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

Georgii Nekhoroshkov

Moscow Institute of Physics and Technology

Course: My first scientific paper
(Strijov's practice)

Expert: A. V. Grabovoy

Consultant: D. D. Dorin

2025

Ensure Biological Image Integrity

Comparing 2 images

Develop a contrastive learning model for pairwise image comparison to:

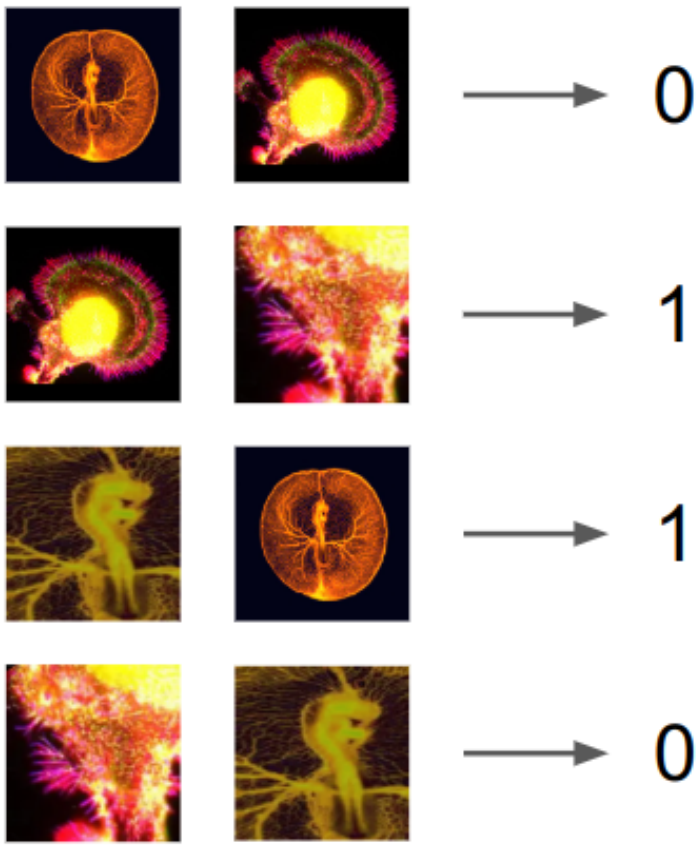
1. Detect alterations (color jittering, crop, rotation, noise)
2. Select pairs of images with the same content
3. Outperform existing state-of-the-art models (Barlow Twins[1], SimCLR[2]) on cell datasets

(a) Original (b) Crop and resize (c) Crop, resize (and flip) (d) Color distort. (drop) (e) Color distort. (jitter)

[1] *J. Zbontar et al.* Barlow Twins: Self-Supervised Learning via Redundancy Reduction // ICML, 2021.

[2] *T. Chen et al.* A Simple Framework for Contrastive Learning of Visual Representations // ICML, 2021.

Detection of Similar Images Despite Modifications



The model should process two images and output a value from [0, 1] – the likelihood that they are identical, up to modifications.

The method must leverage a self-supervised learning approach.

Key Articles

1. **SimCLR**: Chen T. et al. "A Simple Framework for Contrastive Learning of Visual Representations", ICML 2020
2. **Barlow Twins**: Zbontar J. et al. "Barlow Twins: Self-Supervised Learning via Redundancy Reduction", ICML 2021
3. **CLIP**: Radford A. et al. "Learning Transferable Visual Models From Natural Language Supervision", ICML 2021
4. **Siamese Networks**: Melekhov I. et al. "Siamese Network Features for Image Matching", ICPR 2016

Problem Statement

Given biological image dataset

$$\mathcal{D} = \{d_i \in \mathcal{S},\ i \in [0, N)\}, \quad \mathcal{S} \subseteq \mathbb{R}^{H \times W \times C}$$

Pairwise similarity classification

For any $(x, y) \in \mathcal{S} \times \mathcal{S}$, learn mapping:

$$\mathcal{M} : (x, y) \mapsto s \in [0, 1]$$

where:

$$s = \begin{cases} 1, & \textit{similar} \text{ pair (same content pre-alteration)}, \\ 0, & \textit{dissimilar} \text{ pair (different content)} \end{cases}$$

Model Decomposition

Fixed structure

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

where:

$$f : \mathcal{S} \to \mathbb{R}^d \text{ (encoder)}$$

$$h : \mathbb{R}^d \times \mathbb{R}^d \to [0, 1] \text{ (classifier)}$$

Quality metric

Maximize accuracy over pairwise comparisons:

$$\text{Acc} = \frac{1}{|\mathcal{P}|} \sum_{(x,y)\in\mathcal{P}} \mathbb{I}\big(\mathcal{M}(x, y) = I(x, y)\big)$$

where $\mathcal{P}$ is test pairs, $I(x, y)$ ground truth similarity.

Barlow Twins Adaptation (BTA)

Model based on Barlow Twins

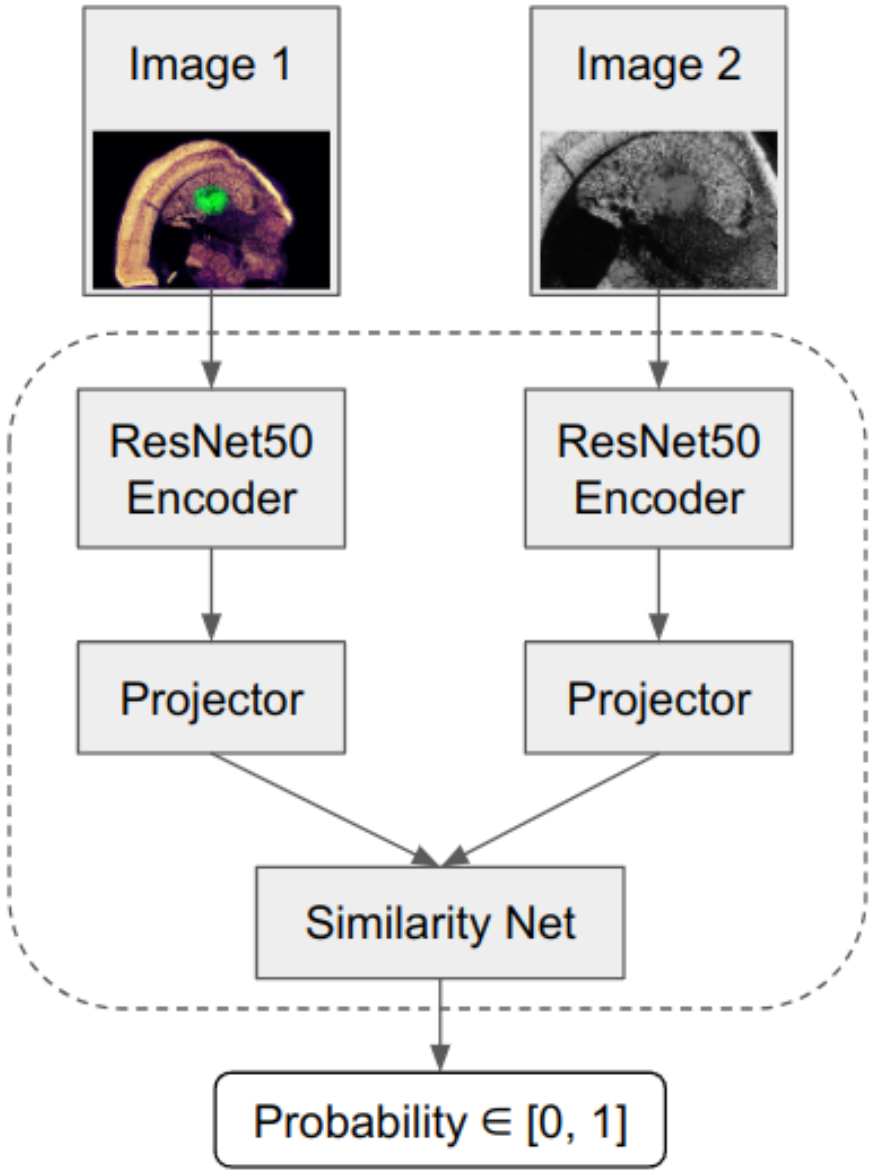
Architecture:

- ResNet-50 backbone
- Projector
- Similarity head

Training specific:

- Parallel image augmentation
- AdamW optimizer with decreasing learning rate
- Performed on a specially selected dataset

Key Innovation:
Custom model's head, training dataset and pipeline



Comparing Training Pipelines

Modifying original learning specifics

Consecutively

$$\mathcal{L}_{proj} = \sum_i (1 - \mathcal{C}_{ii})^2 + \lambda_{proj} \sum_i \sum_{j \neq i} \mathcal{C}_{ij}^2$$

$$\mathcal{C}_{ij} = \frac{\sum_b z^A_{b,i} z^B_{b,j}}{\sqrt{\sum_b (z^A_{b,i})^2} \sqrt{\sum_b (z^B_{b,j})^2}}$$

$$\mathcal{L}_{sim} = BCELoss$$

Parallel

$$\mathcal{L} = \mathcal{L}_{sim} + \lambda \cdot \mathcal{L}_{proj}$$

Experiment Setup

Dataset: 630 biological scans (animal and plant cells)
Train/Test Split: 80%/20%
Training: 100 epochs, AdamW optimizer
($\gamma_{start} = 3 \cdot 10^{-3}, \gamma_{end} = 5 \cdot 10^{-4}$)

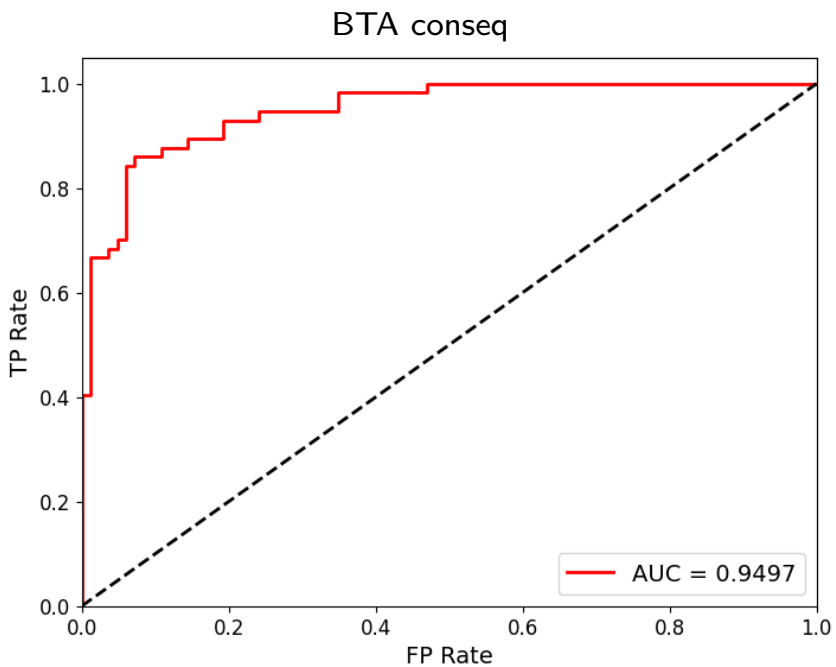
Evaluation Protocol

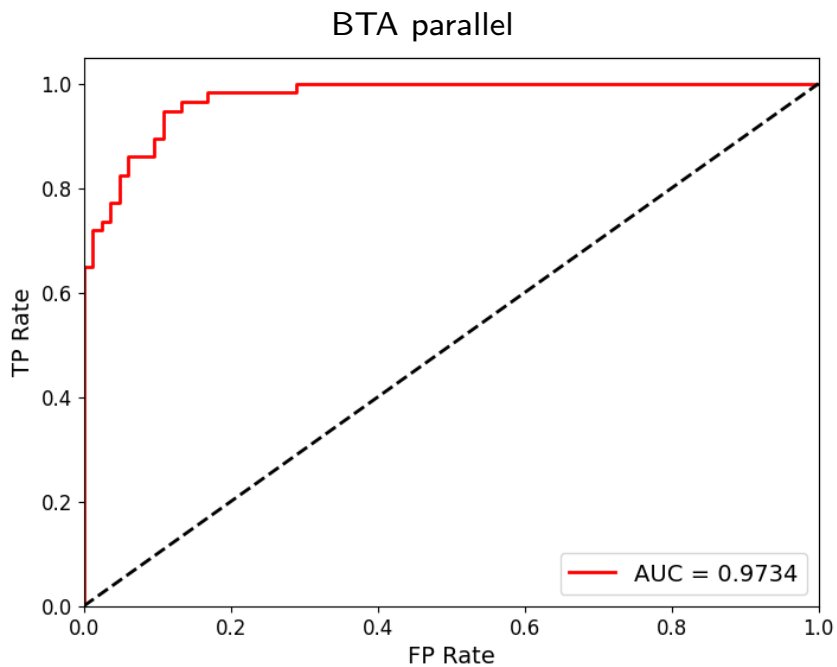
Compare with Barlow Twins and SimCLR baselines
Metrics:

1. Accuracy
2. F1-Score, Precision, Recall
3. AUC-ROC

Significant Accuracy Improvements

Metric	BTA conseq	BTA parallel	BT	SimCLR
Accuracy	0.89	**0.90**	0.68	**0.67**
F1-Score	**0.85**	0.80	**0.48**	0.54
Recall	**0.84**	0.71	**0.43**	0.52
Precision	0.87	**0.92**	0.54	**0.46**
AUC	0.95	**0.97**	**0.69**	0.71





Key Achievements

1. Significant accuracy metrics improvement over state-of-the-art models Barlow Twins and SimCLR
2. Model is robust to 4 types of manual alterations
3. First biological-SSL solution for automated fraud detection and image provenance verification

Research materials are available in GitHub repository

`https://github.com/intsystems/2025-Project-170`