2015/2016 Summer Studentship Project Application Form

Send to: Research Office, University of Otago Christchurch, PO Box 4345, Christchurch, by 5pm on **3 July 2015**

Supervisor Information (First named supervisor will be the contact):	
Supervisor's Name and Title(s): Prof. Martin A Kennedy	
Department: Pathology	Institution: UOC
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Mailing Address:	

Research Category (Choose one category only – to be used for judging the students' presentations):		
	Laboratory	

Project Title (20 words MAXIMUM):

Nanopore sequencing of repeat sequences in human DNA

Project Description:

Introduction:

The MinION nanopore DNA sequencer is a tiny device with extraordinary characteristics. It has the ability to perform high throughput single-molecule sequencing of very long DNA fragments, and it is rapid and relatively simple to set up and run. Although the device has not yet been commercially released, Prof. Kennedy's laboratory has been part of the MinIon Access Programme (MAP) since mid-2014, and has been exploring potential applications for nanopore sequencing since then.

The MinIon offers the possibility of rapid DNA diagnostics and novel applications for research into various genetic disorders. We are interested in using the device to count repeat elements in DNA, including regions involved in neurological disorders such as Huntington disease, Fragile X syndrome, and myotonic dystrophy, as well as examining repeat sequence elements such as microsatellites which may be important regulatory elements in the genome, and telomeres found at the ends of chromosomes. These elements are all of relevance to human disease, but are often difficult to quantify by conventional methods.

Aim:

This project seeks to explore and evaluate the ability of the MinION nanopore sequencer to correctly read and quantify a variety of human repeat DNA tracts.

Method:

The project will begin with PCR amplification of a range of selected repeat tracts from anonymous human DNA. These tracts will include repeat regions involved in human neurological disease, as well as other simple repeat tracts such as microsatellites or VNTR loci. Once a range of these amplicons have been generated, they will be checked by Sanger sequencing, then prepared and run in parallel on the MinION sequencer. These analyses will be supplemented by inclusion of plasmids which contain cloned repeat tracts of known length. Multiple reads of each amplicon will be aligned and examined to establish accuracy, and to determine if the device has difficulty recognizing such repeat sequences. Hypotheses to be tested are that:

1. The MinIon will effectively and accurately read repeat sequences that are not prone to secondary structure formation.
2. GC rich repeats prone to formation of G-quadruplexes and other structures will not be accurately read.
3. Incorporation of deaza-7 dGTP during PCR will alleviate secondary structures and enhance reading of these difficult repeats.
4.

This is a relatively fundamental project to help test out the capabilities of this new and very exciting technology. Knowing whether the device can effectively examine these types of repeated DNA sequences will be of considerable value as the machine holds considerable potential and is being trialled for a very wide range of applications in both the diagnostic and research setting.

The student will be responsible for carrying out all of the laboratory work and data analyses, with supervision from Prof Kennedy, Dr Simone Cree, and other members of the Gene Structure and Function Laboratory.

Student Prerequisites (eg. Medical Student) if applicable:
Prefer a student with genetics training, and some aptitude for bioinformatics.