



THE UNIVERSITY OF
MELBOURNE

Faculty of Medicine,
Dentistry and Health
Sciences

Colorectal Oncogenomics Group

Identifying and investigating subtypes of colorectal cancer.

The Colorectal Oncogenomics Group's research program is focused on the identification of clinically and biologically relevant subtypes of colorectal cancer including hereditary colorectal cancer and polyposis syndromes. The Colorectal Oncogenomics Group uses genomic, epigenomic and transcriptomic profiling integrated with immune cell profiling, histopathological characterisation, environmental/lifestyle risk factors and clinical data to determine the underlying aetiology of colorectal tumourigenesis so that greater steps can be made towards personalised risk stratification for early detection and prevention of this disease.

Opportunity for Honours or Masters:

The Medical Genome Reference Bank as a population control for germline variants in colorectal and prostate cancer

Rare germline DNA variants play an important role in the risk of developing many kinds of cancer. However, the genetic factors influencing the inherited component of cancer risk remain poorly understood. Addressing the "missing heritability" of cancer risk, many cancer research projects are employing whole genome sequencing (WGS) to interrogate the genetic make-up of individuals at very high resolution, however this also yields large numbers of rare variants that can be difficult to interpret in isolation. Population control groups can provide estimations of the prevalence and distribution of DNA variants and can therefore yield useful insights into disease association of individual variants and disease-related genes/pathways. In this project, we propose to use the Medical Genome Reference Bank (MGRB) as a

population control for germline variants in our colorectal and prostate cancer studies. Specifically, we propose to compare the frequency and distribution of germline DNA variants between cohorts of colorectal and prostate cancer patients (including cancer subtypes) against the individuals within the MGRB. We aim to be comprehensive in our consideration of variant types including single nucleotide variants, small insertions and deletions, copy number variants, structural variants, and microsatellite polymorphisms from both nuclear and mitochondrial DNA.



Contact us

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