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Using Artificial Intelligence for Salivary Gland Tumours Subtyping and Risk Stratification

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Summary:

Salivary gland tumours (SGTs) present a diagnostic challenge with over 35 subtypes and a significant overlap in features. Most cases require extensive immunohistochemistry, molecular testing and expert opinions for diagnosis. Most of the markers used in routine practice only aid diagnosis with limited information about prognosis. Furthermore, some of these investigations are only available at a few specialist centres limiting their wider adaptation.

Artificial Intelligence (AI) can obtain 'big data' from whole slide images (WSI) and quantify vast amounts of information about morphological/spatial patterns to discover novel digital biomarkers. However, the use of AI for salivary tumour analysis remains unexplored. We aim to develop AI algorithms for automated differentiation between salivary tumours, predict prognosis and objectively quantify pathological variables on digitally scanned histology images.

Scanned WSI will be used in addition to other relevant stain information. Following initial training of the algorithm, semi-automatic annotations will be performed on further cases. A WSI will be used as an input and segmented/classified it into different regions (i.e. normal, tumour, mitoses, stroma, immune cells, etc.). Each region will be used to extract features that prove significant in the training phase. A random forest classifier will be used to predict the presence of features, and behaviour of the lesion. The optimised algorithm will be applied to the validation/testing cohort to determine accuracy and specificity. Correlation with prognosis will be determined using follow-up data. The potential to predict prognosis will be analysed using survival analyses (e.g. Kaplan-Meier, Hazard Proportion, Random Forest).