The 2022 NIST-Hosted Workshop on Standards for Microbiome and Multi'Omics Measurements

AGENDA

Updated 08/09/2022

Day 1: Tuesday, Aug 23, 2022 (all times in MT)

8:15 – 8:45 AM	**WELCOME Breakfast & INTRODUCTORY REMARKS**
	Welcome, Logistics, NIST & Workshop Overview – Dr. Scott Jackson, Leader of the Complex Microbial Systems Group, Material Measurement Laboratory at the National Institute of Standards and Technology

8:45 – 10:15 AM	**SESSION 1 MODERATOR: SCOTT JACKSON (NIST)**
8:45 AM	V-Establishing the 1st WHO International Reference Reagents for microbiome analysis (Chrysi Sergaki)
9:10 AM	V-Non-Viable bacteria in Microbiome Analyses can Skew Taxonomic Results (Jason Arnold)
9:22 AM	IP-Minimum Requirements for Producing High Performance Whole Cell Microbial Reference Standards for DNA and RNA Applications (Scott Tighe)
9:34 AM	IP-Characterization, Hi-Fi Genome Assembly, and Data Sharing of a True Diversity Microbiome Reference (Raul Cano)
9:46 AM	IP-NIST Stool Reference Material for Multi'omic Analyses (Stephanie Servetas)

10:35

10:15 – 10:35 AM	**Morning BREAK**

10:35 – 12:05 PM	**SESSION 2 MODERATOR: CLAY DAVIS (NIST)**
10:35 AM	V-Linking individual microbial and metabolite biomarkers of Colorectal Cancer using computational models of the gut microbiota metabolism (Ali R. Zomorrodi)
10:45 AM	IP-NIST Calibrant Solution for Fecal Metabolomics (Sandra Da Silva)
10:55 AM	IP-Rapid Microbiome and Multi-Omics Data Analysis: A Case Study on Inflammatory Bowel Disease (Dana Walsh)
11:05 AM	Metabolomics Association of North America- Microbiome Interest Group (MANA-MIG) Panel Discussion: Martha Carlin, BioCollective Andrew Percy, Cambridge isotope laboratories; Mary Lipton, PNNL; Laura-Isobel McCall, Oklahoma U; John Ryals, Consultant; Di wu, UNC; Tucker Hallmark, Avanti Polar Lipids; Maryam Goudarzi, Sciex; Tom Metz, PNNL

12:05 – 1:30 PM	**LUNCH**

1:30 – 2:35 PM	**SESSION 3 MODERATOR: JASON KRALJ (NIST)**
1:30 PM	V-Standardizing Differential Abundance Approaches for Microbiome Data Analysis (Baris Ozdinc)
1:40 PM	IP-Exploring a Novel Microbiome Sampling Technique: A Benchmark Experiment Comparing DNA Yield and Community Profiles Between PDMS and Swab Collection Methods (Pheobe Mankiewicz)
1:50 PM	IP-Identifying driving factors in wastewater processing for monitoring via metagenomics (Ishi Keenum)
2:05 PM	IP-Differential Abundance Analysis from Biased Metagenomic Measurements (Ben Callahan)
2:15 PM	IP-Relative Abundance Estimation under Complex Measurement Error (Amy Willis)

2:25 – 3:05 PM	**DISCUSSION GROUPS SESSION 1 STEPHANIE SERVETAS (NIST)**
2:25 PM	Introduction/Overview IMMSA working groups
2:35 PM	Break out into working groups

3:05 – 3:30 PM	**Coffee BREAK**

3:30 – 4:15 PM	**KEYNOTE 1 MODERATOR: SCOTT TIGHE (UVM)**
	KEYNOTE Phil Hugenhotlz- SeqCode

Day 2: Wednesday, Aug 24, 2022 (all times MT)

8:15 – 8:30 AM	**WELCOME Breakfast & INTRODUCTORY REMARKS**
	Welcome, recap of day 1 Scott Jackson

8:30 – 10:25 AM	**SESSION 4; KEYNOTE 2 MODERATOR: ISHI KEENUM (NIST)**
8:30 AM	**KEYNOTE Rita Colwell**
9:15 AM	V-Risk assessment at the gastrointestinal health and One Health concept (Sangeeta Khare)
9:25 AM	IP-Measuring Antibiotic Resistance Propagation via Horizontal Gene Transfer in Complex Microbial Communities (Nadrat Chowdhury)
9:35 AM	IP-Role of bacterial motility in evolutionary mechanisms for acquired antimicrobial resistance (Lisa Stabryla)
9:45 AM	IP-Summary of microbiome data analysis from statistical point of view (Yan Wang)

9:55 AM	IP-Developing metadata standards to improve omics sample interoperability and data analysis (Montana Smith)
10:05 AM	IP-Metagenomic NGS (MGS) Performance Metrics with an Organism-centric Approach (Jason Kralj)

10:25 – 10:55 AM	**Group Photo & Morning BREAK**

10:55 – 11:40 PM	**Session 5 Moderator: Sandra Da silva (NIST)**
10:55 AM	IP-Standardizing approaches for stable isotope probing (SIP) metagenomics (Rex Malmstrom)
11:10 AM	IP-Characterizing the Gut Microbiome of Dietary Patterns using Pooled Samples: Assessing a Novel Methodological Approach to a Complex Web of Confounders (Leigh Frame)
11:20 AM	IP-Longitudinal Changes in Mental Health Symptoms May Be Associated with the Gut Microbiome in Inpatient Treatment-Seeking Adults with Alcohol Use Disorder (Katherine Maki)
11:30 AM	IP-A Meta-Analysis Study On The Effects Of Breastfeeding Practices On The Gut Microbiome In The Mal-Ed Cohort Study (Aya Kutbi)

11:40 – 12:10 PM	**Discussion Groups Session 2**

12:10– 1:40 PM	**LUNCH**

1:40 – 2:25 PM	**Session 6 Moderator: Stephanie Servetas (NIST)**
1:40 PM	V-Analyses of Mock Community Standards using a Highly Rapid Nanopore Sequencing Protocol (Cory Bernhards)
1:50 PM	IP-Benchmarking DNA recovery rates from aerobiomes sampled with electret filters (Harrison J. Trethowan)
2:00 PM	IP-ASVs/genomes indexing database for integrating datasets from different microbiome studies/Cultured-based quality evaluation of stool collection kits (Liping Zhao)
2:15 PM	IP- Towards Genome Authentication: The ATCC Genome Portal (John Bagnoli)

2:25 – 2:45 PM	**Coffee BREAK**

2:45 – 3:30 PM	**Keynote 3 Moderator: Bharath Prithiviraj (Reckitt)**
	KEYNOTE Jack Gilbert

Day 3: Thursday, Aug 25, 2022 (all times MT)

8:15 – 8:30 AM	**WELCOME Breakfast & INTRODUCTORY REMARKS**
	Welcome, recap of day 2 Scott Jackson

8:30 – 10:20 AM	**Session 7 Moderator: Ishi Keenum (NIST)**
8:30 AM	**KEYNOTE Krista Wigginton**
9:15 AM	IP- Culture-free discovery and host-attribution of phages in diverse microbial ecosystems using high-throughput proximity ligation sequencing (Ivan Liachko)
9:25 AM	V-Performance comparison of host DNA depletion methods to allow direct sequencing of blood samples for pathogen identification (Daniel Evans)
9:35 AM	V-ViOS - an open access systems biology platform for next generation of diagnostic and therapeutic approaches (Momo Vuyisich)
9:45 AM	V-Galileo ONE: Standardizing metagenomics research using a sample-to-result workflow with integrated controls (Meredith Carpenter)

9:55 – 10:25 AM	**Morning BREAK**

10:25 – 12:00 PM	**Discussion Groups Session 3**

12:15 – 1:15 PM	**LUNCH**

1:15 – 2:05 PM	**Discussion Groups Presentations** **Moderator: Stephanie Servetas (NIST)** **Discussion Group Presentation Times and topics subject to change**
1:15 PM	Reference material WG report
1:25 PM	Bioinformatics WG report
1:35 PM	Metabolomics WG report
1:45 PM	Documentary standards WG report
1:55 PM	Enumeration and viability WG report

2:05 – 3:35 PM	**Closing Remarks and End Reception**