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Mohd Hafiz Arzmi · Anwar P. P. Abdul Majeed ·  
Rabiu Muazu Musa · Mohd Azraai Mohd Razman ·  
Hong-Seng Gan · Ismail Mohd Khairuddin ·  
Ahmad Fakhri Ab. Nasir

# Deep Learning in Cancer Diagnostics

A Feature-based Transfer  
Learning Evaluation

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A Feature-based Transfer Learning Evaluation

# Chapter 2

## A VGG16 Feature-Based Transfer Learning Evaluation for the Diagnosis of Oral Squamous Cell Carcinoma (OSCC)



**Abstract** Oral Squamous Cell Carcinoma (OSCC) is the most prevalent type of oral cancer. Early detection of such cancer could increase a patient's survival rate by 83%. This chapter shall explore the use of a feature-based transfer learning model, i.e., VGG16 coupled with different types of conventional machine learning models, viz. Support Vector Machine (SVM), Random Forest as well as  $k$ -Nearest Neighbour ( $k$ NN) as a means to identify OSCC. A total of 990 evenly distributed normal and OSCC histopathological images are split into the 60:20:20 ratio for training, testing and validation, respectively. A testing accuracy of 93% was recorded via the VGG16-RF pipeline from the study. Consequently, the proposed architecture is suitable to be deployed as artificial intelligence-driven computer-aided diagnostics and, in turn, facilitate clinicians for the identification of OSCC.

**Keywords** Computer-Aided Diagnosis · Transfer Learning · Oral Cancer · OSCC

### 2.1 Introduction

It has been reported that oral cancer has the sixth highest occurrence amongst the different types of cancers [1]. The lack of early detection of this form of cancer contributes to a high mortality rate. Nonetheless, it is worth noting that Oral Squamous Cell Carcinoma (OSCC) accounts for more than 90% of oral cases. More often than not, smoking and the consumption of alcohol are deemed to be the main causes of OSCC [2]. As remarked earlier, early detection could allow patients to seek life-prolonging treatments. Traditional means of diagnosing such ailments by oncologists are rather labour-intensive, however, with the aid of computer-aided diagnostics (CAD) powered by artificial intelligence, the aforesaid predicament could be alleviated. Researchers have developed different deep learning architectures for diagnosing normal and malignant characteristics of oral cancer, especially OSCC.

Palaskar et al. [3] compared the efficacy of different transfer learning models, namely ResNet50, InceptionV3 and MobileNet against two conventional Convolutional Neural Network (CNN) models, dubbed as Large CNN and Small CNN in diagnosing histopathological OSCC images. Different sampling technique was

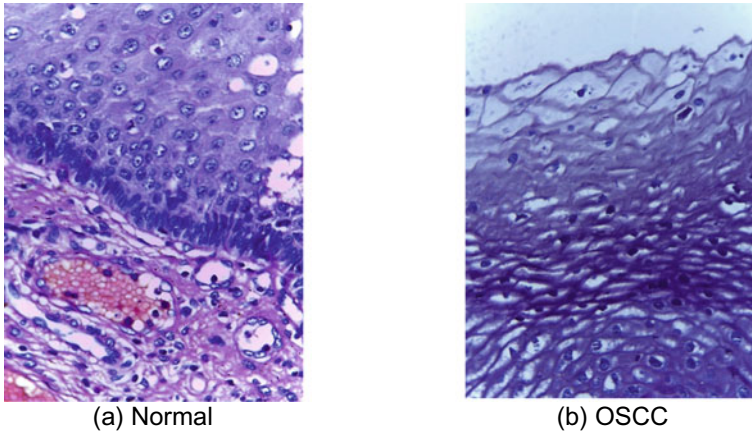
investigated to handle the imbalanced dataset. It was shown from the study that the InceptionV3 transfer learning model is able to classify better against the other evaluated models with a multi-site testing result of 83.66%.

In a recent study, Amin et al. [4] investigated the efficacy of concatenating different transfer learning models, i.e., VGG16, InceptionV3 and ResNet50 and comparing it with its individual models in classifying OSCC. A similar dataset employed by Palaskar et al. that was published by Rahman et al. [5] was used in the study. Hence, owing to the imbalanced dataset, the authors augmented it by oversampling. A total of 120 images was used as a testing dataset and it was shown from the study that the concatenated pipeline outperformed the individual models.

Abdul Rauf et al. [6] evaluated the performance of the InceptionV3 transfer learning model as a feature extractor whilst classifying OSCC images using Support Vector Machine (SVM),  $k$ -Nearest Neighbours ( $k$ NN) and Random Forest (RF) classifiers. It was shown from the study that the InceptionV3-RF pipeline demonstrates a test classification accuracy of 91%, in demarcating the normal and OSCC classes, suggesting that the proposed architecture has an attractive proposition. In this chapter, a feature-based transfer learning approach [7–9] by considering the VGG16 pre-trained CNN model with its fully connected layers replaced by the SVM,  $k$ NN and RF classifiers in the classification of OSCC is investigated.

## 2.2 Methodology

In this study, the histopathological images of the normal and OSCC tissue are obtained from an open-access repository curated by Rahman et al. [5]. It is worth noting that for the present study, the  $400\times$  magnified image set is used. This set contains 201 normal oral cavity images and 495 OSCC images. Owing to the imbalanced nature of the dataset, the normal images were oversampled to equate the total number of the OSCC images, therefore a total of 990 images was used in the study. A sample of the images from the two classes is shown in Fig. 2.1. The proposed architecture in the present investigation is a departure from a typical transfer learning pipeline, i.e., the fully connected layers are swapped with a conventional machine learning model [10, 11]. The features from the VGG16 pre-trained CNN model is then fed to the SVM,  $k$ NN and RF classifiers with its hyperparameters set to default from the scikit-learn library. The analysis was carried out using a Python IDE, namely Spyder 3.3.6, along with its associated Keras 2.3.1 and TensorFlow 1.14.0 libraries in evoking the VGG16 model. The performance of the pipelines is evaluated via the classification accuracies as well as the confusion matrix.



**Fig. 2.1** Histopathological images for (a) Normal tissue (b) OSCC tissue

## 2.3 Results and Discussion

The performance of the evaluated pipelines is shown in Fig. 2.2. It is apparent that the VGG16-RF pipeline outperformed the other pipelines evaluated across all datasets. The VGG16-SVM pipeline performs reasonably well with a reduction of 3% in testing accuracy. The worst performing pipeline is the VGG16- $k$ NN pipeline, suggesting that the default  $k$ NN classifier is unable to discern well the features extracted by the VGG16 model from the histopathological images. A similar observation with regards to the  $k$ NN model is reported in [6] from the features extracted via the InceptionV3 model. The confusion matrix on the test dataset of the evaluated pipelines is depicted in Fig. 2.3. The normal and OSCC classes are denoted as 0, and 1, respectively. It could be seen that no misclassification transpired on the N class across all pipelines. It could be seen that only five of the normal tissues are diagnosed as OSCC for the RF-based pipeline, whilst both the SVM and RF pipelines misdiagnosed six OSCC as normal. Considering the small fraction of misclassification, the proposed pipeline if deployed could significantly facilitate oncologists in the diagnosis of OSCC.

## 2.4 Conclusion

The chapter has demonstrated that the proposed architecture is able to discern the classes of normal and malignant oral tissue reasonably well, particularly the VGG16-RF pipeline. The deployment of such a model could facilitate oncologists in the diagnosis of OSCC, which is undoubtedly one of the most prevalent types of oral cancer.

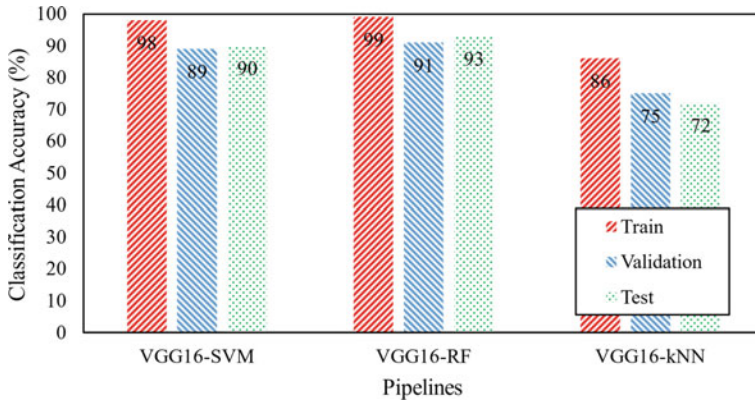


Fig. 2.2 The performance of the different VGG16 pipelines evaluated in terms of classification accuracy

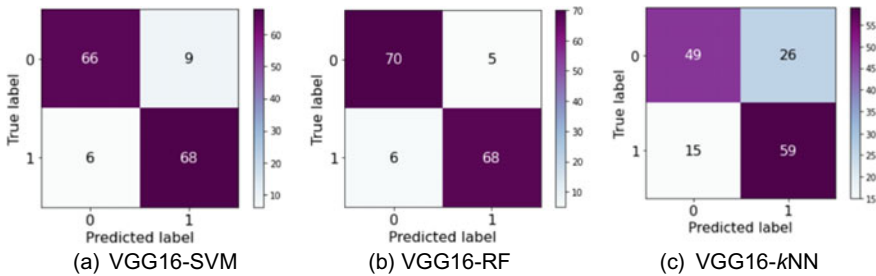


Fig. 2.3 The confusion matrix of pipelines on the testing dataset

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