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Correlated Preference based Weighted Feature Vector using ResNet50 for Accurate Oral Cancer Stage Detection

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ABSTRACT
With 130,000 deaths annually, Oral Cancer (OC) is the eighth most common cancer worldwide in India. The tumors that make up oral cancer can be found in many different places, including the salivary glands, tonsils, neck, face, and mouth. A biopsy, which involves taking a small piece of tissue from one area of the body and analyzing it under a microscope, is one of several diagnostic methods used to diagnose oral cancer. It is possible that the patient's oral glands, face, neck, or mouth will be impacted. The use of histological images in cancer screening aids in the detection and prognosis of abnormalities. Early diagnosis of oral potentially malignant disorders is crucial for improving the morbidity and mortality outcomes from mouth cancer. Early detection is often the key to a successful cure for many conditions, which have a chance of progressing to cancer. The potential applications of computer vision and deep learning algorithms in the detection of oral cancer using photographic images are analyzed to identify oral disorders that could be cancerous. Deep learning is applied in this research that recognized a wide range of oral and mouth diseases, including gum disease, canker sores, cold sores, oral lichen planus, oral thrush, mouth cancer, and oral cancer. When features are used incorrectly or excessively, classification algorithms learn a lot of useless information from images, leading to poor classification accuracy. A correlated preference based weighted feature vector is proposed to extract various types of properties from histopathology images. The texture and deep features obtained from these techniques are used as input vectors by the deep learning model. This research makes use of ResNet-50 architecture that makes use of 50 stackable bottleneck residual pieces. Traditional convolutional and pooling layers preprocess the image in the network's initial layers before the remaining blocks do any more processing. This research proposes a Correlated Preference based Weighted Feature Vector using ResNet50 for accurate Stage Detection (CPbWFV-SD) of oral cancer. The weighted feature vector is used to train the model and the minute change in the feature attribute set is used to identify the stage of the disease. The proposed model when compared with the traditional methods performs better in oral cancer stage detection.

Keywords: Oral Cancer, Histological Images, Deep Learning, Classification Algorithms, Classification Accuracy, Feature Vector, Convolutional and Pooling Layers, Stage Detection.

1. INTRODUCTION

Oral cancers, a subtype of head and neck cancers, account for around 3% of all malignancies diagnosed worldwide. A review of the literature found that this cancer ranks as the sixth most prevalent worldwide [1]. Tobacco, betel nut, and cigarette chewing are the main causes of this disease, which manifests mostly in the nasal passages, throat, and mouth. People in developing countries, especially those in South Asia, have a higher risk of oral cancer because of a lack of education, clinical diagnostic tools, and specialists in the field [2]. Oral cancer symptoms can include problems with chewing or speaking, inflammations or ulcers inside the mouth, and maybe even visible facial markings [3]. One potentially fatal complication of the disease's fast progression is the formation of squamous cell linings, which lead to Oral Squamous Cell Carcinoma (OSCC) [4]. Early detection of these oral malignant lesions greatly reduces the probability that they may develop into cancer. According to research, mouth cancer recurrence rates are high. Therefore, a thorough analysis of its occurrence and progression is necessary for its prognosis [5].

An oral cancer survival study that followed patients for five years found a prognosis rate of between 35% to 50%. The researchers concluded that if all relevant pathological aspects were optimally examined, the disease

survival rate may be increased [6]. For this reason, pathologists place a premium on correctly histologically classifying oral lesions.The cells of the mouth are the incubators for oral cancer [7]. Malignant tumors form when cancer cells gather in one area and have the ability to spread to other areas of the body. It may also spread to other parts of the body, a process known as metastasis [8]. The majority of oral cancer metastases end up in the neck, specifically in lymph nodes. The oral cavity, throat, or mouth cancer is another name for this disease. Changes, abnormal development, or abnormal behavior in oral cells do occur from time to time. These changes may lead to the development of noncancerous tumors such as fibromas and warts [9].Alterations to the cells of the mouth can potentially lead to precancerous disorders. So, while the abnormal cells aren't cancer just yet, they might turn into it if not addressed. Most cases of oral precancerous diseases include leukoplakia and erythroplakia [10].

Identifying Oral Cavity Cancer (OCC) at an early stage is a great way to increase the survival rate of patients [11]. However, the current approach of initial screening is time-consuming and expensive for the average individual, especially in developing countries around the world. The problem is exacerbated because there are insufficient expertise in these domains. Automating the first screening process with Artificial Intelligence (AI) to detect pre-cancerous lesions would be a cost-effective and efficient way to classify patients based on clinical need [12]. The high prevalence of OCC in developing countries is due, in large part, to a lack of education about the disease and an absence of dental professionals and clinical diagnostic tools. This is particularly true in South Central Asia. The roof and floor of the mouth, the tongue, the gums, and the inside lining of the cheeks are the most typical places where OCC appears [13]. Severe oral cancer symptoms include visible scars from procedures and therapies, excruciating pain, difficulties with eating and speaking, and the development of tumors in the mouth. If untreated, OCC can quickly spread to other organs, such as the neck and lungs [14]. The oral cancer images with different stages are shown in Figure 1.

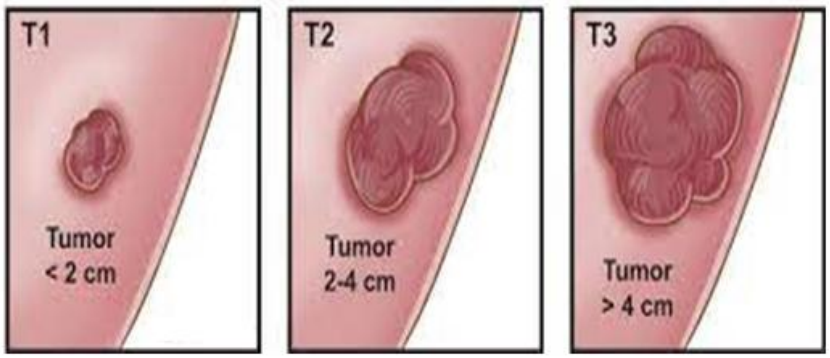

Fig 1: Oral Cancer Images with Different Stages

More than eighty percent of OCCs begin as lesions called Oral Potentially Malignant Disorders (OPMD). OPMDs are the initial sign of a lot of different oral and systemic diseases. Early diagnosis of these OPMD is crucial for reducing the chance of malignant transformation. The topic of tongue lesions has been covered thus far. Classifying OPMDs according to their propensity to develop into oral cancer is challenging and requires specialist knowledge due to the wide variety of tongue lesions [15]. Precancerous tongue lesions might be more properly classified by an automated system, which would be a boon to both patients and clinicians. Patients with limited medical expertise could get potentially life-saving diagnoses using mobile apps, which would be cheaper and faster.The outcomes of conventional methods are subjective due to factors such as the pathologist's level of training, the quality of the microscope used, the amount of time needed to examine each slide, and the staining quality. The subsequent procedure may be postponed or mistaken due to the diagnostic test's findings. In contrast, deep learning-based approaches generate high-quality classification results without requiring human domain experts to manually generate features. When there aren't enough biopsy images, the pathological gold standard to train deep learning models for important features, it becomes problematic to make an accurate diagnosis [16]. Researchers have demonstrated that by integrating deep learning with transfer learning on a limited dataset of biopsy images, pretrained models may be successfully applied to the classification task, thus resolving this issue.

Oral cancer symptoms can include problems with chewing or speaking, inflammations or ulcers inside the mouth, and maybe even visible facial markings. One potentially fatal complication of the disease's fast progression is the formation of squamous cell linings, which lead to OSCC. Early detection of these oral malignant lesions greatly reduces the probability that they may develop into cancer. According to research, mouth cancer recurrence rates are high. Therefore, a thorough analysis of its occurrence and progression is necessary for its prognosis [17]. An oral cancer survival study that followed patients for five years found a prognosis rate of between 35% to 50%. The researchers concluded that if all relevant pathological aspects were

optimally examined, the disease survival rate may be increased. For this reason, pathologists place a premium on correctly histologically classifying oral lesions.The cells of the mouth are the incubators for oral cancer [18]. Malignant tumors form when cancer cells gather in one area and have the ability to spread to other areas of the body. It may also spread to other parts of the body, a process known as metastasis. The majority of oral cancer metastases end up in the neck, specifically in lymph nodes. The oral cavity, throat, or mouth cancer is another name for this disease. Changes, abnormal development, or abnormal behavior in oral cells do occur from time to time. The general process of oral cancer detection is shown in Figure 2.

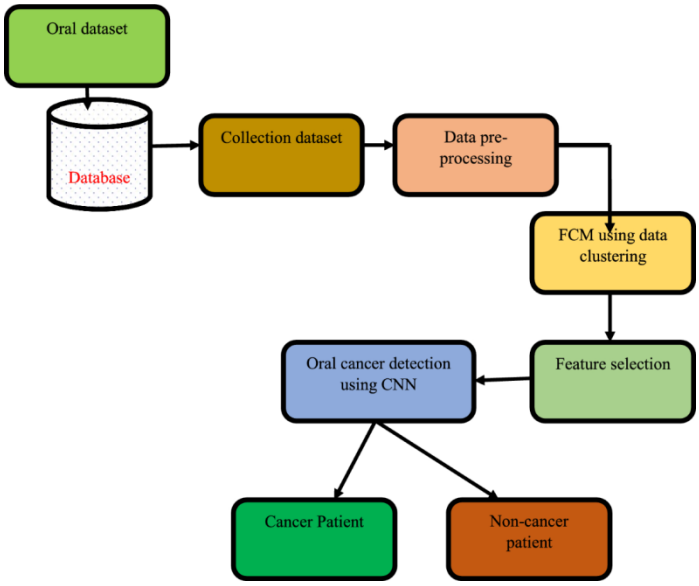

Fig 2: General Process of Oral Cancer Detection

The proposed model makes use of ResNet-50 model for accurate stage detection of oral cancer. ResNet50 can train ultra-deep networks with hundreds of layers since it is built on a deep residual learning framework. The 50 layers that make up ResNet-50 are split into five blocks, with a set of residual blocks contained in each block. By preserving data from previous layers in the residual blocks, the network is able to learn more accurate representations of the input data. The input image is convolutionally processed by the first layer of the network, which is a convolutional layer. The output of the convolutional layer is downsampled by a max-pooling layer that follows. Following the max-pooling layer, a sequence of residual blocks processes the output [19]. Two convolutional layers make up each residual block, with batch normalization and a rectified linear unit (ReLU) activation function following. The input of the residual block is supplemented with the output of the second convolutional layer, and subsequently processed by means of an additional ReLU activation function. After the residual block finishes processing, its result is transmitted to the subsequent block [20]. Finally, the network's last layer is a completely linked one, and it maps the output classes to the last residual block's output. In a fully linked layer, the quantity of output classes is directly proportional to the number of neurons. This research proposes a Correlated Preference based Weighted Feature Vector using ResNet50 for accurate Stage Detection of oral cancer. The weighted feature vector is used to train the model and the minute change in the feature attribute set is used to identify the stage of the disease.

2. LITERATURE SURVEY

Precise subtype and/or stage prediction is of the utmost importance in the fields of cancer diagnosis, treatment, and management. Overfitting, overly complex computing, and traits unrelated to prediction accuracy are some of the issues plaguing most existing genomic profile-based methods. These limitations are mostly brought about by the inherent high dimensionality and small sample size of molecular data. Many people think this is a problem with DNNs and other forms of deep learning that could hinder its use in cancer research and biomedicine. In order to address these issues, Chen et al. [1] presented a Dropfeature-DNNs algorithm that integrates a DNN with an innovative embedded feature selection method. Users can train Dropfeature-DNNs to disregard some genes and other superfluous features; the author modeled them as an iterative AUC optimization problem. For accurate tumor subtype and stage prediction, a subset of features including relevant genes can be obtained when the AUC optimization converges during training. During training, DNNs optimize the feature subset and AUC while simultaneously reducing model complexity and computing expense.

Metastasis, or the spread of abnormal cells to other parts of the body, is a hallmark of cancer. There are potentially billions of cells in the human body where it might begin. The body's necessities are met by these

cells constantly dividing. When cells become damaged or old, they naturally undergo apoptosis, a process that allows new cells to replace them. The secondary dataset that is utilized in this research is derived from Kaggle and contains more than 130,000 images depicting various forms of cancer. The groundbreaking Deep-learning program designed by Omar Bappi et al. [2] can detect and classify early-stage cancer with remarkable accuracy. Eight primary cancer types and twenty-six subcategories are classified by the model using five thousand images. Machine learning, deep learning classifiers such as KNN and SVM, and pre-trained Convolutional Neural Networks are all a part of this strategy, which also includes innovative multimodal designs of coupled CNN-LSTM hybrids. To classify things, the author employed two different approaches. The first move will be to combine the main and subclasses into one. For the second approach, the author forecasted eight primary classes and twenty-six subclasses associated with each using a KNN model, which achieved better results than CNNs in the Lymphoma class. Finally, a fusion strategy that utilizes X-OR gates considerably enhances cancer type confidence while reducing misclassifications when used after prediction.

Computer Vision (CV) and medical image diagnosis have a significant role in healthcare by allowing for the detection of laryngeal cancer on images of the neck area. Studying and identifying abnormal or cancerous tissues in the larynx is important because it is a part of the respiratory and vocal systems. The collected characteristics are classified using a variety of ML and DL algorithms to differentiate between benign and cancerous tissue. CNNs and recurrent neural networks (RNNs) have shown promise in this area. Alrowais et al. [3] presented a novel approach to laryngeal cancer detection and classification by applying the Aquila Optimization Algorithm with Deep Learning (LCDC-AOADL) method to images of the neck region. By evaluating histopathology images, the LCDC-AOADL approach may detect and classify laryngeal cancer. The presented LCDC-AOADL approach employs the Inceptionv3 model for feature extraction. Further, a deep belief network (DBN) model was used by the LCDC-AOADL approach to identify and type LC. In addition, adjusting the DBN model's hyperparameters with the AOA improves the detection rate. The simulation study of the LCDC-AOADL approach is validated using the benchmark Laryngeal dataset.

Using mutational signatures, users can gain a better understanding of the roles played by cancer-associated genes in carcinogenesis pathways. Thus, by utilizing these pathways, precision medicine approaches can discover successful drugs and cures. Different types of cancer exhibit unique patterns of mutation. Some malignancies may have a connection to certain mutations that cause proteins to stop working as they should, which can lead to their accumulation and, eventually, cancer. Therefore, mutations, as a set of characteristics, may prove to be a useful tool for distinguishing between various cancers. There is more than one way to prove mutations. Binary numbers can be used to display the locations of mutations. Another option for feature extraction is to use mutation interpreters. In this study, Abdollahi et al. [4] investigated the tumor types that share a common pattern of trinucleotide mutations. On top of that, the author used NMF to find significant mutational signatures for various cancers. The next step is to identify genes linked to cancer by analyzing the target cancer's notable signatures. The author evaluated the cancer-related genes by analyzing survival and gene expression data across different stages of cancer. A deep learning-based binary classifier, DiaDeL, is also available from us. Using mutational signatures as input features, the DiaDeL model can distinguish between various cancer kinds.

There has been a significant uptick in healthcare research focused on prognosis prediction using digital pathology pictures as a way to enhance patient treatment and make early therapeutic decisions. Efforts to build deep learning approaches to solve the difficulty of prognosis prediction using digital pathology images have been fruitful, and the challenge has recently gained a lot of interest. Whole slide histopathological images (WSIs) still have a ways to go before they can be used for prognosis prediction due to factors like tumor heterogeneity, ROI labeling's high cost, and the massive size of pathological photos. Liu et al. [5] introduced TSDLPP, a novel WSI-based two-stage deep learning system for prognosis prediction. The proposed framework is based on two-stage paradigms, which are using two types of densely connected CNNs, one for general prognosis and another for morphology-specific prognosis to extract different level characteristics from diseased images. The Cancer Genome Atlas (TCGA) datasets for breast cancer prognostic prediction are subsequently processed using TSDLPP.

Identifying OCC at an early stage is a great way to increase the survival rate of patients. However, the current approach of initial screening is time-consuming and expensive for the average individual, especially in developing countries around the world. The problem is exacerbated because there are insufficient expertise in these domains. Automating the first screening process with AI to detect pre-cancerous lesions would be a cost-effective and efficient way to classify patients based on clinical need. Using a limited dataset of clinically annotated photographs, Shamim et al. [6] evaluated six deep convolutional neural network (DCNN) models trained with transfer learning for early diagnosis of oral cancer and directly detected pre-cancerous lesions on the tongue. The DCNN models demonstrated impressive classification results in identifying various tongue lesions, including benign and pre-cancerous ones. The models could also distinguish between five different types of tongue lesions: hairy, fissured, geographic, strawberry, and oral hairy leukoplakia.

Oral cancer ranks sixth in terms of global incidence of cancer. While early detection by screening or treatment

can avert some occurrences of cancer, the vast majority of cases are discovered when the disease has progressed to a lethal stage. The result is a dramatic decline in death rates. In this study, a method is outlined by Goswami et al. [7] for reliably differentiating benign lesions from cancerous ones, as well as precancerous lesions, in the mouth. After exploring color and texture data in five different color spaces, Light Gradient Boosting Machine (LightGBM) uses machine learning to categorize the features retrieved from the data. In comparison to the current gold standard for oral cancer categorization, the overall findings are promising. The testing accuracy, precision, recall, f1-score, and specificity for binary classification were 99.25%, 99.18%, 99.31%, and 99.24%, respectively. The testing accuracy, recall, precision, f1-score, and specificity for multi-class classification were 98.88%, 98.86%, 97.92%, and 99.03%, respectively.

Early metastasis to neighboring lymph nodes is a hallmark of OSCC. Patients with OSCC often have bad prognoses and low survival rates due to cervical lymph metastases. Consequently, a reliable screening technique is needed to quickly determine if OSCC patients have cervical lymph metastases and to develop appropriate treatment plans. Zhang et al. [8] suggested a new method for diagnosing OSCC lymph node metastases using hyperspectral imaging in conjunction with the commonly used hematoxylin-eosin (H&E) stained pathological sections. Accuracy is achieved through a learning and decision-making stage that gradually finishes lesion segmentation from coarse to fine, focuses on cancer and non-cancer nuclei, and so on. A network known as FD-Net is builtto differentiate between cancerous and non-cancerous nuclei during the learning phase. The lesions are effectively segregated utilizing the preceding knowledge throughout the decision-making stage after the segmentation findings have been post-processed. Experimental results show that the proposed FD-Net performs better than its rivals in the OSCC hyperspectral medical image segmentation challenge. The proposed FD-Net method outperforms the alternatives when it comes to segmentation according to the seven quality indicators. The proposed FD-Net method outperforms the DeepLab V3 approach by 1.75 percent, 1.2 percent, 0.3 percent, 1.9%, 0.88%, 4.45%, and 1.9 percent on each of the seven performance measures.

Oral cancer, one of the deadliest forms of cancer, is common in countries with medium or low incomes. Oral cancer might be more efficiently and cheaply diagnosed if machine learning could detect precancerous and malignant tumors earlier. A lot of research has gone into developing a machine-learning algorithm that can accurately detect oral cancer in images. However, they have not yet achieved a level of success in accurately detecting oral cancer. That is why this research aims to shed light on a new way to identify oral cancer in diagnostic images. Sudha et al. [9] introduced a novel and effective approach to oral cancer detection by combining an enhanced deep belief network (DBN) with a CNN. Al-Biruni Earth Radius (BER) Optimization and Particle Swarm Optimization (PSO) are combined to form an optimization method called (PSOBER). Users can use it to fine-tune the parameters of the CNN and DBN designs. The proposed method achieves a remarkable 97.35 percent accuracy, surpassing other competing methods on a standard biological images dataset accessible in the Kaggle repository. Statistical tests, such as one-way analysis-of-variance (ANOVA) and Wilcoxon signed-rank tests, are also run to prove the method's stability and relevance.

3. PROPOSED MODEL

Computer vision and deep learning have recently made great strides, which bode well for the future of supplemental technology that can scan the mouth automatically and give feedback to doctors and patients alike during exams [20]. The majority of the research on image-based automated oral cancer diagnosis has focused on imaging modalities, hyperspectral imaging, and autofluorescence imaging. On the other hand, little research has focused on white-light photography, and most of that research has focused on detecting particular oral lesions. The establishment of screening strategies for oral cancer is greatly impacted by the discovery of OPMD due to its crucial role in improving early diagnosis of the cancer [21]. In this research, the potential of computer vision techniquesare analyzed, particularly as they pertain to photographic images, in the context of establishing an automated system for screening for oral cancer using deep learning [22].

Automated histopathological image analysis has recently attracted the attention of many academics in response to the concerning increase in cancer incidence over the past few years. With state-of-the-art imaging technology, data capture in the medical profession is easier than ever before. The complexity of the data provided by these technologies means that topic experts still need to invest a lot of time to get final diagnosis results [23]. It is necessary to clean and filter this enormous data set, which takes a lot of time and effort, to extract important information while deleting any irrelevant data, because not all data is significant. Researchers in medical image analysis have so discovered a plethora of options to satisfy the demand for trustworthy feature selection and extraction [24]. Researchers have presented both novel and more traditional methods for computer diagnostic systems to utilize feature extraction and selection algorithms, with the goal of better addressing the diverse needs of medical imaging data [25]. Numerous research have proposed different approaches to medical imaging, including geometrical, textural, color-based, shape-based, wavelet-based, and so on.

Feature extraction's main objective is to select the most relevant feature for feeding into the classification algorithm in order to boost its performance [26]. By integrating feature extraction and selection, this research suggests a way to enhance the accuracy of histopathology image classification. Experienced experts must put in

a lot of time and effort to review the histopathological images. In order to create a robust computer-aided medical image diagnostic system, many researchers are integrating deep learning with image processing methods. These strategies let the expert analyze the image quickly and accurately [27]. Another issue with medical image diagnosis is that different feature extraction strategies could yield different categorization results for the same image. This research successfully differentiated between normal and cancerous tissue in the mouth by using a variety of parameters and also stage detection is done accurately [28].

Various levels have yielded both low and high-level features. The final feature vector for deep learning model will be a hybrid of low-level features and high-level features. To do this, deep learning employ both low-level and high-level convolutional layers [29], with the former used to extract low-level information and the latter for high-level tasks. While low-level features are usually rich in information like color, positions, and edges, deep-level features can extract abstract elements like sophisticated geometric patterns and greater shapes [30]. CNNs use deep layer characteristics to classify data. Among the numerous tasks that lower-level features excel at is image classification with complex texture contours. In cases when high-level features are more important, the Feature Fusion method can combine low-level and high-level characteristics into a fused feature vector that contains exceptionally rich semantic information regarding the image. When applied to data, this composite feature vector may lead to better classification accuracy. A feature fusion layer was implanted into ResNet 50 parallel to the layer immediately before the dense layers in order to test the efficacy of feature fusion. The thick layers of ResNet50 are trained to classify these features by feeding them the final sets of the original deep features and the fused deep features.

ResNet-50 is composed of 50 layers, which are organized into 5 blocks. Each block has a group of residual blocks. The residual blocks facilitate the retention of knowledge from preceding layers, hence enhancing the network's ability to acquire more effective representations of the input data. ResNet50 is a highly potent image classification model that can be effectively trained on extensive datasets to attain cutting-edge performance. An important feature of this system is the incorporation of residual connections, which enable the network to learn residual functions that translate the input to the desired output. The inclusion of residual connections allows the network to acquire knowledge from much deeper structures than was previously feasible, without being affected by the issue of vanishing gradients.

The ResNet50 architecture consists of four primary components: the convolutional layers, the identification block, the convolutional block, and the fully linked layers. The convolutional layers extract features from the input image, while the identity block and convolutional block process and change these features. Ultimately, the completely connected layers are employed to carry out the ultimate classification. The convolutional layers of ResNet50 comprise multiple convolutional layers, which are subsequently followed by batch normalization and ReLU activation. These layers have the task of extracting features from the input image, such as edges, textures, and forms. Following the convolutional layers, there are max pooling layers that decrease the spatial dimensions of the feature maps while retaining the crucial information.

Number staging classifies oral cancer into four distinct phases, numbered 1–4. Cancer is classified into four stages: early, intermediate, progressed, and terminal. When cancer is in its earliest stages, it is known as stage 0 or carcinoma in situ (CIS). Calling this precancerous is what some doctors recommend. Even while cancer cells do exist, they are all contained within the mouth's lining. No metastasis has occurred. Precancerous conditions have a significant propensity to progress to aggressive malignancy if left untreated. Invasive cancer begins in its earliest stage, known as Stage 1.The cancer is 2 cm in diameter or less and 5 mm in depth if this is true. No other organs, lymph nodes, or neighboring tissues have been affected. Stage 1 oral cancer is denoted as T1, N0, and M0 in the TNM staging system.

There are a variety of meanings for stage 2, including, the malignancy is less than 2 centimeters in diameter, and its depth ranges from 5 millimeters to 10 millimeters. The depth of the tumor is 10 millimeters or less, and its diameter is between 2 and 4 centimeters. No other organs or lymph nodes are in the vicinity of the original tumor. When it comes to the TNM staging system, stage 2 mouth cancer is equivalent to T2, N0, and M0.

Stage 3 indicatesthat the cancer is more than 2 cm in size but less than 4 cm in diameter and less than 10 mm in depth; it has not metastasized to other organs or regions of the body; or the cancer is more than 4 cm in diameter but less than 10 mm in depth; it has metastasized to other organs or regions of the body; or the cancer is of any size; however, there is cancer in one lymph node on the same side of the neck, and its diameter is less than 3 cm. Stage 3 oral cancer, according to the TNM staging system, is equivalent toN1, M0; T1, 2 or 3; T3, N0, M0

Cancer is considered progressed when it reaches stage 4. There are three sub-stages: 4a, 4b, and 4c.

Level 4a

It may indicate that the cancer has spread to other parts of the body beyond the mouth. One lymph node, no bigger than 3 cm, may also have been affected.The cancer can be of any size, though. One or more lymph nodes on either side of the neck have been affected by the spread. Lymph nodes range in size from 3 to 6 cm.

Level 4b

Malignancy has progressed to neighboring regions, such the jawbone, the base of the skull, or the neck region where the carotid arteries are located.If a cancerous lymph node is more than 6 cm in diameter, the disease has

likely metastasized to the tissues in and around the node. The following conditions are equivalent to stage 4b mouth cancer according to the TNM staging T4b, any N, M0

Level 4c

When cancer has progressed to other organs like the lungs or bones, the prognosis is dire. Stage 4c oral cancer, according to the TNM staging classification, indicates, T, N, and M1 can be any two numbers. The proposed model framework is shown in Figure 3.

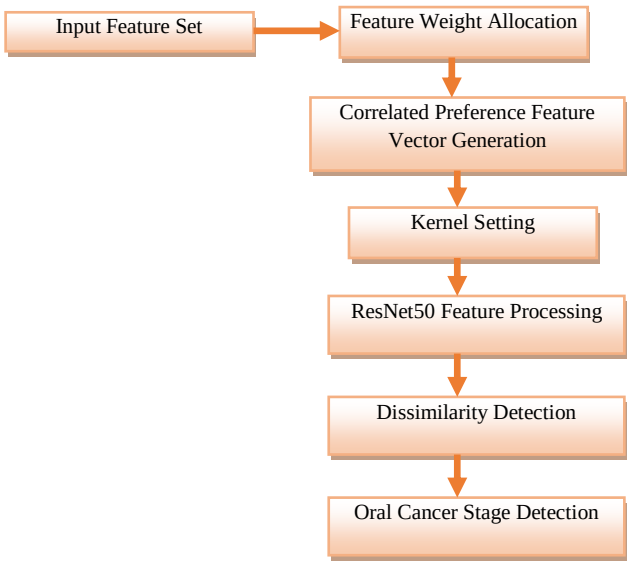

Fig 3: Proposed Model Framework

The identity block and convolutional block are the fundamental components of ResNet50. The identity block is a basic unit that forwards the input through a sequence of convolutional layers and then combines the input with the output. This enables the network to acquire residual functions that transform the input into the desired output. The convolutional block is analogous to the identity block, however with the inclusion of a 1x1 convolutional layer that serves to diminish the quantity of filters before to the 3x3 convolutional layer.The last component of ResNet50 consists of the completely connected layers. These layers have the responsibility of determining the final classification. The final class probabilities are generated by applying a softmax activation function to the output of the last fully connected layer. This research proposes a Correlated Preference based Weighted Feature Vector using ResNet50 for accurate Stage Detection (CPbWFV-SD) of oral cancer. The weighted feature vector is used to train the model and the minute change in the feature attribute set is used to identify the stage of the disease.

Algorithm CPbWFV-SD

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Input: Feature Set {Feaset}

Output: Oral Cancer Stage Detection {Stgset}

Step-1: Initially, the feature extracted from denoised oral images is considered as input and the feature processing is performed. The feature processing will analyze each attribute range of values in the feature set. The feature set processing is performed as

$$FeatP \quad [M] = \sum_{f=1}^{M} getFeaset \qquad (f) + \lim_{f \to M} \left(\delta(f, f+1) + \frac{\gamma(f, f+1) * \tau(f)}{len \quad (Feaset \quad)} \right)^{\mu}$$

Each feature from the dataset is considered and the feature attribute ranges are verified. The getFeaset() model retrieves each feature attribute and the range is analyzed. δ is the model that considers the highest range of values from the prefixed Threshold value and γ is the lowest value than the threshold value.μ is the balancing factor value.

Step-2: Feature weight allocation is the act of giving different amounts of value to different features in a dataset based on a correlation factor. Improving model accuracy is the goal of this method, which involves highlighting significant features and downplaying less impactful or irrelevant ones. The feature weight allocation is performed as

$$FW[M] = \sum_{f=1}^{M} \max\left(FeatP \quad (f)\right) + \beta\left(\delta(f, f+1)\right) + \beta(\gamma(f, f+1) + \frac{\omega(FeatP \quad (f))}{len \quad (FeatP \quad)} \begin{cases} FW \leftarrow setVal & (R)\ if \quad \omega(f) > CFT \\ FW \leftarrow 0 & Ot \ herwise \end{cases}$$

Here β is the model to identify the relation among the features that has high range of values and ω is the model to assign weights to the processed feature set. CFT is the correlation factor threshold.

Step-3: The numerical representations of features related with other alternative features that take correlations among these preferences into consideration are called related preference feature vectors. This method is essential in situations when feature entities' preferences interact with one another, creating intricate relationships that conventional feature vector models would struggle to handle. The correlated preference feature vector generation is performed as

$$CPFV \quad [M] = \sum_{f=1}^{M} getmax \quad \left(FW(f)\right) + \frac{\sum_{f=1}^{M}(FW(f) - \overline{FW(f)})(FW(f) - \overline{FW(f)})}{\sqrt{\sum_{f=1}^{M}(FW(f) - \overline{FW(f)})^2} * \sqrt{\sum_{f=1}^{M}(FW(f+1) - \overline{FW(f+1)})^2}} + \delta(FW(f)$$

Step-4: To build deep convolutional neural networks, ResNet makes use of a specified kernel configuration. Optimizing performance and reducing complexity, such as the vanishing gradient problem typically encountered in very deep networks, is achieved by judicious choice of kernel sizes and configurations. The convolution layers of the ResNet design usually use kernels of size 3×3. Because it preserves spatial information while enabling deeper network levels, this size is frequent. The kernel setting is performed as

$$KerSet \quad [M] = \sum_{f=1}^{M} \lim_{f \to M} \left(CPFV \quad (f) + \frac{\alpha(\mathrm{CPFV(f, f+1)})}{FW(f)} \right)^2 + \frac{K + 2f - R + L}{M}$$

Here α is the model for setting the kernel size and K is the input feature size, f is the feature considered and R is the size of the convolution and L is the padding performed in convolution model.

Step-5: The identity block and the convolutional block are two essential building components that ResNet50 incorporates. In order to learn residual functions, the network can use the identity block to feed inputs into a series of convolutions and then add them back to the output. To optimize feature processing and prevent excessive dimensionality, the convolutional block applies a 3x3 convolution after a 1x1 convolution to reduce the number of filters. At the end of the feature extraction process, there are fully connected layers that use the learnt features to make final classifications. In order to make good decisions when it comes to picture classification, the output of the fully connected layer is usually routed via a softmax activation function after feature processing.

The output feature map OPF for a set of features CPFV, at position x,y is calculated as

$$OPF \quad (x, y) = \sum_{i=1}^{K} \sum_{j=1}^{i} FW(j) * FW(f, f+1) + b$$

Here FW is the feature weight set, $FW(f, f+1)$ is the input set of features, b is the bias and K is the kernel size.

The batch normalization is performed as

$$\bar{i} = \frac{f - \mu}{\sqrt{\eta^2 + \varepsilon}}$$

Here f is the input feature, μ is the mean of the input feature set, ŋ is the feature variance, ε is the feature normalized value.

The ReLU function is performed as

$$y = \max(0, x)$$

The max polling is applied as

$$y(i, j) = \sum_{f=1}^{M} \max_{(f, f+1)\varepsilon \bar{i}} x(i + f, j + f + 1)$$

Step-6: When trying to identify the distinctions between the different stages of oral cancer, feature dissimilarity checks are crucial. Researchers can improve the accuracy of oral cancer type categorization, including pre-cancerous and malignant phases, by carefully analyzing the differences between characteristics retrieved from biopsy images. To improve oral cancer prognostic modeling, strong feature dissimilarity checks should be applied.Improved treatment methods and patient outcomes can be achieved by healthcare practitioners by improving classification accuracy. This highlights the significance of incorporating sophisticated feature analysis into diagnostic workflows.

The dissimilarity matrix is a comprehensive representation of pairwise distinctions between data objects6. To

construct it, first, compile the feature data for each object, available in both quantitative and qualitative formats. Each entry D(i,j) in the matrix corresponds to the calculated dissimilarity between objects i and j.

$$Stgset \quad [M] = \sum_{f=1}^{M}\sum_{i=1}^{f}\frac{\max\left(y(f,f+1)\right)}{M} + \lambda(OPF\ (f)) + \max(\lambda(OPF\ (y,y+1)))$$

$$+ \max(diff\ (y(f,f+1)) \begin{cases} Stgset \leftarrow Val & if\ \max\left(diff\ (f)\right) > ST\ h \\ 0 & Ot\ herwise \end{cases}$$

}

4. RESULTS

Deep learning is being used by an increasing number of dental health care applications to evaluate images of oral tissues. Unfortunately, most images of oral tissues include distracting background details like the patient's clothes, the doctor's hands, and dental instruments, which do not help with the diagnosis. If these parts are still in the image, the processing could not pick up on the potential oral cavity lesions. This issue can be resolved by the model's ability to automatically reduce the full oral tissue image to just the region of interest. Since the best way to improve oral cancer outcomes is by early identification and treatment, there is a great need for advancements in vision-based adjunctive technologies that can identify OPMDs. This could lead to new possibilities for oral cancer screening. The development of cancer is a concern associated with OPMDs. This research focused on the potential of computer vision algorithms to identify OPMD automatically and on their potential applications in the field of oral cancer utilizing images. The most recent advances in deep learning were used to propose a multi-stage model for the detection of oral lesions and stage detection. A detector network is used in the first step, and a classifier network is used in the second stage to categorize the detected region as either benign, OPMD, or cancer and finally the region based stage detection is performed. According to the preliminary results, algorithms based on deep learning can automatically identify and categorize oral lesions in real-time. The proposed model has great potential as a non-invasive, cost-effective method to supplement screening processes and improve OPMD detection.

A dependable OSCC detection technology is urgently needed because this disease affects a large number of individuals. Several different deep learning techniques have been investigated for the purpose of automated oral squamous cell carcinoma identification using oral histopathology images. The unique patch selection technique is used by the proposed OSCC detection method to choose patches that provide important information about the morphology and nuclear density of tissues. ResNet50 model was trained on a dataset of 2000 pictures to utilize the characteristics that were extracted from the patches, which included morphological and textural information. From every input image, a set of overlapping patches with 50% coverage is extracted following contrast enhancement. Afterwards, four regions that contain a high concentration of nuclei are chosen. For accurate feature extraction from the four patches, an approach based on feature fusion is suggested. The proposed model is implemented in python and executed in Google colab. The dataset is considered from the link https://www.kaggle.com/datasets/zaidpy/oral-cancer-dataset. The proposed Correlated Preference based Weighted Feature Vector using ResNet50 for accurate Stage Detection (CPbWFV-SD) is compared with the traditional Effective Cancer Subtype and Stage Prediction via Dropfeature-DNNs (CSSP-DNN) and Novel Deep Learning Approach for Accurate Cancer Type and Subtype Identification (CNN-LSTM). The proposed model performance in stage detection is high when contrasted with the traditional models.

To improve model performance and interpretability, feature selection, a crucial step in deep learning involves picking out a subset of pertinent features from a bigger collection. This method simplifies the model, which in turn reduces the likelihood of overfitting and improves the model's capacity to generalize to new data. The Feature Selection Time Levels are shown in Table and Figure 4.

Table 1: Feature Selection Time Levels

Images Considered	Models Considered		
	CPbWFV-SD Model	CSSP-DNN Model	CNN-LSTM Model
250	14.2	18.4	16.3
500	14.6	18.6	16.5
750	14.8	18.9	16.8
1000	15.0	19.1	17.1
1250	15.3	19.3	17.3
1500	15.6	19.5	17.4

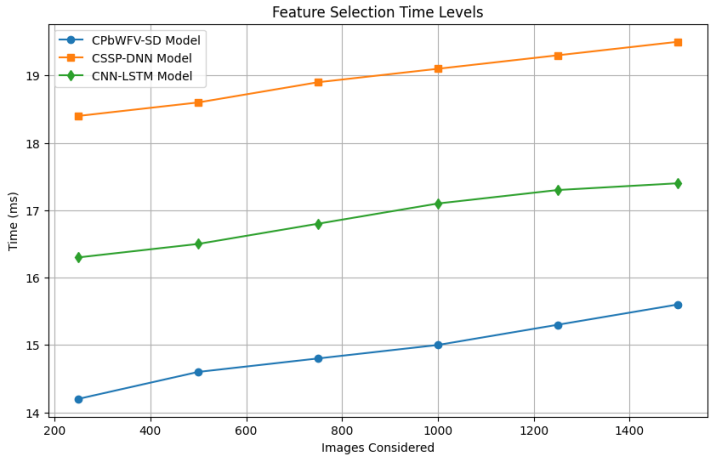

Fig 4: Feature Selection Time Levels

One step in deep learning is feature weight allocation, which involves giving different features varying amounts of weight depending on how well they predict the output. This improves the model's performance and interpretability by allowing it to highlight more useful features while downplaying less significant ones. The Feature Weight Allocation Accuracy Levels is indicated in Table 2 and Figure 5.

Table 2: Feature Weight Allocation Accuracy Levels

Images Considered	Models Considered		
	CPbWFV-SD Model	CSSP-DNN Model	CNN-LSTM Model
250	97.5	94.6	95.1
500	97.8	94.8	95.3
750	98.1	94.9	95.6
1000	98.3	95.1	95.8
1250	98.5	95.3	96.0
1500	98.7	95.6	96.2

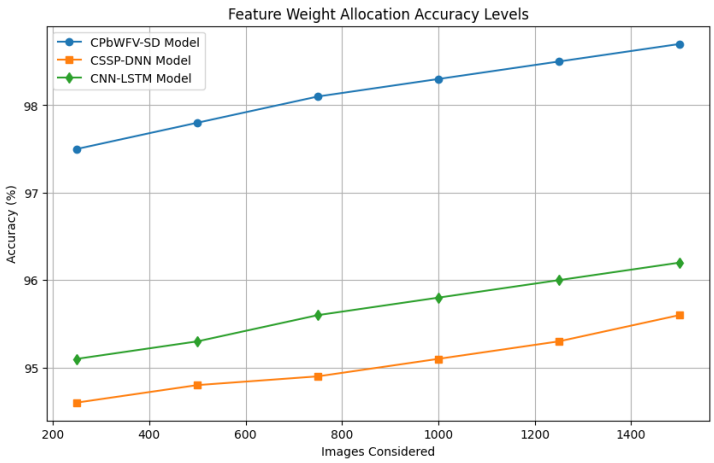

Fig 5: Feature Weight Allocation Accuracy Levels

Deep learning and pattern recognition rely heavily on feature vectors, which are n-dimensional vectors that numerically encode an object's quantifiable attributes. To facilitate efficient data processing and statistical analysis, this vector contains features that stand for distinct observable properties. Duplicate data in a dataset can occur as a result of feature correlation, which means that updates to one feature might foretell updates to another. In order to generate preference feature vectors, it is important to first determine which characteristics to keep based on their influence on model correctness and then assess the correlations among them. For a systematic approach, practitioners can train single-feature models on linked groups and evaluate their performance to decide which characteristics to retain. A better grasp of the connections between features and the dependent variable can be reflected in the intuitive model designs made possible by this approach. The Table 3 and Figure 6 shows the Correlated Preference Feature Vector Generation Accuracy Levels.

Table 3: Correlated Preference Feature Vector Generation Accuracy Levels

Images Considered	Models Considered		
	CPbWFV-SD Model	CSSP-DNN Model	CNN-LSTM Model
250	98.3	95.6	94.8
500	98.4	95.8	95.0
750	98.6	96.0	95.2
1000	98.8	96.2	95.4
1250	99.1	96.4	95.7
1500	99.2	96.5	95.8

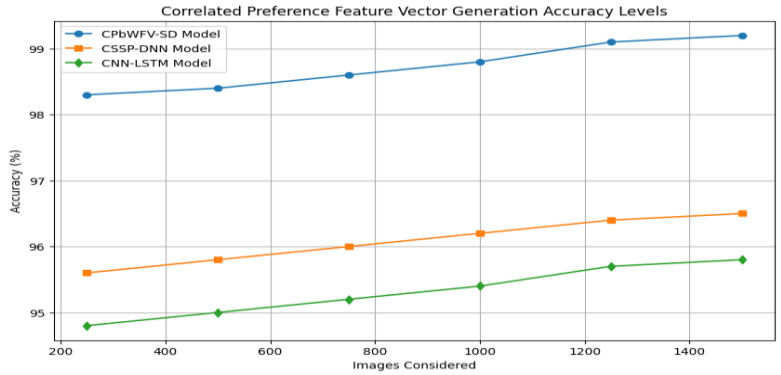

Fig 6: Correlated Preference Feature Vector Generation Accuracy Levels

As a technique in artificial neural networks, hidden layer kernel processing uses the hidden layers as kernel techniques to convert input data into representations in higher dimensions. In order for the network to learn the intricate, non-linear correlations present in the data, this transformation is vital. How inputs are altered as they flow through the network is dictated by the activation functions and weights assigned within the hidden layers, which determine the effectiveness of this process. The Hidden Layer Kernel Processing Time Levels are depicted in Table 4 and Figure 7.

Table 4: Hidden Layer Kernel Processing Time Levels

Images Considered	Models Considered		
	CPbWFV-SD Model	CSSP-DNN Model	CNN-LSTM Model
250	17.5	21.5	20.3
500	17.7	21.7	20.5
750	17.9	21.9	20.7
1000	18.2	22.0	20.9
1250	18.4	22.2	21.1
1500	18.5	22.4	21.3

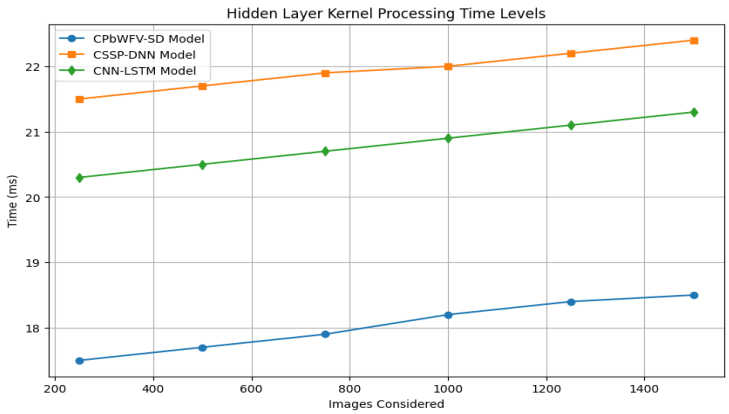

Fig 7: Hidden Layer Kernel Processing Time Levels

The ResNet model's distinctive architecture, a succession of residual blocks housing convolution and pooling layers allows it to extract progressively more complicated features, making it an excellent feature extraction tool. As a whole, the residual blocks help the network learn more complex patterns and correlations by

improving feature representations. Applications like image identification and classification greatly benefit from this hierarchical feature extraction method. The Table 5 and Figure 8 represents the ResNet Processing Accuracy Levels.

Table 5: ResNet Processing Accuracy Levels

Images Considered	Models Considered		
	CPbWFV-SD Model	CSSP-DNN Model	CNN-LSTM Model
250	98.4	95.9	95.3
500	98.6	96.0	95.5
750	98.8	96.2	95.7
1000	99.0	96.4	95.9
1250	99.2	96.6	96.0
1500	99.4	96.8	96.2

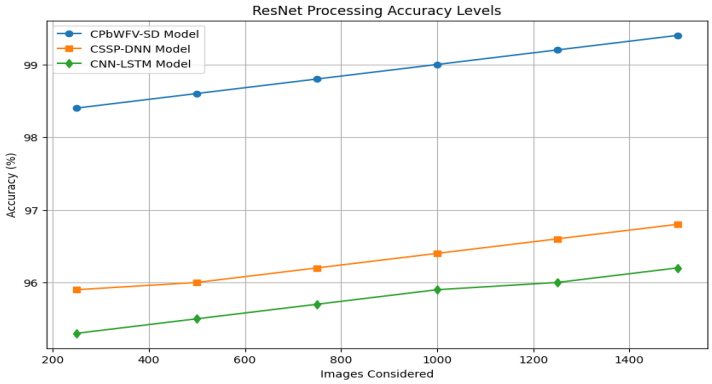

Fig 8: ResNet Processing Accuracy Levels

When comparing multiple data objects, it is crucial to compute their feature dissimilarity in order to quantify the differences between them. In order to find clusters, outliers, and trends in a dataset, this procedure is crucial. The features included in a dataset dictate the dissimilarity metric that is most appropriate. The Feature Dissimilarity Detection Time Levels are indicated in Table 6 and Figure 9.

Table 6: Feature Dissimilarity Detection Time Levels

Images Considered	Models Considered		
	CPbWFV-SD Model	CSSP-DNN Model	CNN-LSTM Model
250	16.1	18.6	20.4
500	16.3	18.7	20.6
750	16.4	18.9	20.8
1000	16.5	19.0	21.0
1250	16.7	19.2	21.3
1500	16.8	19.4	21.5

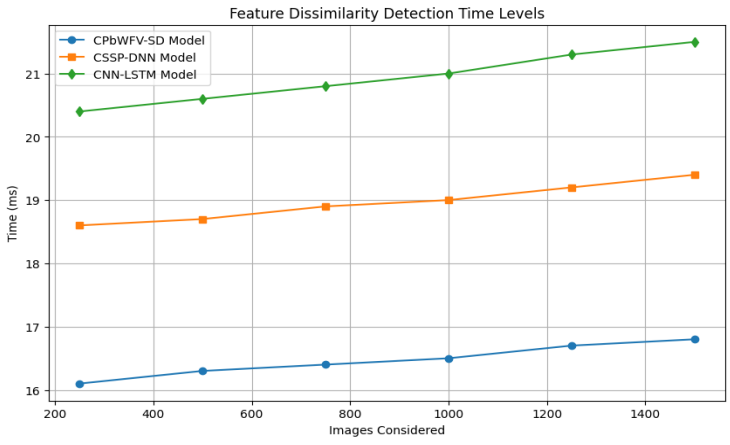

Fig 9: Feature Dissimilarity Detection Time Levels

The development of non-invasive methods that improve detection accuracy has led to innovations such as saliva-based diagnostics and tissue-fluorescence imaging. Oral cancer diagnoses are also being revolutionized by the use of AI in medical data analysis, which is leading to better early detection rates and overall results with accurate stage detection. The Table 7 and Figure 10 represents the Oral Cancer Stage Detection Accuracy Levels.

Table 7: Oral Cancer Stage Detection Accuracy Levels

Images Considered	Models Considered		
	CPbWFV-SD Model	CSSP-DNN Model	CNN-LSTM Model
250	98.3	95.5	94.3
500	98.5	95.7	94.5
750	98.8	95.9	94.7
1000	99.0	96.1	94.9
1250	99.2	96.3	95.0
1500	99.4	96.5	95.2

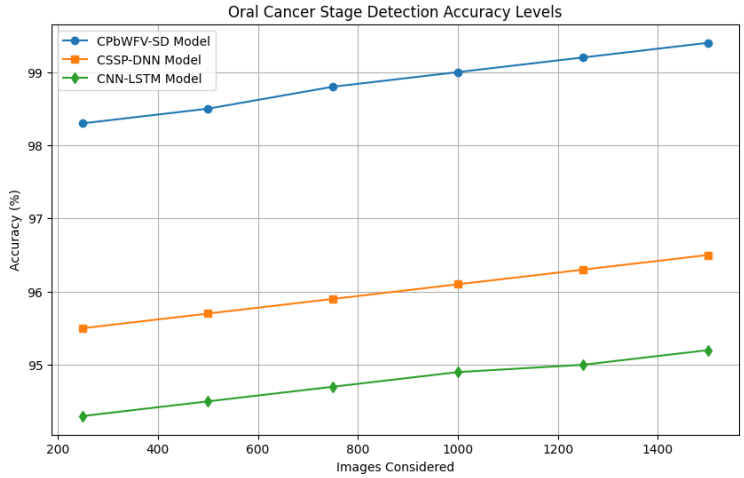

Fig 10: Oral Cancer Stage Detection Accuracy Levels

5. CONCLUSION

The best way to screen for oral cancer is with a comprehensive medical history and physical exam. The areas of the head, neck, mouth, and throat should be palpated and examined visually by the doctor. Digital palpation of nodes in the neck, bimanual palpation of the tongue and floor of the mouth, and examination of the oral and pharyngeal mucosa under good lighting conditions make up the process. Full visualization of the posterior lateral tongue and base requires forceful protraction of the tongue using gauze. The development of OSCC can be influenced by both internal and external factors, including nicotine, alcohol, malnutrition, and anemia. One of the OSCCs that can occur alongside or before OPMD is leukoplakia. Because of this, doctors must accurately classify oral lesions. Using a variety of deep learning methods that leverage recent advancements in deep learning, images of both normal and cancerous oral tissues can be predicted. Primary care doctors and dentists now have a non-invasive tool at their disposal with deep learning technologies that can detect oral pre-cancer and malignancy at an early stage. There have been major advancements in the diagnostic and therapeutic spheres in recent times. However, there is still a low overall survival rate linked to OSCC. Number staging classifies oral cancer into four distinct phases, numbered 1–4. Cancer is classified into four stages: early, intermediate, progressed, and terminal. Therefore, this research appropriately addresses the question of image classification as either normal or symptomatic of oral cancer with accurate stage detection. The proposed model achieved 99.4% accuracy in ResNet Processing and 99.4% accuracy in Oral Cancer Stage Detection. Experiment results show that ResNet50 can distinguish between oral cancer and non-cancerous images and accurate stage detection, and that experimental data and model prediction performance are highly correlated. The results back up the idea of a deep learning pipeline for screening oral cancer, which can automatically identify and categorize various oral lesions in real-time with little processing costs. Adding more examples of challenging lesion types to the dataset will be the focus of future research aimed at improving all of the models.

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