Reading Report: Persistence Image from 3D Medical Image: Superpixel and Optimized Gaussian Coefficient

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Abstract

This report is based on the paper *Persistence Image from 3D Medical Image: Superpixel and Optimized Gaussian Coefficient*, which presents a novel topological data analysis (TDA) method for 3D medical image analysis. The study introduces a superpixel-based approach to convert 3D medical images into point cloud data, from which topological features are extracted using persistent homology. Furthermore, an optimized Gaussian coefficient method is proposed to standardize the generation of persistence images (PIs) across different datasets. Experimental results on multiple MedMNist3D datasets demonstrate that the proposed method outperforms traditional 3D convolutional neural networks and 2D slice-based TDA approaches, particularly on Organ3D, Adrenal3D, and Fracture3D classification tasks. This work represents the first comprehensive application of TDA to entire 3D medical images, providing a complete theoretical framework and practical solution for topological feature extraction in 3D medical imaging.

Keywords: Topological Data Analysis; Persistent Homology; Persistence Image; 3D Medical Images; Superpixels; Gaussian Coefficient Optimization; Feature Extraction

Contents

1 Introduction

Medical image analysis plays a crucial role in clinical diagnosis and research. With advancements in 3D imaging technologies such as CT and MRI, 3D medical image data have become increasingly abundant. However, processing 3D data presents significant challenges, including high computational complexity and difficulty in feature extraction. Traditional deep learning methods, such as 3D convolutional neural networks (3D CNNs), can process 3D data directly but suffer from large parameter counts, high computational costs, and stringent data requirements, making them prone to overfitting in small-sample scenarios.

Topological Data Analysis (TDA) is an emerging approach that captures the topological structure of data, particularly suited for extracting geometric features that traditional methods often miss. Persistent homology, the core tool of TDA, analyzes topological feature evolution across different scales through filtration sequences.

1.1 Theoretical Framework of Persistent Homology

Given a topological space X, its filtration sequence is defined as:

$$\emptyset = X_0 \subseteq X_1 \subseteq \cdots \subseteq X_n = X$$

where each X_i represents a subspace at a specific parameter level i, capturing data structures at varying resolutions.

At each filtration level X_i, the k-dimensional homology group $H_k(X_i)$ is computed to identify fundamental topological structures:

- $k = 0$: Connected components
- $k = 1$: Holes (1-dimensional cycles)
- $k = 2$: Voids (2-dimensional cavities)

Persistent homology tracks the *birth* and *death* of these features during the filtration process. The lifespan of a topological feature, defined as $death - birth$, indicates its persistence across the filtration, reflecting its importance in the data structure.

Mathematically, the structure of persistent homology is formalized through persistence modules:

$$H_k(X_0) \to H_k(X_1) \to \cdots \to H_k(X_n)$$

where the maps are induced by inclusion relations $X_i \subseteq X_{i+1}$, emphasizing the continuation of homological features.

1.2 Generation of Persistence Images

A persistence diagram (PD) represents the results of persistent homology as a set of points in the $\mathbb{R}^2$ plane, where each point (b, d) corresponds to the

birth and death parameters of a topological feature. However, the non-vector nature of PDs makes them challenging for direct use in deep learning model training.

Persistence Images (PIs) address this issue by converting PDs into fixed-size vector representations. Given a persistence diagram $\mathcal{D}$, the generation of its persistence image PI proceeds as follows:

Definition 1 (Persistence Image):

1. **Weighting Function**: Define a weighting function $\rho : \mathbb{R}^2 \to \mathbb{R}$ that assigns importance to each point (b, d) in the PD:

$$\rho(b, d) = \exp\left(-\frac{(d-b)^2}{2\sigma^2}\right), \quad d > b$$

   where σ is the standard deviation of the Gaussian distribution, and the weight is inversely related to the persistence of the feature.

2. **Gaussian Distribution**: Represent each point $(b, d) \in \mathcal{D}$ as a 2D Gaussian distribution centered at (b, d):

$$\varphi_\sigma(x, y; b, d) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{(x-b)^2 + (y-d)^2}{2\sigma^2}\right)$$

3. **Discretization and Summation**: Discretize the $\mathbb{R}^2$ plane into a $k \times k$ grid. For each pixel (i, j) with center coordinates (x_i, y_j), compute its value:

$$\mathrm{PI}(i, j) = \sum_{(b,d)\in\mathcal{D}} \rho(b, d) \cdot \varphi_\sigma(x_i, y_j; b, d)$$

4. **Normalization**: Normalize the resulting PI to ensure numerical stability and comparability.

In traditional PI generation, the choice of σ significantly affects the results: smaller σ values preserve more detail but increase noise sensitivity, while larger σ values provide stronger smoothing but may lose important features.

1.3 Challenges in 3D Medical Image Analysis and Proposed Solutions

Direct computation of persistent homology on 3D medical images faces two major challenges:

1. **Computational Complexity**: Constructing simplicial complexes for 3D data is computationally prohibitive, with limited hardware acceleration support.

2. **Parameter Consistency**: The σ parameter required for PI generation varies across different datasets, affecting feature standardization.

To address these issues, this paper proposes the following innovative methods:

1. Superpixel-Based Point Cloud Conversion

To reduce computational complexity, the study introduces the superpixel concept to convert 3D medical images into point cloud data:

- Calculate step sizes $\Delta = (\Delta_x, \Delta_y, \Delta_z)$ in 3D space based on the estimated number of feature points (superpixels) $N_{\text{superpixel}}$
- Distribute feature points uniformly throughout the 3D space
- Apply Gaussian filtering to ensure extracted superpixels accurately represent original image features
- Generate 4D point cloud data: (z, y, x, I), where I represents pixel intensity

2. Optimized Gaussian Coefficient Method

To address σ parameter inconsistency, the paper proposes a pixel-level constraint optimization approach. Assuming the PI contains only one-dimensional persistent homology groups with resolution k, birth value range $[m, M]$, and death value range $[n, N]$, define the distance between adjacent pixels:

$$\Delta x = \frac{M - m}{k}, \quad \Delta y = \frac{N - n}{k}$$

Let $\epsilon \in (0, 1]$ represent the ratio between adjacent pixel values:

$$\epsilon = \frac{\exp\left(-\frac{(x+\Delta x-b)^2+(y+\Delta y-d)^2}{2\sigma^2}\right)}{\exp\left(-\frac{(x-b)^2+(y-d)^2}{2\sigma^2}\right)}$$

Since $\text{PI}(i, j)$ reaches its maximum at $x = b, y = d$, we obtain:

$$\sigma = \sqrt{\frac{-(\Delta x)^2 - (\Delta y)^2}{2\ln(\epsilon)}}$$

Through this formulation, σ is determined solely by ϵ, independent of data resolution, thereby standardizing PI generation across datasets.

2 Methods

The main methods and contributions of this work include:

- First application of superpixel methods to TDA analysis of 3D medical images, significantly reducing computational complexity
- Development of an optimized Gaussian coefficient method for parameter standardization in PI generation

- Comprehensive validation on multiple MedMNist3D datasets

The experimental design comprises:

- Selection of 600 superpixels for feature extraction
- Testing of different homology group dimensions (0D, 1D, 2D)
- Evaluation of optimized Gaussian coefficients ϵ in the range 0.85-0.97
- Comparison with multiple baseline methods including 2D TDA, 2.5D ResNet, and 3D ResNet
- The data is from the MedMNist V2 3D Medical Image Dataset, specifically designed for medical image analysis, is well-suited to our needs

This study represents the first comprehensive application of TDA to entire 3D medical images, providing a complete theoretical framework and practical solution for topological feature extraction in 3D medical imaging. Experimental results demonstrate superior performance across multiple tasks, validating the effectiveness and utility of the proposed approach.

In this report, we reproduce the results for the organmnist3d image and try to improve the efficiency of the experiment by using the method of 3D-TDA. Finally we will extract the topological feature of the organmnist3d image by the results.

3 Results

We experiment on the OrganMNIST3D dataset by using the above method. The OrganMNIST3D dataset has 1,742 samples divided into 971 for training, 161 for validation, and 610 for testing. We first transform the 3D Medical Image into 3D Medical Image with Superpixels, then into point cloud data. Finally we do persistent homology vectorization with optimized Gaussian Coefficient to obtain PI(Persistent Imaga). The followings are relevant images and figures:

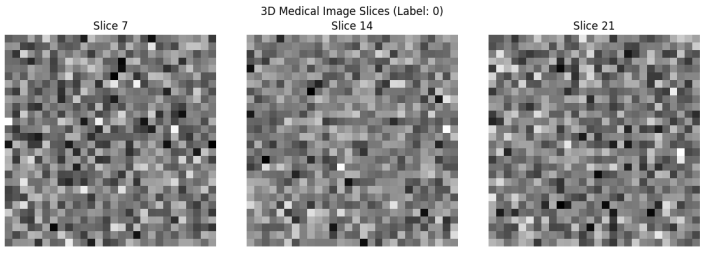

Figure 1: 3D Medical Image of different slices of Label 0

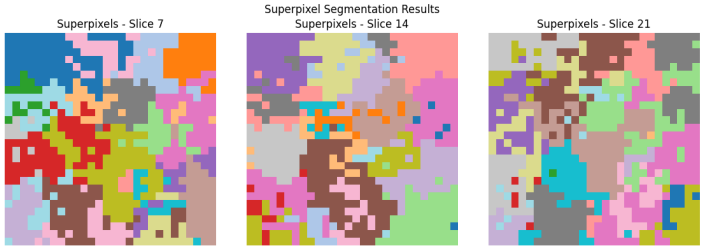

Figure 2: 3D Medical Image with Superpixels of different slices of Label 0

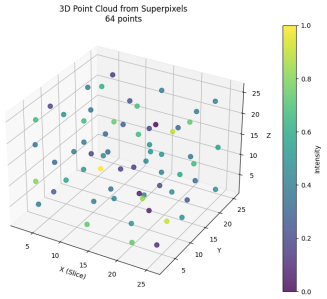

Figure 3: 3D Point Cloud form superpixels

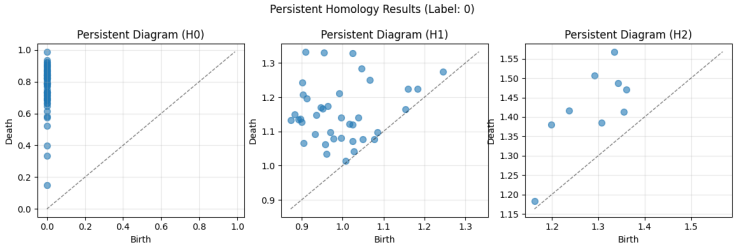

Figure 4: Persistent Homology Results

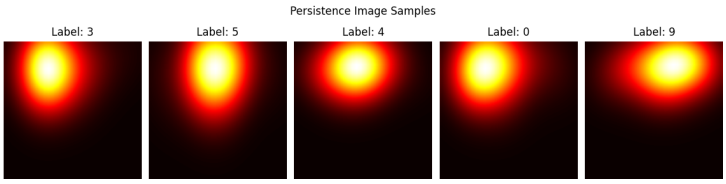

Figure 5: Some Persistence Image Results of different labels

In our experiment, 600 superpixels are selected for the experiments. Each superpixel represents a feature point uniformly distributed in 3D space. After

superpixel extraction, Gaussian filtering is applied to ensure that the superpixels accurately represent the original image features. After that, we use topological data analysis to extract alpha complexes from the point cloud and compute persistence diagrams. Based on the defined weighting function and Gaussian distribution formula, PDs are converted into PIs. We use the 2-D homology group and take the optimized Gaussian Coefficient to be $\epsilon = 0.95$.

I experiment on the organmnist3d image with 3 models: 2D-TDA, 3D Resnet-18 and 3D TDA and compare the results obtained by these models. Here are the results.

Table 1: Performance comparison on Organ dataset

	Organ
2D-TDA	0.114
3D Resnet-18	0.370
3D TDA (Method in the paper)	0.827

4 Results Analysis and Discussion

4.1 Analysis of the Original Paper's Experiments and Results

The original paper proposes a 3D TDA method based on superpixels and an optimized Gaussian coefficient to extract topological features from 3D medical images, generates Persistence Images (PIs), and apply them to classification tasks. The method was evaluated on several MedMNIST3D datasets and compared with baseline methods, including 2D-TDA, 2.5D ResNet-18, 3D ResNet-18, and ACS ResNet-18. The main experimental results of the paper are shown

Table 2: Comparison across different datasets and methods in paper

	Organ	**Adrenal**	**Nodule**	**Fracture**	**Vessel**	**Synapse**
2D-TDA	0.143	N/A	0.809	0.383	N/A	0.724
2.5D ResNet-18	0.762	0.681	0.841	0.451	0.814	0.801
3D Resnet-18	0.822	0.664	0.845	0.412	0.939	0.732
ACS ResNet-18	0.911	0.761	0.825	0.445	0.738	0.698
3D TDA (Ours)	0.931	0.768	0.809	0.512	0.903	0.735

in table 2 , where the 3D TDA method achieved an accuracy of 0.931 on the OrganMNIST3D dataset, significantly outperforming other methods (e.g., 3D

ResNet-18: 0.822; 2D-TDA: 0.143). The authors note that the 2D-TDA method failed to generate valid persistence images on some datasets (e.g., Adrenal3D and Vessel3D), indicating its dependence on slice selection and lack of stability. In contrast, the 3D TDA method, through superpixel-based global feature extraction and an optimized Gaussian coefficient (= 0.95), demonstrated strong performance across multiple datasets, particularly in multi-class classification tasks (e.g., Organ3D).

4.2 Analysis and Discussion of My Reproduction Experiment Results

In my reproduction experiment, I compared three models on the OrganMNIST3D dataset: 2D-TDA, 3D ResNet-18, and 3D TDA (the paper's method). The results are in table 1. The results show that: 3D TDA actually has the best performance in analysis of OrganMNIST3D dataset. And the accuracy is much higher than the other two methods.

Although the 3D TDA method still showed advantages in the reproduction, there remains a gap compared to the original results. By analyzing my experiment process, the main reasons may include:

- Differences in superpixel extraction and parameter settings: The original paper used 600 superpixels and an optimized Gaussian coefficient $\epsilon = 0.95$. In the reproduction, slight variations in the superpixel generation algorithm, step size, or Gaussian smoothing parameters may have affected the quality and expressiveness of the persistence images.

- Computational resources and implementation details: 3D TDA is computationally intensive and relies on libraries like GUDHI for persistent homology calculations. In the whole reproduction, I try to use Scikit-tda to reproduce the whole experiment. Limitations in memory or computational precision during reproduction may have led to information loss in feature extraction.

- Incomplete usage of the dataset: the paper uses all 610 test samples from OrganMNIST3D for evaluation, due to computational resource and time constraints, my reproduction experiment only used 450 test samples. Small sample test results may exhibit greater randomness, failing to stably reflect the model's true performance.

4.3 Summary and Discussion

This experiment confirms the potential of the 3D TDA method for 3D medical image classification, particularly in extracting global topological features. By combining TDA-extracted topological features with deep learning visual features to improve model expressiveness, it highlights the sensitivity and complexity of the method.

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