

INTRODUCTION TO GENOMICS FOR PUBLIC HEALTH AND CLINICAL MICROBIOLOGY

Wednesday 1st May– Friday 3rd May 2019

Microbiological Diagnostic Unit Public Health Laboratory

Doherty Institute, 792 Elizabeth Street, Melbourne VIC 3000

Wednesday 1st May 2019

9:00am – 9:30am	Registration
9:30am – 10:30am	<p>Lecture 1: Introduction and overview of NGS</p> <p>Dr Susan Ballard</p> <ul style="list-style-type: none"> • Builds on a sound understanding of Sanger sequencing • Provides an overview of NGS technologies (Illumina, PacBio, Oxford Nanopore) • Discusses whole genome sequencing versus amplicon and capture based assays.
10:30am – 10:45am	Morning tea
10:45am – 11:45pm	<p>Lab workflow observation and discussion</p> <ul style="list-style-type: none"> • Discussion of different DNA/RNA extraction methods. • Explores the limitations and quality metrics required for DNA/RNA • Consideration for controls and trouble shooting
11:45am – 12:45pm	<p>Lecture 2: Bioinformatics and phylogeny</p> <p>Dr Mark Schultz</p> <ul style="list-style-type: none"> • Sequence data, meta-data, data security and storage. • Provides an overview of bioinformatics tools and available databases used for pathogen characterisation • Discusses relevant bioinformatics issues and limitations
12:45pm – 1:15pm	Lunch

1:15pm – 3:15pm	<p>Lab workflow observation and discussion</p> <ul style="list-style-type: none"> • Observation and discussion of different library preparation methods. • Consideration for controls and trouble shooting
3:15pm – 3:30pm	Afternoon tea
3:30pm – 4:30pm	<p>Lecture 3: Using genomics in clinical and public health I</p> <p>Dr Kristy Horan / Dr Danielle Ingle</p> <ul style="list-style-type: none"> • Explore the complexities of pathogen genomics for Mycobacterium tuberculosis. • Explore the complexities of pathogen genomics for enteric pathogens (Salmonella and E. coli).
4:30pm – 5:00pm	<p>Roundtable discussion</p> <ul style="list-style-type: none"> • A debrief of the days activities. • A discussion of results generated using NGS compared to legacy methodologies (Salmonella, Mtb).
Thursday 2nd May 2019	
9:00am – 10:45am	<p>Lab workflow observation and discussion</p> <ul style="list-style-type: none"> • Observation of sequence library QC • Explores the limitations and quality metrics required for sequence libraries
10:45am – 11:00am	Morning tea
11:00am – 1:00pm	<p>Computer workshop: case studies</p> <ul style="list-style-type: none"> • Using case studies explore and evaluate the accuracy and precision of genomic data.
1:00pm – 1:30pm	Lunch
1:30pm – 2:30pm	<p>Lecture 4: Using genomics in clinical and public health II</p> <p>Dr Deborah Williamson / Dr Norelle Sherry</p> <ul style="list-style-type: none"> • Using pathogen genomics in public health to investigate outbreaks.

	<ul style="list-style-type: none"> Using pathogen genomics in clinical microbiology to investigate AMR
2:30pm – 3:00pm	<p>Roundtable discussion</p> <ul style="list-style-type: none"> Reporting genomic results Discuss the advantages and limitations of genomic data.
3:00pm – 3:15pm	Afternoon tea
3:15pm – 5:00pm	<p>Lab workflow observation and discussion</p> <ul style="list-style-type: none"> Observation of sequence library pooling and Illumina instrument set-up Explore the variety of sequence read lengths and instruments available using Illumina technology.
5:00pm	Close
Friday 3rd May 2019	
9:00am – 10:45am	<p>Lecture 5: Setting up a sequencing laboratory</p> <p>Dr Susan Ballard</p> <ul style="list-style-type: none"> Explores the environmental, equipment and staffing requirements for setting up and managing a sequencing facility. Discussion of Quality, Validation and Accreditation requirements
10:45am – 11:00am	Morning tea
11:00am – 1:00pm	<p>Lab workflow observation and discussion</p> <ul style="list-style-type: none"> Observation of minION sequencing using Oxford Nanopore Explore the limitations and quality metrics required for long read sequencing.
1:00pm – 1:30pm	Lunch
1:30pm – 2:30pm	<p>Lecture 6: Typing pathogens using NGS</p> <p>Dr Susan Ballard / Dr Kristy Horan</p> <ul style="list-style-type: none"> Exploration of different typing schemes using NGS data (in silico MLST, cgMLST, wgMLST).

	<ul style="list-style-type: none"> Using MLST in phylogeny analysis and a comparison with SNP-based typing
2:30pm – 3:00pm	<p>Roundtable discussion</p> <ul style="list-style-type: none"> A debrief of the day's activities A discussion of results generated using NGS compared to legacy methodologies (Listeria, AMR).
3:00pm – 3:15pm	Afternoon tea and close