

Project Title	Automatic quantification of fungal burdens in histology images using deep neural networks
Supervisor	Dr Reiko Tanaka
Theme(s)	Computational and theoretical modelling
Project Type	Desk Based
Project Description	<p>Invasive aspergillosis (IA) is a critical lung disease that is characterised by uncontrolled fungal growth of <i>Aspergillus fumigatus</i> in the lungs. IA occurs in immunocompromised patients, such as patients undergoing chemotherapy, and is treated with antifungal drugs. Due to the increase of antifungal resistance, there is a real need to locate novel treatments.</p> <p>Experiments investigating new IA treatments usually evaluate treatment responses by reported fungal burden. However, the fungal enumeration methods in the community are not standardised, resulting in different quantifications of pulmonary fungal burden, making quantitative evaluation of disease progression often challenging. Quantifying fungal burden in murine models of infection remains a difficult task. The most accurate and sensitive qPCR-based methods cannot capture fungal viability. As a result, the community relies on less sensitive metrics such as conidial forming units (CFUs), which require comparison with histology images. Histological images of murine lung biopsies can give us an idea of disease progression caused by viable fungal burden. However, enumeration of fungal burden, extent of tissue invasion and occlusion of the airspaces is still done manually.</p> <p>Recently, we proposed a fully automated image analysis pipeline to identify the fungal regions on histological images. The histology images are first transformed into different colour space channels that preserve fungi-related colour information. After applying image enhancement methods to accentuate the fungal regions' pixel intensity, the pixels are clustered by their intensity values to identify the fungal region in the image. The results broadly show good agreement with the reference annotations, achieving an average Dice score of 65% across 5-fold cross-validation with an 80/20 train/test split of a dataset of 33 images.</p> <p>This project aims to further improve this pipeline by utilising deep neural networks to automatically detect and classify fungal lesions into "spores" and "hyphaes" and subsequently enumerate them (number of spores and hyphae length). The student is expected to review, implement, and validate the different stages of the image analysis pipeline using off-the-shelf deep-learning and image analysis software packages for segmentation, classification and quantification of "spores" and "hyphae" regions.</p>