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[1], SimCLR[2]) on cell datasets

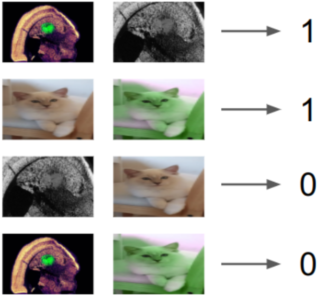
(a) Original (b) Crop and resize (c) Crop, resize (and flip) (d) Color distort. (drop) (e) Color distort. (jitter)

[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.

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.

Literature

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:

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

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

Success criterion

Maximize accuracy over pairwise comparisons:

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

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

Solution

Barlow Twins Adaptation

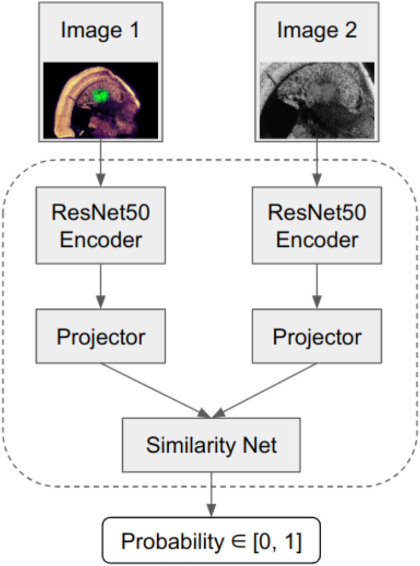
Architecture:

- 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

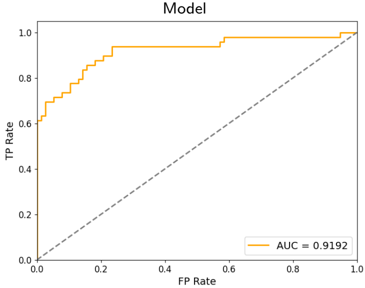
- **Dataset**: 630 biological scans (animal and plant cells)
- **Train/Test Split**: 80%/20%
- **Training**: 100 epochs, AdamW optimizer ($\gamma_{start} = 3 \cdot 10^{-3}, \gamma_{end} = 5 \cdot 10^{-4}$)

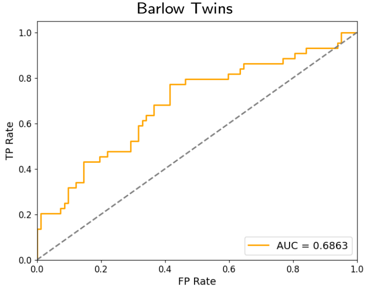
Evaluation Protocol

- 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

Conclusion

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