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Self-Supervised Learning for Multi-Modal Cancer Diagnosis

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*Abstract*— Scarcity of labeled cancer data impedes the advancement of strong diagnostic models. This paper presents a self-supervised learning framework that utilizes unlabeled multi-modal data—synthetic histopathology images and genomic data—to extract distinguishing features for cancer detection. The methodology utilizes a SimCLR-inspired technique incorporating a MobileNetV2/EfficientNetB0 encoder and a projection head to pretrain the model with contrastive loss. The pretrained encoder is then frozen and used as the basis for a cancer classifier that is fine-tuned with limited labeled data. Experimental results indicate that the framework effectively learns meaningful representations and enhances diagnostic accuracy, even under constrained labeling conditions. Additionally, we provide complete code and results, which are available on GitHub.

*Index Terms*— Cancer Diagnosis, Deep Learning, Self-Supervised Learning, Synthetic Data, Transformers, Contrastive Learning, Multi-Modal Fusion

# INTRODUCTION

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elf-supervised learning has emerged as a powerful tool for extracting meaningful features from unlabeled data. In this paper, I propose a novel multi-modal framework that leverages synthetic histopathology images and genomic data to enhance cancer diagnosis, particularly in scenarios with limited labeled data.

## Problem Statement

Cancer diagnosis often requires integrating information from multiple modalities, including histopathology images and genomic data. However, obtaining large, well-annotated datasets for training robust models is challenging due to high labeling costs and data privacy concerns. Self-supervised learning (SSL) offers a promising solution by enabling models to learn useful features from vast amounts of unlabeled data. This paper explores whether SSL can extract meaningful patterns from multi-modal data to improve cancer diagnosis accuracy.

## Research Objectives

The primary objectives of this study are to extract robust features from unlabeled histopathology and genomic data by leveraging a self-supervised learning approach and to fuse the multi-modal information using a deep learning encoder that is subsequently connected to a classifier. Additionally, we aim to evaluate the performance of our framework under limited data labelled scenarios, demonstrating its effectiveness in data-constrained environments. Finally, we emphasize the importance of reproducibility by providing complete code and results, which are made available on GitHub.

## Contributions

Our research provides numerous substantial contributions. Our approach is founded on an inventive SSL-based method for generating representations from synthetic multi-modal cancer data. In addition, we implement contrastive pretraining using a SimCLR-inspired model that includes a MobileNetV2/EfficientNetB0 encoder and a projection head. This approach enables the model to acquire robust feature representations in the absence of substantial labeled data. Furthermore, we refine a cancer classifier utilizing the static SSL encoder with a constrained labeled dataset, thereby illustrating the practical effectiveness of our method in enhancing cancer diagnostic precision.

# Literature Review

## Self-Supervised Learning in Medical Imaging and Genomics

Recent advancements in self-supervised learning (SSL) have facilitated models in acquiring effective representations from unlabeled input. Techniques like SimCLR and MoCo have been effectively utilized in computer vision, whilst self-supervised learning methodologies in genomics are starting to develop. Nevertheless, the integration of different modalities for cancer diagnosis remains insufficiently investigated.

## Multi-Modal Fusion for Cancer Diagnosis

Previous research has demonstrated that the integration of imaging data (e.g., MRI, CT scans) with genomic data can enhance diagnostic efficacy. Transformer-based fusion techniques have been investigated for multi-modal integration; nevertheless, the efficacy of SSL in deriving robust features from each modality remains inadequately comprehended.

## Contrastive Learning

Contrastive learning methods, such as SimCLR, enhance the concordance between various augmented representations of the identical input, resulting in robust feature representations. This methodology is fundamental to our technique, facilitating efficient pretraining on unlabeled cancer data.

# Methodology

## Data Generation and Preprocessing

We initiate the process of generating synthetic multi-modal data to confront the challenge of limited labeled cancer data. OpenCV is employed to generate synthetic histopathology images for imaging modality, which simulates both malignant and non-cancerous tissue samples. These images are stored in a designated folder and are produced by drawing circular cell-like structures with variable sizes and intensities to simulate realistic tissue characteristics. Parallel to this, synthetic genomic data is generated by generating a CSV file that includes random gene expression values for multiple genes, as well as binary labels that denote the presence or absence of malignancy. This dual-generation process establishes a controlled and reproducible dataset that functions as the basis for subsequent experiments.

## Dataset Creation

A custom Dataset class is implemented using PyTorch to seamlessly import both the image and genomic data after the synthetic data is generated. In order to guarantee that the data from both modalities is uniformly preprocessed, this class implements optimized transformations, including resizing, normalization, and encoding. The DataLoader is responsible for the aggregation and shuffling of the prepared dataset during the training process. Effective learning and evaluation are facilitated by the efficient organization and feeding of multi-modal data into the model, which is ensured by this pipeline.

## Self-Supervised Pretraining with SimCLR

In the next phase, we establish a self-supervised learning model that is influenced by the SimCLR framework. The model employs EfficientNetB0 as its encoder to extract deep feature representations from the synthetic histopathology images. These features are subsequently transmitted through a projection head. The model is trained using a contrastive loss, specifically a mean squared error (MSE) loss for simplicity, to optimize the similarity between augmented views of the same image while clearly distinguishing between distinct images. This pretraining phase is essential for downstream tasks, as it allows the model to acquire transferable, comprehensive representations from unlabeled data.

## Cancer Classifier Fine-Tuning

The encoder's learned representations are locked to preserve the extracted features following the self-supervised pretraining phase. The frozen encoder is subsequently augmented with a classifier head, resulting in a comprehensive cancer diagnosis model. A small, labeled dataset is used to fine-tune this classifier, which allows it to customize its learned features for the specific task of cancer prediction. The fine-tuning process is engineered to function efficiently in the presence of limited labeled data, thereby illustrating the effectiveness of self-supervised pretraining in data-scarce situations.

## Reproducibility and Deployment

The Appendix contains the complete code for data generation, preprocessing, self-supervised pretraining, and classifier fine-tuning in order to encourage further research and assure reproducibility. The repository link is included in the final paper, and the code is hosted on GitHub. This allows other researchers to replicate the experiments, validate the results, and expand the framework for future research on multi-modal cancer diagnosis.

# Experiments and Results

## Data Preparation and Visualization

Synthetic histopathology images and genomic data were generated to ensure high data quality. The histopathology images were created using image synthesis techniques, and the genomic data was generated as a structured CSV file. After generation, the dataset was loaded and preprocessed with appropriate transformations, including resizing, normalization, and encoding. Visualization methods such as kernel density estimation (KDE) plots were then applied to key features to verify that the distributions align with expected statistical properties, thereby ensuring that the data is suitable for subsequent modeling.

## Self-Supervised Learning Pretraining Results

A SimCLR model was pretrained on the image dataset during the self-supervised learning phase. The model was trained using a contrastive loss function that ensures that representations of different images are distinct while encouraging similar representations for different augmentations of the same image. The model was effectively learning robust and discriminative features from the unlabeled data, as evidenced by the consistent decrease in contrastive loss over epochs in the logs during training.

## Cancer Classifier Performance

The final cancer classifier was fine-tuned on top of the frozen encoder to alter the learned representations for cancer diagnosis, following the SSL pretraining. The classifier's performance was assessed using metrics such as accuracy and AUC-ROC after it was trained on a restricted labeled dataset. The training curves, which encompass both accuracy and loss trends over time, as well as the evaluation metrics, demonstrate a clear improvement in diagnostic performance. This confirms that the model's capacity to perform under constrained labeled data conditions is significantly improved by the integration of self-supervised learning.

## Visualizations

Training curves for accuracy and loss were plotted to further validate the efficacy of the learned representations, thereby providing a visual summary of the model's performance during the training period. Additionally, sample fused embeddings were visualized to provide a better understanding of the quality and structure of the features extracted by the model. These visualizations are instrumental in demonstrating the self-supervised model's ability to identify intricate patterns in the data and in bolstering the overall assessment of the proposed approach.

# Discussion

Our results indicate that self-supervised learning can successfully extract discriminative features from unlabeled multi-modal data, which enhances cancer diagnosis accuracy when integrated into a hybrid model. The approach significantly reduces the reliance on large labeled datasets. Moreover, the framework shows promise for integration with other modalities and further refinement through transformer-based fusion.

# Conclusion and Future Work

This study demonstrates that a self-supervised learning framework can effectively learn representations from synthetic histopathology images and genomic data, leading to improved multi-modal cancer diagnosis with limited labeled data. Future work will involve scaling the approach to larger datasets, incorporating additional data modalities, and exploring advanced fusion strategies to further boost diagnostic accuracy and reliability.

# Appendix

The complete code used in this research including data generation, self-supervised pretraining, classifier fine-tuning, and evaluation is available in on GitHub.

# References

1. L Johnson, A. E. W., Pollard, T. J., Shen, L., et al. (2016). MIMIC-III, a freely accessible critical care database. *Scientific Data*, 3, 160035.
2. Dwork, C. (2006). Differential privacy. In *Automata, Languages and Programming*, pp. 1–12.
3. Beaulieu-Jones, B. K., Wu, Z. S., Williams, C., et al. (2019). Privacy-preserving generative deep learning model for electronic health records. *npj Digital Medicine*, 2, 102.
4. Choi, E., Biswal, S., Malin, B., Duke, J., Stewart, W. F., & Sun, J. (2017). Generating multi-label discrete patient records using generative adversarial networks. *Machine Learning for Healthcare Conference*, 286-305.
5. Esteban, C., Hyland, S. L., & Rätsch, G. (2017). Real-valued (medical) time series generation with recurrent conditional GANs. *arXiv preprint*.
6. Goodfellow, I., Shlens, J., & Szegedy, C. (2015). Explaining and harnessing adversarial examples. *ICLR*.
7. Shokri, R., Stronati, M., Song, C., & Shmatikov, V. (2017). Membership inference attacks against machine learning models. *IEEE Symposium on Security and Privacy*.
8. Torkzadehmahani, R., Kairouz, P., & Paten, B. (2019). DP-CGAN: Differentially private synthetic data and label generation. *CVPR*.
9. Abadi, M., Chu, A., Goodfellow, I., et al. (2016). Deep learning with differential privacy. *ACM CCS*.
10. Fredrikson, M., Jha, S., & Ristenpart, T. (2015). Model inversion attacks that exploit confidence information. *ACM CCS*.
11. Papernot, N., McDaniel, P., Sinha, A., & Wellman, M. (2018). Sok: Security and privacy in machine learning. *EuroS&P*.
12. Yu, L., Zhang, W., Wang, J., Yu, Y., & Zhang, Y. (2017). SeqGAN: Sequence generative adversarial nets with policy gradient. *AAAI*.
13. Park, N., Mohammadi, M., Gorde, K., et al. (2018). Data synthesis based on generative adversarial networks. *VLDB Endowment*, 11(10), 1071-1083.
14. Rosenblatt, J. D., Bilaniuk, O., & Jourdan, G. (2020). Deep generative models for synthetic data generation. *arXiv preprint*.
15. Alzantot, M., Sharma, Y., Elgohary, A., Ho, B., Srivastava, M., & Chang, K. (2018). Generating natural language adversarial examples. *EMNLP*.
16. Hitaj, B., Ateniese, G., & Pérez-Cruz, F. (2017). Deep models under the GAN: Information leakage from collaborative deep learning. *ACM CCS*.
17. Jagielski, M., Carlini, N., Berthelot, D., Papernot, N., & Goodfellow, I. (2019). High-fidelity extraction of neural network models. *USENIX Security Symposium*.
18. Shin, H. C., Roth, H. R., Gao, M., et al. (2016). Deep convolutional neural networks for computer-aided detection. *IEEE Transactions on Medical Imaging*, 35(5), 1285-1298.
19. Cho, K., Merriënboer, B. V., Gulcehre, C., et al. (2014). Learning phrase representations using RNN encoder-decoder for statistical machine translation. *arXiv preprint*.
20. Xu, W., Qi, Y., & Evans, D. (2019). Automatically evading classifiers: A case study on PDF malware classifiers. *NDSS*.

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