

Applying long-read sequencing technologies to cancer genomes

Project Description

Project duration:	Can accommodate various project durations (PhD, MPhil, Hons)
Description:	Tumour genomes are frequently highly rearranged relative to the corresponding non-tumour genome along with aberrant CpG methylation and gene regulation. Current second-generation sequencing technologies are limited in their ability to resolve genome and transcript structure as well as interrogate genome-wide methylation status. Long-read third-generation sequencing technologies mark a significant improvement in our ability to address these issues and better understand tumour biology. This project will aim to develop and apply novel computational methods for studying tumour rearrangements and aberrations in genome-wide regulatory status in epithelial solid tumours.
Expected outcomes and deliverables:	You will learn about sequencing technology, both in terms of methods for generating data and methods for analysing data. You will further your background in software development, learn how to apply computational methods in genomics, or learn to use existing command-line tools to analyse genomics data depending on your background and specific details of the project.
Suitable for:	Ideally you should have a computational or quantitative background with a working knowledge of genomics. For some students, a background in genetics or genomics and a desire to improve upon their computational background would also be suitable.
Primary Supervisor:	Adam Ewing
Further info:	adam.ewing@mater.uq.edu.au You should contact me prior to submitting an application to discuss your background and areas of interest.