**Quantitative analysis of idiopathic pulmonary fibrosis abnormality from CT imaging**

Zhang, Y.1, Clark, A.R.1, Kumar, H.1, Bartholmai, B.J.2, Tawhai, M.H.1

1Auckland Bioengineering Institute, University of Auckland, Auckland, NZ, 2 Department of Radiology, Mayo Clinic, Minnesota, US.

Idiopathic pulmonary fibrosis (IPF), the most aggressive and frequent form of idiopathic interstitial pneumonias, is a chronic and life-threatening disease of unknown cause. It occurs primarily in middle-aged and elderly adults and more than 200 cases per 1000,000 people over 75 years old are estimated to suffer from IPF. Even worse, the aetiology of IPF remains elusive, and its progression is variable and unpredictable, hence there are no biomarkers that indicate the likely progression of the disease. A successful classification scheme that allows recognition of disease identically across radiology, pulmonary and pathology disciplines still remains difficult.

High-resolution computed tomography (HRCT) has played an essential role in evaluating lung disease through recognizing visual patterns and features of disease regions. In this study, we aim to analyze and characterize IPF tissue abnormalities over time using quantitative methods. The clinical data used in this study comprised HRCT images obtained from 8 patients diagnosed with IPF, and four of them included more than one time point. Tissue regions of HRCT images were classified using CALIPER (Computer-Aided Lung Informatics for Pathology Evaluation and Ratings) software. The classified data was mapped to a statistical shape model, which allows a reliable comparison between different patients or within one patient of different time points. Quantitative approaches was used to analyze tissue density, tissue volume, the spatial distribution of abnormalities, and regional changes in tissue over time. The tissue density, tissue volume and the location of abnormality are all important indexes for representing a quantitative statistical progression of IPF disease. This quantitative analysis would provide consistent potential tissue-level markers to help with the further modeling of mechanical ventilation/perfusion mismatch and impaired gas exchange.