The 12th Global Microbial Identifier Meeting
Nanyang Technological University, Singapore

Lecture Theatre 8, Block NS1, NS1-02-01, 50 Nanyang Avenue, 639798
http://maps.ntu.edu.sg/maps#q:LT8.

Day 1 – Wednesday 12th June 2019

07:45-08:30 Registration		
08:30-08:40	Welcome and opening remarks	Nanyang Technological University (NTU), SG
08:40-09:00	Political progress of the GMI idea at the international stage	Joergen Schlundt, NTU, SG
Singapore's Experience with Next Generation Sequencing (NGS)		
Chair: Joergen Schlundt		
09:00-09:20	The air microbiome: A missing ecosystem?	Stephan Schuster, NTU, SG
09:20-09:40	Tracking AMR evolution in *Acinetobacter spp* in WGS in South East Asia and Globally	Eric Yap, NTU, SG
09:40-10:00	Whole-Genome Sequencing Reveals Plasmid-mediated Transmission and Persistent Healthcare Reservoirs of Carbapenemase-producing Enterobacteriaceae	Oon Tek, TTSH, SG
10:00-10:10	QA and Discussion	
10:10-10:30 Coffee break		
10:30-10:50	Recovery of closed bacterial genomes from complex microbial communities using long read sequencing	Krithika Arumugam, NTU, SG
10:50-11:10	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment	Niranjan Nagarajan, GIS, SG
11:10-11:20	QA and Discussion	
Developing Country's experience in NGS		
Chair: Joergen Schlundt		
11:20-11:40	NGS training and application in Southern Africa	Yasmina Fakim, University of Mauritius, MA
11:40-12:40	Presentation from Developing Country Representatives	Developing Country Representatives
12:40-13:55 Lunch & Illumina Inc. Symposium		
13:55-14:55	Panel discussion on developing country NGS/WGS experience, including presentation on NGS training and application in Southern Africa *continued*	Developing Country Representatives
14:55-15:15 Coffee break		
15:15-17:15	Working group break-out session	
17:15-17:55	Summary of break-out session	Working Group chairs
17:55-1800	Closing remarks	
Conclusion of Day 1		

Day 2 – Thursday 13th June 2019

08:30-08:40	Opening remarks for Day 2	Joergen Schlundt, NTU, SG
Existing Platforms for Sequencing Analysis and Active Systems and (Barriers to) International Data Sharing **Chair: Eric Stevens**		
08:40-09:00	Updates on NCBI pathogen detection browser - *TBC*	Bill Klimke, NCBI, USA – *TBC*
09:00-09:20	Microbial genomics in EFSA activities	Mirko Rossi, EFSA, FI
09:20-09:40	Keeping up with exponentially growing databases and time constraints	Bernhard Y Renard, RKI, DE
09:40-10:00	IRIDA: an extensible and distributed bioinformatics analysis platform - working towards a global interoperable ecosystem for genomic epidemiology	William Hsiao, BCCDC, CA
10:00-10:10	QA and discussion	
10:10-10:30 Coffee break		
Advances in the Use of WGS in Clinical, Public Health and Food Virology **Chair: William Hsiao**		
10:30-10:50	*TBC*	Andreas Nitsche, RKI, DE
10:50-11:10	*TBC*	*TBC*
11:10-11:30	The use of WGS to better understand the human health risks of zoonotic diseases from wildlife and agricultural production systems	Gavin Smith, NUS, SG
11:30-11:50	Pending title	October Sessions, NUS, SG
11:50-12:00	QA and discussion	
12:00-13:00 Lunch		
Advances in the Use of WGS in Clinical, Public Health and Food Bacteriology **Chair: William Hsiao**		
13:00-13:20	Integrating the use of whole-genome sequencing in infectious disease and antimicrobial resistance surveillance in Europe	Marc Jean Struelens, ECDC, SE
13:20-13:40	First steps towards incorporation of WGS data in exposure assessment: Machine learning and Network-Diffusion approaches	Pimlapas (Shinny) Leekitcharoenphon, DTU, DK
13:40-14:00	Pending title	Nancy Chow, CDC, USA
14:00-14:20	NGS applications in the food industry – Present status and perspectives	Renaud Jonquieres, Merieux Nutrisciences, SG
14:20-14:30	QA and Discussion	
14:30-14:50 Coffee break		
New Molecular/Sequence Based Identification Tool for Organism **Chair: Jianguo Xu**		
14:50-15:10	Advances in NGS technologies	Illumina Inc., SG
15:10-15:30	Oxford Nanopore Technologies at the bench, in the field and beyond	Paola De Sessions, Oxford Nanopore Technologies, SG
15:30-15:50	Comprehensive Microbial detection by the combination of Next Generation Sequencing and Microbiome array developed by Thermo Fisher Scientific	Arjun Kandalam, Thermo Fisher Scientific, SG
15:50-16:10	MitochonTrakr and Metagenometrakr	Padmini Ramachandran, FDA, USA
16:10-16:30	Reverse microbial etiology: new strategy for prevention of emerging infectious diseases in future	Jianguo Xu, CDC, CN
16:30-16:50	Whole-genome sequence based species ID using K-mer alignment	Pimlapas (Shinny) Leekitcharoenphon, DTU, DK
16:50-17:10	Genomic Biomarkers to advance Food Safety	Maria Hoffmann, FDA, USA
17:10-17:30	The role of whole genome sequencing in antimicrobial susceptibility testing of bacteria: report from the EUCAST Subcommittee	Matthew Ellington, Public Health England, UK
17:30-17:40	QA and Discussion	
17:40-17:50	Closing remarks	
Conclusion of Day 2		

Day 3 – Friday 14th June 2019

08:30-08:35	Opening remarks for Day 3	Joergen Schlundt, NTU, SG
Advances in the Use of Metagenomics		
Chair: Andreas Nitsche		
08:35-08:55	Mapping everything against everything	Frank Aarestrup, DTU, DK
08:55-09:15	The successes and pitfalls of metagenomics for clinical, public health, and food safety application – a Canadian perspective	Natalie Knox, PHAC, CA
09:15-09:35	Metagenomics profiling for analysis of sequencing data from foods	Luca Cocolin, University of Torino, IT
09:35-09:55	Progression of metagenomics as a tool for routine diagnostics	Robert Schlaberg, University of Utah, USA
09:55-10:15	Culture-independent genome sequencing of Mycobacterium tuberculosis	Nathan Bacchman, University of Sydney, AU
10:15-10:35 Coffee break		
10:35-10:55	COMPARE food PT based on a salmon matrix - wet lab part	Alessandra De Cesare, University of Bologna, IT
10:55-11:15	COMPARE food PT based on a salmon matrix -dry lab part	Dirk Hoper, FLI, DE
11:15-11:25	QA and Discussion	
NGS in One Health – Surveillance and Investigation		
Chair: Marc Struelens, TBC		
11:25-11:45	Investigating a listeriosis outbreak in South Africa	Anthony Smith, NICD, ZA
11:45-12:05	Establishing integrated genomic outbreak investigation and surveillance systems in Germany: Players, challenges and chances	Maria Borowiak, BfR, DE
12:05-12:25	Typing reveals an invasive clone of *Streptococcus agalactiae* in SE Asia, missed for decades	Timothy Barkham, NUS, SG
12:25-13:25 Lunch		
13:25-13:45	How WGS is used for foodborne pathogens: a regulatory perspective	Eric Stevens and Ruth Timme, FDA, USA
13:45-14:05	Epidemiological considerations concerning the use of WGS data for foodborne outbreak investigation	Heather Carleton, CDC, USA
14:05-14:25	The modernization of foodborne disease surveillance in Canada: how we made it happen	Celine A. Nadon, PHAC, CA
14:25-14:45	Application of WGS in surveillance and risk assessment for foodborne pathogens	Kalliopi Rantsiou, University of Turin, IT
14:45-14:55	QA and Discussion	
14:55-15:15 Coffee break		
15:15-17:00	Working group break-out session	
17:00-17:40	Summary of break-out session	Working Group Chairs
17:40-17:55	Finalization of Potential Singapore Statement	
17:55-1800	Closing remarks	
Conclusion of Day 3		

Participation is free of charge, all coffee breaks and lunches will be catered for by sponsors.

Registration is now OPEN:
https://coe.ntu.edu.sg/Research/naftec/UpcomingEvent(s)/GMI%2012/Registration/Pages/Home.aspx

Further details:
www.globalmicrobialidentifier.org