Normal and Neoplastic Salivary Gland Segmentation Using Machine Learning

<u>Ibrahim Alsanie</u>,^{1,2} Eu-Wing Toh,³ Syed Ali Khurram,¹

- ¹Unit of Oral and Maxillofacial Pathology, School of Clinical Dentistry, University of Sheffield.
- ² Department of Oral Medicine and Diagnostic Sciences, College of Dentistry, King Saud University.
- ³ Department of Histopathology, Royal Hallamshire Hospital, Sheffield Teaching Hospitals NHS Foundation Trust.





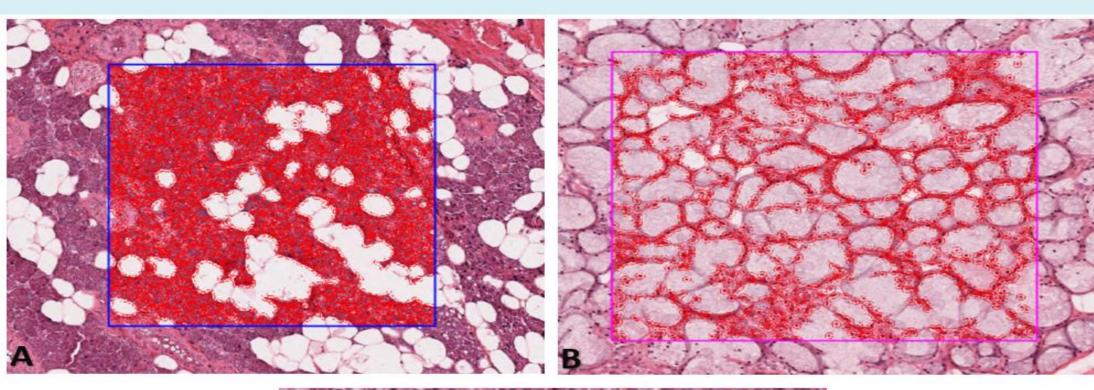


Introduction

- The advent of digital pathology and availability of whole slide images (WSI) has allowed the application of artificial intelligence (AI) and machine learning (ML) to pathology, supported by advancements in computing power and technology. (1)
- Numerous studies have used AI/ML to differentiate between normal and cancerous tissues (2,3,4), such as breast cancer, but its usefulness in salivary gland tumours remains unexplored.
- The aim of this pilot study was to use ML for differentiation between normal salivary gland tissue and salivary gland tumours.

Methods

- Normal salivary gland tissue and salivary gland tumours (SGT) of both benign and malignant were used.
- 90 WSI were used for training and testing in 70 /30 split.
- 60 WSI were used for training and 30 unseen WSI were used to test and validate the classifier and to perform automated analysis and quantification of features.
- An open-source image analysis software (QuPath) was employed, and the representative areas classified into three different classes including normal serous gland, normal mucous gland and tumour.
- Classifier performance was measured using metrics of accuracy, precision, recall and F1 score.



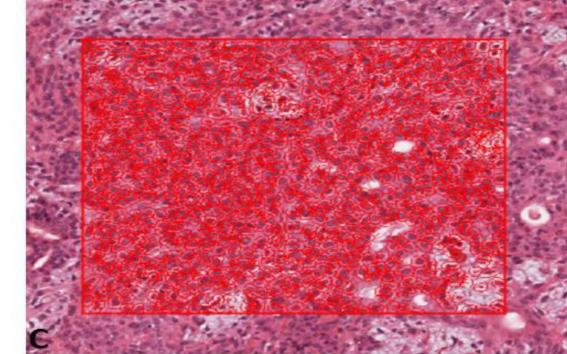


Figure 1: QuPath training set of normal glands serous and mucous as well as tumour. A- blue boxes representing serous gland, B- pink boxes representing mucous section and c- red boxes representing tumour areas.

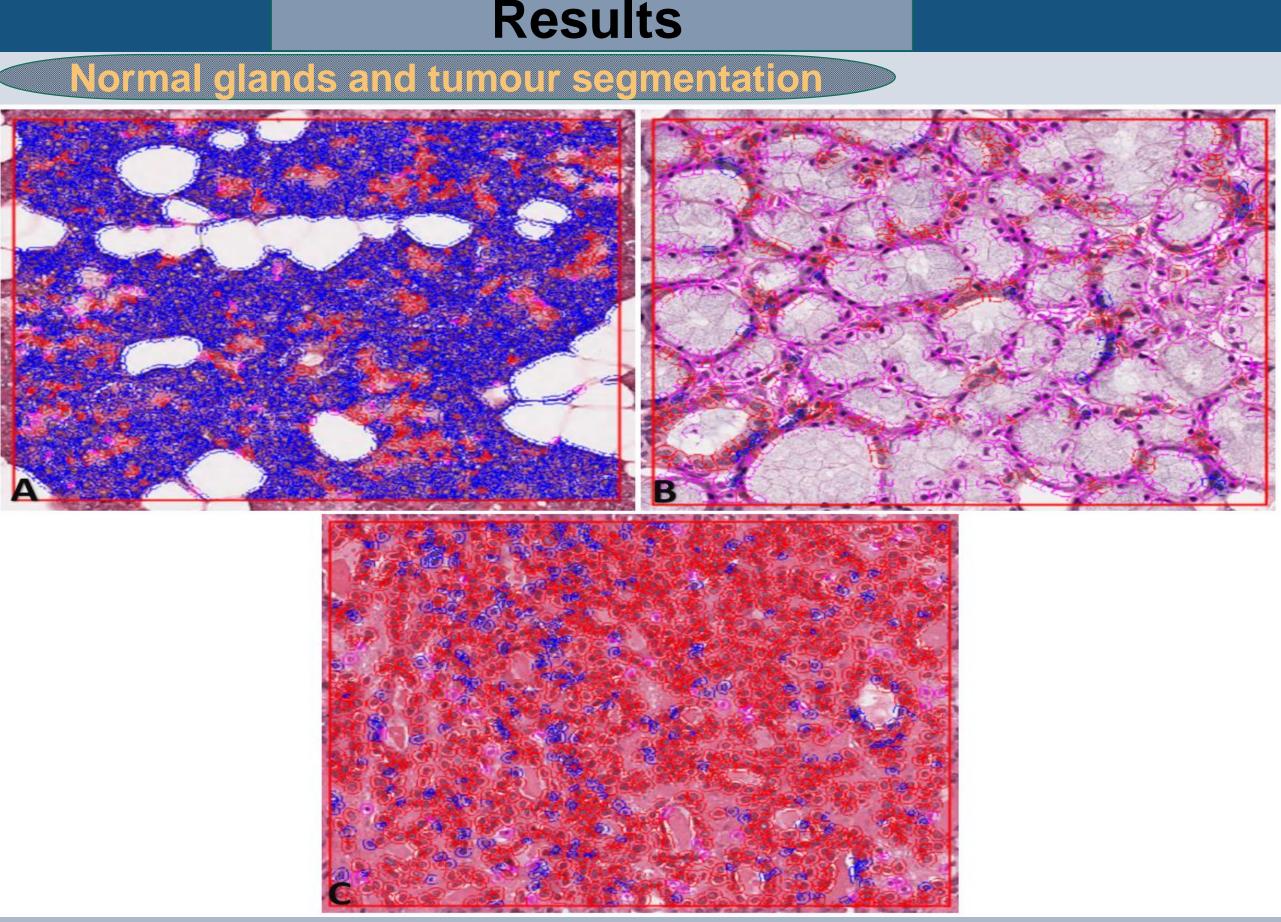


Figure 2: QuPath ROI automatic cell segmentation using trained classifier. A- Blue areas (normal serous gland), B- pink areas (normal mucous gland), C- red areas (tumour)

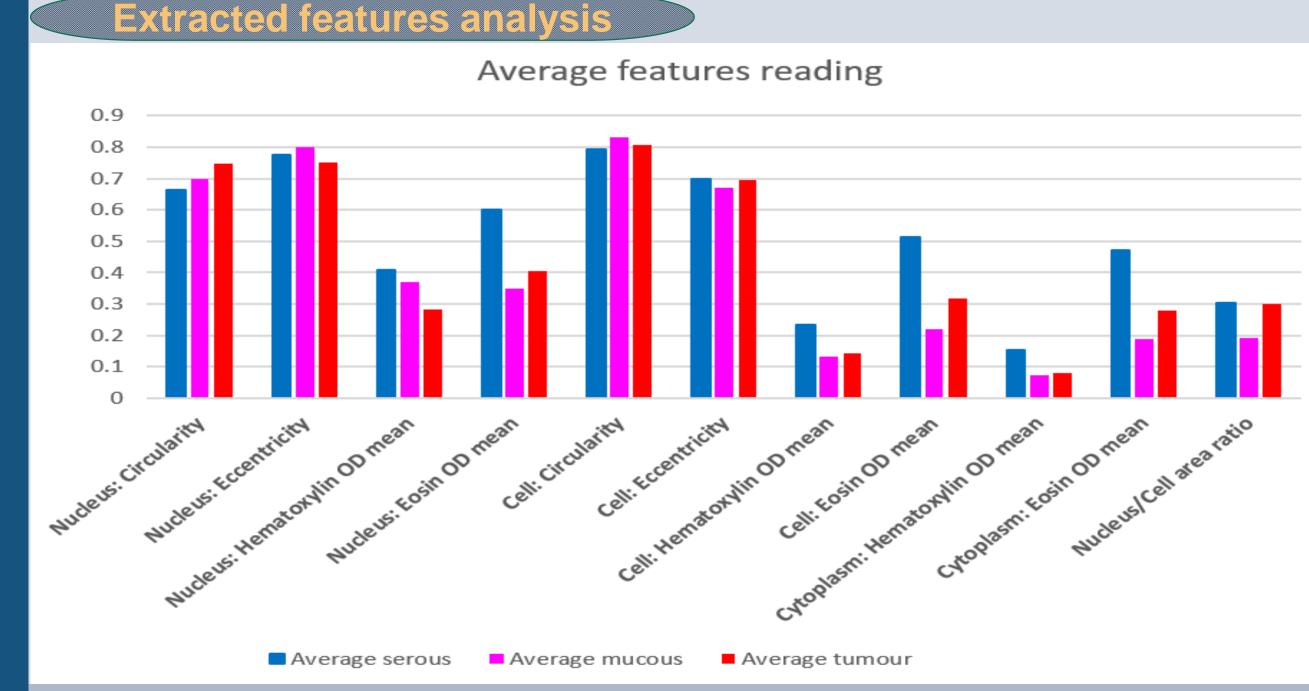


Figure 3: Plot of average reading of extracted features of the test set exported from QuPath for the serous, mucous and tumour classes.

Algorithm performance metrics

Table 1: Segmentation accuracy of the algorithm for the serous, mucous and tumour classes with average reading of 10 WSIs of each class.

classes with average reading of 10 WSIs of each class.				
Cell detection	Serous section	Mucous section	Tumour section	
Serous gland	4447		917	
detections		219		
Mucous gland	164	3572	955	
detections				
Tumour detection	472	888	4131	
Total number of			6003	
detections	5083	4679		
Accuracy	87.4%	76.3%	68.8%	

Table 2: Algorithm performance of the serous, mucous and tumour classes using precision, recall and F1 score.

Precisions	Recall	F1 score
0.775	0.769	0.770

Normal and tumour features analysis

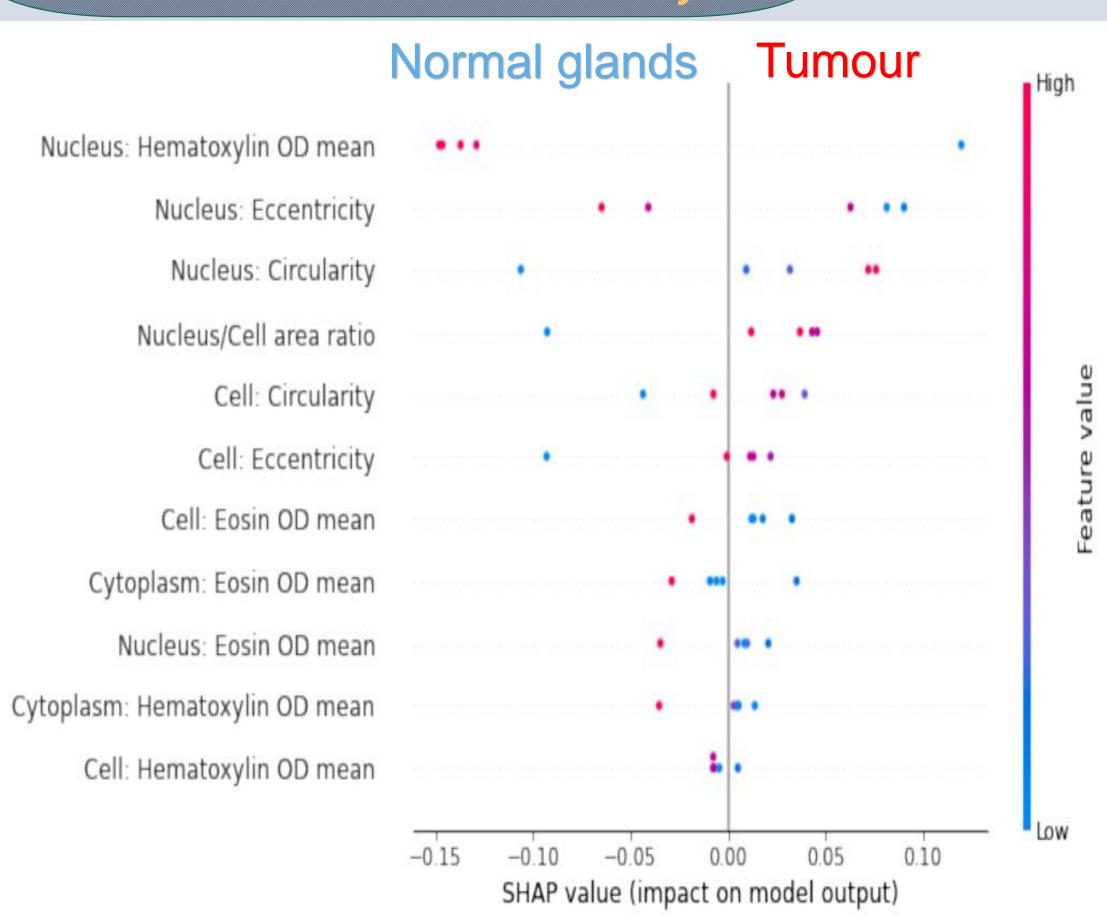


Figure 4: SHAP analysis plot of the extracted features showing that top features were impacted the algorithm judgment towards certain class more. Greater than 0 value on x-axis representing tumour while value less than 0 representing both normal glands. Features are sorted in descending order of their impact on the algorithm.

Conclusion

- Al has enormous potential to aid diagnosis and improve patient care, and our novel data show that Al can be used for analysis and differentiation between normal salivary glands and SGT.
- A larger cohort needs to be analysed to determine the true significance of these findings.

Acknowledgments

Saad Bashir (TIA Centre, University of Warwick) King Saud University, KSA.

References

