



# Department of Biochemistry and Molecular Biology

## PhD Oration



**Friday 17<sup>th</sup> of August**

**3:30-4:30pm**

**Bio21 Institute Auditorium  
30 Flemington Road, Parkville**

**Yu Wan**

Holt Laboratory,  
Department of Biochemistry and Molecular  
Biology. University of Melbourne.

### ***Detecting horizontal co-transfer of antimicrobial resistance genes in bacteria using a network approach***

Acquired multidrug resistance (MDR) in bacteria, which is disseminated through horizontal gene transfer (HGT), is a fast evolving and global threat to infection control and public health. In this study, I am interested in mobile antimicrobial resistance genes (ARGs) that are physically linked in the same DNA molecule, because they are prone to co-mobilise into the same recipient bacterium in a single HGT event, making it an efficient way to spread MDR between bacteria even when they are distantly related. Particularly, I aim to detect horizontally co-transferred ARGs in a large amount of bacterial isolates of the same species using whole-genome sequencing (WGS) and a computation approach, and to identify their vectors using genome assemblies and spatial-temporal information. This oration is comprised of three primary sections. First, I will explain my methodology that integrates association modelling, genomic physical distances and network analysis for collecting evidence of co-transferred ARGs. Next, I will present an implementation of the method as a software package GeneMates and demonstrate validations of this tool using published data sets of *Escherichia coli* and *Salmonella* Typhimurium. Finally, I show an application of GeneMates to a larger data set, a global collection of *Klebsiella pneumoniae*, for the inference of horizontally co-transferred ARGs as well as tracing their configurations with country and year information. In conclusion, this study provides us with a flexible approach for investigating the co-transfer and vectors of acquired ARGs using various WGS data, such as those routinely collected in national diagnostic laboratories for surveillance of antimicrobial resistance. Further, under a proper study design, my approach is applicable to other kinds of bacterial genes and species to address different questions.

*ALL WELCOME. Please join us for Pizza to celebrate this PhD Oration!  
Further information: Matthew Dixon ([matthew.dixon@unimelb.edu.au](mailto:matthew.dixon@unimelb.edu.au))*

