Topological Few Shot Learning for Biomedical Imaging

Philmore Koung
Department of Mathematics ,University of Texas at Dallas
philmore.koung@utdallas.edu

Baris Coskunuzer
Department of Mathematics ,University of Texas at Dallas
coskunuz@utdallas.edu

***Abstract*— Over the past decade, deep learning (DL) methods have become foundational in biomedical imaging. However, their success largely depends on the availability of large, high-quality datasets—an essential yet challenging requirement in computer-aided diagnosis (CAD). These challenges arise due to the scarcity of labeled samples, privacy concerns, and the high costs of data acquisition.**

To tackle this issue, we propose using topological data analysis (TDA), specifically cubical persistence, as an alternative to CNNs in data-constrained settings. Cubical persistence generates direct embeddings of images by capturing topological structures. Our initial experiments indicate that TDA embeddings can significantly enhance CNN performance in data-limited environments.

***Clinical relevance*— In biomedical imaging settings where data is limited, incorporating topological vectors into deep learning models, or utilizing them independently, can improve diagnostic accuracy and reliability, providing a valuable tool for medical fields with limited data availability.**

I. INTRODUCTION

Deep learning has demonstrated significant efficacy in pattern recognition tasks and holds considerable promise in healthcare applications. However, the development of robust deep learning models for computer-aided diagnosis (CAD) faces several challenges, including limited training data, imbalanced datasets, and the complexities of data augmentation [1], [2]. The recent integration of topological data analysis (TDA) into machine learning offers a novel approach to addressing these challenges, particularly in limited data or few-shot scenarios.

II. MATERIALS & METHODS

Cubical persistence, a well-established method in TDA particularly suited for image data, is central to our approach. Given an image $\mathscr{X}$, we create a nested sequence of binary images $\mathscr{X}_1 \subset \cdots \subset \mathscr{X}_N$, tracking the topological changes throughout this sequence [3]. For each image, we then compute 100-dimensional Betti vectors that encapsulate these topological changes.

For our experiments, we used publicly available datasets from the MedMNIST collection (https://medmnist.com). To ensure balanced class representation, we randomly sampled an equal number of images for each class. The data was divided using an 80/20 train/test split, with 20% of the training set further allocated for validation.

1. Vanilla CNN: We employed the untrained base network ResNet50 to extract high-level features from the image data. After global average pooling, two fully connected layers with 128 and 64 units, respectively, and ReLU activation was applied.

TABLE I
AUC PERFORMANCES FOR OUR MODELS WITH DIFFERENT SPLITS.

	BLOOD			BREAST		
Split	**CNN**	**TDA**	**CNN+TDA**	**CNN**	**TDA**	**CNN+TDA**
80/20	50.68	76.52	**77.04**	56.25	**87.75**	78.25
200/50	80.41	83.63	**87.12**	58.36	75.56	**81.34**
400/100	65.09	**87.24**	86.56	70.72	71.76	**72.01**
	PNEUMONIA			**DERMA**		
Split	**CNN**	**TDA**	**CNN+TDA**	**CNN**	**TDA**	**CNN+TDA**
80/20	52.75	**72.00**	65.25	50.65	59.73	**63.79**
200/50	81.08	65.24	**88.99**	62.21	58.84	**63.11**
400/100	86.84	70.89	**88.56**	66.29	57.62	**68.70**

2. Vanilla-TDA: For the topological features, we used a Multi-Layer Perceptron (MLP) with two dense layers, containing 128 and 64 units and ReLU activation functions.
3. CNN+TDA: We combined the outputs from the CNN and MLP into a final dense layer, utilizing the softmax activation function.

All models were trained using the Adam optimizer, categorical cross-entropy loss function, a batch size of 32, and 100 epochs.

III. RESULTS

We present our results in Table I. Our results show a consistent increase from our vanilla CNN model to our TDA + CNN model and MLP. Across our 3 different dataset sizes, we can see vast improvements in AUC. One notable observation is the standalone performance of TDA method is shoulder to shoulder with CNN models.

IV. DISCUSSION & CONCLUSION

Our preliminary experiments demonstrate that integrating topological vectors can result in more robust and accurate models than conventional CNNs in scarce data settings, addressing a critical need in biomedical imaging. We aim to expand this study by applying the approach to additional datasets, and subtler integration methods with state-of-the-art deep learning models to further assess the effectiveness of combining TDA and DL techniques in biomedical imaging settings with limited data.

REFERENCES

[1] J. Kotia *et al.*, "Few shot learning for medical imaging," *Machine learning algorithms for industrial applications*, pp. 107–132, 2021.
[2] R. Schäfer *et al.*, "Overcoming data scarcity in biomedical imaging with a foundational multi-task model," *Nature Computational Science*, pp. 1–15, 2024.
[3] A. Yadav *et al.*, "Histopathological cancer detection with topological signatures," in *2023 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*. IEEE, 2023, pp. 1610–1619.