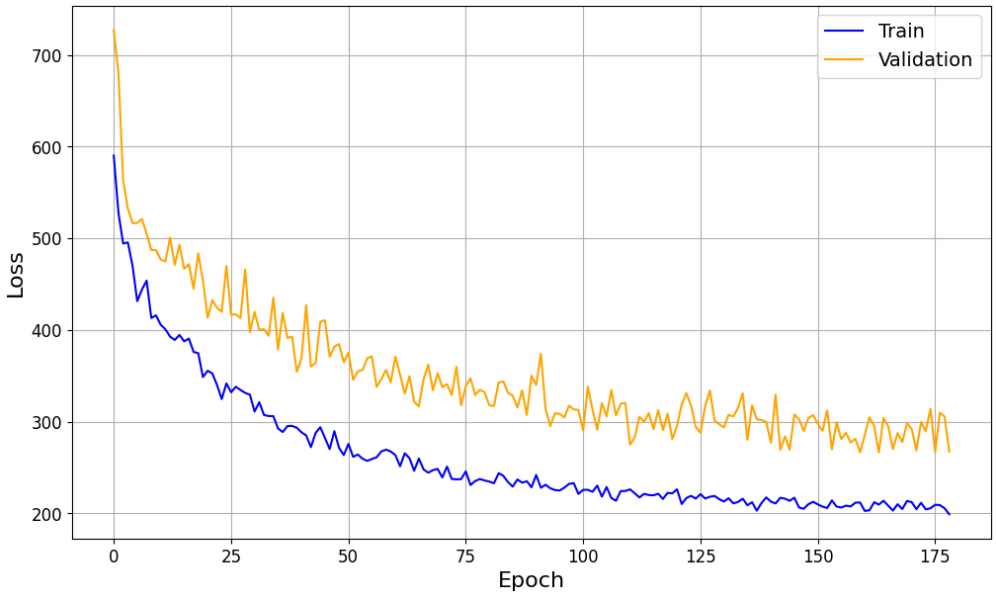

Figure 1: Graph of the loss function for training and validation samples. The experiment was conducted over 180 epochs. The validation loss decreases alongside the training loss, indicating that the model can be trained further. Training takes approximately 25 minutes on a Google Colab GPU.

4 Method

DRAFT

The problem of detecting reused biological and medical images is rooted in the complexity of distinguishing between similar images while remaining invariant to various transformations. The dataset consists of biological snapshots from publicly available sources, we will store them as an array D with elements $d_i \in [0, 256)^{l \times l \times 3}$, where l is the length of images sides. Let us define the *solution* – a method which meant to solve the stated problem. Also we will use the termini *model* – the machine learning solution, which is proposed in our work.

Structure of the model is the same as in `Barlow Twins` [3]. It takes a batch of images X, each image x_i is being augmented in two ways, producing two modified pictures y_i^A and y_i^B for each original. The resulted two batches of distorted images Y^A and Y^B are then fed to a deep network function f_θ, and the produced embeddings Z^A and Z^B are used to evaluate loss function $\mathcal{L}$ with the following formula, proposed in `Barlow Twins` [3]:

$$\mathcal{L}(Z^A, Z^B) = \sum_i (1 - \zeta_{ii})^2 + \lambda \sum_i \sum_{j \neq i} \zeta_{ij}^2$$

where λ is the positive constant, and ζ_{ij} – cross-correlation matrix, computed between the outputs of the two identical networks along the batch dimension:

$$\zeta_{ij} = \frac{\sum_b z_{b,i}^A z_{b,j}^B}{\sqrt{\sum_b (z_{b,i}^A)^2} \sqrt{\sum_b (z_{b,j}^B)^2}}$$

For the further simplicity, we will refer to a pair of images with the same content before alterations as a *similar* pair, otherwise it will be called *dissimilar*. The idea behind this loss function is to minimize the distance between similar pairs embeddings and to make it bigger for dissimilar.

The model is trained on the 70% dataset D data, then validated on another 10% and tested on the remaining 20% – let D_{test} be this part. For accuracy evaluation, we follow the widely used linear evaluation protocol (here comes the links from [1]).

5 Related Work

Topic #1. TODO

Topic #2. TODO

6 Preliminaries

6.1 General notation

In this section, we introduce the general notation used in the rest of the paper and the basic assumptions.

6.2 Assumptions

TODO

7 Experiments

To verify the theoretical estimates obtained, we conducted a detailed empirical study...

8 Discussion

TODO

9 Conclusion

TODO

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A Appendix / supplemental material

A.1 Additional experiments

TODO