

# RESEARCH SEMINAR

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## Microbial sequencing and bioinformatics pipelines for public health genomics

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Hosted by Assoc. Prof. Chew Eng Hui

### Abstract

As humans, we share our existence with a complex community of microbial partners; fungal, viral and bacterial. At the Genome Institute of Singapore (GIS), the GIS Efficient Rapid Microbial Sequencing (GERMS) platform utilizes both wet lab and dry lab tools to genetically characterize these populations and how they impact our lives. The principal goal of the platform is to enable industrial and academic partners to use microbial genomics for a variety of applications. We have used our tools to help medicinal chemists with data mining after rational drug design with Novartis (1), used comparative genomics and transcriptomics to decipher novel gene families that can explain how that fungi can survive on lipids from the skin, and potentially serve as therapeutic targets with P&G (2). We have recently helped International Business Machines (IBM) and the Institute of Bioengineering and Nanotechnology (IBN) A\*STAR to decipher if their new polymer could be developed into an antimicrobial drug for antibiotic-resistant infections. To determine whether the bacteria would develop any resistance to the polymer we used our functional genomics capabilities (3).

We also collaborate with academics in South East Asia such as the Oxford Clinical Research Unit in Vietnam and NUS in Singapore to understand microbial causes for the infectious diseases prominent in this part of the world. In July of 2016, we combined genomics with traditional epidemiology during a Group A Streptococcus outbreak in a local mental health hospital (4). Together we identified that there was a single strain causing an outbreak in a particular ward but not throughout the hospital. In the absence of genomics, the infection control team was considering hospital-wide antibiotic prophylaxis. However, the higher resolution of whole genome sequencing enabled a targeted intervention to control the outbreak, saving the hospital money and saving many patients from unnecessary antibiotic treatment. Importantly, we helped perform the genome sequencing and analysis on a time scale fast enough to impact infection control interventions.

The world of genomics and the data mining process is an ever changing and challenging landscape. However, if we stay on top of the innovative wet lab methods and current bioinformatics tools available the power of informing public health through genomics is vast.

## References

1. Exploring the mode of action of bioactive compounds by microfluidic transcriptional profiling in mycobacteria. PLoS One, 2013 PMID 23935951
2. Genus-wide comparative genomics of *Malassezia* delineates its phylogeny, physiology, and niche adaptation on human skin. PLoS Genetics, 2015 PMID 26539826
3. A macromolecular approach to eradicate multidrug resistant bacterial infections while mitigating drug resistance onset. Nature Communications, 2018 PMID 29500445
4. An outbreak of streptococcus pyogenes in a mental health facility: Advantage of well -timed whole genome sequencing over emm typing. Infection Control Hospital Epidemiology, 2018 PMID: 29739475

## Biography



Paola Flórez de Sessions holds a PhD from Duke University where she helped elucidate the mechanism of action of an oncolytic virus called PVS-RIPO, which targets glioblastomas. She did postdoctoral studies at the Novartis Institute for Tropical Diseases in Singapore, where she was exposed and extremely interested in the world of bioinformatics. She is currently the Genome Institute of Singapore (GIS) Efficient Rapid Microbial Sequencing (GERMS) Platform Leader at GIS. The GERMS team is able to offer a complete package, from project design to sample handling, sequencing strategies, cutting-edge analysis pipelines and comprehensive interpretation. GERMS specialized in small genomes: viral, bacterial, parasites and fungal entities and their genomic peculiarities for both industrial purposes as well and public health genomics.