

EEG-Based Emotion Recognition Using a Parallel Spatiotemporal Graph Attention Network

Jiawei Zhang¹, Xin Yan², Lingtao Tang³, Liguo Dong^{4,*}, Yuzhu Guo^{1,5,6,*}

¹ School of Automation Science and Electrical Engineering, Beihang University, Beijing, China

² Sino-French Engineer School, Beihang University, Beijing, China

³ School of Biomedical Engineering, Capital Medical University, Beijing, China

⁴ Department of Neurology, The Affiliated Hospital of Xuzhou Medical University, Xuzhou, Jiangsu, China

⁵ Beihang University-BoardWare-Barco BAloT Brain and Intelligence Joint Laboratory, Beijing, China

⁶ Beijing Key Laboratory of Brain-Computer Interface and Neuromodulation Therapy for Brain Disorders, Beijing, China

***Correspondence:** Liguo Dong, Department of Neurology, The Affiliated Hospital of Xuzhou Medical University, Xuzhou, Jiangsu 221002, China.

E-Mail: dongliguo@xzhmu.edu.cn

Yuzhu Guo, School of Automation Science and Electrical Engineering, Beihang University, Beijing 100191, China.

E-Mail: yuzhuguo@buaa.edu.cn

Abstract

Background: Electroencephalography (EEG)-based emotion recognition is a core technology for intelligent healthcare, supporting critical applications from early affective disorder screening to closed-loop neurorehabilitation. Graph Neural Networks (GNNs) are widely used for this task due to their strength in modeling non-Euclidean brain network topology. However, existing GNNs rely on static, uniform topologies, overlooking dynamic brain connectivity reorganization during emotional processing and neglecting unique contributions of distinct EEG frequency bands, limiting the clinical utility.

Materials and methods: This paper proposes a Parallel Spatiotemporal Graph Attention network (PSGA). It constructs spatiotemporal graphs through temporally jointed segments to capture dynamic functional connectivity and attention-based cross-temporal associations, adopts frequency band-specific parallel graph attention modules to learn dynamic time-varying topological structures, and aggregates node connections to enhance model interpretability.

Results: In cross-trial and cross-subject settings on the SJTU Emotion EEG Dataset (SEED), PSGA achieved $85.59\% \pm 12.34\%$ and $78.85\% \pm 11.56\%$ accuracy, exceeding the best baselines by 3.04% and 14.45%. On Database for Emotion Analysis using Physiological Signals (DEAP), it attained $65.30\% \pm 7.20\%$ for valence and $70.34\% \pm 9.82\%$ for arousal (cross-trial), with stable performance. Identified emotional brain patterns aligned with neuroscience findings.

Conclusion: PSGA can extract emotion-related EEG features through parallel spatiotemporal graph modeling. It provides a new perspective for exploring emotional brain mechanisms and shows potential for practical intelligent healthcare applications.

Keywords: EEG emotion recognition; Graph Attention Network; dynamic connectivity

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Introduction

Emotion recognition is a core enabling technology for intelligent healthcare, as affective states are closely tied to mental health status, neurorehabilitation outcomes, and quality of life for patients with affective and neuropsychiatric disorders. Accurate emotion decoding not only advances our understanding of human cognitive and affective mechanisms, but also directly supports a wide range of clinical intelligent healthcare applications, including early risk stratification of depression and anxiety disorders, closed-loop neuromodulation for neurorehabilitation, and personalized mental health intervention. Compared to subjective self-report scales and non-physiological modalities, electroencephalography (EEG) signals non-invasively capture the dynamic functional interactions between distributed brain regions, offering objective, quantifiable neurobiological markers of emotional responses^[1]. This objectivity addresses a key limitation of traditional clinical assessment, making EEG-based emotion recognition a foundational tool for data-driven intelligent healthcare systems.

To translate EEG emotion recognition into reliable clinical intelligent healthcare tools, developing deep learning models grounded in neuroscience principles has become a critical research priority. A growing body of work has focused on decoding emotional states by modeling functional connectivity in brain networks, which aligns model design with the underlying neurophysiology of emotion processing^[2–4].

Connectivity in brain networks refers to the dynamic coordination of neural activities across distributed brain regions, a core biomarker for affective and neuropsychiatric disorders in clinical neuroscience. It primarily encompasses two complementary dimensions: functional and effective connectivity^[5]. Functional connectivity describes the temporal correlation or statistical dependency between spatially separated neural units, while effective connectivity characterizes the causal, directional influence of one neural region on another, defining the regulatory pathways that underpin emotional processing^[6]. In this paper, we follow the standard definition that effective connectivity refers to causal and directional influence. Unless otherwise specified, we use the term connectivity to describe model-inferred interaction

patterns or associations rather than causal effective connectivity.

Leveraging these network neuroscience insights, Graph Neural Network (GNN) frameworks have been developed for EEG emotion recognition, laying a technical foundation for intelligent healthcare applications. Related advances in intelligent healthcare also highlight the importance of interpretability and generalization^[7,8]. For example, Song et al.^[9] proposed an EEG-based multi-channel signal recognition algorithm utilizing a dynamic graph convolutional neural network (DGCNN), which constructs a graph using various electrode channels. Zhong et al.^[10] proposed a Regularized Graph Neural Network (RGNN) that leverages the biological topology of EEG channels to enhance emotion recognition, incorporating neuroscience-inspired adjacency matrices and novel regularization strategies. Wang et al.^[11] proposed a transformer-based model for emotion recognition using EEG, designed to hierarchically capture spatial dependencies from electrode-level to brain-region-level, overcoming limitations of conventional convolutional and recurrent networks in capturing long-range dependencies.

Despite significant advancements, few studies on EEG emotion recognition consider time-varying connectivity patterns across different time points within the brain. This oversight can lead to the loss of critical information and lead to poor interpretability^[12].

With the impressive performance of large models in natural language processing and computer vision tasks, increasingly complex architectures have also been introduced into EEG-based emotion recognition^[13]. The growing complexity of these models often makes their internal mechanisms difficult to interpret^[14], which limits the applications of these models, especially in clinical scenarios. Therefore, when designing models related to brain–computer interfaces (BCIs), it is expected to balance the model performance and interpretability effectively to ensure both effectiveness and transparency.

In this study, we propose a Parallel Spatiotemporal Graph Attention network (PSGA) for EEG-based emotion recognition, using band-pass filtered EEG signals and differential entropy (DE) features as inputs. By incorporating a fully-connected graph attention mechanism

across three consecutive time segments, this model aggregates information along spatial, temporal, and spectral dimensions, resulting in an efficient and interpretable GNN. The primary contributions of this study are as follows:

Temporally jointed EEG segments were used as inputs: fully connected graphs across time segments enable modeling attention-based cross-temporal associations of EEG signals.

A parallel spatiotemporal graph attention neural network structure: the Graph Attention Network (GAT) is utilized for emotion-related feature extraction. It is characterized by its ability to capture global dependencies among graph nodes and highlight salient features, along with its flexibility, adaptability, and computational efficiency. Parallel GAT streams process each EEG band and DE separately, avoiding band mixing and boosting emotion recognition.

Frequency band specific connectivity: Parallel GAT modules learn different graphical topologies for each frequency band, which is physiologically plausible.

Enhanced interpretability: visualization reveals key regions and connection patterns aligned with neuroscience.

The remainder of this paper is organized as follows. Section 2 reviews related works. Section 3 details our model architecture and sample construction methods. In Section 4, we present our experimental setup, sensitivity analysis, results, and ablation studies in depth. Finally, the interpretability of the model is discussed in Section 5 and conclusions are drawn in Section 6.

Related work

EEG-based emotion recognition has attracted significant attention due to its potential applications in BCIs and affective computing. Traditional methods often struggle to capture the complex spatial and temporal dependencies inherent in EEG signals. In recent years, researchers have increasingly turned to Graph Convolutional Neural Networks (GCNs) to model non-Euclidean data structures like brain connectivity patterns. The graph convolution operations are generally divided into spectral-based and

spatial-based methods^[15]. Spectral-based graph convolutions perform information aggregation in the frequency domain of the graph, while spatial graph convolutions aggregate information from neighboring nodes, similar to how traditional image convolutions gather data from adjacent pixels. Both approaches have their own advantages and are commonly used for EEG signal classification^[16,17]. For example, Ding et al.^[18] use spectral graph convolution to build a local-global-graph network (LGGNet) to model cooperative brain activity. Qiu et al.^[19] integrate complex brain networks with spatial graph convolution to enhance EEG emotion recognition.

Research suggests that spectral graph convolution is more suitable for tasks involving node classification and link prediction, while spatial graph convolution is better suited for tasks involving graph classification and node clustering^[20]. Additionally, compared to spectral methods, spatial graph convolution operates directly within a node's neighborhoods, providing higher computational efficiency, better capture of local information, and scalability for large graphs^[21]. Therefore, this study primarily utilizes spatial graph convolution to build a spatiotemporal dynamic GNN model.

Graph attention mechanism is another type of spatial graph convolution model, first introduced by Veličković et al. in 2018^[22]. The main idea behind this mechanism is to address the limitations of traditional graph convolution by using an attention mechanism, allowing the model to adaptively assign different importance weights to various node relationships. Unlike other graph networks, GAT calculates the attention weights based on the feature representations of the nodes, rather than relying on information from the edges. This unique capability of the graph attention mechanism has been widely applied in numerous fields, including social network analysis^[23], bioinformatics^[24], and recommendation systems^[25]. In these applications, GATs are highly valued for their ability to capture complex inter-node relationships.

In EEG analysis, capturing the spatiotemporal dependencies of dynamic brain networks is crucial for understanding brain activity. To this end, Spatiotemporal Graph Attention has potential advantages in extracting both temporal and spatial features, which can help uncover richer dynamic connectivity information in EEG signals^[26]. Related

approaches have already achieved significant results in spatiotemporal modeling, for example, Li et al.^[27] introduce a spatiotemporal graph convolutional network, which learns the latent structure among EEG channels for improved classification accuracy, outperforming existing methods. Satipi et al.^[28] developed a Spatiotemporal Attention Neural Network (STANN) that combines convolutional networks and attention-based LSTM to enhance EEG emotion recognition, while also leveraging graph signal processing to capture inter-channel relationships, achieving state-of-the-art performance in both binary and four-class emotion classification. These studies provide a strong theoretical foundation for applying spatiotemporal graph attention in the EEG domain.

However, GAT has rarely been used in EEG analysis. Existing models that use GATs for EEG-based emotion recognition have not fully leveraged the potential of GATs. For instance, CR-GAT^[29] treats each sample as a single node for node classification, thereby overlooking the spatial relationships between different EEG channels. Similarly, the EEG-GAT model by Demir et al.^[30] combines information from all frequency bands and applies convolutional layers to extract temporal and frequency features before using GAT, compromising the interpretability of the GAT model. In this paper, we demonstrate the advantages of GATs in EEG information aggregation and emotion recognition.

Materials and methodology

Datasets

SJTU Emotion EEG Dataset (SEED) and Database for Emotion Analysis using Physiological Signals (DEAP) are widely used publicly available datasets in emotion recognition. These datasets were used for model training and model evaluation.

The SEED dataset, developed by the Brain-like Computing and Machine Intelligence Lab (BCMI) at Shanghai Jiao Tong University, includes EEG recordings from 15 participants as they watched emotionally charged movie clips (categorized as positive, neutral, and negative)^[31]. Each clip lasted between 3 to 5 minutes. Data were collected using a 62-channel ESI NeuroScan device with a sampling rate of 1 kHz, later downsampled to 200 Hz. A bandpass filter of 0–75 Hz was applied to remove artifacts, resulting in five distinct frequency bands.

The DEAP dataset, released in 2012 by a consortium of universities^[32], is a multimodal dataset designed for analyzing human emotional states. It includes EEG, eye-tracking, electromyography, and temperature recordings from 32 participants as they viewed 40 one-minute excerpts of music videos. Additionally, facial expression videos were recorded for 22 participants. After watching each video, participants rated it on a continuous scale from 1 to 9 for valence, arousal, dominance, and liking. The EEG data in the DEAP dataset were collected using 32 electrodes positioned according to the international 10–20 system, with a sampling rate of 512 Hz. Following preprocessing, the data were downsampled to 128 Hz, and artifacts were removed. Each trial lasted 63 seconds, with the final 3 seconds capturing resting-state EEG signals while participants completed the emotion rating questionnaire, which was considered the baseline. A bandpass filter of 4–45 Hz was applied, resulting in four frequency bands.

Based on the differing characteristics of the two datasets, the selected features for each are summarized in Table 1.

In this paper, the average of the resting-state DE features of every frequency band and every channel is used as the baseline to correct the DE features. In the DEAP dataset,

Table 1: Feature selection of two datasets.

Dataset	Original EEG					DE feature	
	δ	θ	α	β	γ	Baseline calibrated	Non-calibrated
SEED	√	√	√	√	√	×	√
DEAP	×	√	√	√	√	√	×

Abbreviations: EEG, electroencephalography; DE, differential entropy; SEED, SJTU Emotion EEG Dataset; DEAP, Database for Emotion Analysis using Physiological Signals.

for each trial, the final 3 s baseline period was used to compute the baseline DE for each channel and frequency band. The task EEG data were then segmented into samples, and the DE features were extracted for each segment. The baseline DE of the corresponding trial was subtracted from the DE features of each segment. This procedure aims to reduce inter-trial baseline variation in band-specific EEG energy.

Graph definition

Before introducing our model structure, we define the spatial network used in this paper as G . The constructed EEG spatial network is represented as $G = (V, E)$. To capture dynamic connectivity, the graph is constructed by connecting nodes across three consecutive time segments. Thus, the set of vertices V contains $3 \times N$ nodes, where N is the number of EEG channels. The set of edges E initially forms a fully-connected graph, resulting in $|E| = (3 \times N)^2$ edges before any pooling operation. The graph signal matrix in this study is denoted as $X_G \in R^{3N \times C}$, where C is the number of features per node and $3N$ is the total number of nodes. So the problem addressed in this study can be described as learning a mapping function through a deep learning model that maps a series of spatiotemporal network graphs X_G to a level of emotion. The specific model structure is discussed in ascending order of scale in the next subsections. The motivation for connecting nodes across three consecutive time segments is to embed both spatial and temporal information into a single graph. Specifically, edges within the same time slice model spatial functional connectivity, while edges across different time slices capture temporal propagation patterns. Although this construction enables the model to utilize delayed feature interactions, the resulting attention coefficients are not directly interpretable as directed causal flows; instead, they quantify the importance of each node-node relationship in the context of the classification task.

Model structure

The proposed model employs two GAT modules to aggregate emotional information from input signals across each frequency band. Compared to conventional feature extraction modules like CNN and GCNN, the GAT module demonstrates greater proficiency in capturing

global dependencies among nodes and emphasizing salient features. Moreover, the GAT module supports adaptive learning by dynamically adjusting attention weight allocation according to varying input data, thereby improving its flexibility and adaptability. This section first elaborates on the architectural specifics and cardinal advantages of the GAT module, subsequently delineates the feature-extraction unit dedicated to each input frequency band, and concludes by presenting the overall framework of the proposed model.

GAT module

The core component of our EEG-based emotion recognition model is designed as a graph attention module to capture the spatiotemporal dynamics of brain activity. Based on the hypothesis that connectivity between different brain regions changes dynamically, our module first constructs a microstate-inspired input graph. Then, a multi-head attention mechanism is employed to assign edge values that adapt to changes in node features. Finally, we apply top-K pooling to make the model lighter and faster.

(a) Input graph construction

In the context of EEG-based emotion recognition, microstate analysis offers a framework for understanding the brain's rapid transitions between quasi-stable states, each lasting approximately tens to hundreds of milliseconds^[33]. These microstates are thought to represent the brain's fundamental units of information processing. Inspired by microstate analysis, we can construct input graphs that capture both spatial and temporal dynamics of EEG signals.

As illustrated in Figure 1a, the input graph for the GAT module is depicted, with only three channels shown for clarity. This approach involves creating fully connected graphs across time, allowing for the modeling of attention-based cross-temporal associations between EEG signals at different time points. By incorporating cross-temporal edges within the graph structure, we can model spatial relationships among channels at each time slice while capturing dynamic signal trends over time. This method more comprehensively reflects the spatiotemporal dependencies of EEG signals under varying emotional states, significantly enhancing the

completeness and expressiveness of features in the emotion recognition process. Such integration of microstate analysis with GAT facilitates a more nuanced understanding of the brain's functional connectivity patterns, thereby improving the accuracy and robustness of emotion recognition systems.

(b) Feature aggregation

As shown in Figure 1b, here we provide a detailed explanation of the GAT mechanism. The input to the module is a set of feature vectors for each node, denoted as: $h = \{\vec{h}_1, \vec{h}_2, \dots, \vec{h}_N\}$, where N represents the number of EEG channels, and $\vec{h}_i \in R^F$ represents the feature vector of a single node.

The graph attention layer uses a self-attention mechanism to calculate attention coefficients for the input feature

vectors. To make the coefficients between different nodes comparable, the attention coefficients are normalized using a Softmax function, as expressed by the following equation:

$$e_{ij} = a(W\vec{h}_i, W\vec{h}_j), \alpha_{ij} = \text{Softmax}_j(e_{ij}) = \frac{\exp(e_{ij})}{\sum_{k \in \mathcal{N}_i} \exp(e_{ik})}$$

where e_{ij} represents the importance of node i to node j and α_{ij} is the normalized attention score. This process is illustrated in the first two images of Figure 1. In the implementation of the graph attention mechanism, a non-linear component is introduced, and the attention score is calculated using the following formula:

$$\alpha_{ij} = \frac{\exp\left(\text{LeakyReLU}\left(\vec{a}^T [W\vec{h}_i \parallel W\vec{h}_j]\right)\right)}{\sum_{k \in \mathcal{N}_i} \exp\left(\text{LeakyReLU}\left(\vec{a}^T [W\vec{h}_i \parallel W\vec{h}_k]\right)\right)}$$

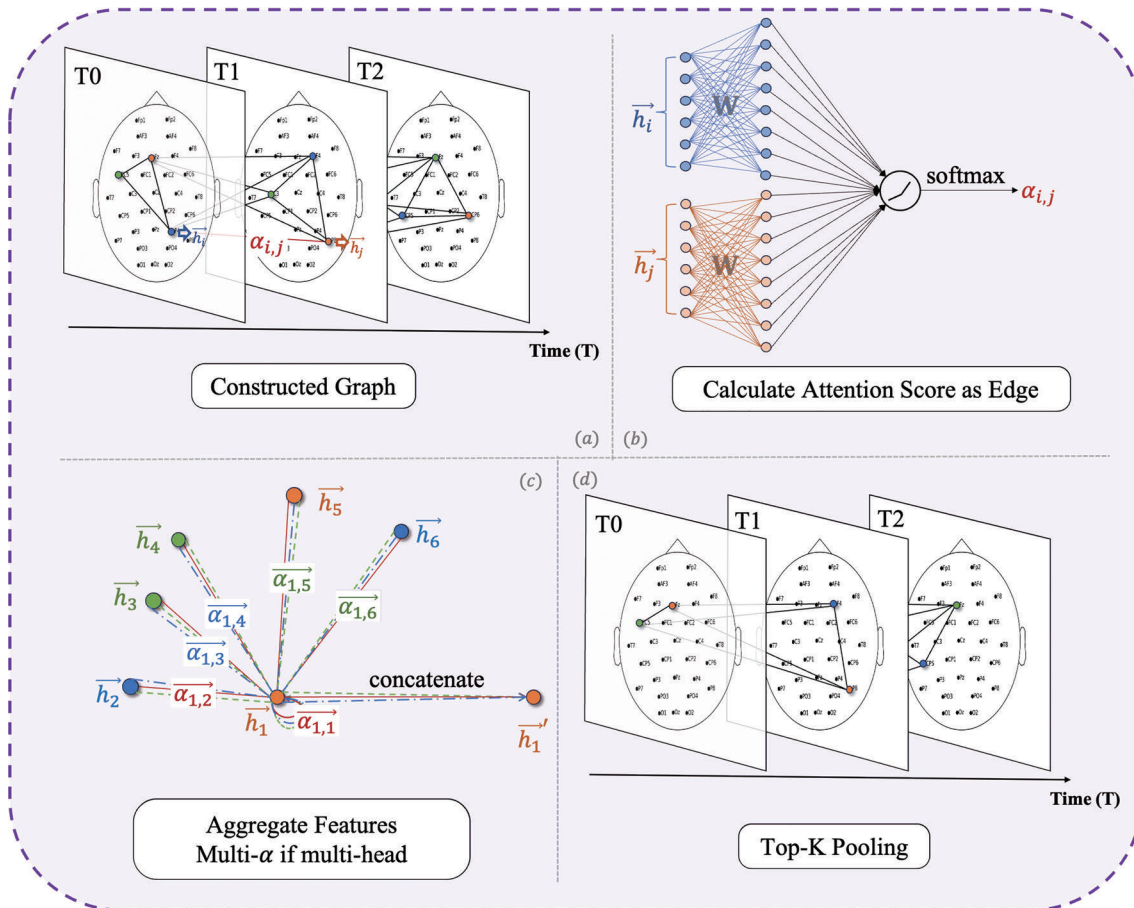


Figure 1: Details of GAT module. GAT, Graph Attention Network.

where $||$ denotes concatenation. After nodes i and j are linearly transformed, their features will be concatenated to calculate the attention score. The resulting score undergoes a linear transformation and normalization, and then serves as the edge connection strength in the convolution process for computing node features.

(c) Multi-head attention mechanism

To enhance feature representation, the GAT module uses a multi-head attention mechanism (Figure 1c), allowing each head to capture different aspects of the data. The attention scores from each head weight the features, which are then concatenated to produce the final output for each node. In our model, the first GAT module employs a multi-head mechanism, while the second module uses a single head. This structure ensures a rich feature representation by leveraging both multi-head and single-head attention mechanisms.

(d) Top-K pooling layer

An excessive number of features often increases computational complexity, raises the risk of overfitting, and reduces model interpretability. Many studies have observed feature redundancy in EEG signals for emotion recognition tasks^[34], meaning that emotion recognition is often related to only a small number of channels or features. For example, Xu et al.^[35] demonstrated that using just 12 features could achieve higher accuracy than using a larger set, while Uttam Singh et al.^[36] applied a meta-heuristic algorithm for channel selection on the DEAP dataset, achieving better results using a few selected EEG channels compared to using all channels.

We use a fully connected graph as the model input, where each node is connected to many neighbors. This often introduces redundant information and noise, which presents challenges for efficient transmission and training. Graph condensation has emerged as a solution, condensing large graphs into compact yet representative structures. This technique accelerates training and reduces irrelevant information while preserving emotion-related data. Drawing inspiration from traditional convolutional pooling, graph pooling has been widely adopted for graph simplification^[37].

According to Chen et al.^[38], pooling plays a crucial role in the proposed model by refining the EEG-based graph structure, selectively aggregating information from less-important to more-important nodes.

Consequently, a Top-K pooling layer is used to remove unnecessary information. This layer adaptively selects a subset of nodes to form a downsampled graph, shown in Figure 1d. It consists of three main steps: a score generator, a node selector, and graph coarsening^[39]. The score generator assigns a score to each node, the node selector picks the top- K nodes with the highest scores, and graph coarsening regenerates the feature and adjacency matrices based on the selected nodes.

First, we define a trainable projection vector p . For each node and its feature vector X , the scalar projection of X onto p is given by $\frac{X \cdot p}{|p|}$. This projection, $y = \frac{X \cdot p}{|p|}$, serves as the scoring function, retaining the top 50% of nodes with the highest scores: $\text{Index} = \text{top}_k(y)$.

The coarsened feature matrix is then computed by element-wise multiplying the original features of the retained nodes with their scores, activated through a tanh function: $X' = (X \odot \tanh(y))_{\text{Index}}$.

The coarsened adjacency matrix A' retains the weights from the original adjacency matrix based on the selected indices: $A' = A_{\{\text{Index}, \text{Index}\}}$. This method has implementations available in both PyTorch^[40] and TensorFlow frameworks^[41].

Feature extraction unit for each frequency band

Two GAT modules are serially connected to construct a feature extraction unit for each frequency band. Given that each frequency band may have a different spatial topology and play a distinct role in EEG emotion^[31], we hypothesize that each band exhibits unique patterns during emotional transformations. Thus, in our study, different frequency bands EEG and the DE features are used to construct multiple sub-graphs, allowing each sub-graph to learn its topology.

A feature extraction unit, composed of two serially connected GAT modules, is dedicated to each frequency

band (Figure 2). This design is motivated by the physiological plausibility that different frequency bands exhibit distinct spatial topologies and functional roles in emotional processing^[31]. Therefore, we allow each band-specific sub-graph to learn its own unique connectivity patterns. Each of these sub-graphs is constructed from three consecutive time steps (as defined in Section 3.2) to inherently model cross-temporal dynamics.

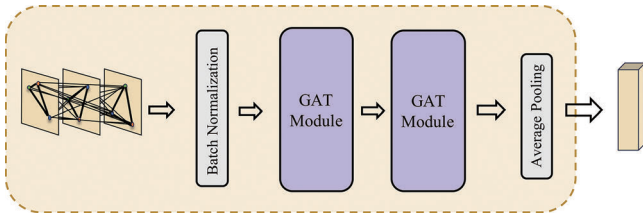


Figure 2: Feature extraction of each sub-graph. GAT, Graph Attention Network.

To effectively capture cross-temporal connectivity, sub-graphs are connected with a step size of three to form larger subgraphs. After batch normalization, each subgraph is fed into two sequential GAT modules individually for information aggregation. After applying average pooling, we obtain a set of embeddings corresponding to each subgraph.

Overall model structure

The network is designed with a focus on parallel spatio-temporal modeling and a balance between model capacity and computational complexity, while maintaining a relatively shallow architecture. These characteristics make the model straightforward to implement and consistent with the initial design objectives. Inspired by brain activity mechanisms, the network uses parallel graph-attention branches to extract and utilize critical information from

graph-structured data for emotion recognition. Although the model does not achieve the lowest computational cost among compared methods, its parallel architecture provides a reasonable trade-off between spatiotemporal modeling capability and computational burden, which may help reduce overfitting risk and support generalization. Its potential application to other BCI tasks is currently under exploration.

The overall architecture of the model is illustrated in Figure 3. Each fully connected subgraph is processed through a separate feature extraction unit to model dynamic connectivity and generate corresponding embeddings. These embeddings are then concatenated and fed into a forward layer that maps the features to emotion labels.

Experimental study

In this section, the proposed model is validated on two public datasets and compared with the edge models to illustrate the effectiveness of the model. Three ablation studies have also been conducted to further demonstrate the correctness of the proposed strategies.

Experimental settings

All algorithmic experiments in this study were conducted under a computational experimental setup based on the public DEAP and SEED datasets, following a standardized pipeline including preprocessing, sample construction, model training, and evaluation. The flow chart is shown in Figure 4.

The algorithmic experiments were conducted on a Dell Precision workstation equipped with an Intel(R)

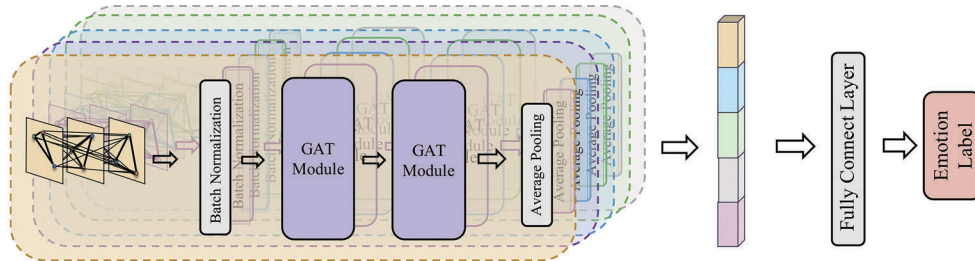


Figure 3: Model structure of PSGA. PSGA, Parallel Spatiotemporal Graph Attention network; GAT, Graph Attention Network.

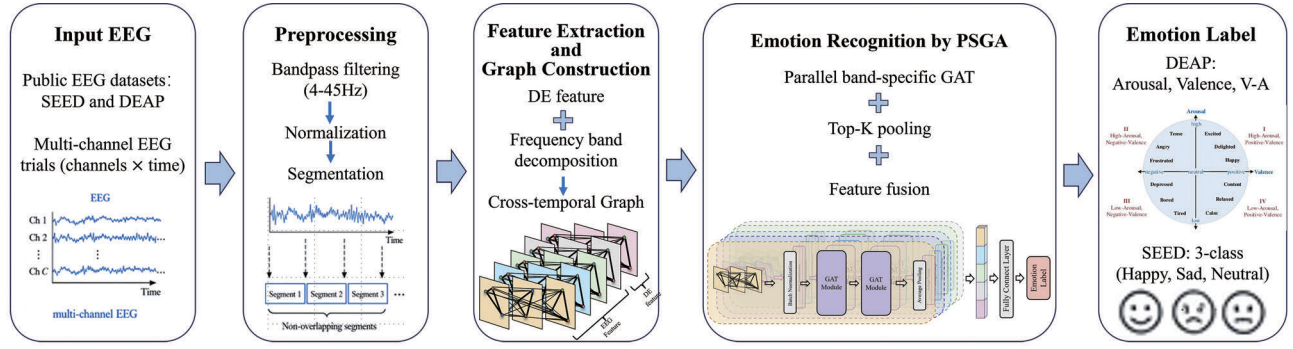


Figure 4: Flow Chart of EEG-based emotion recognition by PSGA. EEG, electroencephalography; SEED, SJTU Emotion EEG Dataset; DEAP, Database for Emotion Analysis using Physiological Signals; DE, differential entropy; GAT, Graph Attention Network.

Xeon(R) Gold 6133 CPU running at 2.50 GHz and two NVIDIA GeForce RTX 3090 GPUs. Our workstation ran PyTorch 2.1.1 with CUDA 12.1, using Python 3.9.

In this study, Weights & Biases was employed to log training details, performance metrics, and parameter tuning for all models, ensuring reproducibility and transparency in the experimental process^[42].

Sensitivity analysis

Determination of embedding length

Selecting an appropriate time window length to construct samples is a critical step in this study. Since there is no theoretical framework to directly inform this choice, experimental methods are typically employed to determine the optimal length. Selecting a time

window that is too long may introduce excessive noise, potentially affecting the accuracy of the final analysis. Research indicates that causal connectivity effects in the brain primarily occur within time windows of tens to hundreds of milliseconds^[43]. Based on this finding, we tested several data lengths within this range and conducted extensive experiments on four representative participants to identify the optimal window length. By systematically analyzing the results for each time window, we determined the most suitable length for subsequent analysis. This empirical approach aims to optimize data processing while minimizing noise interference, thereby enhancing the accuracy and reliability of the study. Figure 5 presents the results of the time window selection experiment.

Experimental results indicate that for the DEAP dataset,

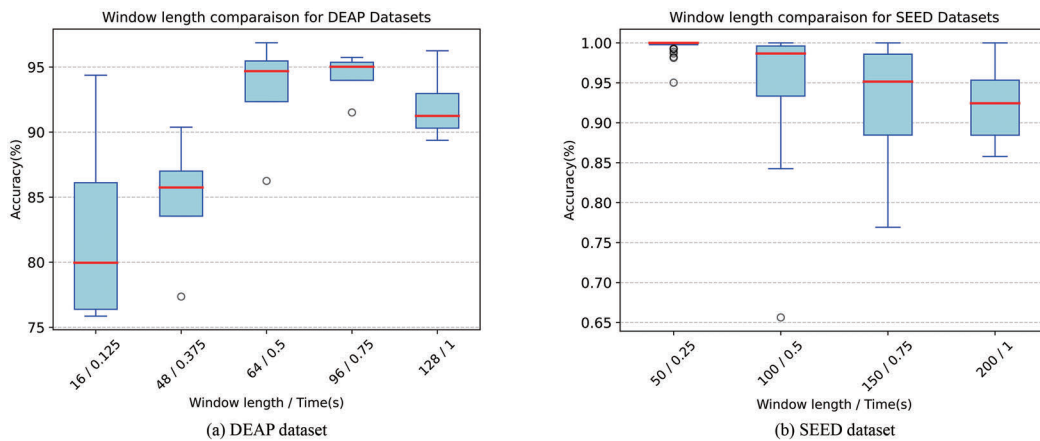


Figure 5: Window length comparison results. DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset.

the average accuracy improves significantly when the sample length exceeds 500 ms. Conversely, for the SEED dataset, the highest average accuracy is achieved with a sample length of 250 ms. Consequently, a sample length of 96 was selected for further experiments on the DEAP dataset, while a length of 50 was chosen for the SEED dataset.

The choice of window length is intended to balance temporal resolution and the reliability of band-specific feature estimation. In general, longer windows provide more stable estimates for lower-frequency oscillations, whereas shorter windows preserve finer temporal variations that may be relevant to transient emotional dynamics. Therefore, the window sizes used in this work should be interpreted as empirically supported operating points under the current preprocessing and modeling framework, rather than theoretically universal optima.

Specifically, the selected 96-sample window for DEAP (750 ms at 128 Hz) provides several oscillatory cycles for theta/alpha activity while maintaining short-term sensitivity, whereas the 50-sample window for SEED (250 ms at 200 Hz) emphasizes finer temporal responsiveness. Since our model jointly constructs graphs from three consecutive segments, the effective temporal context is larger than a single-window duration.

Sensitivity analysis of hyperparameter

Sensitivity analyses were further conducted for key hyperparameters, including the number of attention heads, hidden dimension, and the Top-K pooling ratio.

The results indicate that PSGA remains reasonably stable across a range of settings, while the best performance is obtained with 8 attention heads, hidden dimension 32, and Top-K ratio 0.3, as shown in Figure 6. Based on this analysis, the above configuration was selected as the final setting for the subsequent experiments. The refined hyperparameter configuration identified here was adopted in the subsequent cross-trial and cross-subject experiments.

Results

Extensive experiments on two public datasets demonstrate that PSGA achieves competitive performance. The model implementation is publicly available at GitHub website (Anais-Y/restart).

To improve reproducibility, we summarize the module-wise architecture, hyperparameter settings, and computational experimental setup in Table 2. The final values of key hyperparameters, including the number of attention heads, hidden dimension, and Top-K pooling ratio, were selected according to the sensitivity analysis.

This section first presents the results of shuffled subject-dependent experiment on the DEAP dataset and a comparison with baseline models, followed by the results and baseline comparison on the SEED dataset shown in Table 3 and Table 4.

The confusion matrix of the model is shown in Figure 7. For both datasets, the model accurately identifies various emotion types with high precision. Notably, it is particularly

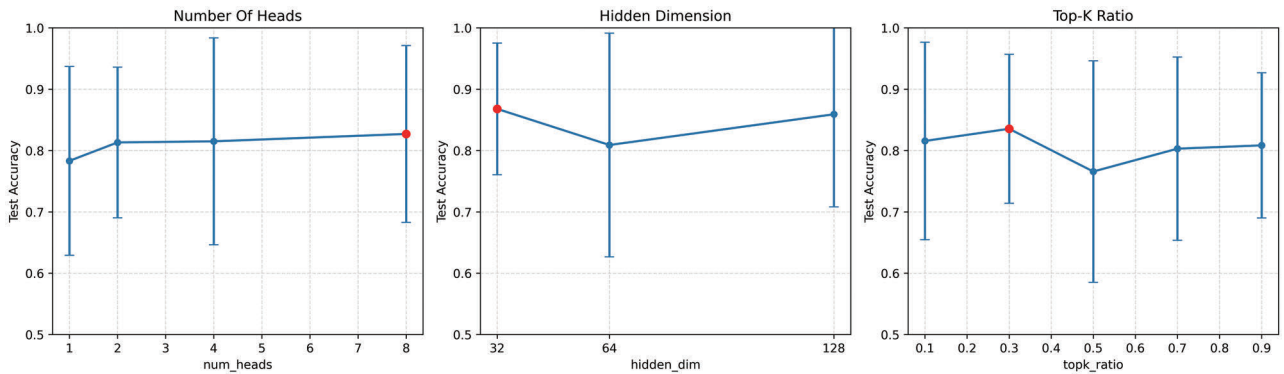


Figure 6: Sensitivity analysis of PSGA. PSGA, Parallel Spatiotemporal Graph Attention network.

Table 2: Parameter of PSGA.

Module/Component	Parameter	Value
DEAP	Sampling rate	128 Hz
SEED	Sampling rate	200 Hz
Segmentation	Overlap	Non-overlapping
Segmentation	Window length	0.75 s DEAP, 0.25 s SEED (shuffled) 1 s (cross-trial and cross-subject)
Spatiotemporal graph	Number of consecutive segments	3
Node feature	Feature type	DE + 4 bands (DEAP) DE + 5 bands (SEED)
First GAT layer	Number of attention heads	8
Hidden representation	Hidden dimension	32
Top-K pooling	Pooling ratio	0.3
Output layer	Number of classes	4 (DEAP) 3 (SEED)
Loss function	Type	Cross entropy
Early stopping	Patience	20 epochs
Optimizer	Type	Adam

Abbreviations: PSGA, Parallel Spatiotemporal Graph Attention network; GAT, Graph Attention Network; DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset.

Table 3: Comparison on DEAP dataset with other models.

Model	Year	Valence Acc (%)	Arousal Acc (%)	Four-class Acc (%)
4D-CRNN ^[44]	2020	94.22	94.58	—
DGCNN ^[9]	2020	86.93	86.21	—
BiDCCN ^[45]	2021	94.38	94.72	—
EEG-GCN ^[46]	2022	91.86	91.81	86.71
ACRNN ^[47]	2023	93.72	93.38	—
GLFANet ^[48]	2023	94.53	94.91	92.92
EESCN ^[49]	2024	94.56	94.81	—
TFCNN-BiGRU ^[50]	2024	96.40	96.40	92.90
ESC-GAN ^[51]	2024	96.33	96.68	—
PSGA (Ours)	2024	97.20	96.50	95.54

Abbreviations: DEAP, Database for Emotion Analysis using Physiological Signals; 4D-CRNN, 4D Convolutional Recurrent Neural Network; DGCNN, Dynamical Graph Convolutional Neural Networks; BiDCCN, Bi-hemisphere Discrepancy Convolutional Neural Network; EEG-GCN, Spatio-Temporal and Self-Adaptive Graph Convolutional Networks; ACRNN, Attention-based Convolutional Recurrent Neural Network; GLFANet, Global to Local Feature Aggregation Network; EESCN, Emo-EEG SpikeConvNet; TFCNN-BiGRU, Time Frequency Convolutional Neural Network- Bidirectional Gated Recurrent Unit; ESC-GAN, Emotional Subspace Constrained Generative Adversarial Networks; PSGA, Parallel Spatiotemporal Graph Attention network.

effective in recognizing non-extreme emotions, such as neutral states, and emotions with high arousal but low valence, or vice versa, compared to other emotion categories.

Table 4: Comparison on SEED dataset with other models.

Model	Year	Three-Class Acc (%)
4D-CRNN ^[44]	2020	94.74
DGCNN ^[9]	2020	90.40
ATDD-LSTM ^[52]	2022	90.92
EEG-GCN ^[46]	2022	85.65
RGNN ^[10]	2023	94.24
GLFANet ^[48]	2023	93.19
DCPCNet ^[53]	2023	90.04
TFCNN-BiGRU ^[50]	2024	93.11
ESC-GAN ^[51]	2024	97.14
PSGA (Ours)	2024	94.68

Abbreviations: SEED, SJTU Emotion EEG Dataset; 4D-CRNN, 4D Convolutional Recurrent Neural Network; DGCNN, Dynamical Graph Convolutional Neural Networks; ATDD-LSTM, Attention-based Long Short-Term Memory with Domain Discriminator; EEG-GCN, Spatio-Temporal and Self-Adaptive Graph Convolutional Networks; RGNN, Regularized Graph Neural Network; GLFANet, Global to Local Feature Aggregation Network; DCPCNet, Depthwise Convolution and Pointwise Convolution; TFCNN-BiGRU, Time Frequency Convolutional Neural Network-Bidirectional Gated Recurrent Unit; ESC-GAN, Emotional Subspace Constrained Generative Adversarial Networks; PSGA, Parallel Spatiotemporal Graph Attention network.

The experimental results consistently demonstrate PSGA’s competitive performance in both binary (valence/arousal) and multi-class classification tasks across the DEAP and SEED datasets. These results suggest that the proposed

spatiotemporal graph modeling strategy is effective for capturing emotion-related EEG patterns under the evaluated settings.

Additionally, we applied t-SNE to reduce the dimensionality of the final features and visualized them on a two-dimensional plane. As illustrated in Figure 8, the features appear cluttered prior to being processed by the model. However, after aggregation, they are evenly distributed across distinct regions on the plane.

To avoid potential temporal leakage, we additionally evaluate PSGA under trial-wise subject-dependent and subject independent protocol. To fairly compare PSGA with other models, we conducted the experiments following the experimental settings in LibEER^[54]. In the cross-trial setting, trials are first split in a stratified manner at the trial level before segmentation. Specifically, for each subject in SEED dataset, the 45 trials (3 sessions $\times$ 15 trials) are stratified over the joint (session, emotion) cells, resulting in a balanced 60/20/20 trial split for each cell in the train/validation/test sets. In the LOSO cross-subject setting, one subject is left out for testing while the remaining subjects are used for training, and the final result is averaged over all subjects. All subsequent subject-dependent and subject-independent experiments were re-conducted using the best-performing hyperparameter configuration identified above. The results

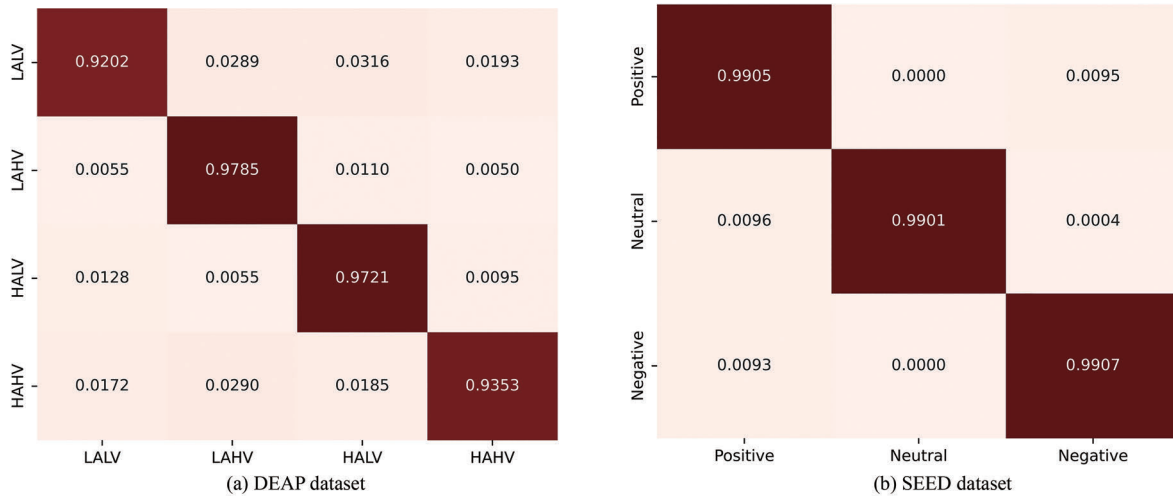


Figure 7: Confusion matrix of PSGA on DEAP and SEED dataset. PSGA, Parallel Spatiotemporal Graph Attention network; DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset; LALV, low arousal and low valence; LAHV, low arousal and high valence; HALV, high arousal and low valence; HAHV, high arousal and high valence.

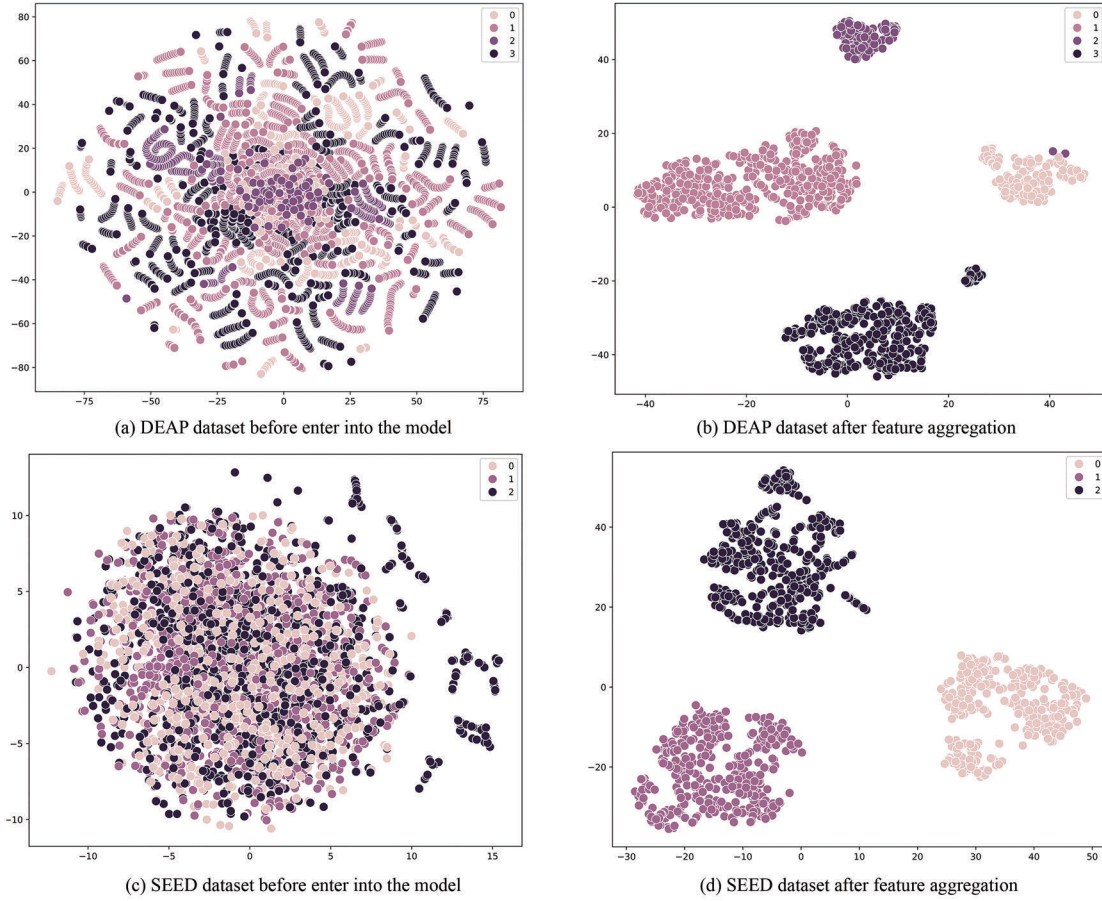


Figure 8: T-SNE visualization. T-SNE, T-distributed Stochastic Neighbor Embedding; DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset.

of trial-wise subject-dependent experiment on SEED and DEAP are shown in Table 5 and Table 6, respectively.

The trial-wise subject-dependent results further show that PSGA remains competitive under a more rigorous leakage-controlled evaluation protocol. Compared with the original shuffled split, this setting provides a more conservative and reliable assessment, while still demonstrating the effectiveness of PSGA in modeling emotion-related EEG patterns. The training and validation curves are shown in Figure 9.

To further evaluate practical generalization ability, we also conducted leave-one-subject-out subject-independent experiments. Under this cross-subject setting, PSGA achieves $78.85\% \pm 11.56\%$ on SEED, shown in Table 7. On DEAP, PSGA achieves $54.92\% \pm 7.10\%$ on DEAP-V, $52.42\% \pm 13.49\%$ on DEAP-A, and $32.83\% \pm 9.20\%$ on DEAP-VA, shown in Table 8. These additional results

Table 5: Subject-dependent cross-trial comparison on SEED dataset.

Model	Year	Three-Class Acc (%)
DGCNN ^[9]	2020	82.55 ± 15.61
GCBNet ^[55]	2022	80.56 ± 16.98
GCBNet_BLS ^[55]	2022	76.64 ± 17.44
RGNN ^[10]	2023	76.55 ± 16.92
NSAL-DGAT ^[56]	2023	78.62 ± 17.48
PSGA (Ours)	2024	85.59 ± 12.34

Abbreviations: SEED, SJTU Emotion EEG Dataset; DGCNN, Dynamical Graph Convolutional Neural Networks; GCBNet, Graph Convolutional Broad Network; GCBNet_BLS, Graph Convolutional Broad Network_Broad Learning System; RGNN, Regularized Graph Neural Networks; NSAL-DGAT, Neighborhood Semantic Aware Learning-based Dynamic Graph Attention convolution; PSGA, Parallel Spatiotemporal Graph Attention network.

provide a more comprehensive evaluation of PSGA beyond within-subject performance and better support

Table 6: Subject-dependent cross-trial comparison on DEAP dataset.

Model	Year	Valence Acc (%)	Arousal Acc (%)	V-A Acc (%)
DGCNN ^[9]	2020	56.07 $\pm$ 17.15	62.68 $\pm$ 19.66	41.86 $\pm$ 11.57
GCBNet ^[55]	2022	56.49 $\pm$ 18.17	65.95 $\pm$ 17.61	38.80 $\pm$ 16.23
GCBNet_BLS ^[55]	2022	57.02 $\pm$ 15.07	61.07 $\pm$ 16.56	37.51 $\pm$ 15.29
RGNN ^[10]	2023	55.90 $\pm$ 16.24	66.09 $\pm$ 13.91	44.53 $\pm$ 14.35
NSAL-DGAT ^[56]	2023	52.21 $\pm$ 16.19	60.31 $\pm$ 17.29	38.78 $\pm$ 15.64
PSGA (Ours)	2024	65.30 $\pm$ 7.20	70.34 $\pm$ 9.82	44.83 $\pm$ 11.51

Abbreviations: DEAP, Database for Emotion Analysis using Physiological Signals; DGCNN, Dynamical Graph Convolutional Neural Networks; GCBNet, Graph Convolutional Broad Network; GCBNet_BLS, Graph Convolutional Broad Network_Broad Learning System; RGNN, Regularized Graph Neural Networks; NSAL-DGAT, Neighborhood Semantic Aware Learning-based Dynamic Graph Attention convolution; PSGA, Parallel Spatiotemporal Graph Attention network.

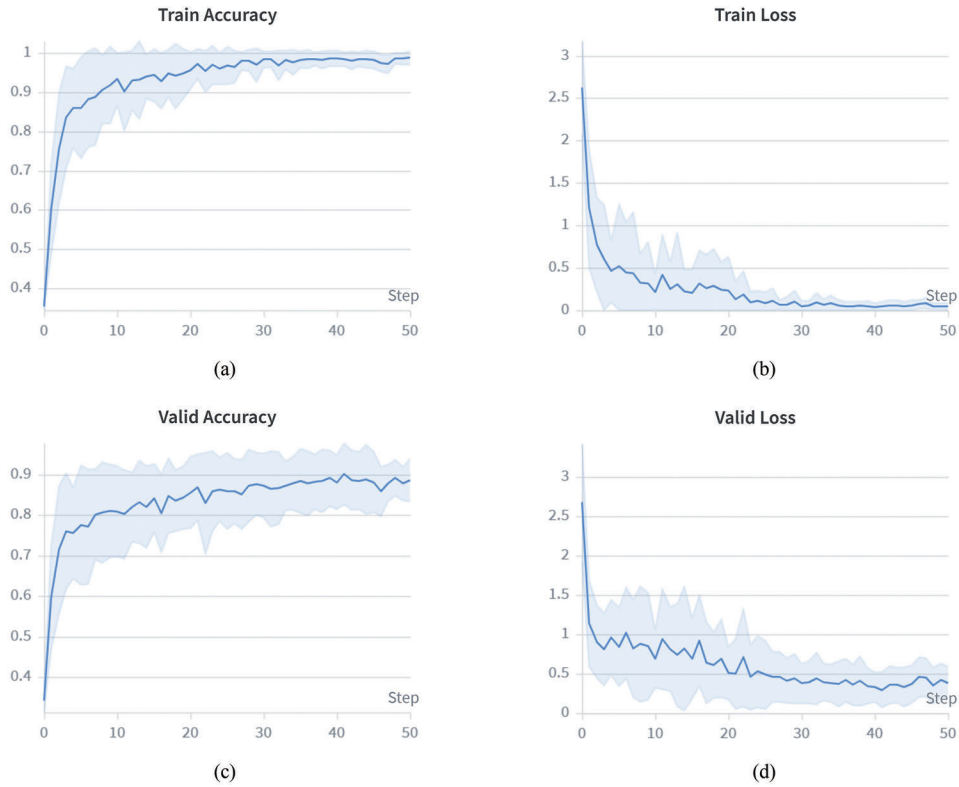


Figure 9: Curves of training and validation. (a) Average train accuracy of SEED; (b) Average train loss of SEED; (c) Average valid accuracy of SEED; (d) Average valid loss of SEED. SEED, SJTU Emotion EEG Dataset.

its potential relevance for intelligent healthcare applications.

The subject-independent results further indicate that PSGA retains competitive cross-subject generalization under a more realistic evaluation setting. These findings provide a more comprehensive assessment beyond

subject-dependent experiments and support the potential applicability of PSGA in practical intelligent healthcare scenarios.

Ablation experiments

In this section, extensive experiments are conducted to

Table 7: Subject-independent comparison on SEED dataset.

Model	Year	Three-class Acc (%)
DGCNN ^[9]	2020	60.87 ± 15.62
GCBNet ^[55]	2022	56.32 ± 14.73
GCBNet_BLS ^[55]	2022	56.32 ± 9.91
RGNN ^[10]	2023	59.45 ± 15.28
NSAL-DGAT ^[56]	2023	64.40 ± 19.00
PSGA (Ours)	2024	78.85 ± 11.56

Abbreviations: SEED, SJTU Emotion EEG Dataset; DGCNN, Dynamical Graph Convolutional Neural Networks; GCBNet, Graph Convolutional Broad Network; GCBNet_BLS, Graph Convolutional Broad Network_Broad Learning System; RGNN, Regularized Graph Neural Networks; NSAL-DGAT, Neighborhood Semantic Aware Learning-based Dynamic Graph Attention convolution; PSGA, Parallel Spatiotemporal Graph Attention network.

validate the role of the cross-temporal connections graph, the impact of graph pooling on the model, and the effectiveness of learning topology across frequency bands.

Effectiveness of cross temporal connections

A key innovation of this study is the introduction of a fully connected cross-temporal graph network to model attention-based dynamic connectivity patterns during emotional changes in the brain. To validate the impact of cross-temporal connections, we conducted ablation experiments comparing models with and without these connections. By keeping other parameters constant, we assessed classification accuracy using three connected time slices versus a single time slice, with the results as follows:

The results shown in Table 9 indicate that, for both the DEAP and SEED datasets, the classification accuracy achieved with three connected time slices consistently surpassed that obtained with a single time slice, regardless of whether samples were fully randomized or grouped by trial.

In these experiments, all conditions, including the random seed used for sample partitioning, were kept consistent across the two experimental groups. This ensured that cross-temporal connections were the only variable, thereby demonstrating that these connections provide additional information crucial for emotion classification.

Effectiveness of graph pooling

As demonstrated by Nakisa et al.^[57], different frequency bands and channel combinations of EEG signals can generate a substantial number of features. However, an excess of features can increase computational complexity and the risk of overfitting. Thus, selecting essential features while eliminating redundancy and noise is crucial for enhancing model robustness and interpretability. This study leverages graph pooling to reduce redundant information and improve network efficiency. Notably, while pooling enhances efficiency, it does not directly reduce the total number of parameters, as Top-K pooling requires training a scoring function to select nodes, thereby introducing additional trainable parameters.

This subsection first compares changes in parameter count and accuracy on both datasets before and after pooling. It then analyzes the impact of including

Table 8: Subject-independent Comparison on DEAP dataset.

Model	Year	Valence Acc (%)	Arousal Acc (%)	V-A Acc (%)
DGCNN ^[9]	2020	49.91 ± 7.48	49.91 ± 9.27	25.66 ± 8.22
GCBNet ^[55]	2022	53.58 ± 8.72	50.05 ± 10.60	30.92 ± 12.73
GCBNet_BLS ^[55]	2022	52.34 ± 4.51	50.59 ± 19.22	20.49 ± 11.13
RGNN ^[10]	2023	52.65 ± 8.09	46.85 ± 16.25	22.40 ± 12.36
NSAL-DGAT ^[56]	2023	52.22 ± 11.83	50.94 ± 9.60	26.44 ± 14.74
PSGA (Ours)	2024	54.92 ± 7.10	52.42 ± 13.49	32.83 ± 9.20

Abbreviations: DEAP, Database for Emotion Analysis using Physiological Signals; DGCNN, Dynamical Graph Convolutional Neural Networks; GCBNet, Graph Convolutional Broad Network; GCBNet_BLS, Graph Convolutional Broad Network_Broad Learning System; RGNN, Regularized Graph Neural Networks; NSAL-DGAT, Neighborhood Semantic Aware Learning-based Dynamic Graph Attention convolution; PSGA, Parallel Spatiotemporal Graph Attention network.

Table 9: Cross-time frame effect experiment results.

Dataset	Single time frame	Three times frames	Change
DEAP	92.31%	95.54%	+3.23%
SEED-shuffle	84.43%	94.68%	+10.25%
SEED-cross-trial	71.18%	85.59%	+14.41%

Abbreviations: DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset.

versus excluding pooling layers on model performance. Table 10 presents the trainable parameter counts for both datasets with and without compression, using hidden layer dimensions of 128 and 4 attention heads.

Table 10: Model parameter changes before and after pooling.

Dataset	Parameters before compression	Parameters after compression	Change
DEAP	269,888	279,676	+3.63%
SEED	534,573	544,347	+1.83%

Abbreviations: DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset.

Additionally, we assessed the model’s computational efficiency by measuring its computational load. The results indicate that, although the number of trainable parameters increased, the overall computational complexity was significantly reduced. Table 11 presents the changes in Floating Point Operations (FLOPs) before and after applying graph pooling. FLOPs represent the total number of floating-point calculations performed during a model’s forward pass and are commonly used to evaluate model efficiency—the lower the FLOPs, the faster the computation speed.

Table 11: Changes in model computation (FLOPs) before and after pooling.

Dataset	FLOPs before compression	FLOPs after compression	Change
DEAP	14,943,232	10,249,472	−31.4%
SEED	42,378,960	30,248,928	−28.6%

Abbreviations: FLOPs, Floating Point Operations; DEAP, Database for Emotion Analysis using Physiological Signals; SEED, The SJTU Emotion EEG Dataset.

Table 12 shows the change in model accuracy before and after adding the compression layer.

Table 12: Model accuracy changes before and after pooling.

Dataset	Accuracy before compression	Accuracy after compression	Change
DEAP	95.13%	95.54%	+0.41%
SEED-shuffle	94.52%	94.68%	+0.16%
SEED-cross-trial	81.71%	85.59%	+3.88%

Abbreviations: DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset.

As seen in the comparison tables, the computational load of the model with pooling is only two-thirds that of the model without pooling, resulting in a substantial increase in computation speed. Meanwhile, model accuracy remains stable or even slightly improves with pooling, demonstrating that a single graph pooling step can enhance model efficiency.

Effectiveness of band-specific connectivity

Numerous studies have demonstrated that EEG signals from different frequency bands have varying impacts on emotion classification. Therefore, we hypothesize that the connections and brain regions involved may also differ across frequency bands. Simply merging all signals after band separation could lead to misleading conclusions. To examine the effect of aggregating features by frequency band, we conducted an ablation study by replacing the distinct graph attention layers for each frequency band with a shared-weight graph attention mechanism. The results are presented in Table 13.

The experimental results indicate that incorporating

Table 13: Model accuracy comparison of mixed and separate frequency bands.

Dataset	Accuracy of mixed bands	Accuracy of separate bands	Change
DEAP	84.68%	95.54%	+10.86%
SEED	90.21%	94.68%	+4.37%

Abbreviations: DEAP, Database for Emotion Analysis using Physiological Signals; SEED, SJTU Emotion EEG Dataset.

frequency-specific brain connectivity features significantly enhances model performance, particularly for the DEAP dataset. Specifically, the average accuracy on the DEAP dataset increased by 10.86% with frequency separation, while the SEED dataset showed a more modest improvement of 4.37%. We attribute this difference to the varying contributions of features in each dataset to the classification task. Feature importance analysis reveals that for the SEED dataset, using only DE features achieves over 90% classification accuracy, whereas the DEAP dataset achieves only 77% under the same conditions. This suggests that the SEED dataset relies heavily on DE features, making the additional benefits of frequency separation less pronounced. However, even in this case, frequency separation still contributes to a performance improvement.

Discussion

Deep learning models based on neural networks and backpropagation algorithms have achieved great success across various fields. However, their lack of interpretability has limited their application in sensitive areas such as healthcare. This is why many domains that prioritize interpretability still prefer traditional machine learning or simpler neural networks. As a result, interpretability in neural networks is gaining increasing attention. Interpretation refers to the process of mapping abstract concepts to domains understandable to humans^[58], while interpretability is often defined as the degree to which an observer can understand the reasons behind a model's

decisions^[59]. In other words, the more readily a model's decision-making can be understood through existing human knowledge, the more interpretable it is.

This study enhances model interpretability to some extent by deconstructing the graph attention mechanism and using a simpler network structure. This section will present insights into brain mechanisms related to emotion that were discovered through the model.

Rich club effect

As described in the principles of the graph attention mechanism, the model calculates attention scores between nodes to generate aggregated representations, with these scores reflecting each node's relative importance to some extent. Many interpretability studies on graph attention mechanisms utilize average attention scores as importance weights^[60].

By visualizing the attention scores of an intermediate layer in the GAT, we observed that only a few nodes exhibited particularly strong connections with others. This suggests that these nodes are more closely associated with emotional changes, reflecting the “rich club effect” observed in neuroscience. According to Griffa et al.^[61], brain neural networks exhibit a characteristic in which highly connected elements occupy central positions in the network and tend to form strong connections with one another, creating a “rich club.”

In Figure 10, we present the connection strengths for

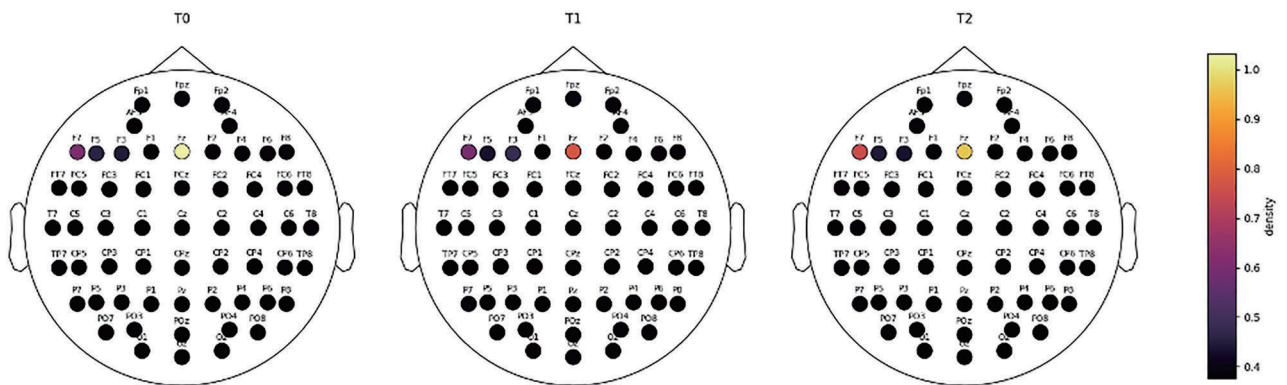


Figure 10: Rich club effect on SEED dataset. SEED, SJTU Emotion EEG Dataset.

EEG nodes in the theta frequency band for a specific participant of SEED dataset. The node positions correspond to EEG channel locations, and the color intensity indicates connection strength. Since each sample includes three connected time slices, three brain diagrams are displayed. Notably, connections within each time slice are concentrated on a few key nodes, and the changes in node colors over time illustrate how the central nodes evolve with emotional shifts. This clustering pattern was consistently observed across all participants and frequency bands in both datasets.

Similarly, we noted the same clustering effect among participants in the DEAP dataset, shown in Figure 11. The consistency of this pattern across different datasets and participants further underscores the model’s interpretability and reliability.

Channels and brain regions related to emotional changes

The brain mechanisms underlying emotional changes have long been a focus of research. By capturing electrical activity on the cerebral cortex, EEG signals reveal how different brain regions respond to emotional stimuli. Machine learning methods can detect subtle differences and inter-channel connections that are difficult to observe manually, making them invaluable in neuroscience research. For example, Zheng and Lu^[31] found that positive emotions increase energy in the gamma and beta bands, while neutral emotions elevate energy in the alpha band. These insights advance our

understanding of biological and neurological processes, offering new perspectives for future research.

Additionally, Wang et al.^[62] highlighted key channels and brain regions associated with emotions, noting distinct asymmetries in emotional responses between anterior and posterior regions, as well as between the left and right hemispheres. For instance, the frontal cortex exhibits stronger responses compared to other areas^[63,64], and the left hemisphere often responds more intensely than the right^[65]. The connection strengths learned by our model align with these observations.

To provide quantitative evidence beyond qualitative visualization, we further conduct a functional-connectivity consistency analysis. We follow the standard definition that effective connectivity refers to causal and directional influence; therefore, the attention weights learned on a fully connected graph should be interpreted as attention-based interaction/association patterns rather than causal effective connectivity.

Specifically, we extract the first-layer GAT attention weights and compare them with a classical functional connectivity measure, magnitude-squared coherence, computed from the same band-pass filtered EEG segments used as model inputs. To ensure a well-defined comparison, we restrict the analysis to intra-slice spatial edges (i.e., channel–channel connections within each temporal slice) and average the resulting connectivity matrices across the three temporal slices.

We then assess edge-wise agreement using Spearman’s

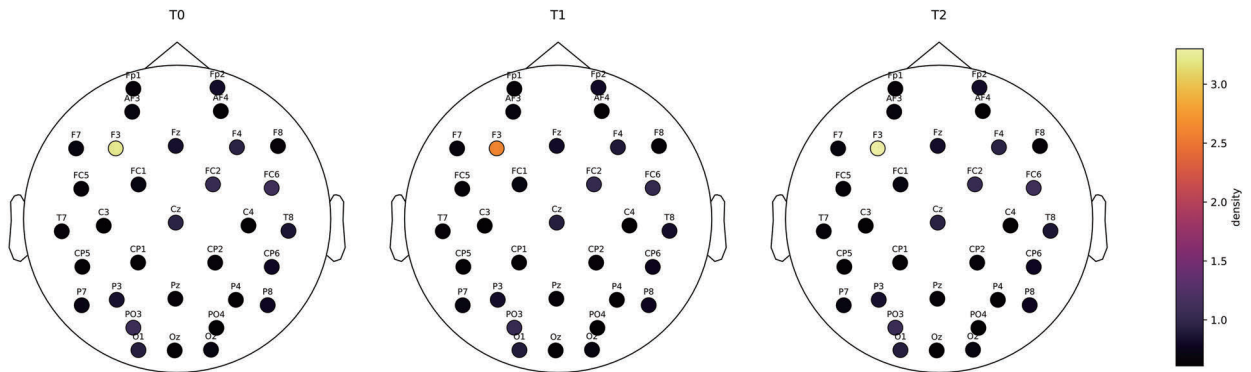


Figure 11: Rich club effect on DEAP dataset. DEAP, Database for Emotion Analysis using Physiological Signals.

rank correlation and a Top-10% edge-set overlap (Jaccard index), and evaluate statistical significance via a permutation test by randomly permuting the coherence edge vector (200 permutations per sample). On three SEED trial-wise runs ($n = 30$ correctly classified test graphs per band), we observe significant alignment between attention-based connectivity patterns and coherence across all five frequency bands, as summarized in Table 14. Notably, the permutation P -values are identical ($P = 0.004975$) because, with 200 permutations, the smallest attainable P -value is $1/(200 + 1) = 0.004975$, which is reached when the observed statistic exceeds all permuted values.

Regarding EEG channels linked to emotions, there is general consensus that the frontal, occipital, and temporal lobes play crucial roles in emotional processing, with the frontal and temporal lobes having the most significant influence. For example, Huang et al.^[66] explored the hierarchical affective regions hypothesis, linking emotional mechanisms in the brain to the frontal, temporal,

and parietal lobes using deep learning algorithms and functional MRI (fMRI).

Figure 12 and Figure 13 display the average attention scores from a selected subgraph for two randomly chosen participants. In Participant A, primary channels related to emotion classification are concentrated in the prefrontal cortex, while in Participant B, they are focused in the frontal and left temporal lobes, with the left hemisphere showing greater involvement in emotional processing than the right. This observation aligns with previous research findings and is even more pronounced in the topographic maps shown in Figure 14.

While there are commonalities in emotional responses across individuals, significant individual differences remain, and no single universal pattern for emotional changes has been identified. For instance, Priyasad et al.^[67] also analyzed channel weights across participants using attention scores, finding pronounced individual variability. Our study observed a similar phenomenon: although the

Table 14: Quantitative alignment between attention-based connectivity patterns and functional connectivity on SEED.

Band	n	Spearman ρ	Permutation	Top-10% Jaccard	Permutation
Delta	30	0.4196 ± 0.2050	0.004975	0.2549 ± 0.1386	0.004975
Theta	30	0.4616 ± 0.2072	0.004975	0.3221 ± 0.0736	0.004975
Alpha	30	0.2707 ± 0.2645	0.004975	0.2001 ± 0.1372	0.004975
Beta	30	0.3261 ± 0.2260	0.004975	0.1789 ± 0.1152	0.004975
Gamma	30	0.4198 ± 0.1796	0.004975	0.2842 ± 0.0900	0.004975

Abbreviations: SEED, SJTU Emotion EEG Dataset.

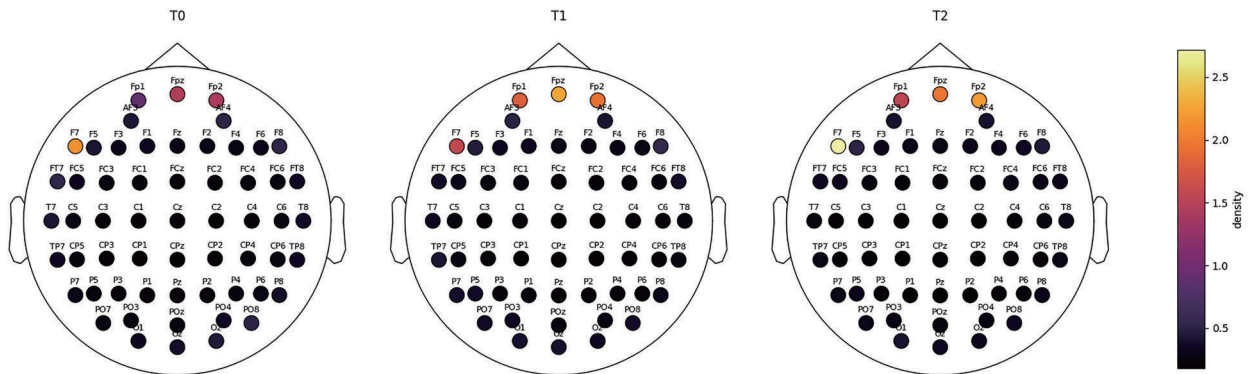


Figure 12: Participant A's attention score distribution.

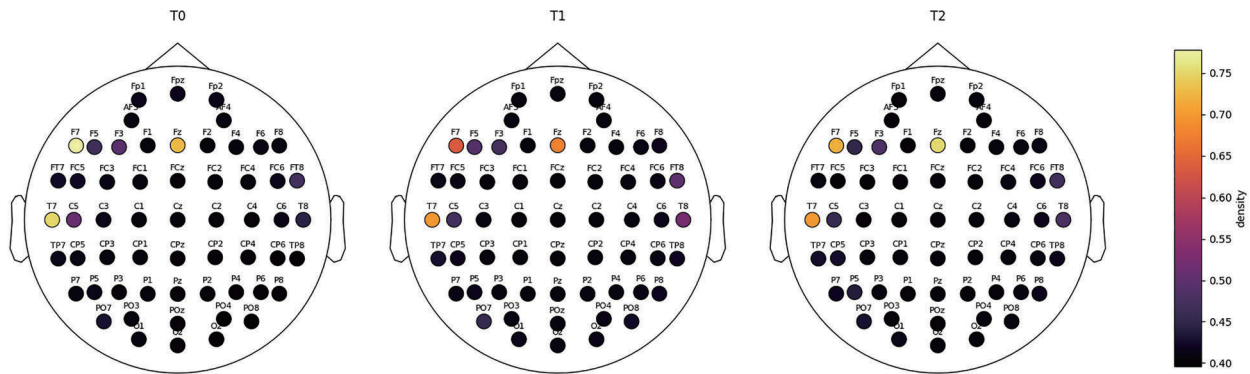


Figure 13: Participant B's attention score distribution.

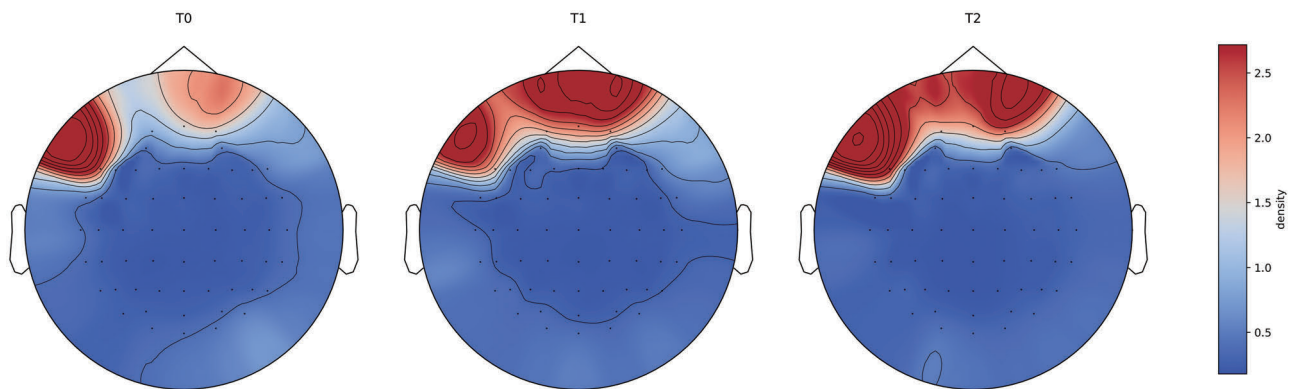


Figure 14: Topomap of one subject.

most influential channels are located in the aforementioned brain regions, the number and distribution of key channels vary notably across individuals.

Continuation of emotion changes

In methods for interpreting graph convolutional networks, beyond visualizing connection strengths between nodes, another approach involves visualizing the features learned by the model. In this study, we explored this technique by mapping each sample's features (prior to final labeling) onto a two-dimensional plane over time. This was achieved by applying average pooling across all features after the fully connected layer, as shown in the figure below.

This study employed hard labels without smoothing. The model was trained on mixed samples without incorporating temporal dependencies between them, meaning

the model did not recognize the sequential order of samples. Despite this, as shown in Figure 15, samples with the same label exhibited continuously evolving features: neutral emotion samples were spatially positioned between positive and negative emotions, with earlier samples in each trial appearing closer to the previous trial and later samples closer to the subsequent trial. This indicates a degree of continuity in the change of emotional features.

Ultimately, the model assigns emotion labels by applying a weighted sum across all features in the graph. This weighting process amplifies feature differences, thereby enhancing the accuracy of the model's classifications.

Conclusion

In this paper, we proposed PSGA, a unified framework for EEG-based emotion recognition that integrates

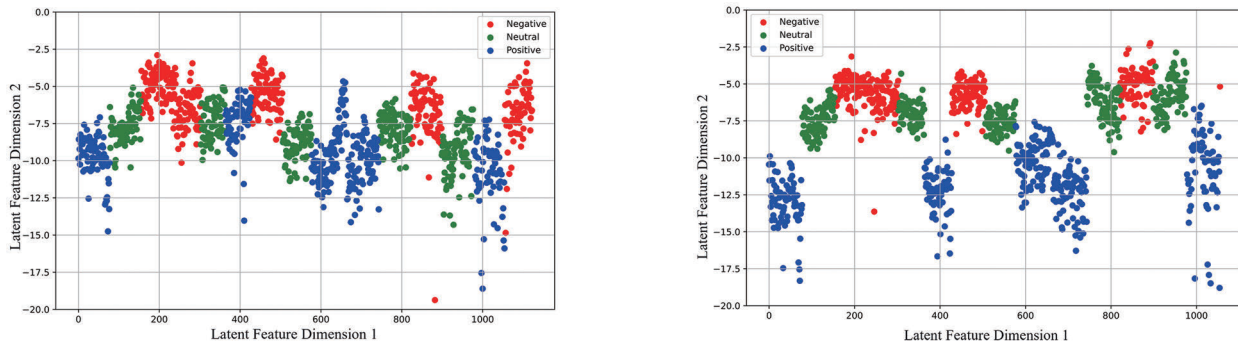


Figure 15: Continuation of emotion changes. (a) Feature distribution of subject A (b) Feature distribution of subject B.

cross-temporal graph construction, band-specific parallel attention modeling, and graph pooling. Experimental results on the DEAP and SEED datasets demonstrated that PSGA achieves competitive and relatively stable performance under both cross-trial and cross-subject evaluation settings. The effectiveness of PSGA is mainly attributed to its ability to capture temporal dependencies and frequency-specific information in EEG signals, while graph pooling improves computational efficiency under the current architecture. Furthermore, the attention analysis revealed emotion-related brain patterns broadly consistent with prior neuroscience findings, supporting the potential of PSGA for affective computing applications. Nevertheless, the current interpretability analysis remains largely qualitative, the adopted datasets may not fully reflect clinically extreme affective conditions, and longer-term emotional dynamics still require further investigation. Future work will focus on more rigorous neuroscientific validation, robustness under real-world conditions, and evaluation on more clinically relevant affective states.

Author contributions

Jiawei Zhang: experimental study, writing, results validation, revision, Xin Yan: methodology, investigation, writing, Lingtao Tang: writing, Liguang Dong: methodology, review, editing, Yuzhu Guo: conceptualization, methodology, review, editing.

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Data availability statement

No new datasets were generated or analyzed during the current study. All analyses in this work were performed on two publicly available EEG emotion recognition datasets:

- DEAP Dataset: a publicly available multimodal dataset for emotion analysis using physiological signals, accessible via its official website after completing the required End User License Agreement (EULA) application process as specified by the dataset administrators.
- SEED Dataset: the SJTU Emotion EEG Dataset (SEED), a publicly available academic EEG emotion recognition dataset provided by the Brain-Like Computing and Machine Intelligence (BCMI) Laboratory of Shanghai Jiao Tong University, accessible via its official website under the dataset's open access terms for non-commercial academic research.

Ethics statement

Not applicable.

AI statement

The authors used GPT-5 as a language-editing tool to improve grammar, clarity, and readability. The AI tool

was not used for data analysis, data generation, image processing, or scientific content creation. All outputs were carefully reviewed and verified by the authors, who take full responsibility for the final content.

Conflicts of interest

Yuzhu Guo serves as a member of the Editorial Board of this journal. He was not involved in the editorial review or decision-making process for this manuscript. All editorial decisions were made independently by other members of the Editorial Board who have no conflicts of interest.

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