**Breast Cancer Detection using Histopathological Images**

Esha Gangam

Department of Information Science and Technology, University at Albany, SUNY, NY, USA.

E-mail:egangam@albany.edu

**Abstract**

Breast cancer remains one of the leading causes of mortality among women worldwide. Accurate and early detection is critical for improving prognosis and treatment outcomes. In this study, we propose two graph-based deep learning approaches for breast cancer classification using histopathological images. The first method utilizes a standard Graph Convolutional Network (GCN) over superpixel-derived image graphs, while the second introduces an Adversarial Graph Convolutional Network with Contrastive Learning (AGCL), incorporating edge masking and projection-based contrastive objectives. Both models convert image segments into graph representations to learn structural and contextual patterns. Results demonstrate that AGCL significantly outperforms the baseline GCN, achieving 90.0% test accuracy and 0.9856 AUC, showcasing the potential of adversarial contrastive learning in graph-based medical image analysis.

**Keywords:** Breast cancer, histopathology, graph neural networks, GCN, contrastive learning, AGCL, superpixel segmentation.

**1. Introduction**

[1] Breast cancer remains the most commonly diagnosed cancer and the second leading cause of cancer-related mortality among women worldwide, emphasizing the urgent need for effective and early diagnostic strategies. Among various diagnostic modalities, **histopathological image analysis** plays a crucial role by providing microscopic-level insights into cellular morphology and the structural organization of tissue, which are essential for distinguishing between benign and malignant states.

Traditionally, **Convolutional Neural Networks (CNNs)** have been widely employed for medical image classification tasks due to their impressive performance in extracting hierarchical spatial features [2]. However, CNNs often operate on regular grid-based pixel data and thus may struggle to model complex spatial dependencies and relational structures inherent in histopathological tissues. This limitation hinders their ability to fully capture the topological and contextual nuances within localized regions of interest.

[3] To address these challenges, recent advancements have turned toward **Graph Neural Networks (GNNs)**, which provide a powerful framework for learning over irregular, non-Euclidean data structures. In the context of histopathological image analysis, converting images into graph representations enables a more structured and interpretable form of learning. Here, **superpixel segmentation** serves as a key preprocessing step, partitioning the image into perceptually meaningful regions [4]. These superpixels are represented as nodes in a graph, while the spatial or functional relationships between them are encoded as edges—thereby preserving both visual coherence and spatial topology.

This study explores and compares two GNN-based models for **binary breast cancer classification**: a baseline **3-layer Graph Convolutional Network (GCN)** and an advanced **Adversarial Graph Convolutional Network with Contrastive Learning (AGCL)** [5]. The AGCL approach introduces adversarial perturbations and a contrastive loss mechanism to improve representation robustness and discriminative power in the graph space. By conducting a comprehensive experimental evaluation, this work aims to assess the relative strengths of both models and investigate the potential of contrastive learning in enhancing graph-based histopathological image classification [6]. Ultimately, this research contributes to the development of more accurate, explainable, and robust computational tools for breast cancer diagnosis.

**2. Literature Review**

[7] Graph-based methods for histopathological image analysis have gained traction in recent years. Prior work like scGNN and GLAE has shown that converting image data into graph structures enhances feature representation, particularly in medical imaging domains where spatial and semantic relationships are essential. Recent studies have also highlighted the advantages of integrating contrastive learning with GCNs to improve robustness and representation quality under noise and adversarial perturbations. While many existing approaches use attention mechanisms or graph transformers, adversarial edge perturbation with contrastive objectives remains underexplored in histopathological classification.

[8] Contrastive learning has recently achieved state-of-the-art results in self-supervised image representation. This work extends contrastive methods to the supervised setting, introducing Supervised Contrastive (SupCon) loss, which pulls together same-class samples and pushes apart different-class ones in embedding space. SupCon outperforms traditional cross-entropy loss across datasets and model variants, offering improved accuracy, robustness to data corruption, and stability across hyperparameters. Using ResNet-200 on ImageNet, it achieves 81.4% top-1 accuracy, surpassing previous benchmarks. The method is simple to implement and publicly available.

[9] The pathological mechanisms of ADHD remain unclear, complicating accurate diagnosis. Functional MRI (fMRI) is commonly used to study brain connectomes, but existing models often underutilize graph structural information. To address this, we propose a dynamic graph convolutional network (dGCN) that captures sparse, dynamic brain region connections and includes a novel convolutional readout layer. Our model outperforms existing methods in ADHD diagnosis and highlights abnormalities in the temporal pole, gyrus rectus, and cerebellar gyri. These connectomic patterns correlate with ADHD symptom severity, demonstrating dGCN’s potential for precise, network-based mental disorder diagnosis.

[10] Deep learning (DL) offers powerful solutions for digital pathology (DP) tasks like detection, segmentation, and classification. Unlike traditional handcrafted methods, DL learns features automatically but lacks clear guidance on challenges like magnification, annotation errors, and training data selection. This study addresses these gaps using seven DP tasks with a single DL framework (Caffe), achieving high performance across all tasks. It represents the largest DL study in DP to date, with detailed instructions and open-source resources provided.

[11] Disease diagnosis benefits from medical imaging, but interpreting complex patterns like irregular lesion distribution remains challenging for traditional CNNs. Graph Neural Networks (GNNs) address this by modeling images as graphs, capturing spatial and relational structures between regions of interest. GNNs aggregate node and edge features to learn meaningful patterns, improving diagnostic accuracy. This makes them well-suited for diseases involving complex anatomical or network changes.

[12] Cervical cancer is a major health concern but is highly preventable through cytology and HPV testing. Computer-aided diagnosis (CAD) systems help automate screening, addressing challenges like manual workload and variability. While CNN-based models are effective for cell classification, they often overlook spatial relationships between suspicious and surrounding cells in whole slide images (WSIs). To improve diagnostic accuracy, we propose a two-stage framework using Local and Global Graph Attention Networks (GATs), combined with supervised contrastive learning. This approach captures contextual cell relationships and enhances WSI-level classification. Our method outperforms previous models with improved accuracy and robustness across multiple analysis levels.

[13] Recent deep learning advancements have transformed histopathology image analysis, with CNNs widely used for tasks like segmentation and classification. However, CNNs struggle to capture complex spatial relationships in tissue structures. Graph Neural Networks (GNNs), especially Graph Convolutional Networks (GCNs), overcome this by modeling cells and regions as nodes and edges, preserving spatial and relational context. GNNs support tasks like cell classification, tissue analysis, and whole-slide image diagnosis with improved interpretability. Attention mechanisms and graph customization enable more accurate and explainable outcomes. This shift from pixel-based to graph-based processing marks a major advancement in digital pathology.

[14] Pathological examination is key to cancer diagnosis, and the rise of digital imaging has driven the development of computational histopathology. Early methods relied on manual feature extraction with limited success. The introduction of AI and deep learning improved performance, but traditional CNNs still struggle to capture rich contextual and biological information. Graph-based models, due to their structural advantages, are better suited for analyzing histopathology images and have shown promising results. This article reviews existing graph-based approaches, proposes a novel graph construction method, categorizes learning paradigms, and outlines clinical applications, challenges, and future directions.

[15] Unsupervised learning, especially self-supervised learning, is valuable for medical image analysis due to the scarcity of labeled data. This study applies the contrastive self-supervised method SimCLR to 57 unlabeled histopathology datasets. Pretraining on diverse, multi-organ datasets with varying staining and resolution significantly improves feature quality. More training images also enhance downstream task performance. Networks pretrained on histopathology data outperform ImageNet-pretrained models, boosting F1 scores by over 28% on average. These findings highlight the potential of contrastive learning in digital pathology.

[16] The spatial arrangement of different cell types, such as tumor-infiltrating lymphocytes and tumor boundaries, plays a key role in cancer detection and characterization. Traditional CNNs struggle to explicitly capture these spatial patterns in histopathology images. To address this, the study proposes using Graph Convolutional Networks (GCNs) by representing tissue sections as multi-attributed spatial graphs, where cells are nodes with high-dimensional features and edges represent spatial proximity. Using nuclei detected from H&E-stained images, this graph-based approach effectively models both cell appearance and spatial context. The method achieves competitive performance with Inception-v3 CNNs on the BACH breast cancer dataset for classifying cancerous vs. non-cancerous and in situ vs. invasive cases.

**3. Materials and Methods**

**3.1 Dataset**

The dataset used in this study is the publicly available Breast Histopathology Images dataset from Kaggle. It contains labeled 50x50 pixel image patches categorized as:

* Class 0: Non-cancerous
* Class 1: Cancerous (Invasive Ductal Carcinoma)

We selected a balanced subset of 2000 images (1000 per class) across 10 patient directories for both models. The dataset was split into 70% training, 15% validation, and 15% testing.

**3.2 Graph Construction**

Each image is converted into a graph using SLIC superpixel segmentation, where superpixels become nodes. Node features are the mean RGB (GCN) or LAB (AGCL) color values. Edges are formed by spatial adjacency between superpixels. For consistency, the number of segments was fixed at 30 for GCN and 60 for AGCL.

**3.3 Model Architectures**

**3.3.1 Graph Convolutional Network (GCN):**

[17] The **Graph Convolutional Network (GCN)** is a foundational model in the domain of graph-based deep learning, particularly effective for tasks where spatial relationships and structural dependencies are important, such as in histopathological image analysis. In this study, a three-layer GCN is employed as the baseline model. Each layer of the GCN performs a message-passing operation, wherein the features of a node are updated by aggregating the features of its neighboring nodes. This operation is followed by a non-linear activation function, specifically ReLU, to enable the model to learn complex patterns in the data. After passing through the three GCN layers, a global pooling operation—typically mean or max pooling is applied to summarize the information from all nodes into a single fixed-size representation for the entire graph [18]. This graph-level representation is then passed through a linear layer that performs binary classification, distinguishing, for example, between cancerous and non-cancerous tissue samples. While this approach captures important structural information and node-level features, its performance may be limited by its sensitivity to noisy graph structures and its reliance on fixed connectivity patterns defined by the graph's adjacency matrix.

**3.3.2 Adversarial Graph Convolutional Network with Contrastive Learning (AGCL):**

[19] The **Adversarial Graph Convolutional Network with Contrastive Learning (AGCL)** introduces a more sophisticated and robust approach to graph-based learning. This model enhances the learning process through two key innovations: adversarial edge masking and contrastive learning. In the AGCL framework, a two-layer GCN is used as the encoder, with each layer followed by batch normalization to improve training stability and generalization. The first enhancement, adversarial edge masking, involves using a learned multi-layer perceptron (MLP) to mask edges in the graph during training. This mimics structural noise that may naturally occur in real-world histopathological graphs, such as missing or spurious connections between tissue regions. By learning under such perturbations, the model becomes more resilient and capable of extracting robust features. The second enhancement is the application of a contrastive loss in addition to the standard classification loss. The model generates two views of each graph—one original and one perturbed—and learns to make their feature embeddings similar in the representation space while keeping embeddings from different graphs distinct [20]. A projection head maps these embeddings into a space suited for contrastive learning, and a separate MLP is responsible for the final classification. This contrastive framework encourages the model to learn invariant and discriminative features that generalize well across variable and noisy graph structures, making AGCL a powerful tool for complex medical image analysis tasks.

**4. Results and Evaluation**

**4.1 Evaluation Metrics**

To evaluate the performance of our graph-based models in classifying breast cancer from histopathological images, we used a combination of five well-established metrics: Accuracy, Macro F1-score, Weighted F1-score, Cohen’s Kappa, and Area Under the ROC Curve (AUC).

**4.1.1. Accuracy:**

Accuracy serves as a fundamental performance indicator, measuring the proportion of correctly classified image patches among all predictions. In this context, it reflects how effectively the model distinguishes between cancerous and non-cancerous tissue samples based on the graph-encoded features. A high accuracy value indicates that the model has successfully learned relevant patterns in tissue morphology and structure.

**4.1.2. Macro F1-score:**

However, since binary classification tasks involving medical data may face issues like subtle class imbalance or varying complexity across samples, accuracy alone does not capture the full diagnostic capability of the model. To address this, we also employed the Macro F1-score, which provides the harmonic mean of precision and recall calculated independently for each class and averaged. This ensures equal treatment of both classes regardless of the sample size.

**4.1.3. Weighted F1**:

The weighted F1-score extends the Macro F1 approach by incorporating the support (i.e., the number of true instances) of each class into the calculation. This metric ensures that the overall performance reflects the contribution of each class based on its prevalence in the dataset. In medical image datasets where class distributions may vary slightly, the Weighted F1-score helps provide a balanced evaluation that accounts for such skew, especially when one class might have more subtle or varied morphological characteristics.

**4.1.4. Cohen’s Kappa**:

Cohen’s Kappa measures the level of agreement between the model’s predictions and the actual labels, while adjusting for the possibility of agreement occurring by chance. This is particularly useful in healthcare scenarios where achieving consistent agreement is critical. A higher Kappa score indicates strong reliability and confirms that the model is not merely benefiting from class priors or random guessing, but is genuinely learning discriminative features.

**4.1.5. AUC**:

The AUC (Area Under the Curve) metric evaluates the model's ability to distinguish between the two classes across various decision thresholds. It is derived from the Receiver Operating Characteristic (ROC) curve, which plots true positive rate against false positive rate. A higher AUC value suggests strong discriminative capability, making it a critical metric for assessing the robustness and reliability of the model in medical image diagnosis.  
**4.2 GCN Results**

The baseline Graph Convolutional Network (GCN) model demonstrated strong performance in classifying histopathological image graphs. After training on 2000 balanced samples for 50 epochs with optimized superpixel segmentation, the model achieved an **accuracy of 81.25%**, reflecting its overall ability to distinguish between cancerous and non-cancerous tissue.

In terms of class-wise balance, the model recorded a **Macro F1-score of 0.8125**, indicating that it performed consistently across both classes, regardless of their distribution. The **Weighted F1-score**, which considers the number of samples per class, also reached **0.8125**, confirming that the model handled class prevalence effectively and avoided bias toward any particular category.

The **Cohen’s Kappa coefficient** was **0.625**, which signifies a substantial level of agreement between the model's predictions and the ground truth labels, even after accounting for the possibility of chance agreement. This metric underscores the model's reliability in making consistent, clinically meaningful predictions.

Lastly, the model achieved an **AUC (Area Under the ROC Curve) of 0.8988**, highlighting its strong discriminative power in separating the two classes across different threshold values. This high AUC indicates that the model is effective at balancing sensitivity and specificity — an important consideration in diagnostic applications where both false positives and false negatives carry significant risk.

**4.3 AGCL Results**

The Adversarial Graph Convolutional Network with Contrastive Learning (AGCL) substantially outperformed the baseline GCN model across all evaluation metrics. By incorporating adversarial edge masking and contrastive representation learning, the model achieved a significantly higher **accuracy of 90.00%**, indicating strong generalization and improved classification reliability on unseen histopathological samples.

The **Macro F1-score** reached **0.8901**, demonstrating that the AGCL model was highly effective at balancing precision and recall across both cancerous and non-cancerous classes, irrespective of sample size. Similarly, the **Weighted F1-score** was **0.8989**, reflecting the model's robust performance even when accounting for class distribution, and further confirming its resilience to data variation.

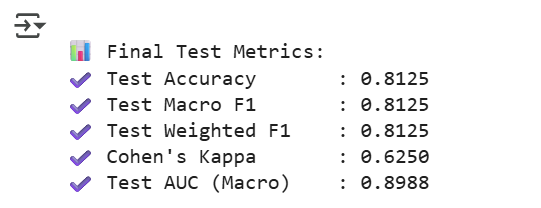
The model achieved a **Cohen’s Kappa coefficient of 0.7805**, which represents a substantial improvement in inter-rater reliability compared to the GCN model. This metric reinforces that AGCL’s predictions align closely with ground truth labels beyond what would be expected by chance, highlighting its consistency and diagnostic trustworthiness.

Most notably, AGCL yielded an **AUC of 0.9856**, indicating excellent discriminative capability. This near-perfect score demonstrates that the model can reliably differentiate between the two classes across a wide range of thresholds a critical requirement for clinical applications where early and accurate cancer detection is vital.

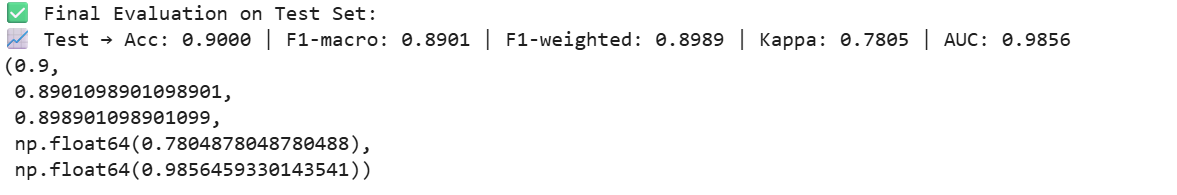
The AGCL model outperformed GCN across all metrics. Adversarial edge masking improved generalization, while contrastive learning enhanced feature robustness. The high AUC demonstrates AGCL’s reliability in separating cancerous from non-cancerous samples.

**4.4 Experimental Results**

4.4.1.GCN Model:



4.4.2.AGCL Model:



**4.5 Comparative Table**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Model | Accuracy | Macro F1 | Weighted F1 | Cohen’s Kappa | AUC |
| GCN | 0.8125 | 0.8125 | 0.8125 | 0.6250 | 0.8988 |
| AGCL | 0.9000 | 0.8901 | 0.8989 | 0.7805 | 0.9856 |

**5. Conclusion**

This study demonstrates that representing histopathological images as graphs significantly enhances breast cancer detection. While the GCN baseline provides solid classification accuracy, incorporating adversarial edge perturbations and contrastive learning in the AGCL model yields notably improved performance. These findings suggest that future research in medical imaging should further explore adversarial learning strategies in graph-based domains for enhanced interpretability and robustness.

**References**

[1] K. Zhao, B. Duka, H. Xie, D. J. Oathes, V. Calhoun, and Y. Zhang, “A dynamic graph convolutional neural network framework reveals new insights into connectome dysfunctions in ADHD,” *NeuroImage*, vol. 246, p. 118774, Feb. 2022, doi: 10.1016/j.neuroimage.2021.118774.

[2] S. Zhang *et al.*, “A-GCL: Adversarial graph contrastive learning for fMRI analysis to diagnose neurodevelopmental disorders,” *Med. Image Anal.*, vol. 90, p. 102932, Dec. 2023, doi: 10.1016/j.media.2023.102932.

[3] A. Janowczyk and A. Madabhushi, “Deep learning for digital pathology image analysis: A comprehensive tutorial with selected use cases,” *J. Pathol. Inform.*, vol. 7, no. 1, p. 29, Jan. 2016, doi: 10.4103/2153-3539.186902.

[4] P. Veličković, G. Cucurull, A. Casanova, A. Romero, P. Liò, and Y. Bengio, “Graph Attention Networks,” 2017, *arXiv*. doi: 10.48550/ARXIV.1710.10903.

[5] K. Xu, W. Hu, J. Leskovec, and S. Jegelka, “How Powerful are Graph Neural Networks?,” 2018, *arXiv*. doi: 10.48550/ARXIV.1810.00826.

[6] T. N. Kipf and M. Welling, “Semi-Supervised Classification with Graph Convolutional Networks,” 2016, *arXiv*. doi: 10.48550/ARXIV.1609.02907.

[7] P. Khosla *et al.*, “Supervised Contrastive Learning,” 2020, *arXiv*. doi: 10.48550/ARXIV.2004.11362.

[8] O. Ronneberger, P. Fischer, and T. Brox, “U-Net: Convolutional Networks for Biomedical Image Segmentation,” 2015, *arXiv*. doi: 10.48550/ARXIV.1505.04597.

[9] K. Shanmugam and H. Rajaguru, “Enhanced Superpixel-Guided ResNet Framework with Optimized Deep-Weighted Averaging-Based Feature Fusion for Lung Cancer Detection in Histopathological Images,” *Diagnostics*, vol. 15, no. 7, p. 805, Mar. 2025, doi: 10.3390/diagnostics15070805.

[10] J.-H. Bae *et al.*, “Superpixel Image Classification with Graph Convolutional Neural Networks Based on Learnable Positional Embedding,” *Appl. Sci.*, vol. 12, no. 18, p. 9176, Sep. 2022, doi: 10.3390/app12189176.

[11] L. Zhang, Y. Zhao, T. Che, S. Li, and X. Wang, “Graph neural networks for image‐guided disease diagnosis: A review,” *iRADIOLOGY*, vol. 1, no. 2, pp. 151–166, Jun. 2023, doi: 10.1002/ird3.20.

[12] M. Fei, X. Zhang, D. Chen, Z. Song, Q. Wang, and L. Zhang, “Whole slide cervical cancer classification via graph attention networks and contrastive learning,” *Neurocomputing*, vol. 613, p. 128787, Jan. 2025, doi: 10.1016/j.neucom.2024.128787.

[13] D. Ahmedt-Aristizabal, M. A. Armin, S. Denman, C. Fookes, and L. Petersson, “A survey on graph-based deep learning for computational histopathology,” *Comput. Med. Imaging Graph.*, vol. 95, p. 102027, Jan. 2022, doi: 10.1016/j.compmedimag.2021.102027.

[14] X. Meng and T. Zou, “Clinical applications of graph neural networks in computational histopathology: A review,” *Comput. Biol. Med.*, vol. 164, p. 107201, Sep. 2023, doi: 10.1016/j.compbiomed.2023.107201.

[15] O. Ciga, T. Xu, and A. L. Martel, “Self supervised contrastive learning for digital histopathology,” 2020, *arXiv*. doi: 10.48550/ARXIV.2011.13971.

[16] S. Gadiya, D. Anand, and A. Sethi, “Histographs: Graphs in Histopathology,” 2019, *arXiv*. doi: 10.48550/ARXIV.1908.05020.

[17] J. Zhou *et al.*, “Graph neural networks: A review of methods and applications,” *AI Open*, vol. 1, pp. 57–81, 2020, doi: 10.1016/j.aiopen.2021.01.001.

[18] Z. Wu, S. Pan, F. Chen, G. Long, C. Zhang, and P. S. Yu, “A Comprehensive Survey on Graph Neural Networks,” *IEEE Trans. Neural Netw. Learn. Syst.*, vol. 32, no. 1, pp. 4–24, Jan. 2021, doi: 10.1109/TNNLS.2020.2978386.

[19] Z. Chen, M. Trabelsi, J. Heflin, D. Yin, and B. D. Davison, “MGNETS: Multi-Graph Neural Networks for Table Search,” in *Proceedings of the 30th ACM International Conference on Information & Knowledge Management*, Virtual Event Queensland Australia: ACM, Oct. 2021, pp. 2945–2949. doi: 10.1145/3459637.3482140.

[20] W. Jin, Y. Ma, X. Liu, X. Tang, S. Wang, and J. Tang, “Graph Structure Learning for Robust Graph Neural Networks,” in *Proceedings of the 26th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining*, in KDD ’20. New York, NY, USA: Association for Computing Machinery, Aug. 2020, pp. 66–74. doi: 10.1145/3394486.3403049.