

DeepCon⁺ based Deep Learning Architecture for Histopathology Image Classification

Jayprakash Upadhyay¹, and Dr. Sudeep Sharma²

^{1,2}Shri Ram Institute of Science and Technology, Jabalpur

Abstract

Histopathological image classification is challenging due to substantial intra-class variability and similarities between tissue categories. This paper presents a DeepCon⁺ framework for colorectal cancer tissue classification. First, a pretrained Xception network is used to extract deep feature vectors from the images. Principal Component Analysis (PCA) is used to reduce the feature dimensionality while retaining 95% of the original information. Subsequently, class-wise K-means clustering decomposes the eight original tissue classes into 16 subclasses to represent intra-class variations more effectively. A pretrained Xception-based CNN is then fine-tuned using transfer learning to classify the decomposed subclasses. This coarse-learning stage enables the model to learn more discriminative representations of heterogeneous tissue patterns. The overall framework aims to improve feature representation and classification by combining deep feature extraction, dimensionality reduction, class-wise clustering, and subclass-level learning. Its effectiveness can be assessed using standard classification metrics, including accuracy, precision, recall, and F1-score. The experimental analysis performed on the colorectal histopathology dataset reveals that the proposed Deep Con⁺ framework markedly surpasses the initial Deep Con model and traditional CNN benchmarks, attaining enhanced classification accuracy and increased F1-score for all tissue categories.

Keywords: Histopathological Image Classification, DeepCon⁺, Coarse-to-Fine Learning, Class Decomposition, Attention Mechanism, Subclass Learning, Deep Learning.

I.Introduction

Histopathological image analysis plays a vital role in computer-assisted medical diagnosis by enabling the identification and classification of tissue structures associated with various diseases, particularly cancer. Accurate tissue classification supports pathological assessment and facilitates the development of automated diagnostic systems. Over the years, several approaches based on image processing, machine learning, and deep learning have been investigated to improve histopathological image analysis. Despite considerable progress, accurate classification remains challenging due to variations in tissue morphology, staining inconsistencies, complex cellular structures, and similarities between different tissue categories.

Traditional image processing techniques, such as thresholding, edge detection, morphological operations, and texture analysis, have been widely used to identify tissue structures and extract relevant image information. However, these methods often depend on predefined rules and manually selected parameters, limiting their adaptability to complex histopathological images. Machine learning techniques, including Support Vector Machines (SVM), Random Forest, and k-Nearest Neighbors (k-NN), have also been employed for tissue

classification using handcrafted features such as color, texture, and shape. Although these methods can provide effective classification under controlled conditions, their performance depends heavily on feature quality and feature selection. Moreover, handcrafted representations may fail to capture the subtle morphological variations and complex spatial relationships present in histopathological images. With advances in computational capabilities, deep learning methods have emerged as powerful alternatives for automated feature extraction and tissue classification. Convolutional neural networks (CNNs), including ResNet, DenseNet, and EfficientNet, can learn hierarchical representations directly from image data. More recently, Transformer-based architectures have been explored to capture long-range dependencies and contextual relationships among tissue regions. Despite their advantages, conventional deep learning models may struggle with substantial intra-class variability, inter-class similarity, limited training data, and differences in staining and image acquisition. Furthermore, standard classification approaches generally assign each image to a predefined class without explicitly modelling the fine-grained variations that exist within that category. Attention mechanisms can emphasize informative features, but attention alone may not sufficiently resolve these classification ambiguities.

To overcome these limitations, this paper proposes DeepCon⁺, a coarse-to-fine deep learning framework for histopathological tissue classification. The framework integrates attention-guided feature extraction with class decomposition to learn more discriminative tissue representations. Initially, stain-sensitive and geometry-aware data augmentation is applied to improve robustness against variations in tissue appearance. Subsequently, CNN-based architectures extract discriminative features, while channel and spatial attention mechanisms emphasize diagnostically relevant regions. A feature-space class decomposition strategy then divides the original tissue categories into visually consistent subclasses through dimensionality reduction and clustering. The model learns to distinguish these subclasses before mapping the predictions back to their corresponding original categories. This approach aims to capture fine-grained morphological variations and reduce confusion among visually similar tissue patterns. The main contributions of this paper are summarized as follows:

1. To develop a deep feature extraction framework using pretrained convolutional neural networks (e.g., Xception and InceptionV3) to capture discriminative texture and structural patterns from colorectal histopathology images.
2. To reduce feature redundancy and computational complexity by applying Principal Component Analysis (PCA) on deep feature embeddings while preserving the most informative components.
3. To perform class decomposition using unsupervised clustering (K-means) to divide each original tissue class into multiple homogeneous sub-classes, thereby reducing intra-class variance.
4. To implement a coarse-to-fine transfer learning strategy, where the model is first trained on decomposed sub-classes and subsequently fine-tuned on the original class labels.
5. To evaluate and compare classification performance before and after class decomposition using standard metrics such as accuracy, precision, recall, F1-score, and confusion matrix.

II.Problem Statement

Histopathological tissue classification is a challenging task due to the complex morphology of tissue structures, substantial intra-class variability, and visual similarities between different tissue categories. Although deep learning techniques have achieved promising results in automated tissue classification, their performance may be affected by variations in staining, tissue preparation, image acquisition, and the availability of representative training samples. These variations can lead to inconsistent feature representations and reduce the generalization capability of trained models. Furthermore, conventional classification approaches may struggle to distinguish subtle morphological differences within heterogeneous tissue categories, particularly when different subclasses share similar textural and structural characteristics.

Existing methods, such as DeepCon, address class variability through class decomposition and learnable composition. However, further investigation is needed into integrating attention-guided feature extraction with fine-grained subclass learning to improve discrimination between visually similar tissue patterns. Without sufficiently discriminative representations, complex tissue categories may be incorrectly classified, affecting class-wise performance and prediction reliability. In addition, robustness to staining and structural variations requires systematic evaluation using appropriate experimental settings and performance metrics. Therefore, the problem addressed in this paper is how to develop a robust histopathological tissue classification framework that can capture intra-class morphological diversity, emphasize diagnostically relevant image regions, and distinguish visually similar tissue categories. To address this problem, DeepCon⁺ is proposed as a coarse-to-fine deep learning framework that combines attention-guided feature extraction with feature-space class decomposition and subclass-level supervision. The framework aims to learn fine-grained tissue representations and map subclass predictions to their corresponding original categories, thereby improving tissue discrimination and classification robustness.

III. Convolutional Neural Network (CNN)

The Convolutional Neural Network (CNN) is used to extract discriminative features from histopathological images. The input image passes through multiple convolutional layers, where filters learn local patterns such as edges, textures, cellular structures, and tissue boundaries. Activation functions, such as ReLU, introduce non-linearity, while pooling layers reduce spatial dimensions and computational complexity. In deeper layers, the CNN learns high-level morphological features that help distinguish tissue categories. The Fig. 1 shows the block diagram of CNN-Based Feature Extraction. A pretrained CNN, such as ResNet, DenseNet, or EfficientNet, can be used through transfer learning to leverage features learned from large image datasets. An attention mechanism, such as SE or CBAM, may further emphasize informative feature channels or spatial regions. The resulting feature maps are then used for subclass discovery and fine-grained classification.

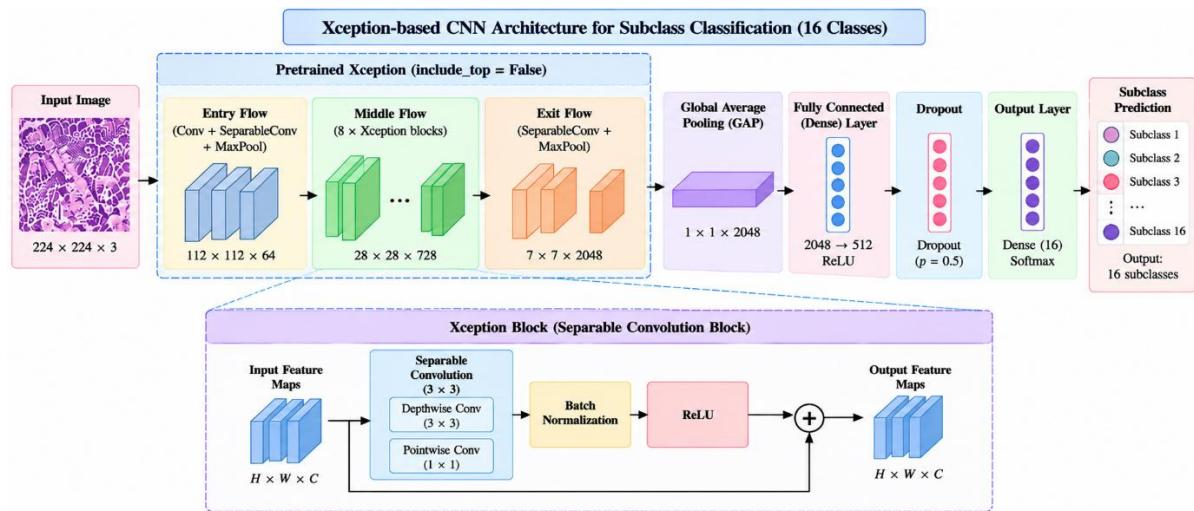


Fig. 1: Block Diagram of CNN-Based Feature Extraction.

IV. Proposed Model Architecture

The proposed model architecture for DeepCon+ is shown in Fig.2. The proposed DeepCon+ framework consists of sequential stages for histopathological tissue classification. First, colorectal histopathological images are collected with their original class labels. During preprocessing, images are resized, normalized, and subjected to stain or color normalization to reduce variations in image appearance. Strong data augmentation, including rotation, flipping, zooming, color jittering, elastic deformation, MixUp, and CutMix, is then applied to improve the diversity of training samples.

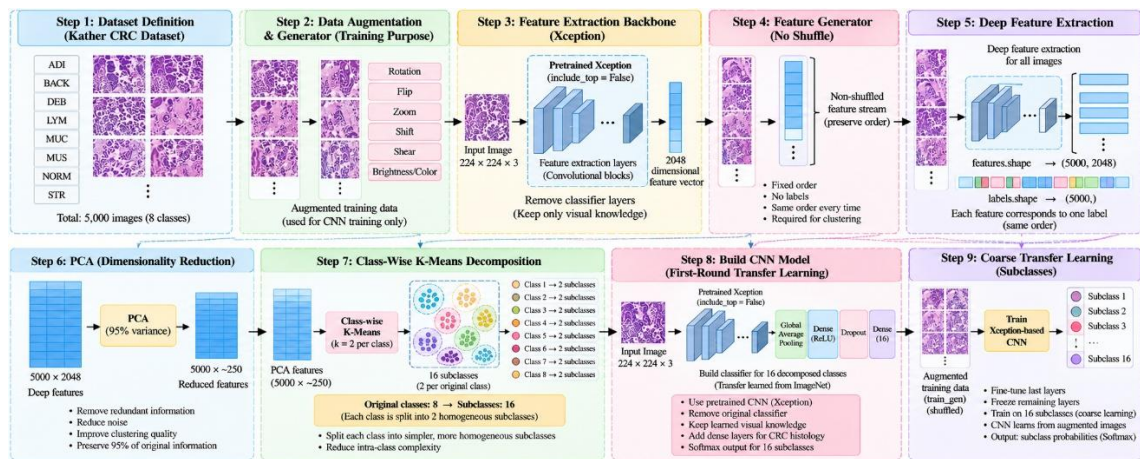


Fig.2: Architecture of the proposed model.

Next, a pretrained CNN backbone, such as EfficientNet or Xception, extracts discriminative deep features from the images. Principal Component Analysis (PCA) reduces the dimensionality of these features, facilitating subsequent clustering. In the class decomposition stage, K-means clustering divides each original tissue category into visually similar subclasses, enabling the model to capture intra-class variability. The hybrid CNN-transformer module is subsequently trained using subclass labels, with suitable loss functions, gradual layer unfreezing, and learning-rate scheduling. During inference, the predicted subclasses are mapped to their corresponding original

tissue categories. The trained DeepCon⁺ model then generates the final tissue classification predictions. Finally, its performance is evaluated using accuracy, precision, recall, and F1-score.

Algorithm 1: DeepCon⁺ for Histopathological Tissue Classification

Input:

- Histopathological image dataset with original class labels.
- Pretrained CNN backbone.
- Number of clusters for each original class.

Output:

- Trained DeepCon⁺ model.
- Predicted class labels for test images.

Procedure:

1. Initialize the pretrained CNN backbone.
2. Resize and normalize all images using ImageNet statistics.
3. Apply geometric, color-based, and elastic augmentations to training images.
4. For each training image, extract deep features
5. For each original class
 1. Collect class-specific features
 2. Apply PCA to reduce feature dimensionality.
 3. Cluster the reduced features using K-means with clusters.
 4. Assign subclass labels to the corresponding training images.
6. Construct the subclass-labelled training dataset.
7. Replace the final classification layer to predict all generated subclasses.
8. Train the CNN subclass labels, a selected classification loss, AdamW, and a learning-rate scheduler.
9. Fine-tune the backbone using gradual layer unfreezing and validation-based model selection.
10. Establish the mapping (g(s)) from every subclass (s) to its original class.
11. For each test image
 1. Apply the required preprocessing.
 2. Obtain subclass probabilities.
 3. Aggregate probabilities by original class:
 4. Predict the original class:
12. Optionally average original-class probabilities across independently trained models and test-time augmentations.
13. Evaluate predictions using accuracy, precision, recall, and macro F1-score.
14. Return the trained DeepCon⁺ model and final test predictions.

End Algorithm

V.Results and Discussion

The performance of the proposed DeepCon⁺ model is evaluated on the colorectal cancer (CRC) histopathology dataset containing eight tissue classes: Tumor, Stroma, Complex, Lympho, Debris, Mucosa, Adipose, and Empty. The proposed model is compared with the existing DeepCon framework using classification accuracy and macro F1-score. The experimental outcomes demonstrate that DeepCon⁺ achieved an accuracy of 96.00%, compared with 93.10% for DeepCon as shown in Fig 4. Similarly, the F1-score increased from 93.13% to 96.04%. These results correspond to absolute improvements of 2.90 and 2.91 %, respectively. The consistent improvement across both metrics suggests that the proposed model contribute to more effective tissue classification and better overall class-wise performance.

Table I:Perfoemance comparisons.

Results Parameters	Existing Method (DeepCon)	Proposed Method (Enhanced DeepCon)
Accuracy in %	93.10	96.00
Macro-F1 in %	93.13	96.04

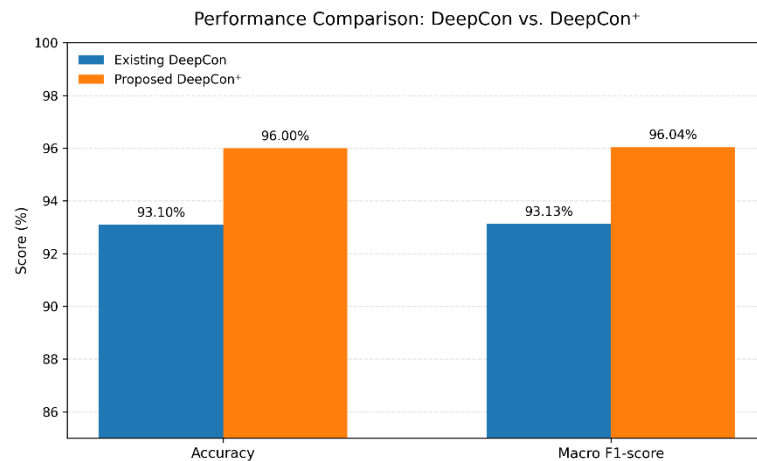


Fig. 4: Performance Comparison of DeepCon and DeepCon* .

A. Class-Wise Performance Analysis:

The proposed DeepCon⁺ framework demonstrates consistent performance improvements across most tissue categories, particularly in clinically critical and visually complex classes as shown in Fig .5 and Table II.

- i. **Tumor tissue** shows a substantial increase in F1-score from 94.00% to 97.60%, highlighting improved discrimination of malignant regions.
- ii. **Stroma and Lympho** classes gain nearly 4–5%, reflecting better modeling of structurally similar connective and immune tissues.
- iii. **Complex tissue**, traditionally challenging due to mixed patterns and ambiguous boundaries, exhibits a notable improvement from 84.00% to 88.97%, confirming the effectiveness of subclass decomposition and attention mechanisms.
- iv. **Debris and Mucosa** achieve near-perfect classification, with F1-scores exceeding 98%, indicating enhanced robustness to staining variations and noise.

A minor reduction is observed for **Adipose and Empty** classes. This marginal decrease (<0.5%) can be attributed to increased model sensitivity toward diagnostically relevant structures, leading to occasional confusion in visually sparse regions. However, these variations are negligible and do not impact the overall performance, as reflected by the improved macro F1-score.

Table II: F1-Score comparisons of Classes.

Classes	F1-Score of Existing models (%)	F1-Score of proposed models (%)
Tumor	94.00	97.60
Stroma	90.00	93.93
Complex	84.00	88.97
Lympho	91.00	95.87
Debris	95.00	98.02
Mucosa	95.00	98.80
Adipose	98.00	97.56
Empty	98.00	97.60

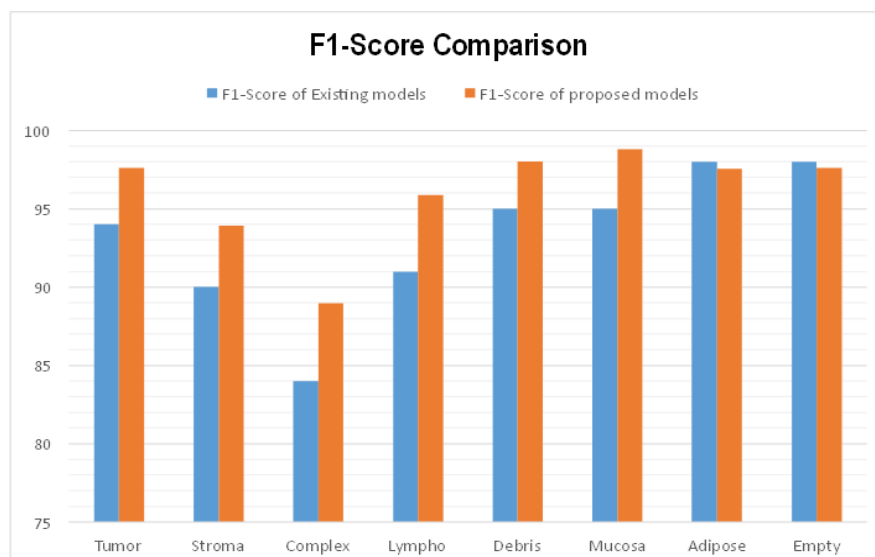


Fig. 5: F1-Score for classes.

VI. Conclusion

In this paper DeepCon⁺ model is proposed for colorectal histopathological tissue classification using class decomposition, dimensionality reduction, and refined subclass-to-class mapping. The proposed method achieved 96.00% accuracy and a 96.04% macro F1-score, outperforming the baseline DeepCon model. Improvements were observed in six of eight tissue classes, particularly Complex, Tumor, Stroma, and Lympho. These results demonstrate the potential of DeepCon⁺ to improve tissue classification, although further validation is required to establish its generalizability. Future work will focus on multi-scale feature learning, Vision Transformer hybrid architectures, and improved subclass decomposition. The framework will also be evaluated on independent histopathology datasets to assess its robustness and generalizability.

References

- [1] Y. Xiand P. Xu, "Global colorectal cancer burden in 2020 and projections to 2040," *Translational Oncol.*, vol. 14, no. 10, Oct. 2021, Art. no. 101174.
- [2] D.Hong,B.Zhang,H.Li,Y.Li,J.Yao,C.Li,M.Werner,J.Chanussot,A.Zipf, and X.X.Zhu,"Cross-citymatters: Amultimodalremotesensingbenchmarkdatasetforcross-city semantic segmentation using high resolution domain adaptation networks," *Remote Sens. Environ.*, vol. 299, Dec. 2023, Art. No. 113856.
- [3] D.Hong,B.Zhang,X.Li,Y.Li,C.Li,J.Yao,N.Yokoya,H.Li,P.Ghamisi,X.Jia, A. Plaza, P. Gamba, J. A. Benediktsson, and J. Chanussot, "SpectralGPT: Spectral remote sensing foundation model," *IEEE Trans. Pattern Anal. Mach. Intell.*, early access, Apr. 3, 2024, doi: 10.1109/TPAMI.2024.3362475.
- [4] D. Hong, C. Li, B. Zhang, N. Yokoya, J. A. Benediktsson and J. Chanussot, "Multimodal artificial intelligence foundation models: Unleashing the power of remote sensing big data in Earth observation," *Innov. Geosci.* vol. 2, no. 1, 2024, Art. no. 100055.
- [5] M.Jahanifar,A.Shepard,N.Zamanitajeddin,R.M.S.Bashir,M.Bilal, S.A.Khurram, F. Minhas, and N. Rajpoot, "Stain-robust mitotic figure detection for the mitosis domain generalization challenge," in *Proc. MICCAI*, Mar. 2022, pp. 48–52.
- [6] N.A.Koohbanani, B.Unnikrishnan, S.A.Khurram, P.Krishnaswamy and N.Rajpoot, "Self-path: Self-supervision for classification of pathology images with limited annotations," *IEEE Trans. Med. Imag.*, vol. 40, no. 10, pp. 2845–2856, Oct. 2021.

- [7] F. Ciompi, O. Geessink, B. E. Bejnordi, G. S. de Souza, A. Baidoshvili, G. Litjens, B. van Ginneken, I. Nagtegaal, and J. van der Laak, "The importance of stain normalization in colorectal tissue classification with convolutional networks," in *Proc. IEEE 14th Int. Symp. Biomed. Imag. Apr. 2017*, pp. 160–163.
- [8] X. Wu, Y. Li, X. Chen, Y. Huang, L. He, K. Zhao, X. Huang, W. Zhang, Y. Huang, Y. Li, M. Dong, J. Huang, T. Xia, C. Liang, and Z. Liu, "Deep learning features improve the performance of a radiomics signature for predicting Kras status in patients with colorectal cancer," *Academic Radiol.*, vol. 27, no. 11, pp. e254–e262, Nov. 2020.
- [9] K. Suzuki, "Overview of deep learning in medical imaging," *Radiological Phys. Technol.*, vol. 10, no. 3, pp. 257–273, Jul. 2017.
- [10] S. Poudel, Y. J. Kim, D. M. Vo, and S.-W. Lee, "Colorectal disease classification using efficiently scaled dilation in convolutional neural network," *IEEE Access*, vol. 8, pp. 99227–99238, 2020.
- [11] E. F. Ohata, J. V. S. D. Chagas, G. M. Bezerra, M. M. Hassan, V. H. C. de Albuquerque, and P. P. R. Filho, "A novel transfer learning approach for the classification of histological images of colorectal cancer," *J. Supercomputer.*, vol. 77, no. 9, pp. 9494–9519, Feb. 2021.
- [12] V. Rachapudi and G. Lavanya Devi, "Improved convolutional neural network-based histopathological image classification," *Evol. Intell.* vol. 14, no. 3, pp. 1337–1343, Sep. 2021.
- [13] T. T. L. Vuong, Q. D. Vu, M. Jahanifar, S. Graham, J. T. Kwak, and N. Rajpoot, "IMPaSh: A novel domain-shift resistant representation for colorectal cancer tissue classification," in *Proc. ECCV*, Feb. 2023, pp. 543–555.
- [14] J. N. Kather, J. Krisam, P. Charoentong, T. Luedde, E. Herpel, C.-A. Weis, T. Gaiser, A. Marx, N. A. Valous, D. Ferber, L. Jansen, C. C. Reyes-Aldasoro, I. Zörnig, D. Jäger, H. Brenner, J. Chang-Claude, M. Hoffmeister, and N. Halama, "Predicting survival from colorectal cancer histology slides using deep learning: A retrospective multicenter study," *PLOS Med.*, vol. 16, no. 1, Jan. 2019, Art. no. e1002730.
- [15] Z. Gu, W. Li, J. Huo, L. Wang, and Y. GAO, "LoFGAN: Fusing local representations for few-shot image generation," in *Proc. IEEE/CVF Int. Conf. Comput. Vis. (ICCV)*, Oct. 2021, pp. 8443–8451.
- [16] A. Kumar, A. K. Bhunia, S. Narayan, H. Cholakal, R. M. Anwer, J. Laaksonen, and F. S. Khan, "Cross-modulated few-shot image generation for colorectal tissue classification," in *Proc. ICCV*, Oct. 2023, pp. 128–137.
- [17] M. Nergiz, "Federated learning-based colorectal cancer classification by convolutional neural networks and general visual representation learning," *Int. J. Image Syst. Technol.*, vol. 33, no. 3, pp. 951–964, May 2023.
- [18] W. Yu, N. Xu, N. Huang, and H. Chen, "Bridging the gap: Geometry-centric discriminative manifold distribution alignment for enhanced classification in colorectal cancer imaging," *Comput. Biol. Med.*, vol. 170, Mar. 2024, Art. No. 107998.
- [19] Z. Cao *et al.*, "A Novel Colorectal Histopathological Image Classification Method Based on Progressive Multi-Granularity Feature Fusion of Patch," in *IEEE Access*, vol. 12, pp. 68981–68998, 2024, doi: 10.1109/ACCESS.2024.3401240.
- [20] Centers for Disease Control and Prevention. (2022). United States Cancer Statistics: Data Visualizations. [Online]. Available: <https://gis.cdc.gov/Cancer/USCS/#/At A Glance>.