

Exploring Digital Pathology for Tongue Tumour Tissue analysis using machine vision Techniques: An automated Approach

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Exploring Digital Pathology for Tongue Tumour Tissue analysis using machine vision Techniques: An automated Approach

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Abstract

Background

In the healthcare domain, artificial intelligence automated systems set the benchmark solutions for diagnosing the disorders in humans. The influence of automated systems is emerging in the field of pathology for the diagnosis and grading of neoplastic tumors precisely. The challenges faced by existing manual microscopic tissue screening procedures includes more time-consuming and classifying dysplasia tumors is highly complex.

Objective

An automated tissue analysis model is newly proposed to overcome the issues faced in the manual microscopic tissue screening process for predicting UADT tongue tumor sites and grade classification. The proposed model is implemented in two phases for tongue tumor tissue analysis. In phase 1, a unique way of exploring the morphological characteristics in tissue samples is proposed and developed to identify benign, malignant, and dysplasia tumors. Different image processing frameworks were developed, (i) to extract non-neoplastic epithelial regions from whole slide tissue samples for tumor severity detection and (ii) to detect and normalize stain artifacts present in the tissue samples for cell and nuclei detection.

Methods

A new Contrast Stretched Convolutional Neural Network (CSCNN) classification model was proposed to classify tongue tumor sites and their gradings. In the first stage, a novel image preprocessing framework was developed to extract the cell and nuclei shape. The decorrelation contrast stretching technique was used to enhance the quality of the image for neoplastic cell annotation. In the second stage, the Contrast Stretched Convolutional Neural Network model was newly developed to assist the pathologists to identify the normality of neoplastic tumors.

Results

The proposed CSCNN model performance was also compared with other state-of-the-art transfer learning CNN models like ‘VGG16’, ‘VGG19’, ‘MobileNetv2’, ‘Xception’, ‘InceptionV3’, and ‘ResNet 50’. It was observed that the proposed CNN model was able to achieve maximum classification accuracy of 98% with 0.2% validation loss.

Keywords: UADT biopsy image; CSCNN; Image analysis; Transfer learning; Classification.

1. Introduction

Tumors are defined as an irregular cell proliferation in the human body. The term "tumor" is derived from the word "neoplasia." Radiation or cancer-causing substances can cause the change of a normal cell into an anaplastic cell. Lesions are classified into two types: benign and malignant. In most cases, benign tumors are restricted to one region with no invasions, but malignant tumor cells penetrate and navigate to another location in the living organism, through either a lymphatic node or the bloodstream, and it is termed as cancer. Cancer diagnosis through biopsy is recognized as one of the most essential procedures throughout the world. Microscopic examination is essential in determining the motions and invasions of malignant tumors. Detection and classification of malignant tumors is very important. Oral cancer is officially ranked second among all deadly malignancies, according to the World Cancer Society [1]. UADT cancer is the sixth most common noncommunicable illness in the world. The primary risk factor for UADT cancer is rising because of consuming tobacco-related products [2]. “Squamous Cell Carcinoma” (SCC) is a primary type of skin cancer that occurs on the outer layer of lips, ears, nose, hands, and legs due to exposure to sunlight. Particularly in the United States, common victims of squamous cell carcinoma are noted to be men rather than women. The SCC can also be found on the inner surface of the epithelial tissues. UADT oral cavity SCC is the most frequent type of cancer that occurs often in both men and women. Approximately 90% of the tumors occur on the surface of the epithelium. Basically, a benign tumor turns to high-grade carcinoma (malignant cases) due to a breach of the basement membrane epithelium. The traditional microscopic tumor tissue analysis procedure is considered the golden standard to report the diagnostic result for various tumors in the human body. The manual microscopic analysis of tumor tissue samples or digital pathology tissue analysis requires proper morphological and cytological features. To collect the significant features, high-quality tissue samples must be prepared as shown in Figure 1.

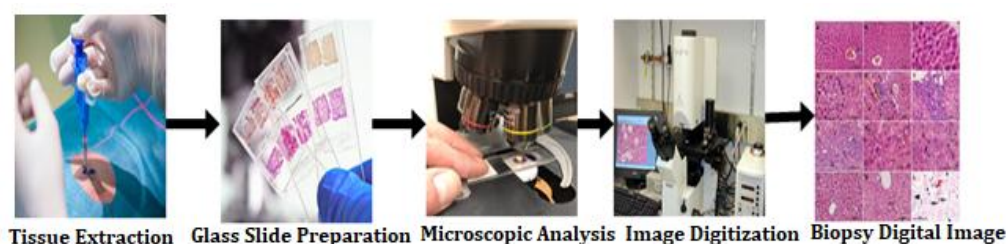


Figure.1 Biopsy Tissue glass slide processing steps

During the tissue analysis process, pathologists frequently monitor the biopsy glass slides to examine for the improper fixations and counterfactual tissue processing. The imprudent slide preparation results in shattered tissue that causes morphological loss and leads to tumor grade misclassification. Different histopathology artifacts are prefixation and fixation artifacts, biopsy tissue-processing artifacts, floating and mounting artifacts, and staining artifacts as shown in figure 2.

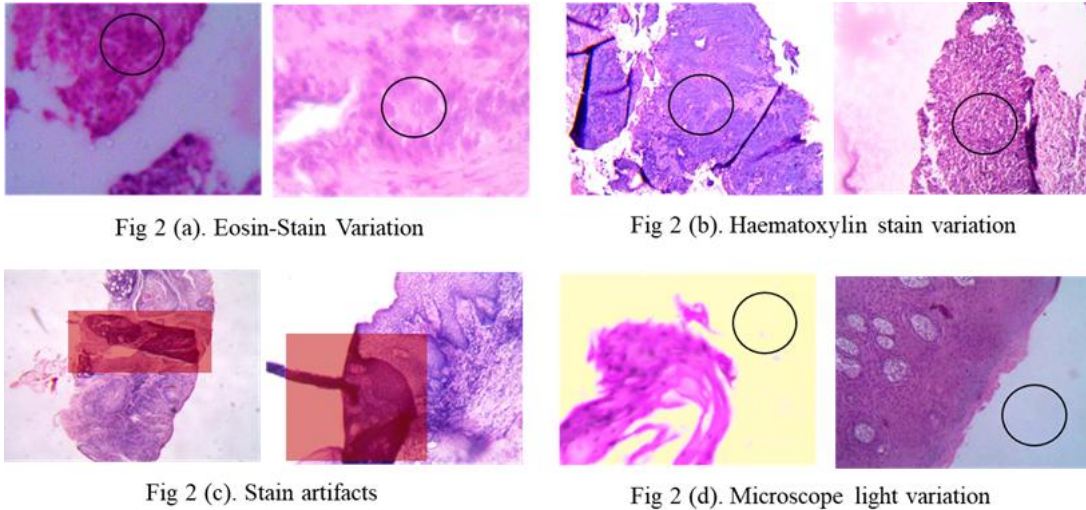


Figure. 2 Histopathology variations in biopsy digital images

The research work includes the cutting-edge Computer Aided Diagnostic Model to classify Upper Aerodigestive Tract (UADT) tumor gradings using Deep Convolutional Neural Network. The core idea behind the research work is to provide an automated system for morphological characteristic analysis of digital biopsy tissue samples to rectify the traditional tissue preparation problems and pathological problems. The cutting-edge deep convolutional neural network model is proposed to classify tongue tumor gradings. The goal is to assist the pathologists to predict the tumor gradings automatically and to reduce the observer variability problems using an automated tissue analysis process called digital pathology. The newly developed automated model will help the clinicians and pathologists i). to diagnose the tumors (an answer to what is wrong), ii). to find the prognosis (what is going to happen in the future) and treatment (an idea for what to do), and iii). to prevent the misclassification of tumor grades (an ideal solution to avoid the spread of tumors and reduce the level of metastasis). The research work is divided into three phases to address the problems faced in traditional pathology. In phase one, different image processing frameworks were introduced for morphological and characteristic analysis of both normal and abnormal biopsy tissue samples and to solve the stain artifacts problems in tissue slides. The proposed framework consists of step-by-step image preprocessing techniques to extract the region of interest from the tissue samples. In the second phase, a contrast-stretched convolutional neural network model was proposed to classify the UADT oral cavity and nasal cavity tumor gradings individually. Finally, the proposed CSCNN model was utilized to classify four classes of UADT tumor gradings as benign, malignant, and dysplasia-type tumors.

2. Literature review

The section explores various cancer tissue analysis methods and feature extraction techniques used for tumour grade classification. The review contains the detailed insights and importance of Artificial intelligence and machine learning in the healthcare domain.

Massimo Salvi & et al has studied about the impact of image processing techniques on the digital pathology samples. Various deep learning methodologies are analysed for the classification of tissue analysis made. Challenges involved in handling the digital pathology is analysed along with the necessary pre-processing and the post processing needed for handling of the tissue samples. Pre-processing and postprocessing algorithms for detection and classification of different types of cancer are discussed in the study. Through this work it is evident that many techniques of image processing and deep learning methods are very helpful in extracting useful results from Digital pathology which helps the human in the process of detection, segmentation and classification of different cancer types.[3]

Maxime Calka & et al has designed a biomechanical model of human tongue. It is done by 3-layer recurrent neural network model. The model is constructed for two different muscle activation in the tongue.[4]

Rasheed Omobolaji Alabi & et al proposed a model to detect the early-stage oral tongue cancer by using machine learning algorithm. Four machine learning algorithms were compared and analysed for finding the early risk associated with detecting a tongue cancer. WHO grade, tumor budding, Lymphocytic host response, depth of invasion is the few parameters analysed with machine learning algorithms. Support vector machine, naïve bayes, decision forest and boosted decision tree are the algorithms used for performance analysis.[5]

Sangjune Laurence Lee & et al researched-on computer assisted image analysis for oral tongue squamous cell carcinoma. Instead, a manual tissue analysis, his method automated the analysis procedure. Immunohistochemistry is a surgical pathology, that is being digitized, on tissue micro array. The TMA slides of the patients are digitized and it was used for study. Tissue samples are automatically segmented by image analysis. The tissue count is observed to be high and accurate in the digital analysis than manual procedure.[6]

Carlos M. Chiesa-Estomba & et al reviewed on the various machine learning algorithms that helped to identify the oral cavity squamous cell carcinoma. The study revealed the usage of the Machine learning tool to predict the different stages or levels of the cancer. Tumor, node, metastasis which was concentrated in manual analysis was analysed using through different ML Algorithms and it requires more amount of data for training to acquire better performance and throughput.[7]. Hakan Weislander et al. [8] proposed the three-step pipeline to predict the tumours from whole slide images using deep learning concepts. On analysis the prediction has shown that the region of interest with low resolution images has decreased the computation time. The proposed three-step pipeline consisting of a bounding box for ROI with low resolution and ROI was subjected to sub-region with mid resolution. The calibration of segmented subregion was done to increase the confidence level using conformal prediction. The experiment demonstrates the validation on Recall, Precision and F1 score as 89 %, 87 %, 87 % that has increased the confidence interval range from 0.8 to 1. Junfeng Gao & et al researched about the usage of computer vision in healthcare application for predictive analysis and therapy for different medical images. Deep learning techniques CNN, auto encoders, deep neural network were the methods used for many medical image

classifications and analysis. SVM and clustering was used for tongue tumour diagnosis.[9] Xaviera A. López-Cortés & et al. made a detailed study on the oral cancer with respect to the various machine learning applications. Detailed study was related to detection, prognosis, diagnosis, prevention of oral cancer using different algorithms like XGBOOST, SVM, LDA, KNN, ANN, LR, CNN. Inputs were different tissue micro array, spectral data and infrared thermal imaging. [10]. The contributions of existing image processing, machine learning and deep learning techniques for various oral cancer imaging modalities and tumour diagnosis are discussed in table 1.

Table1: Comparative performance analysis of existing digital pathology models

Author & Year Title	Dataset Used	Technology Used	Results Acquired	Proposed Model Disadvantages	Suggestions
Aftab et al. (2025) AI in Oncology: Transforming Cancer Detection through Machine Learning and Deep Learning Applications [11].	Public oncology datasets from TCGA	Authors used CNNs, SVMs, Ensemble Learning, Transfer Learning models	Achieved an accuracy of 93% for multi-modal cancer detection.	Lack of clinical validation; mixed data quality.	Standardize datasets; validate models on various populations.
Vinay et al. (2025) Artificial Intelligence in Oral Cancer: A Comprehensive Scoping Review of Diagnostic and Prognostic Apps [12].	Aggregated studies between (2000 - 2024)	AI models (CNNs, Decision Trees, Random Forests), Prognostic Models	Proposed model achieved Sensitivity: 92%; Specificity: 89%.	There are significant differences in the methods used across studies, as well as the issue of very small sample sizes.	Develop standardized assessment frameworks; increase datasets.
Khanagar et al. (2023) Application and Performance of AI in Oral Cancer Diagnosis Using Histopathological Images [13].	TCGA, proprietary histopathology datasets	CNNs (ResNet, EfficientNet), Attention Mechanisms	Accuracy ranges between 85 % and 98%; Sensitivity: 94%.	The overfitting threats are severe, especially considering that the datasets lack diversity.	Apply data augmentation; enhance generalization ability.
Wankhade et al. (2024) Advanced Deep Learning Algorithms in Oral Cancer Detection: Techniques and Applications [14].	Oral cancer image repositories	ResNet, VGGNet, YOLO architectures	Accuracy achieved 95%, Detection increases at the early stages.	There are also high processing costs involved with these analyses, as well as a requirement for specialized equipment.	Optimize model structures for efficiency; investigate lightweight DL models.
Mirfendereski et al. (2025) AI and Diagnosis of Oral Cavity Cancer from Clinical Photographs [15].	Clinical photograph databases	Image-based DL models (InceptionV3, Multi-task Learning, Attention Mechanisms)	The proposed model achieved the Sensitivity: 94%; Specificity: 85%.	There is a lot of variability in both the quality of images taken and the conditions under which lighting takes place.	Standardize imaging protocols; enhance preprocessing methods.

Li et al. (2024) Development of an Oral Cancer Detection System Through Deep Learning [16].	Proprietary oral image dataset	U-Net for segmentation, YOLO for object detection	Accuracy: 93%; High precision in lesion classification.	There is also limited validation in real-world environments, leading to overfitting being a result of the sparse datasets used in many cases.	Apply transfer learning; perform multi-center trials for validation
Sahoo et al. (2024) Diagnostic Performance of AI in Detecting OPMDs and Oral Cancer: A Meta-Analysis [17].	Literature-derived datasets	Hybrid Models (CNN + ML), Ensemble Learning	Sensitivity: 87%; Specificity: 81%; AUC: 0.9758.	Lack of standardized metrics is another issue, as well as heterogeneity seen in study designs.	Implement uniform assessment metrics; emphasize hybrid model optimization.
de Chauveron et al. (2024) AI for OSCC Detection Based on Oral Photographs: A Literature Review [18].	Literature-derived datasets	ViT, GANs, Multi-modal Fusion	Accuracy: 90%; Sensitivity: 85%.	Variability is also seen across different investigations, further resulting in a limited representation of demographics.	Perform multi-center clinical trials on heterogeneous populations.
Pereira-Prado et al. (2023) AI for Image Analysis in Oral Squamous Cell Carcinoma: A Review [19].	Histopathology datasets	CNNs, Attention Mechanisms	Accuracy: 96% in tumor margin detection.	there is a lack of transparency in the processes used, as well as a lack of explainability of the decisions made by the models.	Incorporate interpretable AI frameworks; enhance decision-making transparency.
Yaduvanshi et al. (2024) Automatic Oral Cancer Detection Using Modified Texture Descriptor and ML Algorithms [20].	Oral cancer image datasets	Texture-based ML algorithms (SVM, RF), Feature Engineering	Accuracy: 89%; highly sensitive for certain lesion types.	Manual feature engineering constrains scalability and flexibility.	Adopt texture-based methods and DL for end-to-end learning pipelines.
Nieri et al. (2025) Diagnosis of Oral Cancer With Deep Learning: A Comparative Test Accuracy Review [21].	Public datasets (e.g., Kaggle)	InceptionV3, DenseNet	Model performance differs between architectures (78% and 95%).	High computational requirements for training complex models.	Simplify the various architectures that are necessary for effective clinical deployment as well as for applications that require real-time processing and responsiveness.

Appavu (2025) Oral Cancer Detection Using Hybrid AI Deep Learning Methods [22].	Histopathology datasets	Hybrid Models combining CNNs with SVM	Accuracy: 97%; Improved malignant vs benign classification accuracy.	High computational expenses; slow inference times because of hybrid complexity.	Optimize the hybrid architectures currently in use, focusing on enhancing their efficiency and significantly reducing inference times to improve performance.
Agrawal et al. (2025) Early Detection of Oral Cavity Cancer: Risk Factors and Latest Diagnostic Techniques [23].	Literature synthesis	Risk Assessment Tools using ML/DL & Biomarker Identification Tools	Survival rates for stage diagnosis; diagnostic techniques for early stages innovative.	Limited integration with clinical workflows.	Develop advanced artificial intelligence tools that are fully compatible with electronic health record systems to facilitate seamless integration.
Kumar et al. (2025) Deep Learning Framework for Early Detection of Oral Cancer [24].	Proprietary oral imaging dataset	Custom CNN framework	Accuracy: 91%; Early-stage detection improvements.	Scarcity of data for rare subtypes.	Promote and support open-data initiatives that foster collaborative research efforts among scientists and researchers in the field.
Prithvidhar et al. (2025) Comparative Analysis of Oral Cancer Detection Using Histopathological Images [25].	Histopathology datasets	Traditional ML vs. DL models	DL performs better than ML (92% and 78% accuracy).	Variability in staining protocols.	Standardize the processes involved in staining and preprocessing pipelines to ensure consistency and reliability across different applications.
Chowdhury et al. (2025) Role of AI in Diagnosis of Oral Squamous Cell Carcinoma: A Systematic Review [26].	Aggregated studies (2015 to 2024)	AI models (DL, radiomics)	Good diagnostic accuracy but minimal external validation.	Bias in retrospective studies.	Conduct prospective studies that include a diverse range of cohorts to gather comprehensive data and insights.

Ramani et al. (2025) CNN-Based Real-Time Diagnosis of Oral Epithelial Dysplasia Using Confocal Microscopy [27].	High-resolution confocal microscopy images	CNNs (ResNet, EfficientNet)	Accuracy: 94%; Dysplasia detection in real time.	Needs specialized imaging hardware.	Adapt existing models so that they are suitable for standard imaging modalities, such as those provided by smartphone cameras, to increase accessibility.
Naderi Yaghouti et al. (2025) AI for Ovarian Cancer Detection: Review (2013 to 2023) [28].	Mixed medical imaging datasets	DL models (UNet, GANs)	95% precision in tumor identification (focus on ovarian cancer).	Limited cross-cancer applicability.	Validate the developed models specifically for datasets that pertain to oral cancer, ensuring accuracy and relevance in this important area of study.
Warin & Suebnukarn (2024) Deep Learning in Oral Cancer: A Systematic Review [29].	54 studies between the year(2000 to 2023)	DL architectures (CNNs, RNNs)	Pooled accuracy: 85 %; high diagnostic odds ratio (2549.08).	Reproducibility issues; absence of open-source code.	Encourage the sharing of open-source models as well as benchmarking practices to foster transparency and improvement within the research community.

3. Materials and Methods

The process of automated neoplastic tumour classification consists of image pre-processing technique for image enhancement from highly correlated pixels in the tissue samples, removal of noise from the biopsy samples, eliminating the background and normalizing the stain artefacts. The augmentation of data helps in rectifying the data imbalance problems and also to maintain the equal number of training samples in each UADT neoplastic and non-neoplastic tumour classes. After data augmentation auto features are extracted by the proposed CSCNN deep learning model. Next the classification is carried out based on the gradings of tumours in UADT.

In the healthcare domain, the deep learning automated system sets the benchmark for diagnosing disorders in humans. The influence of the automated systems is viewed to be more in statistics and also in diagnosing the neoplastic tumour. The proposed model for predicting UADT tumours and grade classification of neoplasm was

carried out by step-by-step process. The proposed model will assist the pathologists with an automated platform. The problem identified was addressed to assist the para clinicians in the analysis of biopsy sample images to diagnose diseases automatically. The research includes the grade classification of the oral cavity and nasal cavity tumours. An efficient supervised “Contrast Stretched Convolutional Neural Network” (CSCNN) classification model was proposed and implemented with different microscopy magnified biopsy sample images. Three microscopic magnifications like, 4X, 10X, and 40X biopsy image samples were used for tumour grade classification. Neoplastic and non-neoplastic epithelial tissues were analysed and extracted using 4X magnification. The spread of neoplastic epithelium was extracted and analysed using 10X microscopy magnification. Normal and abnormal nuclei morphology was assessed and extracted with 40X magnification. The distinct magnifications utilized in viewing the biopsy tissue samples supports in analysing benign, malignant and dysplastic tumours.

3.1. Dataset Description

The UADT tissue sample database has 5,170 “Haematoxylin and Eosin stain “Whole Slide Images (WSI) and the patches. The dataset comprises different microscope magnifications such as, 4X scanner magnification, 10X low power magnifications and 40X high power magnifications.

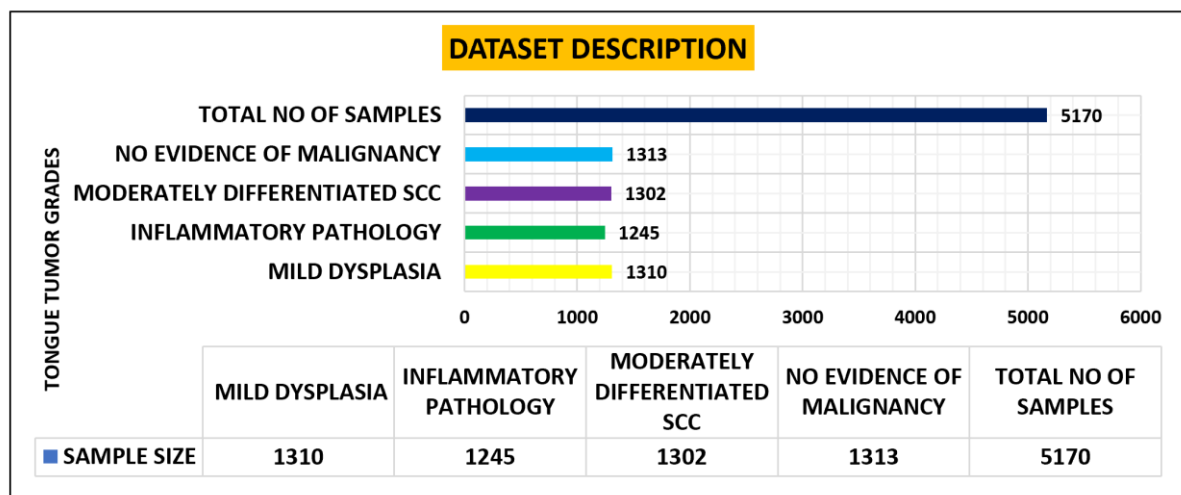


Figure 3. Dataset Description

Figure 3 shows the tongue tumour dataset distribution in four different grading's like, inflammatory pathology (chronic type inflammation), No evidence of malignancy (No gross appearance of abnormal cell and nuclei), moderately differentiated (stage 2 – Squamous Cell Carcinoma), Dysplasia Tumour (Mild chances of transformation to Squamous cell carcinoma).

The process of biopsy digital image acquisition is shown in Figure 3. UADT tumour biopsy tissue samples were collected from the pathology department, "Vellore Medical College Hospital, Tamil Nadu, India. Ref. No. 1258, (H&FW (MCA3) / dept. Dt: 18-05-2018).

3.1.1. Structure of the Dataset

The data set consists of Haematoxylin and Eosin (H&E) stained Whole Slide (WS) images and its corresponding patches. High-quality images lead to detailed, precise visual representations of tissue structure, a factor that plays a crucial role in ensuring safe and precise classification and diagnosis in medical tests.

3.1.2. Microscopic Magnifications

To ensure that we have a comprehensive and complete analysis, the dataset has been prepared with great care so that it contains images taken at three different and distinct magnifications using an optical light microscope as shown in figure 4.

- Scanner View (4X magnification): It gives a wide view of the tissue sample.
- Low Power (10X magnification): This power setting of magnification produces an intermediate amount of detail that is most useful when viewing structural elements.
- High Power (40X magnification): This provides a distinct and clearer image of the different cellular elements and the complex structures present in tissues.

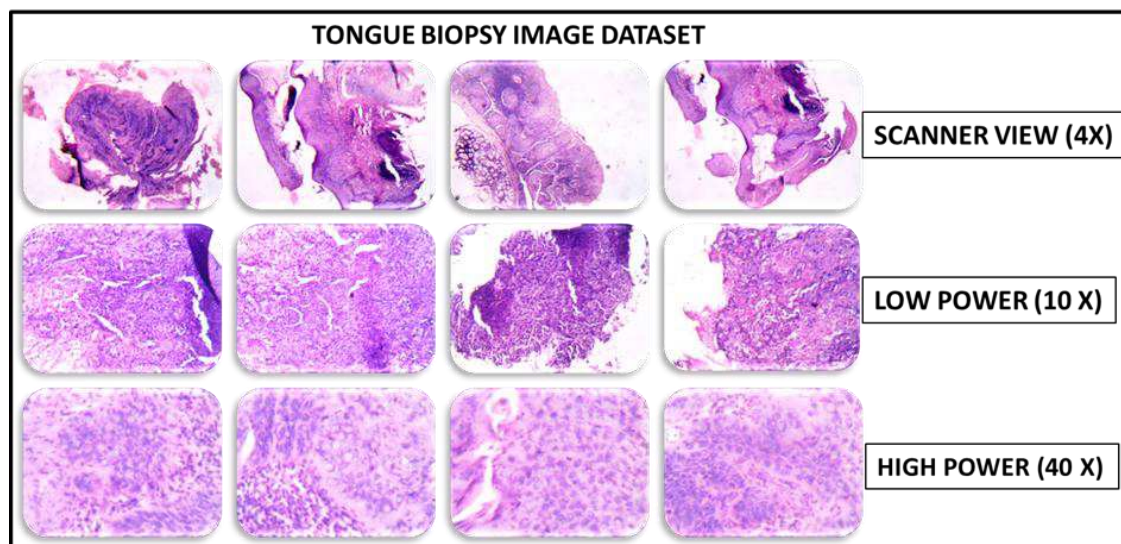


Figure.4 Tongue biopsy digital images.

Tongue tumour biopsy samples were collected with three different magnifications as 4X, 10X and 40X Zooming in MAGNUS light microscopy.

3.2. Pre-processing

The critical tumour diagnosis is carried out in histopathology traditional tissue analysis for cancer microscopic investigation process. The artifacts present in the tissue samples lead to misclassification as there is loss of morphological characteristics in UDT biopsy images. The hidden characteristics of tissue morphology can be enhanced and identified using multispectral images colour separation methodology called decorrelation contrast stretching [30]. The bubble and stain artifacts can be identified by applying the decorrelation (décor) stretching on the H&E stain biopsy samples. By applying decorrelation technique, the unnecessary background details can be normalized.

The process of decorrelation contrast stretching is:

The colour channel can be improved with higher intensity by décor stretching technique and this stretching of colour contrast highlights the highly correlated pixel present in the biopsy samples.

The highly correlated pixels denote the dysplastic tumour cell and nuclei pixels.

Step 1: Let the input sample image be $I_m=1$, and channels $C_n=3$; with ‘n’ as number of pixels; $P_{m,o}$ – value of kth pixel for channel ‘ C_n ’.

Step 2: Evaluate the sum of pixels of RGB channels.

$$SUMO_{b,cl} = \sum_{m=1}^n (P_{m,cl} \times P_{m,b}) \quad (1)$$

Step 3: calculate the covariance matrix for three channels (R, G, B)

(i). Evaluation of covariance of a single matrix is depicted in equation 2.

s, t – mean value of given sample image; u_i, v_i – is the individual pixel of the image.

$$cov_{s,t} = \frac{\sum_{i=1}^n (xi-x') (yi-y')}{N-1} \quad (2)$$

$$Cov_{cl,b} = \frac{1}{N-1} [SUMO_{b,cl} - \frac{1}{n} \times SUMO_{b,cl} \times SUMO_{cl}] \quad (3)$$

Step 4: The correlation matrix of all the three distinct channels is evaluated by equation 4.

$$Corr_{cl,b} = \frac{Cov_{cl,b}}{(Cov_{b,b} \times Cov_{cl,cl})^{1/2}} \quad (4)$$

Step 5: Evaluate the rotation matrix ‘RT’ (Eigenvectors from evaluating the correlation matrix).

Step 6: The stretching vector ‘SV’ can be evaluated by reciprocating every eigenvalue that is multiplied with ‘ σ ’ (standard deviation).

Step 7: The transformation matrix ‘TM’ can be evaluated by combining the stretching and Rotation matrix.

Transformation matrix ‘TM’ can be acquired as a contrast-enhanced image by evaluating the matrix multiplication as given in equation 5.

$$TM = RT \cdot SV \quad (5)$$

For experimental analysis, Decorrelation contrast stretching is applied on the biopsy WS image. The intensity of the pixels in the epithelium is enhanced, artifacts are normalized, unnecessary background details in the samples are eliminated by significantly improving the intensity of the pixels as shown in figure 5(b). Following contrast enhancement, Sobel edge detection is applied to separate the asymmetrical outlines and silhouette appearances as shown in figure 5(c). Then RGB color inversion technique is applied to highlight the ROI present in the tissue samples as epithelium and connective tendons of biopsy samples, the enhanced water blobs and stain artifacts edges are as shown in Figure 5(d).

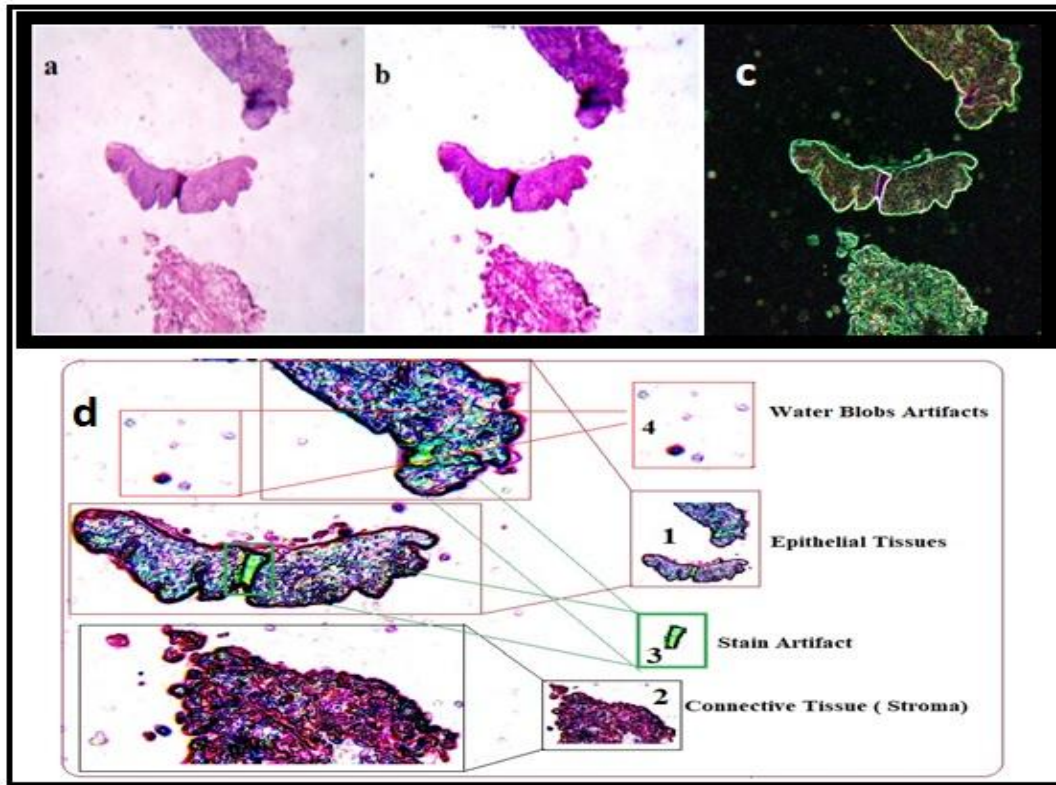


Figure. 5. Cell and nuclei ROI extraction process

3.3. Cell and Nuclei Annotation

To distinguish effectively and efficiently what are termed normal cells from what are termed abnormal cells, and also from nuclei in the images of tongue tumor biopsies, a sophisticated two-stage image processing technique has been suggested. This new technique utilizes the application of edge detection and inversion color methods, which are separately optimized to be most visible on the cellular structure within the tissue sample. The specific techniques of this system are as follows:

Step 1: Performed Edge Detection with the Sobel Operator

The Sobel operator technique is then systematically used on the biopsy image in an attempt to successfully detect and highlight edges of various regions that are present in the tissue. The specific operator performs a gradient calculation of the pixel intensity by considering both the horizontal and vertical directions, thereby placing emphasis on those regions where there is a sudden change in intensity values. By enhancing the edges appropriately, the step detects significant cell and nuclear boundaries, and it becomes very easy to detect and see their structural changes as shown in figure 6.

This new two-stage method significantly improves image quality from biopsy substantially by systematically separating and emphasizing key structural information in them. Not only does this enhancement help in the accurate identification of tongue tumor pathology, it also facilitates more thorough examination of such diseases. Furthermore, this method is a fundamental methodology that provides the basis for further machine learning-based classification tasks as well as aiding manual diagnostic interpretation by medical practitioners.

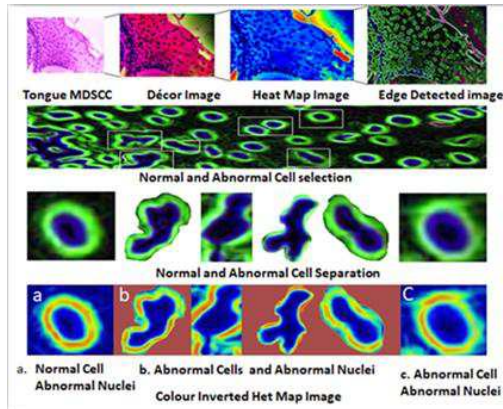


Figure 6(a). Image processing framework for cell and nuclei annotation and extraction

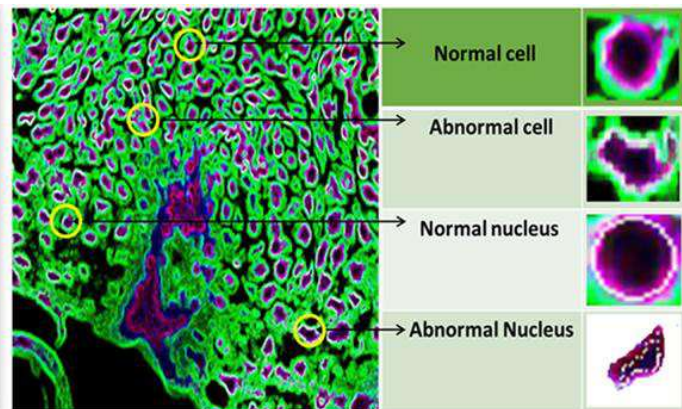


Figure 6(b). Cell and nuclei shape detection

Figure 6. Cell and nuclei annotation using image processing framework

Epithelial cell Analysis Framework using ImageJ

To facilitate more accurate measurement of tongue tumor biopsy image samples, an image processing pipeline in three steps was created using ImageJ image processing tool, an open-source, NIH-funded image analysis software. The process of these steps, which is performed in a sequence which is optimized for increased clarity and contrast of microscopic cellular details with edge enhancement and adaptive thresholding as shown in figure 7.

Step 1: RGB Image Conversion to Grayscale

The first step concerns the conversion of high-resolution RGB images to their grayscale equivalent. The conversion simplifies the visual complexity by removing color information, hence focusing on light intensity levels. Grayscale representation not only makes computational processing easier but also makes subtle textural and structural information more accessible and essential for the detection of pathological patterns in biopsy samples as shown in figure 7(a).

Step 2: Application of Sobel Operator

The Sobel operator processes the grayscale image to strengthen its edges. The method calculates gradients along horizontal and vertical axes which reveals areas where intensity undergoes major changes. Edge enhancement in this processing step enables easier detection of cell and nucleus boundaries which helps determine the normality or abnormality of structures as shown in figure 7(b).

Step 3: Global Thresholding

The edge-enhanced image undergoes global thresholding with a threshold value $T=127$. This operation segments the image into binary regions by separating pixels into two categories: The global thresholding operation divides the image into two main parts by labeling pixels above the threshold value as foreground elements and pixels below the threshold value as background elements. The thresholding process separates cellular components and nuclei effectively which allows for precise examination of pathological features as shown in figure 7(c).

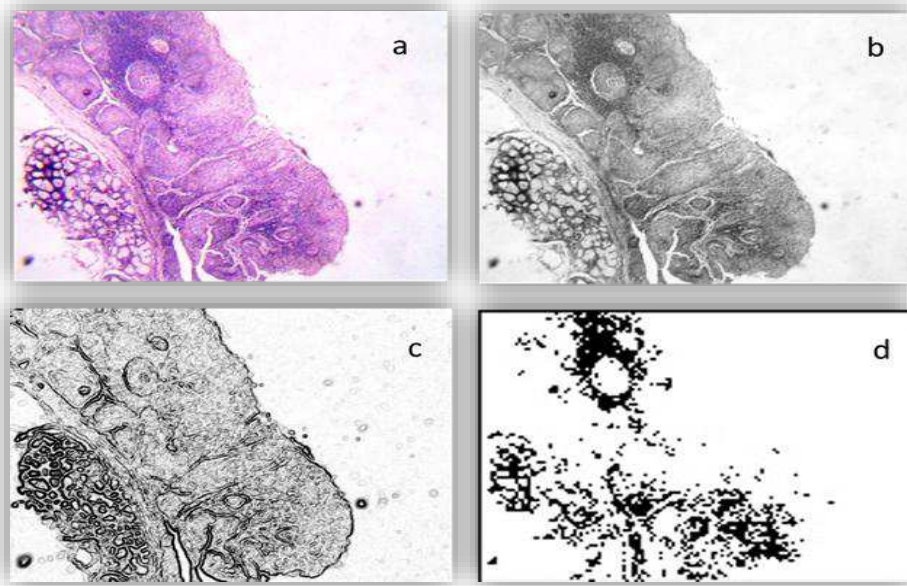


Figure 7. Epithelial (Abnormal) tissue extraction

7(a)- Original glass slide biopsy image, 7(b) RGB to grayscale conversion, 7(c) Sobel edge detection, 7(d) Global thresholding.

The dedicated MAGVISION and FIJI microscopic image analysis tools were compared with IMAGE J tool to analyze and identify the best epithelial abnormal tissue spreading, as the epithelium is the backbone of finding abnormalities in tissue samples and analysing the spread of tumors. The analysis revealed that the IMAGE J tool performed well in identifying the epithelial tissues in the entire slide images as shown in figure 8.

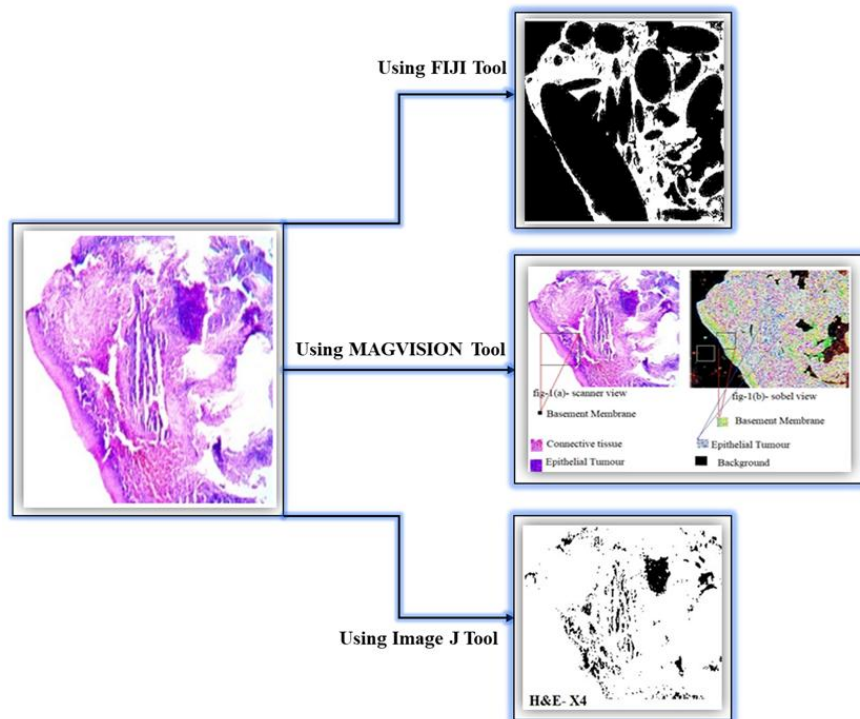


Figure 8. Comparative analysis of image analysis tools.

3.4. Data Augmentation

To avoid the data imbalance problem and to improve the classification accuracy, the proposed method uses data augmentation technique. Augmentation is a type of geometric transformation technique used to increase the overall samples in the dataset and to maintain the equal number of samples in each class. Different geometric transformations like Rotation, Width shift, Height shift, Shear, Zoom and Horizontal flip with maximum ranges like 25-degree interlude for each rotation, 0.2 range for width shift, height shift as 0.3, shear range as 0.2 and zooming range as 0.2. each augmentation technique threshold values are fixed based on the trial-and-error method as shown in Figure 9. But when we increased or changed these threshold values too much, the images started losing important details or became distorted, as you can see in the figure 10 below.

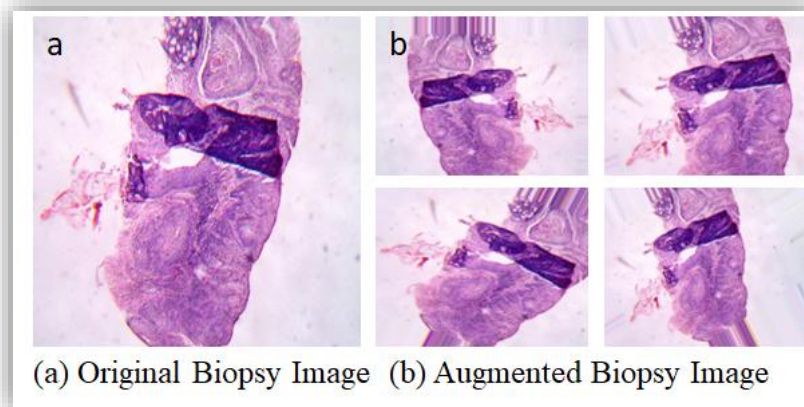


Figure. 9 Augmented biopsy image samples

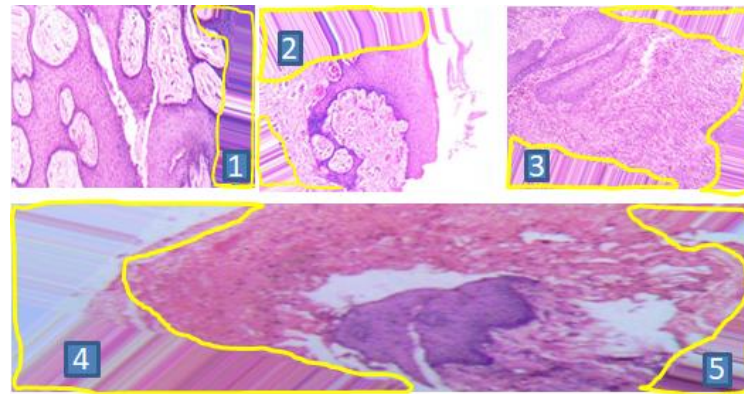


Figure 10. Distorted image samples

3.5. Proposed model Framework

We proposed CSCNN (Contrast Stretched Convolutional Neural Network), a custom architecture tailored for the categorization of tongue tumor biopsy samples. CSCNN is not a deep model; rather, it has been specifically designed to address the distinct requirements of medical image analysis, particularly the interpretation of biopsy slides at different microscopic magnifications.

3.5.1. Clinical History and Dataset Structure

Diagnosis of tumour by histopathological examination involves examination of tissues under microscopes at various levels of zoom. The UDT dataset employed in this study comprises 5,170 biopsy images, each of which was taken at one of three levels of magnification:

- 4X provides a general overview of tissue architecture and surface epithelium.
- 10X facilitates the visualization of epithelial proliferation and structural remodelling.
- 40X provides comprehensive insights at the cellular level, encompassing nuclear alterations associated with malignancy.

The various zoom scales concentrate on distinct biological features, and their combined analysis enhances the understanding of tumor growth. Multi-resolution visual data like this are not processed in conventional CNN models, which prompted to build a new model that can handle multi-resolution input efficiently.

3.5.2. Distinctive Aspects of CSCNN

All the layers of CSCNN are fully learnable with no untrainable parameters. The model doesn't possess any pre-trained weights or frozen layers from other data. Rather, it learns comprehensively from the histological patterns in the training set. It avoids the overfitting to non-medical features and enhances relevance to the clinical domain. The CSCNN architecture consists of a sequence of convolutional and pooling layers that are optimized to perceive patterns at all three magnification levels. This allows the model to learn and aggregate features at multiple spatial resolutions, providing better tumour classification.

3.5.3. Architecture Transparency

For medical applications, interpretability is as important as accuracy. CSCNN avoids the application of batch normalization or dropout layers since these tend to introduce internal behaviour that is difficult to track. This makes learning transparent and the model's decisions auditable and comprehensible by clinicians.

3.5.4. Controls Color Inconsistencies

Biopsy samples may be quite color varied based on variations in H&E staining protocols. Rather than using manually applied normalization procedures, filters of DSCNN learn to normalize automatically based on variations in colors, minimizing preprocessing needs and enhancing dataset strength from sources.

The model consists of four major layers such as input layer, convolution layers, pooling layers and fully connected dense layer for classification and it is shown in Figure 11.

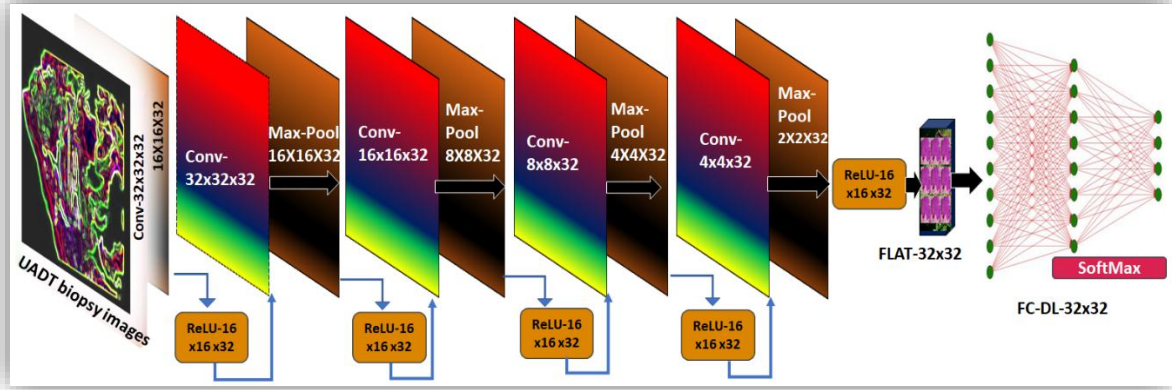


Figure.11. Contrast Stretched CNN architecture

Let C be the classifier, $C(U) = V$, where U is an actual input and the predicted label V is the actual class of V . The UDT tongue tumour dataset consists of 5,170 oral cavity biopsy sample images extracted from WS and Patches. From the observation of an existing standardized computer aided design Convolution Neural Network model, the problem is identified to assist the clinicians in the analysis of medical sample images for automated disease diagnosis. The research incurs the grade classification of the oral cavity tumours, supervised CSCNN classification model which is implemented with distinct microscopy magnified biopsy sample images. The distinct magnification 4X extracts and analyses the neoplastic and non-neoplastic epithelium. The spread of neoplastic epithelium can be extracted and analysed in 10X microscopy magnification. The extraction of normal, neoplastic and abnormal nuclei morphology can be assessed in 40X magnification. These distinct magnifications are the key factors that are used for analysing dysplastic tumours from biopsy digital images. Figure 12 shows the step-by-step CNN layer parameter extraction process.

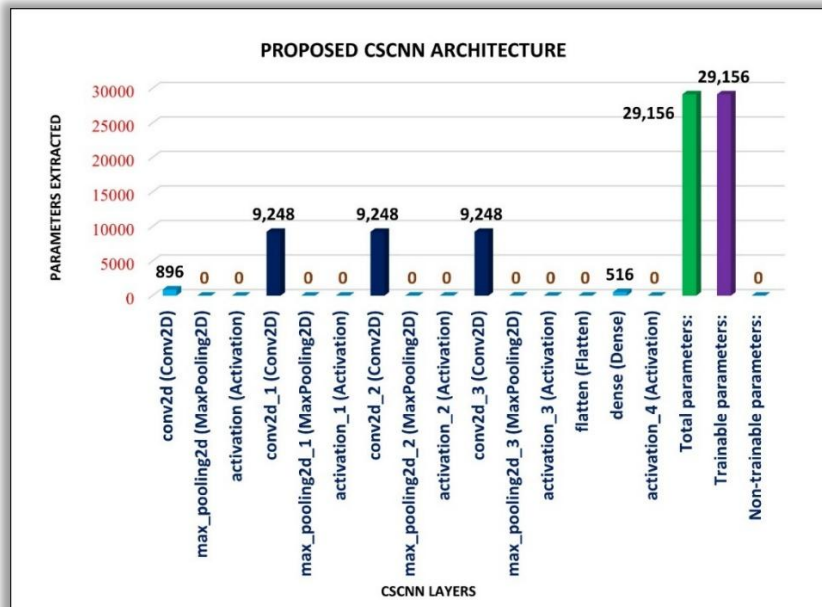


Figure 12. CSCNN Architecture and parameter extraction process

3.5.5. Proposed Architecture Insight

The model is composed with 160 convolution layers as 32x32, 16x16, 8x8, 4x4, 2x2 sizes; 160 max pooling filters as 16x16, 8x8, 4x4, 2x2 and 1x1 sizes and the model extracts 29,156 trainable parameters for classification.

Traditional CNNs typically have a limited number of convolution blocks (3–6 layers) with increasing depth. In contrast, our model has 160 convolution layers—a deliberate design to facilitate deeper abstraction of texture, morphology, and structure at every spatial resolution. This results in:

- More profound semantic comprehension, essential in advanced fields such as histopathology.
- Multi-scale feature enrichment, both capturing local and global patterns.

3.5.6. Pooling with Semantic Preservation

Max-pooling layers from 16×16 to 1×1 are assigned in quantities to be evenly distributed against each spatial down sampling step. This method ensures a controlled spatial information reduction in lieu of radically reducing feature maps, preserving edge, shape, and density information so critical to biomedical classification. Although deep models are typically overparameterized, this architecture is able to efficiently employ only 29,156 trainable parameters—testament to the efficiency of parameters without compromising model performance. This is especially convenient for use in clinical environments with limited computational resources.

3.6. Proposed Framework and Operational Mechanism

Let the input image be denoted as,

$$I = [I_{x,y,z}] \text{ for } x \in [1, h], y \in [1, w], c \in [1, D] \quad (6)$$

Where, H is the image height,

W is the width,

C is the number of channels (e.g., 3 for RGB).

1. Convolution Operation

Each convolutional layer transforms the input via a localized feature aggregation function ϕ

$$\Psi_{u,v}^{(k)} = \phi^{(k)}(I_{[u:u+\delta-1],[v:v+\delta-1],:}) = \sum_{d=1}^D \sum_{i=0}^{\delta-1} \sum_{j=0}^{\delta-1} K_{i,j,d}^{(k)} \cdot I_{u+i,v+j,d} + \beta^{(k)} \quad (7)$$

Where:

δ is the kernel size (typically 3×3),

$K^{(k)}$ is the learnable kernel matrix at layer k,

$\beta^{(k)}$ is the bias term,

$\Psi^{(k)}$ is the resulting feature map.

This specific operation has the purpose to create a novel spatial representation which effectively highlights and presents localized pattern. These patterns can consist of any significant feature like edges, the shape of epithelial tissue, or contrast differences that may exist.

2. Non-Linearity – Piecewise Activation

Each feature map is passed through an activation function $\Gamma(\cdot)$ applied element-wise:

each feature map is passed through an activation function

A non-linear function that represents non-additive interactions in the network, complex multi-cellular structures and gradients.

$$\gamma_{u,v}^{(k)} = \Gamma(\Psi_{u,v}^{(k)}) = \begin{cases} (\Psi_{u,v}^{(k)}) & \text{if } (\Psi_{u,v}^{(k)}) > 0 \\ 0, & \text{otherwise} \end{cases} \quad (8)$$

3. Max Pooling operation is applied to compress the feature map (Down sampling)

This reduces the spatial dimension while keeping the most salient activation—especially important for sparse features such as tumor nuclei.

$$\pi_{m,n}^{(k)} = \max \left\{ \gamma_{x,y}^{(k)} \mid \in R_{m,n} \right\} \quad (9)$$

Where $R_{m,n}$ is the receptive pooling region (2 X2) applied at the centre position of the image (m, n).

4. Fully connected layer

The output tensor is vectorized after the pooling layer which passes through the dense layer.

$$\eta_j = \sum_{i=1}^q w_{j,i} \cdot z_i + \theta_j \text{ for } j = 1, \dots, C \quad (10)$$

Where:

C is the number of classes,

$w_{j,i}$ are the weights generated for training

For class j , θ_j is the bias applied in the fully connected dense layer.

Finally, the possible class probability distribution is calculated from the predicted class

$$\hat{y} = \arg \max \hat{p}_j \quad (11)$$

4. Results and Discussion

In this section, we provide the results of the proposed Contrast Stretched CNN classifiers on UADT tongue biopsy image from four different classes. The dataset is divided as 3619 slide images for training, 1034 images for testing, and 517 biopsy images for validation. The proposed CNN model has achieved the highest classification accuracy of 98 % with 0.02 validation loss is shown in figure 13.

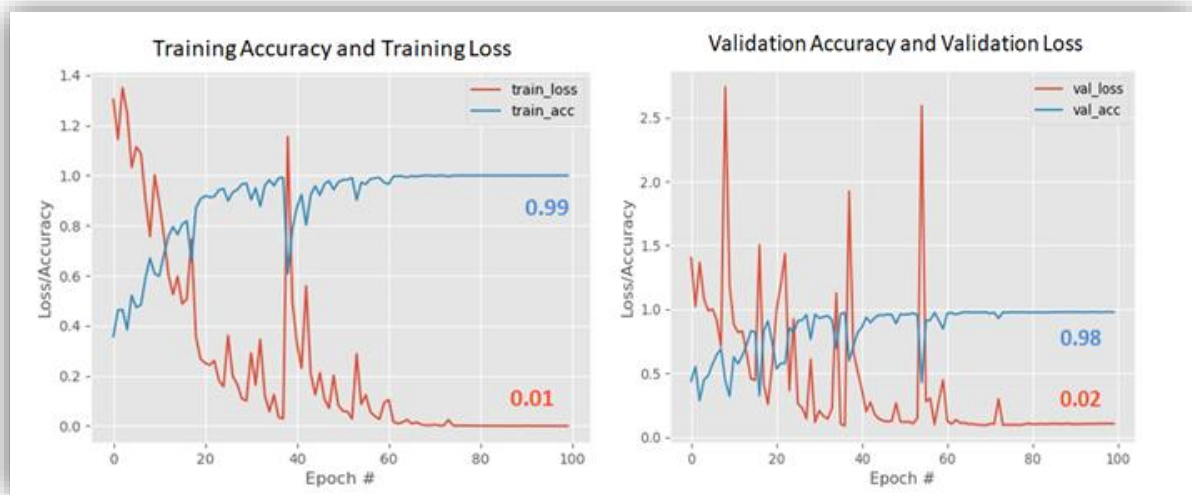


Figure 13. Performance analysis of Proposed CSCNN Model

Table 2. Tongue tumour performance evaluation metrics.

Tongue Tumour classes	precision	recall	f1-score	support			
Inflammatory	1	0.99	1	245			
No evidence of malignancy	0.95	0.97	0.96	259			
Moderately differentiated	0.97	0.96	0.97	270			
Tongue Mild dysplasia	0.99	0.99	0.99	260			
Average accuracy	0.98			1034			
Macro avg.	0.98	0.98	0.98	1034			
Weighted avg.	0.98	0.98	0.98	1034			
colour Gradient of Accuracy - ranges from {95% to 100%}							
	95	96	97	98	99	100	

Table 2 shows the performance analysis of proposed CSCNN model for tongue tumour classification. The dataset is tested with six model performance evaluation metrics like precision, recall, F1-score, average accuracy, macro average accuracy and weighted average accuracy and it was recorded with 98 % classification accuracy.

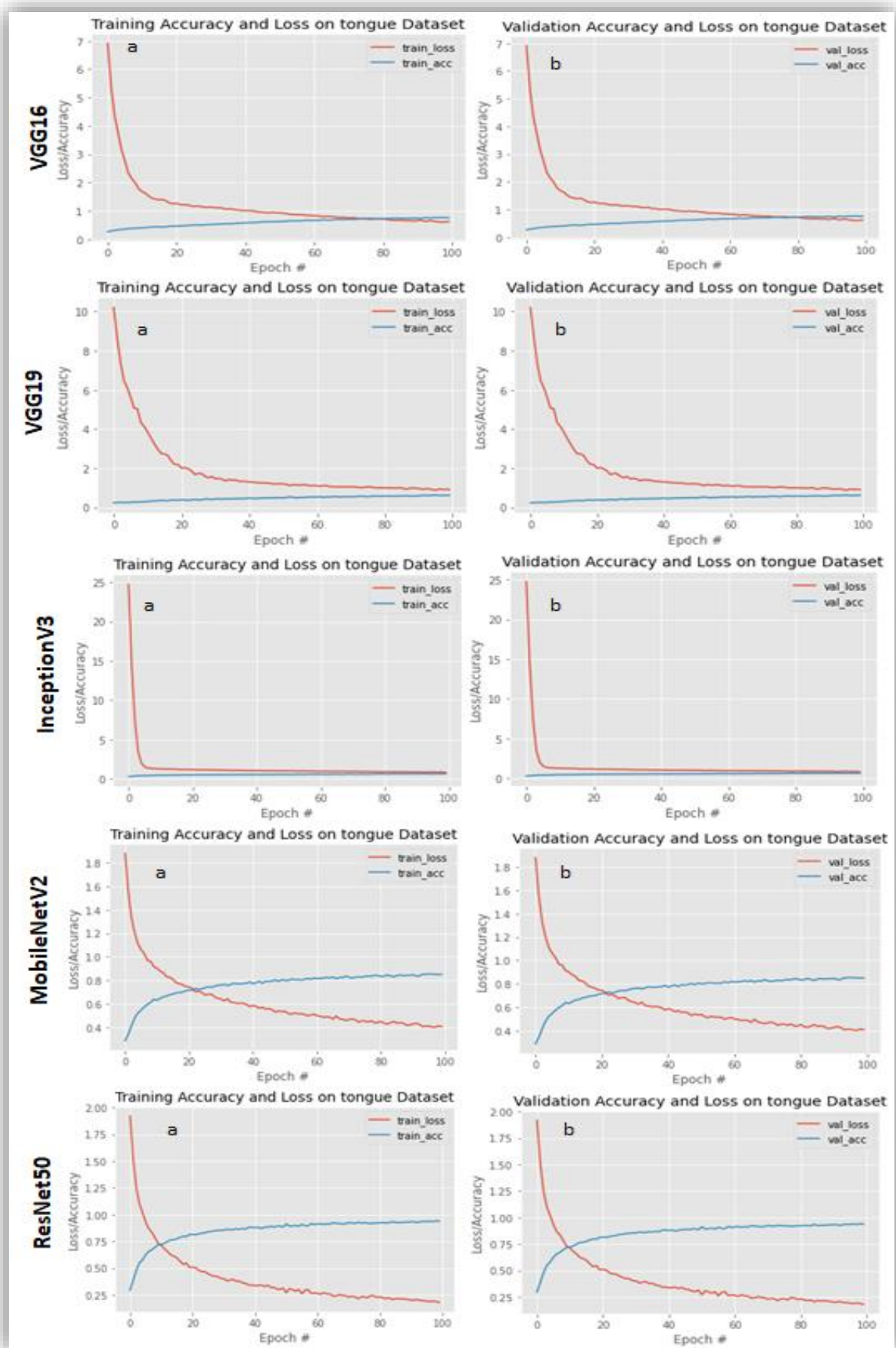


Figure 14. Performance analysis of Transfer Learning Model

Performance Optimization and Observations

To enhance the accuracy and performance of the proposed deep learning model used for epithelial tissue classification, different optimization strategies were utilized at the training level. The following are the most important findings, real modifications executed to address the following problems, and resulting solutions in the below table 3

In the proposed CNN model, the pooling layers were inserted after every convolutional operation. However, it led to the sudden reduction in image resolution, finally causing the elimination of fine edge features during feature extraction. To offset this loss of quality, the model architecture was altered to include a higher number of trainable parameters. In the original configuration, with 100 epochs of training, the model achieved a training accuracy of 78.41% and a validation accuracy of 83.73%, which was a moderate level of feature learning.

Later, other activation functions were explored after the pooling layers. Replacing the conventional Sigmoid and Tanh activations with ReLU showed the following advantages. Using Sigmoid and Tanh functions caused a drastic drop in weight gradients during training. To resolve this problem, the weight parameters were set from 0.15 to 0.53, which helped in stabilizing the training process.

In the end, it was apparent that the use of the ReLU activation function had several significant benefits, most notably in that it resulted in improved gradient flow as well as sparser activations throughout the neural network framework. This improvement was significant in that it then allowed for a significant acceleration of the overall training process, which is essential in creating successful machine learning models.

Further improvement was observed with the addition of Dropout and Batch Normalization layers. This further minimized overfitting, improved generalization, and reduced the training time significantly. With this final configuration, the model attained a validation accuracy of 98.29% and training accuracy of 99.13% in 8 seconds per epoch, along with improved loss metrics. The results collectively indicate the importance of careful architectural calibration as well as the choice of activation functions in the achievement of optimal performance in deep convolutional neural networks, particularly in biomedical image analysis.

Rationale for Setting 100 Epochs as Benchmark

To balance performance improvement and computational cost, 100 epochs were used as the reference for training the model. The training and validation accuracies of the model always reached a point of stabilization and convergence within the range provided, which was the foundation of empirical observations that were established from initial experiments. Increasing the epoch beyond 100 slightly increasing the computational cost.

Table. 3 Proposed model hyper parameters tuning

Metrics	Observation	Solutions	Outcome
After every convolution operation we applied pooling layer	Edge feature loss	The image resolution is reduced rapidly for each layer in feature extraction process	Increased trainable parameters
No of Epoch =100: {32s 79ms/ Epoch} Training loss: 0.6285 – Training accuracy: 0.7841 – validation loss: 0.4573 - Validation accuracy: 0.8373			

After pooling layer Sigmoid and tanh activation functions were applied	Observation: Drastic decrease in weights may leads to overfitting.	Increased the initial Weight from 0.15 to 0.53 Used ReLU activation to produce high sparce Neural network	Increased gradient of the weights. Observation: (Fast training)
No of Epochs= 100: {18s 44ms/Epoch} Training loss: 0.0209 – Training accuracy: 0.9929 – validation loss: 0.1588 – validation accuracy: 0.9629			
Additional Features	1. Dropout	2. Batch normalization	Observation: Fast training; Increased accuracy
No of Epochs= 100: {2s 17ms/Epoch} Training loss: 0.0201 – Training accuracy: 0.9913 – validation loss: 0.1483 – validation accuracy: 0.9829			

5. Conclusion and Future work

The performance of the proposed models CSCNN model for UADT tongue tumour biopsy dataset was tested and analysed using the predictive model performance metrics precision, recall, F1-score and accuracy. The model was trained and tested with 100 epochs. The proposed model is capable of addressing the manual microscopic tissue analysis problems and interobserver variability problems faced by the pathologists. The proposed automated tissue analysis model successfully addresses the limitations of manual microscopic tissue screening in the prediction and classification of UADT tongue tumors. Through a two-phase approach, the model efficiently identifies benign, malignant, and dysplastic tumors by leveraging advanced image processing techniques. By introducing a novel Contrast Stretched Convolutional Neural Network (CSCNN) model, the research significantly improves the detection and grading accuracy of neoplastic tumors, specifically in the oral and nasal cavities.

The decorrelation contrast stretching technique enhances image quality for precise tumor identification, while the CSCNN model achieves superior classification accuracy compared to other established pre-trained CNN models such as VGG16, VGG19, MobileNetv2, Xception, InceptionV3, and ResNet 50 as shown in figure 14. With the classification accuracy of 98% and a validation loss of 0.2%, the model proves to be reliable in aiding pathologists in tumor diagnosis and grading, thus setting a new standard for automated pathology analysis.

The proposed work lays a strong foundation for future advancements in automated cancer diagnosis and offers a scalable solution to enhance the efficiency and precision of tumor screening, potentially reducing human error and improving patient outcomes. Although the proposed model displayed outstanding performance, its computational cost is deserving for further study, especially in processing heterogeneous multi-modal data samples.

Statements and Declarations

Conflict of interest The authors have no competing interests to declare that are relevant to the content of this article.

Data availability The data that support the findings of this study are not openly available due to reasons of sensitivity and are available from the corresponding author upon reasonable request.

Ethics approval and consent to participate Not applicable.

Clinical trial number: Not applicable.

Consent for publication Not applicable.

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Author contributions P.M. made substantial contributions to the conception and design of the work, analysis and interpretation of data; M.C. and G.M. drafted the work and revised it critically for important intellectual content; P.GB. approved the version to be published.

References

1. American Cancer Society. (2025). Cancer Facts & Figures 2025. Atlanta, GA: American Cancer Society, Inc. <https://www.cancer.org/research/cancer-facts-statistics/all-cancer-facts-figures/2025-cancer-facts-figures.html>
2. World Cancer Research Fund International. (n.d.). Mouth and Oral Cancer. <https://www.wcrf.org/dietandcancer/mouth-and-oral-cancer/>.
3. Salvi, M., Acharya, U. R., Molinari, F., & Meiburger, K. M. (2021). The impact of pre- and post-image processing techniques on deep learning frameworks: A comprehensive review for digital pathology image analysis. *Computers in Biology and Medicine*, 128, 104129. <https://doi.org/10.1016/j.combiomed.2020.104129>.
4. Calka, M., Perrier, P., Ohayon, J., Grivot-Boichon, C., Rochette, M., & Payan, Y. (2021). Machine-learning based model order reduction of a biomechanical model of the human tongue. *Computer Methods and Programs in Biomedicine*, 198, 105786. <https://doi.org/10.1016/j.cmpb.2020.105786>
5. Alabi, R. O., Mäkitie, A. A., Pirinen, M., Elmusrati, M., Leivo, I., & Almangush, A. (2021). Comparison of nomogram with machine learning techniques for prediction of overall survival in patients with tongue cancer. *International journal of medical informatics*, 145, 104313. <https://doi.org/10.1016/j.ijmedinf.2020.104313>

6. Lee, S. L., Cabanero, M., Hyrcza, M., Butler, M., Liu, F. F., Hansen, A., ... & Bratman, S. V. (2019). Computer-assisted image analysis of the tumor microenvironment on an oral tongue squamous cell carcinoma tissue microarray. *Clinical and Translational Radiation Oncology*, 17, 32-39. <https://doi.org/10.1016/j.ctro.2019.05.001>
7. Chiesa-Estomba, C. M., Graña, M., Medela, A., Sistiaga-Suarez, J. A., Lechien, J. R., Calvo-Henriquez, C., ... & Fagan, J. J. (2022). Machine learning algorithms as a computer-assisted decision tool for oral cancer prognosis and management decisions: a systematic review. *ORL*, 84(4), 278-288. <https://doi.org/10.1159/000520672>
8. Wieslander, H., Harrison, P. J., Skogberg, G., Jackson, S., Friden, M., Karlsson, J., Spjuth, O., and Wahlby, C. (2021). Deep Learning With Conformal Prediction for Hierarchical Analysis of Large-Scale Whole-Slide Tissue Images. *IEEE Journal of Biomedical and Health Informatics*, 25(2), 371–380. <https://doi.org/10.1109/jbhi.2020.2996300>.
9. Gao, J., Yang, Y., Lin, P., & Park, D. S. (2018). Computer vision in healthcare applications. *Journal of healthcare engineering*, 2018, 5157020. <https://doi.org/10.1155/2018/5157020>
10. López-Cortés, X. A., Matamala, F., Venegas, B., & Rivera, C. (2022). Machine-learning applications in oral cancer: A systematic review. *Applied Sciences*, 12(11), 5715. <https://doi.org/10.3390/app12115715>
11. Aftab, M., Mehmood, F., Zhang, C., Nadeem, A., Dong, Z., Jiang, Y., & Liu, K. (2025). AI in Oncology: Transforming Cancer Detection through Machine Learning and Deep Learning Applications. <https://doi.org/10.48550/arXiv.2501.15489>
12. Vinay, V., Jodalli, P., Chavan, M. S., Buddhikot, C. S., Luke, A. M., Ingafou, M. S. H., ... & Testarelli, L. (2025). Artificial Intelligence in Oral Cancer: A Comprehensive Scoping Review of Diagnostic and Prognostic Applications. *Diagnostics*, 15(3), 280. <https://doi.org/10.3390/diagnostics15030280>
13. Khanagar, S. B., Alkadi, L., Alghilan, M. A., Kalagi, S., Awawdeh, M., Bijai, L. K., ... & Singh, O. G. (2023). Application and performance of artificial intelligence (AI) in oral cancer diagnosis and prediction using histopathological images: a systematic review. *Biomedicines*, 11(6), 1612. <https://doi.org/10.3390/biomedicines11061612>
14. Wankhade, D., Dhawale, C., & Meshram, M. (2024). Advanced deep learning algorithms in oral cancer detection: Techniques and applications. *Journal of Environmental Science and Health, Part C*, 1-26. <https://doi.org/10.1080/26896583.2024.2445957>
15. Mirfendereski, P., Li, G. Y., Pearson, A. T., & Kerr, A. R. (2025). Artificial intelligence and the diagnosis of oral cavity cancer and oral potentially malignant disorders from clinical photographs: a narrative review. *Frontiers in Oral Health*, 6, 1569567. <https://doi.org/10.3389/froh.2025.1569567>
16. Li, L., Pu, C., Tao, J., Zhu, L., Hu, S., Qiao, B., ... & Zhang, H. (2024). Development of an oral cancer detection system through deep learning. *BMC Oral Health*, 24(1), 1-10. <https://doi.org/10.1186/s12903-024-05195-5>

17. Sahoo, R. K., Sahoo, K. C., Dash, G. C., Kumar, G., Baliarsingh, S. K., Panda, B., & Pati, S. (2024). Diagnostic performance of artificial intelligence in detecting oral potentially malignant disorders and oral cancer using medical diagnostic imaging: a systematic review and meta-analysis. *Frontiers in Oral Health*, 5, 1494867. <https://doi.org/10.3389/froh.2025.1569567>
18. de Chauveron, J., Unger, M., Lescaille, G., Wendling, L., Kurtz, C., & Rochefort, J. (2024). Artificial intelligence for oral squamous cell carcinoma detection based on oral photographs: A comprehensive literature review. *Cancer Medicine*, 13(1), e6822. <https://doi.org/10.1002/cam4.6822>
19. Pereira-Prado, V., Martins-Silveira, F., Sicco, E., Hochmann, J., Isiordia-Espinoza, M. A., González, R. G., ... & Bologna-Molina, R. (2023). Artificial intelligence for image analysis in oral squamous cell carcinoma: a review. *Diagnostics*, 13(14), 2416. <https://doi.org/10.3390/diagnostics13142416>
20. Yaduvanshi, V., Murugan, R., & Goel, T. (2024). Automatic oral cancer detection and classification using modified local texture descriptor and machine learning algorithms. *Multimedia Tools and Applications*, 1-25. <https://doi.org/10.1007/s11042-024-19040-y>
21. Nieri, M., Serni, L., Clauser, T., Paoletti, C., & Franchi, L. (2025). Diagnosis of Oral Cancer With Deep Learning. A Comparative Test Accuracy Systematic Review. *Oral Diseases*. <https://doi.org/10.1111/odi.15330>
22. Appavu, N. (2025, February). Oral Cancer Histopathological Detection and Diagnosis Using Hybrid AI Deep Learning Methods. In *2025 3rd International Conference on Intelligent Data Communication Technologies and Internet of Things (IDCIoT)* (pp. 2061-2067). IEEE. <https://doi.org/10.1109/IDCIOT64235.2025.10915019>
23. Agrawal, R., Tofighbakhsh, A., Davidson, J., & Gabriele, J. (2025). Early Detection of Oral Cavity Cancer: A Comprehensive Literature Review of Risk Factors and Latest Techniques in Diagnosis. *Current Surgery Reports*, 13(1), 15. <https://doi.org/10.1007/s40137-024-00442-8>
24. Kumar, J., Pandey, V., & Tiwari, R. K. (2025). Deep Learning Framework for Early Detection of Oral Cancer. In *AI and Green Technology Applications in Society* (pp. 353-372). IGI Global Scientific Publishing. DOI: 10.4018/979-8-3693-9879-1.ch013
25. Prithvidhar, P., Anusha, S., Vamshi, G., Munisekhar, V., & Vaghasana, M. (2025). Comparative analysis of oral cancer detection using histopathological images. In *Digital Transformation and Sustainability of Business* (pp. 166-169). CRC Press. <https://doi.org/10.1201/9781003606185>
26. Chowdhury, T., Kasralikar, P., Syed, A. A., Tumati, R., Patel, S., Kommineni, D., & Syed, A. A. (2025). Role of Artificial Intelligence in the Diagnosis of Oral Squamous Cell Carcinoma: A Systematic Review. *Cureus*, 17(4). <https://doi.org/10.7759/cureus.81800>
27. Ramani, R. S., Tan, I., Bussau, L., O'Reilly, L. A., Silke, J., Angel, C., ... & Yap, T. (2025). Convolutional neural networks for accurate real-time diagnosis of oral epithelial dysplasia and oral squamous cell carcinoma using high-resolution in vivo confocal microscopy. *Scientific Reports*, 15(1), 2555. <https://doi.org/10.1038/s41598-025-86400-5>

28. Naderi Yaghouti, A. R., Shalbaf, A., Alizadehsani, R., Tan, R. S., Vijayanathan, A., Yeong, C. H., & Acharya, U. R. (2025). Artificial Intelligence for Ovarian Cancer Detection with Medical Images: A Review of the Last Decade (2013–2023). *Archives of Computational Methods in Engineering*, 1-32. <https://doi.org/10.1007/s11831-025-10268-x>
29. Warin, K., Suebnukarn, S. (2024), Deep learning in oral cancer- a systematic review. *BMC Oral Health* 24, 212. <https://doi.org/10.1186/s12903-024-03993-5>
30. Rothery, D. A. (1987), Decorrelation stretching as an aid to image interpretation, *International Journal of Remote Sensing*, vol. 8, pp. 1253-1254. <https://doi.org/10.1080/01431168708954771>