

Time Table

April 24 th , THU (Day 1)		
8:30-9:30	Registration	/Centennial Hall, Yonsei University
9:25-9:40	Opening	/Centennial Hall, Yonsei University
KEYNOTE 1		
		CHAIR: Yong-Sun BAHN, Yonsei University
9:40-10:20	[K1] Microbiome data science: Unveiling microbial, viral, and functional diversity Nikos C. KYRPIDES, Joint Genome Institute, Lawrence Berkeley National Laboratory	
10:20-10:35	Coffee Break	
Session 1. Protein and Metabolic Network Analysis in Microbiomes		
		CHAIR: Donghyuk SHIN, Yonsei University
10:35-11:00	[H1] Protein interactions in human pathogens revealed through deep learning Minkyung BAEK, Seoul National University	
11:00-11:25	[H2] Identification of key metabolic microbiota from the human microbiome and their correlation with health and disease Che Ok JEON, Chung-Ang University	
11:25-11:50	[H3] Metabuli: Sensitive and specific metagenomic classification via joint analysis of amino acid and DNA Jaebeom KIM, Seoul National University	
11:50-12:10	[P1] Multi-label classification with masked loss for predicting multi-antibiotic resistance in mixed-species MALDI-TOF MS profile Youngjun PARK, Max Planck Institute for Biology of Ageing	
12:10-13:30	Lunch & Poster Viewing	
12:45-13:20	Lightning Talks	@Global Lounge, The Commons, Yonsei University
		CHAIR: Jongbum JEON, Korea Bioinformation Center
	[Po-01] Enhancing metagenomic classification through query read grouping in Metabuli Luna Sung-eun JANG, Seoul National University	
	[Po-02] HRGV: Human reference gut virome catalog of metagenome-assembled viral genomes Han-June KIM, Yonsei University	
	[Po-05] Genomic diversity and underlying metabolic variations of the human gut microbiome between populations at single nucleotide resolution – Quanbin DONG, Nanjing Medical University	
	[Po-08] SNP-Based machine learning model enhances prediction of immune checkpoint inhibitor response – Jae Woo BAEK, GIST	
	[Po-10] Identification of antimicrobial peptides using knowledgeable multi-layer encoders Kyoungmin LEE, DGIST	
	[Po-12] Metacontam: Negative control-free decontamination tool for metagenomic analysis Junwoo JO, GIST	
	[Po-13] Paradoxical dynamics of antibiotic resistant bacteria with quantitative metagenome-assembled genome profiling - Min-Ji KIM, Kyungpook National University	
Session 2. Core Microbiome and Health Correlations		
		CHAIR: Joo-Hong PARK, Seoul National University
13:30-13:55	[H4] Protein relational stability for identifying core members in microbiomes Liping ZHAO, Rutgers University	
13:55-14:20	[H5] Understanding the human microbiome through multi-omics analysis from an ecological perspective Bong-Soo KIM, Ewha Womans University	
14:20-14:45	[H6] mi-Mic: A novel multi-layer statistical test for microbiota-disease associations Yoram LOUZOUN, Bar-Ilan University	
14:45-15:10	[H7] Microbiome confounders and quantitative profiling challenge predicted microbial targets in colorectal cancer development Raul Tito TADEO, KU Leuven	

15:10-15:30	Group Photo & Yonsei Campus Tour	
15:30-15:45	Coffee Break	
KEYNOTE 2		
		CHAIR: Heenam Stanley KIM, Korea University
15:45-16:25	[K2] Uncharacterized dark matter in the human microbiome and beyond Curtis HUTTENHOWER , Harvard University	
Session 3. Metagenomics Data Analysis and Applications		
		CHAIR: Sunjae LEE, Gwangju Institute of Science and Technology
16:25-16:50	[H8] High-quality genomic catalogs of the human microbiome for the era of microbiome medicine Insuk LEE , Yonsei University	
16:50-17:15	[H9] Microbial network inference for longitudinal microbiome studies with LUPINE Saritha KODIKARA , The University of Melbourne	
17:15-17:35	[P2] Accurate and lightweight taxonomic profiling of long read sequenced metagenomes with Lemur and magnet Nicolae SAPOVAL , Rice University	
17:35-17:55	[P3] Dynamic contrastive learning with pretrained deep language model enhances metagenome binning for contigs Bohao ZOU , Hong Kong Baptist University	
18:00-20:00	Poster Session & Satellite Reception	

April 25th, FRI (Day 2)		
8:30-9:40	Registration	/Centennial Hall, Yonsei University
KEYNOTE 3		
		CHAIR: Jang-Cheon CHO, Inha University
9:40-10:20	[K3] Strain and SNV-level resolved microbial genetic diversity in human health and disease Jingyuan FU , University Medical Center Groningen	
10:20-10:35	Coffee Break	
Session 4. Computational Tools and Algorithms for Microbiome Analysis		
		CHAIR: Jongsik CHUN, CJ Bioscience
10:35-11:00	[H10] Processing-bias correction with DEBIAS-M and implications for analyzing the microbiome in cancer Tal KOREM , Columbia University	
11:00-11:25	[H11] Rapid species-level metagenome profiling and containment estimation with sylph Jim SHAW , Dana-Farber Cancer Institute, Harvard Medical School	
11:25-11:45	[P4] CAMP: A modular metagenomics analysis system for integrated multi-step data exploration Lauren MAK , Weill Cornell Medicine	
11:45-12:05	[P5] Using lossless compression algorithms to improve metagenomics binning and accelerate genome taxonomic classification Itai SHARON , MIGAL-Galilee Research Institute	
12:05-13:30	Lunch & Poster Viewing	

12:45-13:20 **Lightning Talks** @Global Lounge, The Commons, Yonsei University

CHAIR: Minsik Kim, Yonsei University

- [Po-03] PHLAME: A live benchmark for evaluating host-phenotype prediction from gut metagenomics data – **Netta BARAK**, The Hebrew University of Jerusalem
- [Po-04] Comparison of the utility of several gut microbiome DNA standard materials to interpret for NGS analysis verification of human fecal samples – **Suenie PARK**, Biowave
- [Po-06] Investigating geographic and environmental effects on soil metagenomes by correlating GIS data with microbial abundance – **Nicole BROWN**, Johns Hopkins University
- [Po-07] Planetary microbiome structure and gene flow across habitats mediated by generalists **Chan Yeong KIM**, European Molecular Biology Laboratory
- [Po-09] Long-read sequencing in soil metagenomics: advances in assembly, limitations in taxonomic classification – **Matthew NGUYEN**, Johns Hopkins University
- [Po-11] From fear to fascination: Agar art as a science communication tool for microbial awareness – **Jeeyoung LEE**, Yonsei University
- [Po-14] Narrow- and broad-spectrum antibiotics dramatically alter the intestinal bacterial, viral and metabolomic composition of healthy volunteers – **Daniel R. Mende**, Keio University

Session 5. Environmental Microbiome Responses

CHAIR: Sukhwan YOON, Korea Advanced Institute of Science and Technology

- 13:30-13:55 [H12] Viral ecology and evolution in a freshwater lake over three decades
Karthik ANANTHARAMAN, University of Wisconsin-Madison
- 13:55-14:20 [H13] Bovine gut microbiome: Effect of castration and fecal microbiota transplantation
Jin-Woo BAE, Kyung Hee University
- 14:20-14:45 [H14] FoodSeq: A genomic biomarker of diet
Lawrence Anthony DAVID, Duke University
- 14:45-15:05 [P6] A shift from heterotrophy to autotrophy underlies microbial adaptation to global desert ecosystems
Pok Man LEUNG, Monash University
- 15:05-15:25 [P7] Functional regimes define the response of the soil microbiome to environmental change
Kiseok Keith LEE, University of Chicago

15:25-15:45 **Coffee Break**

Session 6. Human Microbiome Studies

CHAIR: Hong KOH, Yonsei University College of Medicine

- 15:45-16:10 [H15] Gut microbiome report to prognosticate liver diseases
Ki Tae SUK, Hallym University Medical Center
- 16:10-16:35 [H16] Gut microbiota in IBS: Pathogenic insights and FMT-based therapeutics
Qi SU, The Chinese University of Hong Kong
- 16:35-17:00 [H17] Explainable AI (XAI) for gut microbiome-based colorectal cancer classification
Takuji YAMADA, Tokyo Institute of Technology
- 17:00-17:20 [P8] Longitudinal oropharyngeal microbial signatures in patients undergoing allogeneic hematopoietic stem cell transplantation
Yan YAN, Shanghai Institute of Immunity and Infection, Chinese Academy of Sciences

Closing