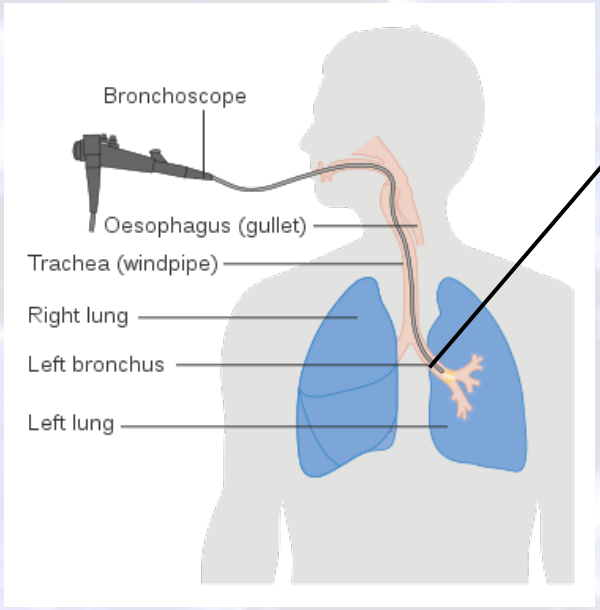
Transcriptional analysis of the local immune response in Community Acquired Pneumonia (CAP)

Background

- Community acquired pneumonia (CAP) is a pathogen-driven inflammatory process that occurs in the lower respiratory tract and impairs lung function.
- It is associated with high mortality and morbidity in Australia and worldwide. The most common causative agents for CAP are bacteria, followed by viruses.
- CAP is diagnosed within 48 hours of hospital admission and is defined based on examination of patient history, biomarker evidence of infection and chest radiography.
- While immunological processes have been classically studied from the peripheral blood, in this project we will study the localized immune response by studying bronchoalveolar lavage (BAL) fluid from intubated patients with CAP in the Intensive Care Unit (ICU), and controls.
- The research aim for this honors project is to determine the localize immune and epithelial transcriptome in CAP patients.
- The project will involve extraction of RNA from BAL samples and RNA expression profiling using Nanostring 770-plex “Immunology gene panel”. We will then conduct bulk RNA sequencing which will be predominated by epithelial signals determined using bioinformatics tools such as gene enrichment analysis.
- Ultimately, we plan on defining what constitutes a superior response to CAP versus a poor localized immune response. Such insights may have important implications for patient prognosis, risk stratification and the development of novel treatment strategies.

Methodology



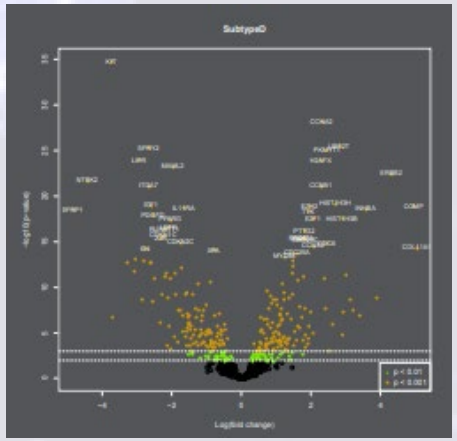
BAL fluid from 3 patient groups:

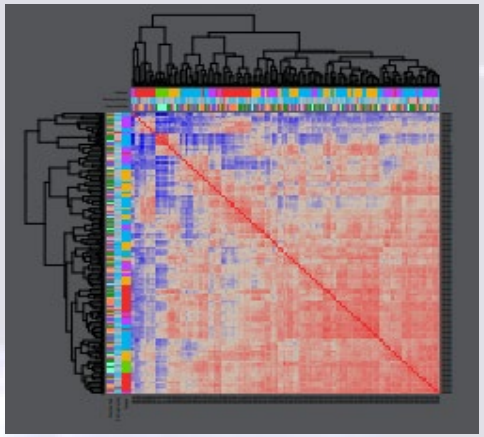
1) **CAP (bacterial and viral)**
2) **Systemic inflammation no primary lung disease e.g. pancreatitis, trauma**
2) **Intubated with no inflammation or infection e.g. neurosurgical patients**

RNA extraction and Nanostring

Data analysis using bioinformatics pipeline

Analysis





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