

BlockGCN: Redefine Topology Awareness for Skeleton-Based Action Recognition

Supplementary Material

A. Supplementary Material Structure

This supplementary material provides additional technical explanations and experimental validations to support and expand upon the main text of our work. The contents are organized as follows:

1. Detailed elaboration of the dynamic topological encoding scheme, Sec. B.
 - (a) Definition and illustration of essential terms and concepts, Sec. B.1.
 - (b) Theoretical foundation and methodology of persistent homology analysis for graph-structured data, Sec. B.2.
 - (c) Comprehensive explanation of the adopted vectorization representation strategy, Sec. B.3.
2. In-depth discussion of the hyperparameter settings and optimization of BlockGCN, Sec. C.
3. Extended experimental validations and analysis, Sec. D.
 - (a) Evaluation and comparison of single modality performance, Sec. D.1.
 - (b) Investigation of the impact of different graph distance metrics on model performance, Sec. D.2.
 - (c) Visual exploration and interpretation of the learned feature representations, Sec. D.4.

B. Technical Preliminaries

B.1. Fundamentals of Algebraic Topology

Topological data analysis (TDA) [54] leverages algebraic topology tools, such as persistent homology [22], to extract topological features, including connected components and cycles, from graph data that persist across multiple scales [2]. These topological descriptors have been shown to be effective representations for graph classification tasks [52, 75]. Furthermore, integrating these topological features with deep learning architectures has achieved significant success in enhancing the representational power of the models [18, 31, 47, 69, 72, 75]. In this section, we first introduce the core notations and concepts, followed by a general description of persistent homology analysis for graph data, and finally present a toy demonstration for intuitive understanding. For more detailed descriptions and formal illustrations of these techniques, we refer the reader to the corresponding literature in computational topology and topological data analysis [9, 23, 28].

Simplicial Complex: A simplicial complex is composed of simplices of different dimensions, such as vertices (0-simplices), edges (1-simplices), triangles (2-simplices), and tetrahedra (3-simplices). Given a k -simplex denoted as

$\sigma = [v_0, \dots, v_k]$, deleting one of its vertices v_i results in a $(k-1)$ -simplex $[v_0, \dots, \hat{v}_i, \dots, v_k]$ (\hat{v}_i denotes the deleted vertex), which is called the i -th *face* of σ . A simplicial complex \mathcal{K} is defined as a set of simplices of varying dimensions that satisfies the following conditions:

1. Any face τ of a simplex $\sigma \in \mathcal{K}$ is also in \mathcal{K} (i.e., $\tau \in \mathcal{K}$).
2. If $\sigma_1, \sigma_2 \in \mathcal{K}$ and $\sigma_1 \cap \sigma_2 \neq \emptyset$, then $\sigma_1 \cap \sigma_2$ is a face of both σ_1 and σ_2 .

A graph \mathcal{G} is a simplicial complex \mathcal{K} consisting only of vertices (0-simplices) and edges (1-simplices).

Boundary Map: Given a simplicial complex \mathcal{K} , consider the vector space $C_\kappa(\mathcal{K})$ generated with \mathbb{Z}_2 (the field with two elements). The boundary map is denoted as $\partial_\kappa : C_\kappa(\mathcal{K}) \rightarrow C_{\kappa-1}(\mathcal{K})$. For a k -simplex $\sigma = [v_0, \dots, v_k] \in \mathcal{K}$, the boundary map is defined as:

$$\partial_\kappa(\sigma) := \sum_{i=0}^k (v_0, \dots, v_{i-1}, v_{i+1}, \dots, v_k) \quad (7)$$

In other words, each vertex v_i of the simplex is omitted once. The boundary operator ∂ is a homomorphism between the simplicial chain groups, providing a precise way to define connectivity [31].

Homology: Homology theory employs commutative algebra tools to study topological features, such as connected components ($\kappa = 0$) and cycles ($\kappa = 1$) in a graph [23], using the boundary operator. The κ -th homology group $\mathbb{H}_\kappa(\mathcal{K})$ of a simplicial complex \mathcal{K} is defined as the quotient group:

$$\mathbb{H}_\kappa(\mathcal{K}) := \ker \partial_\kappa / \text{im} \partial_{\kappa+1} \quad (8)$$

The elements in $\ker(\partial_\kappa)$ and $\text{im}(\partial_{\kappa+1})$ are called κ -cycles and κ -boundaries, respectively. The resulting homology groups $\mathbb{H}_\kappa(\mathcal{K})$ are topological invariants that remain unchanged under homeomorphisms and encode intrinsic information [28].

Betti Numbers: Betti numbers, defined as the ranks of the homology groups, serve as simpler invariants for classifying topological spaces. For $\mathbb{H}_\kappa(\mathcal{K})$, the 0-th Betti number $\beta_0 = \text{rank} \mathbb{H}_0(\mathcal{K})$ represents the number of connected components, while the 1-st Betti number $\beta_1 = \text{rank} \mathbb{H}_1(\mathcal{K})$ represents the number of cycles when $\kappa = 0$ and $\kappa = 1$, respectively. However, these counting-based topological summaries are too coarse to capture the complexity of graph structures. To address this limitation, a persistent version of homology-based topological invariant analysis is proposed, as described in the following section.

B.2. Persistent Homology Analysis for Graphs

In this subsection, we provide an overview of the persistent homology analysis for graphs, followed by an intuitive demonstration using a 5-node graph example. We then introduce the key notations and concepts for further reference.

Intuitive Demonstration: Consider an undirected graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ with a vertex set \mathcal{V} and an edge set $\mathcal{E} \subseteq \mathcal{V} \times \mathcal{V}$. Given a threshold value ϵ , we can obtain a series of graphs by setting the edge weights $w_{ij}^{(\epsilon)}$ to 1 if $w_{ij} > \epsilon$, and 0 otherwise. Treating the graph \mathcal{G} as a simplicial complex \mathcal{K} , we generate a sequence of simplicial complexes, termed as a *filtration*, $\{\mathcal{K}^i\}_{i=0}^m$, where $\emptyset = \mathcal{K}^0 \subseteq \mathcal{K}^1 \subseteq \dots \subseteq \mathcal{K}^m = \mathcal{K}$, by increasing the threshold value ϵ . As the filtration parameter increases, more edges are removed from the graph. In extreme cases, when $\epsilon \rightarrow -\infty$, the graph becomes complete, and when $\epsilon \rightarrow \infty$, the graph reduces to a vertex set \mathcal{V} . For each sub-complex, we record the topological invariants, such as connected components and cycles, to describe the graph structure. During this filtration process, each topological object (i.e., homology) may appear at a specific ϵ_i and disappear at another value ϵ_j . The interval $\{\epsilon_i, \epsilon_j\}$ is called its *persistence*. *Persistent homology* analysis captures the global structure of graphs by recording these paired filtration values in the nested sequence. *Persistence barcodes* and *persistence diagrams* are used to represent the paired set $\{(b_i^{(0)}, d_i^{(0)})\}_{i=1}^n$, where $\mathcal{D}_i^{(0)} = (b_i^{(0)}, d_i^{(0)})$ and $b_i^{(0)}, d_i^{(0)} \in \{\epsilon_0, \epsilon_1, \dots, \epsilon_k\}$ for connected components, and superscripts equal to 1 for cycles.

Figure 7 presents an intuitive demonstration of a 5-node graph filtration with threshold values $\epsilon = 0, 1, \dots, 9$. As ϵ increases from 0 to 9, edges gradually appear, forming different combinations of connected components and cycles. For example, when ϵ increases from 0 to 1, the number of connected components decreases from 5 to 4 as one edge emerges. When ϵ increases from 2 to 3, a cycle appears and persists until $\epsilon = 9$. Through this counting and recording process, the geometrical structure of a weighted graph is explored globally.

Persistent Homology: Given a filtration of \mathcal{K} denoted as $\{\mathcal{K}^i\}_{i=0}^m$, we have a corresponding sequence of chain complexes $C_\kappa(\mathcal{K}^i)$. The concept of homology groups is extended from $\mathbb{H}_\kappa^i(\mathcal{K}) := \ker \partial_\kappa^i / \text{im} \partial_\kappa^{i+1}$ (dependent on a single simplicial complex \mathcal{K}^i) to its persistent version (from \mathcal{K}^i to \mathcal{K}^j) as:

$$\mathbb{H}_\kappa^{i,j}(\mathcal{K}) := \ker \partial_\kappa^j / (\text{im} \partial_\kappa^j \cap \ker \partial_\kappa^i) \quad (9)$$

The ranks of all the homology groups $\beta_\kappa^{i,j} = \mathbb{H}_\kappa^{i,j}(\mathcal{K})$ (namely the κ -th persistent Betti numbers) capture the number of homological features of dimensionality κ (e.g., connected components for $\kappa = 0$, cycles for $\kappa = 1$, etc.) that persist from i to (at least) j [29].

Persistence Barcodes of Filtration: For simplification,

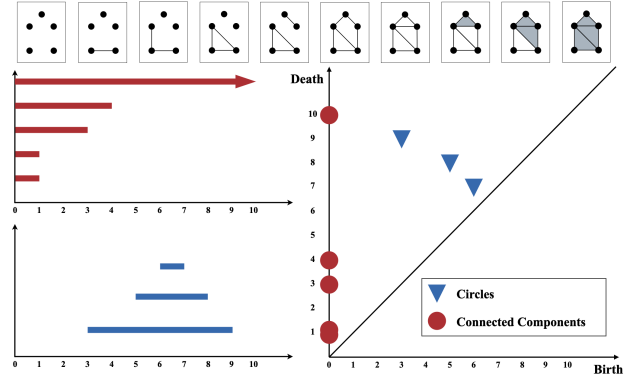


Figure 7. A graph filtration with $\epsilon = 0, 1, 2, 3, 4, 5, 6, 7, 8, 9$ (from left to right): (a) the persistence barcodes of connected components (up) and cycles (down); (b) corresponding persistent diagram of connected components (red disk) and cycles (blue triangle). [Best viewed in zoom and color]

we use \mathbb{R}^2 of $\{\mathcal{D}_1^{(0)}, \mathcal{D}_2^{(0)}, \dots, \mathcal{D}_p^{(0)}\}$, where $\mathcal{D}_i^{(0)} = \{(b_i^{(0)}, d_i^{(0)})\}$, to denote the barcodes extracted from \mathcal{K} . Formally, the filtration sequence of \mathcal{K} can be defined using a vertex filter function $f : \mathbb{V} \rightarrow \mathbb{R}$ with the filtration values $\epsilon_1 < \epsilon_2 \dots \epsilon_m$, where $\epsilon_i \in \{f(v) : \{v\} \in \mathcal{K}\}$. With function f , the filtration of \mathcal{K} is:

$$\mathcal{K}^{f,0} = \emptyset, \quad \mathcal{K}^{f,i} = \{\sigma \in \mathcal{K} : \max_{v \in \sigma} f(v) \leq \epsilon_i\} \quad (10)$$

for $1 \leq i \leq m$. Then, for the filtration of \mathcal{K} and homology dimension κ ($\kappa = 0, 1$ in this work), we obtain the persistence barcode representation $\{\mathcal{D}_i^{(0)}\}_{i=1}^m = \{(b_i^{(0)}, d_i^{(0)})\}_{i=1}^m$, which we denote as \mathcal{B} .

B.3. Vectorization Representation

The inconsistency of using persistence barcodes $\{(b_i^{(0)}, d_i^{(0)})\}_{i=1}^m$ in machine learning tasks has led to the development of various vectorization approaches, including statistical analysis [4, 46], kernel methods [6, 11, 36, 38, 51], distance metrics [15, 45], and \mathbb{R}^d elements [1, 3, 5, 8, 33].

Recently, learning-based techniques have been proposed to facilitate the integration of such graph descriptions into modern deep learning architectures by introducing learnable weights for each barcode [29, 31]. Typical embedding functions include the *rational hat* function [29], point transformation-based techniques [7], and the *DeepSets* approach [71] adopted in [31].

For computational efficiency and ease of implementation, we employ the *rational hat* function, as described in [29], for vectorization extraction due to its differentiability and expressive power in representing graphs. Mathematically, the *barcode coordinate function* maps a barcode in \mathcal{B} to a real value by aggregating the points in the persistence

Table 9. Default Hyperparameters for BlockGCN on NTU RGB+D, NTU RGB+D 120, and Northwestern-UCLA.

Config.	NTU RGB+D 60 and 120	NW-UCLA
random choose	False	True
random rotation	True	False
window size	64	52
weight decay	4e-4	3e-4
base lr	0.05	0.05
lr decay rate	0.1	0.1
lr decay epoch	110, 120	90 100
warm up epoch	5	5
batch size	64	16
num. epochs	140	120
optimizer	Nesterov Accelerated Gradient	Nesterov Accelerated Gradient

Table 10. Classification Accuracy (%) of BlockGCN using Different Modalities on NTU RGB+D, NTU RGB+D 120, and Northwestern-UCLA Dataset.

Modality	NTU-RGB+D		NTU-RGB+D 120		NW-UCLA
	X-Sub	X-View	X-Sub	X-Set	
Joint	90.9	95.4	86.9	88.2	95.5
Bone	91.3	95.3	88.1	89.3	93.3
Motion	88.7	93.3	82.7	84.6	92.9
Bone Motion	88.3	92.6	83.0	84.8	88.8
Ensembled	93.1	97.0	90.3	91.5	96.9

diagram via a weighted sum:

$$\Psi : \mathbb{B} \rightarrow \mathbb{R} \quad \mathcal{B} \rightarrow \sum_{(b,d) \in \mathcal{B}} s(b, d) \quad (11)$$

where $s : \mathbb{R}^2 \rightarrow \mathbb{R}$ is a differentiable function that vanishes on the diagonal of \mathbb{R}^2 . The rational hat structure element from [30] is defined as:

$$p \in \mathcal{B} \quad p \rightarrow \frac{1}{1 + \|p - c\|_1} - \frac{1}{1 + \|r\| - \|p - c\|_1} \quad (12)$$

where $c \in \mathbb{R}^2$ and $r \in \mathbb{R}$ are learnable parameters. This function evaluates the "centrality" of each point $p \in \mathbb{B}$ with respect to a learned center c and a learned shift/radius r .

In our implementation, we adopt the modified version of the *rational hat* function provided in the *Pytorch-topological*² library, which is based on the original implementation by [29]. This vectorization approach allows us to transform the persistence barcodes into fixed-length feature vectors that can be readily integrated with deep learning models, such as the BlockGCN architecture used in our work. By learning the parameters of the *rational hat* function, we can adaptively capture the most informative topological features for the given graph classification task, enhancing the expressive power and discriminative capability of our model.

²<https://pypi.org/project/torch-topological/>

C. Hyperparameter Settings

In this section, we provide the default hyperparameter settings used for training our BlockGCN model on the NTU RGB+D, NTU RGB+D 120, and Northwestern-UCLA datasets. Throughout our experiments, we consistently train a 10-layer BlockGCN with a maximum channel dimension of 256. Table 9 presents the default hyperparameters for our BlockGCN model on these datasets. These hyperparameter settings have been carefully tuned to achieve optimal performance on each dataset while maintaining a balance between model complexity and computational efficiency. By using consistent hyperparameter settings across all experiments, we ensure a fair comparison and evaluation of our BlockGCN model's performance on different datasets and modalities.

D. Extended Experimental Results

In this section, we present additional experimental results to provide a more comprehensive evaluation of our BlockGCN model's performance on various datasets and modalities.

D.1. Single Modality Performance

To gain further insights into the contribution of each modality to the overall performance of our BlockGCN model, we conduct experiments training the model on each single modality separately. Table 10 provides detailed results of our BlockGCN's performance on each modality for the different benchmark datasets. These results demonstrate the

effectiveness of our BlockGCN model in learning discriminative features from individual modalities, such as skeleton, RGB, depth, and infrared data. By examining the performance on each modality, we can identify the strengths and weaknesses of our model in capturing modality-specific information and guide future research efforts towards improving the fusion of multi-modal features. The single modality performance also serves as a baseline for evaluating the benefit of multi-modal fusion in our BlockGCN model. By comparing the results of single modality training with those of multi-modal fusion, we can quantify the synergistic effect of combining complementary information from different modalities to enhance the overall recognition accuracy.

D.2. Selection of Graph Distance for Static Topological Encoding

In the main text, we discuss the use of relative distances between joint pairs on the graph to symbolize graph topology. Theoretically, any proper graph distance can serve this purpose. In our work, we investigate two common graph distances for our Static Topological Encoding: the shortest path distance and the distance in the level structure [19]. Table 11 compares these two distances. Interestingly, both distances lead to an equivalent improvement, suggesting that they fundamentally convey the same information, i.e., bone connectivity. To streamline our approach, we default to employing the shortest path distance.

The choice of graph distance for Static Topological Encoding is an important consideration, as it directly influences the model’s ability to capture the intrinsic topology of the skeleton graph. By comparing the performance of different graph distances, we can identify the most informative and computationally efficient representation for encoding the graph topology. The equivalent improvement observed when using either the shortest path distance or the distance in the level structure indicates that both distances effectively capture the essential connectivity information of the skeleton graph. This finding simplifies the implementation of our Static Topological Encoding, as we can focus on using the shortest path distance without compromising the model’s performance.

Table 11. Comparing different graph distances for our Static Topological Encoding.

Graph Distance		Acc(%)
shortest path distance	level difference	
-	-	86.7
✓	-	86.9
-	✓	86.9

D.3. Choice of Simplicial Complex

In addition to the graph distance, we also explore the choice of simplicial complex for persistent homology analysis used in our dynamic topological encoding. Table 12 shows the comparison between two commonly used simplicial complexes: the Vietoris-Rips Complex and the Cubical Complex. The results indicate that using the Cubical Complex leads to a slight decrease of 0.2% in accuracy and significantly longer run time compared to the Vietoris-Rips Complex. Based on these findings, we adopt the Vietoris-Rips Complex for our dynamic topological encoding.

The choice of simplicial complex is crucial for efficient and effective persistent homology analysis. The Vietoris-Rips Complex, which is based on pairwise distances between points, provides a good balance between topological expressiveness and computational efficiency. On the other hand, the Cubical Complex, which is based on a cubical grid, may introduce additional computational overhead without providing significant benefits in terms of accuracy. By selecting the Vietoris-Rips Complex for our dynamic topological encoding, we ensure that our model can efficiently capture the evolving topological features of the skeleton graph over time, while maintaining high recognition accuracy.

Table 12. Comparing different simplicial complexes.

Vietoris-Rips Complex	Cubical Complex	Acc(%)
✓	-	86.9
-	✓	86.7

D.4. Visualization of Learned Representations

To gain further insights into the learned representations of our BlockGCN model, we provide additional visualizations of the Static Topological Encodings and the learned adjacency matrices.

Figure 8 presents more examples of the learned Static Topological Encodings, showcasing the model’s ability to capture the intrinsic topology of the skeleton graph. These visualizations illustrate how our model learns to encode the relative distances between joint pairs, effectively representing the connectivity information of the skeleton.

Figure 9 visualizes the learned adjacency matrices of our BlockGCN model. These matrices represent the learned graph structure and the strength of connections between different joints. By examining these visualizations, we can gain insights into how our model adapts the graph structure to better capture the dependencies and relationships between joints for action recognition. The visualizations of the learned Static Topological Encodings and adjacency matrices provide a qualitative assessment of our BlockGCN model’s learning process.

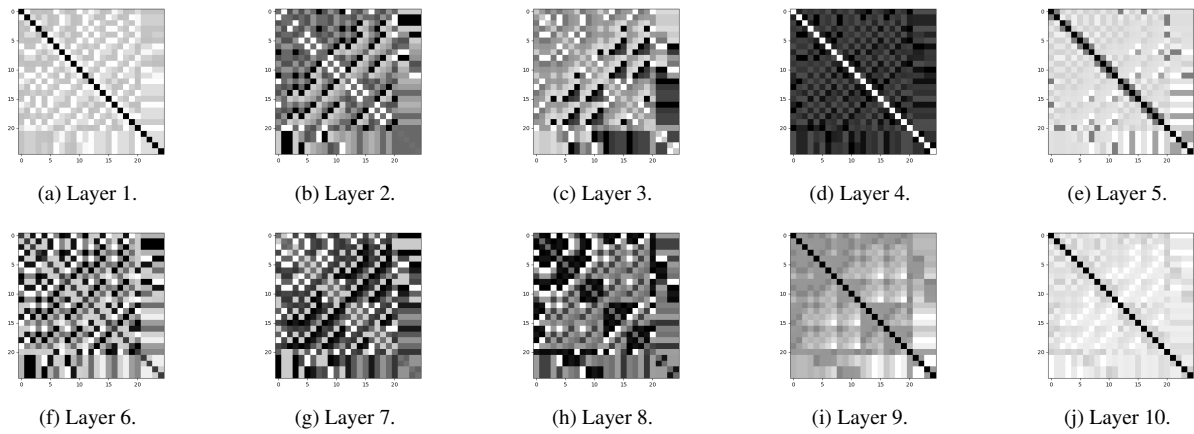


Figure 8. The learned Static Topological Encodings of our BlockGCN at each layer. It can be seen that the learned weights are diverse and adapted to different levels of semantics.

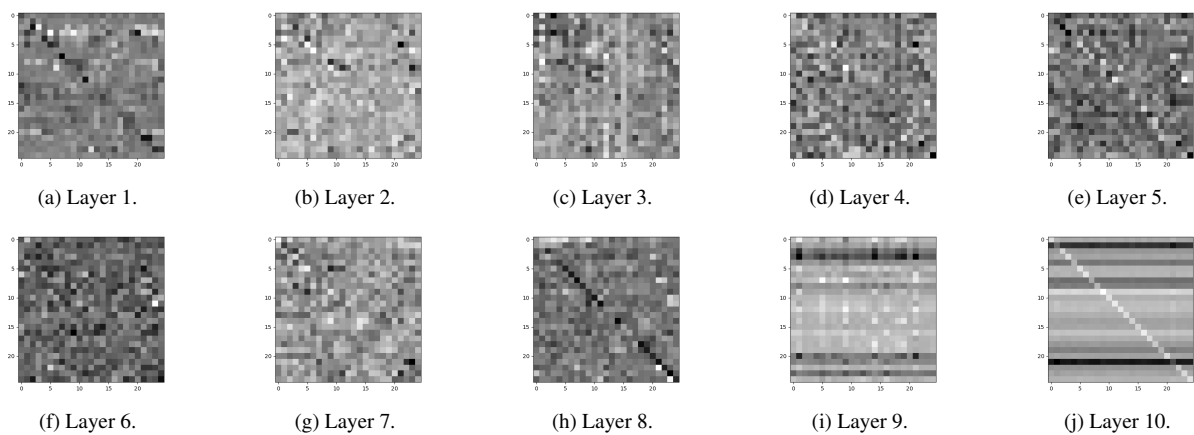


Figure 9. The learned adjacency matrices of the GCN baseline model at each layer (Darker colors stand for larger weights). It can be seen that the learned weights vary dramatically among different layers and deviate far from the bone connections, which are used for initialization.

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