ResNet50-Driven Correlated Preference Weighted Features for Accurate Oral Cancer Stage Detection

ResNet50 based Oral Cancer Stage Detection

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Abstract. The eighth most frequent disease in the globe in India is oral cancer (OC), which kills 130,000 people every year. Oral cancerous tumors can arise in a variety of locations, such as the tonsils, salivary glands, neck, face, and mouth. Histological pictures are useful for cancer screening because they can find abnormalities and determine their prognosis. It is necessary to reduce the morbidity and mortality caused by mouth cancer, early detection of oral problems that could be cancerous. Misuse or over-reliance on features causes classification algorithms to absorb irrelevant data from images, resulting in inaccurate classifications. The deep learning model takes as input vectors the texture and deep features that are retrieved from these methods. The 50 stackable bottleneck residual pieces used in the ResNet-50 design are the basis of this research. First, the network's traditional convolutional and pooling layers preprocess the picture before the other blocks do any processing. For precise oral cancer stage detection, this study suggests a ResNet50-based Correlated Preference based Weighted Feature Vector (CPbWFV-SD). Train the model using the weighted feature vector; then, utilize the smallest change in the feature attribute set to determine the disease stage. When it comes to detecting the stage of oral cancer, the proposed model outperforms the conventional methods.

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

1 Introduction

As a subset of head and neck cancers, oral cancers are responsible for around 3% of all malignancies identified globally. According to a literature study, this cancer is the sixth most common cancer in the world [1]. The nasal passages, throat, and mouth are the most common sites of manifestation of this condition, which is primarily caused by chewing tobacco, betel nut, or cigarettes. The absence of training, clinical

R. Vasanth Kumar Mehta et al. (eds.), *Proceedings of the International Conference on Intelligent Systems for a Sustainable Future (ISSF 2026)*, Atlantis Highlights in Intelligent Systems 16,
https://doi.org/10.2991/978-94-6239-693-7_10

diagnostic resources, and oral cancer experts puts people in underdeveloped nations, particularly in South Asia, at a greater risk of developing the disease [2]. Discomfort with eating or speaking, sores or ulcers inside the mouth, and perhaps even noticeable facial marks are all signs of oral cancer [3]. The rapid development of oral squamous cell carcinoma (OSCC) is a potentially deadly consequence of the disease's rapid pace [4]. If these oral malignant tumors are caught early on, they have a far lower chance of turning into cancer. Research indicates that the recurrence rates of oral cancer are really high. In order to determine its prognosis, it is essential to conduct a comprehensive examination of its occurrence and course [5].

The prognosis rate for oral cancer was 35% to 50% according to a five-year survival study. According to the study's findings, the disease survival rate could be improved with a thorough investigation of all pertinent pathological factors [6]. That is why it is so important for pathologists to appropriately histologically categorize oral lesions. The oral cells provide a favorable environment for the development of oral cancer [7]. A malignant tumor develops when cancer cells congregate in one spot and acquire metastasis potential. Metastasis refers to the possibility of the cancer spreading to other organs or regions of the body [8]. Lymph nodes in the neck are the final destination for most mouth cancer metastases. Cancer of the mouth, throat, or oral cavity is another term for it. Occasionally, oral cells might undergo changes, abnormal development, or abnormal activity. Noncancerous growths like fibromas and warts can form as a result of these alterations [9]. Changes to the mouth's cells may cause precancerous diseases. Therefore, the aberrant cells aren't cancer just yet, but they may become cancer if left untreated. Leukoplakia and erythroplakia are the most common forms of oral precancerous disorders [10].

Early detection of oral cavity cancer (OCC) greatly improves patient survival rates [11,12]. Nevertheless, initial screening as it is now is both costly and time-consuming for the typical person, particularly in underdeveloped nations all over the globe. There is a severe lack of competence in these areas, which makes the problem worse. An efficient and cost-effective method of patient classification according to clinical necessity could be to automate the initial screening with AI to identify pre-cancerous lesions [13,14]. Oral Potentially Malignant Disorders (OPMD) lesions are the origin of almost 80% of oral cancers. OPMDs are the first indicator of various systemic and oral disease. The risk of malignant transformation can be significantly reduced with early detection of this OPMD. We have covered tongue lesions thus far. Different types of tongue lesions make it difficult to categorize OPMDs according to their likelihood of progressing to oral cancer [15]. The authors of this study suggest a ResNet50-based Weighted Feature Vector that is Correlated Preference based for precise oral cancer stage detection. Train the model using the weighted feature vector; then, utilize the smallest change in the feature attribute set to determine the disease stage.

2 Literature Survey

Chen et al. [1] tackled these problems by combining a DNN with a novel embedded feature selection approach. Impressively, the revolutionary Deep-learning algo-

rithm developed by Omar Bappi et al. [2] can identify and categorize early-stage cancer. Using 5,000 photos, the program classifies eight main cancer types and twenty-six subgroups. This approach incorporates state-of-the-art multimodal designs of linked CNN-LSTM hybrids, as well as machine learning, deep learning classifiers like KNN and SVM, and pre-trained Convolutional Neural Networks. The author used two distinct methods to arrange items into categories.

Convolutional neural networks (CNNs) and RNNs have demonstrated potential in this domain. Using the Aquila Optimization Algorithm with Deep Learning (LCDC-AOADL) method on neck area pictures, Alrowais et al. [3] introduced a new way to detect and classify laryngeal cancer. The LCDC-AOADL method shows promise for the detection and classification of laryngeal cancer through the evaluation of histopathology pictures. For feature extraction, the offered LCDC-AOADL method makes use of the Inceptionv3 model. Abdollahi et al. [4] looked into the different kinds of tumors that have a similar pattern of trinucleotide mutations. Further, the author discovered important mutational markers for different tumors using NMF. Analyzing the prominent signatures of the target cancer will allow us to find genes associated to the disease. The author assessed the genes involved in cancer by looking at survival and gene expression data from various stages of the disease.

3 Proposed Model

The primary goal of feature extraction is to improve the performance of the classification algorithm by feeding it with the most relevant features. This study proposes a method to improve the precision of histopathology picture categorization by combining feature extraction and selection. The four main parts of the ResNet50 architecture are the fully linked layers, the identification block, the convolutional blocks, and the convolutional blocks. In order to process and alter the features extracted from the input image by the convolutional layers, the identity block and convolutional block work together. The Figure 1 shows the proposed model architecture.

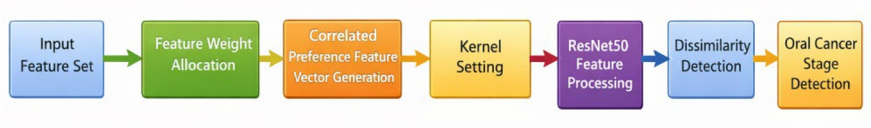

Fig.1. Proposed Model Framework

For precise oral cancer stage detection, this study suggests a ResNet50-based Correlated Preference based Weighted Feature Vector (CPbWFV-SD). Train the model using the weighted feature vector; then, utilize the smallest change in the feature attribute set to determine the disease stage.

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

$$FeatP[N] = \sum_{k=1}^{N} getFeaset(k) + \lim_{k \to N} \left(\phi(k, k+1) + \frac{\psi(k, k+1) * \theta(k)}{len(Feaset)} \right)^{\eta}$$

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.$\phi$is the model that considers the highest range of values from the prefixed Threshold value and $\psi$is the lowest value than the threshold value.η is the balancing factor value.

Step-2: The feature weight allocation is performed as

$$FW[N] = \sum_{k=1}^{N} \max\left(FeatP(k)\right) + \theta\left(\varepsilon(k, k+1)\right) + \theta(\kappa(k, k+1) + \frac{\rho\ (FeatP(k))}{len(FeatP)} \begin{cases} FW \leftarrow setVal(Z) & if\ \rho\ (k) > CFT \\ FW \leftarrow 0 & Otherwise \end{cases}$$

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

Step-3: The correlated preference feature vector generation is performed as

$$CPFV[N] = \sum_{k=1}^{N} getmax\left(FW(k)\right) + \frac{\sum_{k=1}^{N} (FW(k) - \overline{FW(k)})(FW(k) - \overline{FW(k)})}{\sqrt{\sum_{k=1}^{N} (FW(k) - \overline{FW(k)})^2} * \sqrt{\sum_{k=1}^{N} (FW(k+1) - \overline{FW(k+1)})^2}} + \varepsilon(FW(k)$$

Step-4: 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

$$KerSet[N] = \sum_{k=1}^{N} \lim_{k \to N} \left(CPFV(k) + \frac{\lambda(CPFV(k,k+1))}{FW(k)} \right)^2 + \frac{S+2k-Z+D}{N}$$

Here λ is the model for setting the kernel size and S is the input feature size, f is the feature considered and Z is the size of the convolution and D is the padding performed in convolution model.

Step-5: The output feature map OPF for a set of features CPFV, at position x,y is calculated as

$$OPF(x, y) = \sum_{a=1}^{S} \sum_{b=1}^{a} FW(b) * FW(k, k+1) + c$$

Here FW is the feature weight set, $FW(k, k+1)$is the input set of features, c is the bias and S is the kernel size. The batch normalization is performed as

$$\bar{\imath} = \frac{k - \mu}{\sqrt{\eta^2 + \varepsilon}}$$

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

$$y(r,s) = \sum_{k=1}^{N} \max_{(k,k+1)\varepsilon\bar{\imath}} x(r+k, s+k+1)$$

Step-6: 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.

$$Stgset[N] = \sum_{k=1}^{N}\sum_{r=1}^{k} \frac{\max(z(k,k+1))}{M} + \lambda(OPF(k)) + \max(\lambda(OPF(z,z+1))) + \max(diff(z(k,k+1)) \begin{cases} Stgset \leftarrow Val & if \max(diff(k)) > STh \\ 0 & Otherwise \end{cases}$$

}

4 Results

In order to make use of the morphological and textural information that was extracted from the patches, the ResNet50 model was trained on a dataset of 2000 photographs. After applying contrast enhancement to each input image, a collection of overlapping patches with 50% coverage is extracted. A subsequent step involves selecting four areas with a high nucleus density. Google Colab is used to run the model that is implemented using the Python programming language. At https://www.kaggle.com/datasets/zaidpy/oral-cancer-dataset, you can find the dataset in question. We compare the proposed CPbWFV-SD, which uses ResNet50 for accurate stage detection, to two existing methods: CSSP-DNN, which uses drop feature DNNs for effective cancer subtype and stage prediction. Figure 2 display the levels of accuracy for the generation of the Correlated Preference Feature Vectors.

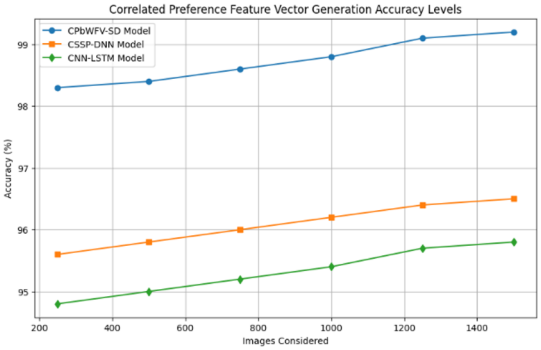

Fig.2. Correlated Preference Feature Vector Generation Accuracy Levels

Hierarchical feature extraction is a powerful tool for applications like picture recognition and categorization. Figure 3 show the levels of accuracy for ResNet processing.

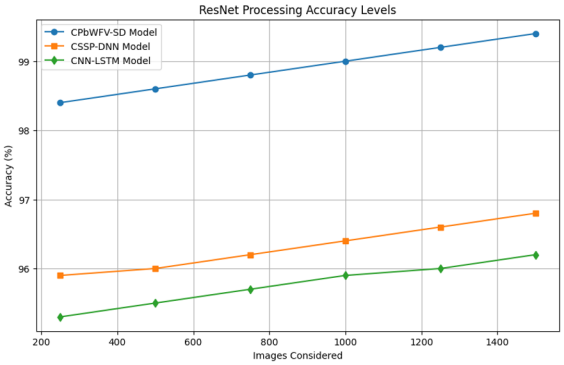

Fig.3. ResNet Processing Accuracy Levels

The application of artificial intelligence (AI) to the analysis of medical data is also transforming the way oral cancer is diagnosed. This is resulting in more accurate stage identification and higher rates of early diagnosis. Oral cancer stage detection accuracy levels are shown in Figure 4.

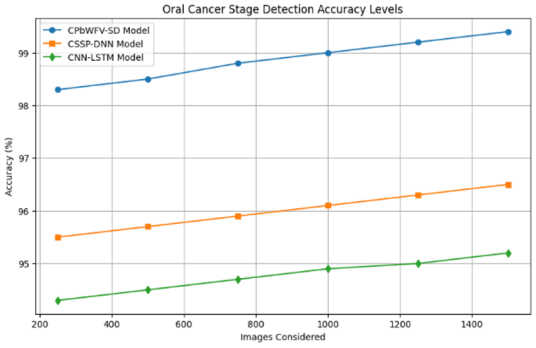

Fig.4. Oral Cancer Stage Detection Accuracy Levels

5 Conclusion

Oral cancer screenings should always begin with a thorough medical history and physical examination. It is important for the clinician to view and palpate the areas of the neck, mouth, and throat. There are four distinct phases of cancer: early, middle, advanced, and terminal. Image classification as normal or indicative of oral cancer with accurate stage detection is thus an appropriate subject that this research effec-

tively addresses. Both the ResNet Processing and Oral Cancer Stage Detection metrics were hit by the suggested model, which reached 99.4 percent accuracy. The findings of the experiments demonstrate that ResNet50 is capable of accurately detecting stages of oral cancer and non-cancerous images, and that there is a strong correlation between the experimental data and the model's prediction ability. These findings provide credence to the concept of a deep learning pipeline that might detect and classify different types of oral lesions in real-time with little processing costs, making it an ideal tool for screening oral cancer. Future study will focus on enhancing all of the models by adding more examples of hard lesion types to the dataset.

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