SUMMER RESEARCH 2024/25
PROJECT ABSTRACT

THE UNIVERSITY OF WAIKATO
Te Whare Wānanga o Waikato

PROJECT # 62

SUPERVISOR/S: Dr William Kelton

PROJECT TITLE: Computationally assisted engineering of antibody fragments

FIELD: Biotechnology/Health

DIVISION/SCHOOL: HECS - Te Aka Mātuatua School of Science

PROJECT LOCATION: Hamilton

PROJECT ABSTRACT:

Antibodies and antibody fragments are already widely used as therapeutics and diagnostic reagents and yet the demand for engineered antibodies with high affinity and target specificity continues to increase. A key challenge in discovering these new variants is searching a vast protein sequence space to find the most optimal amino acid changes. Experimental techniques are currently limited physically by the number of unique variants that can be created in cells. To expand beyond this limitation, computational methods represent a path to understanding how mutations made to antibodies have an influence on their performance as binding agents.

This project seeks to optimise the use of deep sequencing data from protein engineering experiments for the training of machine learning models. We will use nanopore sequencing to evaluate the results from a series of completed antibody panning experiments. We will specifically evaluate the training of new base calling algorithms to improve readout accuracy from the nanopore sequencer. Processed data from these experiments will inform the most efficient ways to generate datasets that train ML models for antibody discovery. This project, supervised by Dr William Kelton (Te Huataki Waiora Te Huataki Waiora School of Health / Te Aka Matuatua Te Aka Mātuatua School of Science) and Kyrin Hanning, aims to accelerate the rate at which we discover new antibodies.

STUDENT SKILLS:

- Computational skills in Unix, Python
- Molecular biology techniques such as ELISA analysis
- Ideally but not required, experience with next-generation sequencing data

PROJECT TASKS:

1. Nanopore sequencing of nanobody libraries from phage panning experiments
2. Establish nanopore base calling algorithms in house
3. Compare and benchmark library generation approaches for training of ML models
4. Variant validation by ELISA
5. Poster creation

EXPECTED OUTCOMES:

- Student's Research Poster (as per clause 6 of the Scholarship regulations)
- Generation of nanopore datasets from model nanobody affinity maturation experiments.
- Benchmarking of various library design strategies for predictive ML accuracy based on nanobody sequence.