

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

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

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# Goal of research

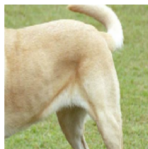
## Ensure biological image integrity

Develop a contrastive learning model for pairwise image comparison to:

- ▶ Detect alterations (color jittering, crop, rotation, noise)
- ▶ Select pairs of images with the same content
- ▶ Outperform existing state-of-the-art models (Barlow Twins<sup>1</sup>, SimCLR<sup>2</sup>) on cell datasets



(a) Original



(b) Crop and resize



(c) Crop, resize (and flip)



(d) Color distort. (drop)



(e) Color distort. (jitter)

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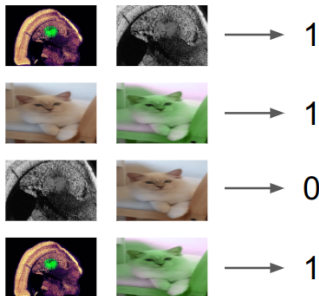
<sup>1</sup>J. Zbontar et al. Barlow Twins: Self-Supervised Learning via Redundancy Reduction // ICML, 2021.

<sup>2</sup>T. Chen et al. A Simple Framework for Contrastive Learning of Visual Representations // ICML, 2021.

# One-slide talk

## The problem

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

- ▶ **SimCLR**: Chen T. et al. "A Simple Framework for Contrastive Learning of Visual Representations", ICML 2020
- ▶ **Barlow Twins**: Zbontar J. et al. "Barlow Twins: Self-Supervised Learning via Redundancy Reduction", ICML 2021
- ▶ **CLIP**: Radford A. et al. "Learning Transferable Visual Models From Natural Language Supervision", ICML 2021
- ▶ **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:

- ▶  $s = 1$ : *similar* pair (same content pre-alteration)
- ▶  $s = 0$ : *dissimilar* pair (different content)

# Problem statement

## Model decomposition

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

where:

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

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

## Success criterion

Maximize accuracy over pairwise comparisons:

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

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

# Solution

## Barlow Twins Adaptation

Architecture:

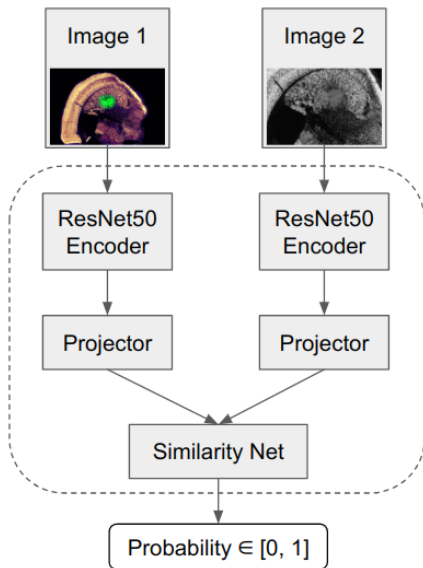
- ▶ ResNet-50 backbone
- ▶ Projector
- ▶ Similarity head

Training specific:

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

**Key Innovation:**

Custom model's head and dataset



# Computational experiment

## Experimental Setup

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

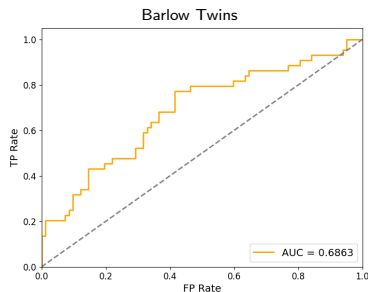
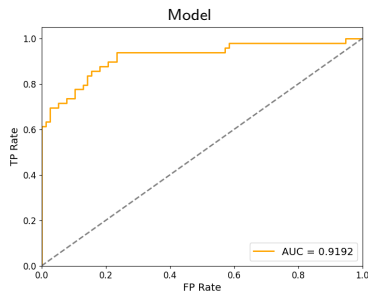
## Evaluation Protocol

- ▶ Compare with Barlow Twins baseline
- ▶ Metrics:
  - ▶ Accuracy
  - ▶ F1-Score, Precision, Recall
  - ▶ AUC-ROC



# Computational Experiment

## ROC-AUC Comparison



## Performance Metrics

Metric	Model	Barlow Twins
Accuracy	0.85	0.68
F1-Score	0.80	0.48
Precision	0.82	0.54
Recall	0.78	0.43
AUC	0.92	0.69

- ▶ All metrics computed on test set (20% data)
- ▶ Threshold = 0.5 for binary classification

## Key achievements

- ▶ Significant accuracy metrics improvement over state-of-the-art model
- ▶ Robust to 4 types of manual alterations
- ▶ First biological-SSL solution for:
  - ▶ Automated fraud detection
  - ▶ Image provenance verification