Second Workshop in Statistical and Algorithmic Challenges in Microbiome Data Analysis
The Broad Institute of MIT and Harvard, February 16 + 17, 2017
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Workshop Program
Thursday, February 16, 2017

8-9am

Registration in The Broad Lobby
Breakfast for all attendees in the Broad Lobby

Welcoming Remarks   9am

Eric Alm (MIT, Center for Microbiome Informatics and Therapeutics)
Richard Bonneau (Simons Center for Data Analysis, Simons Foundation)
Christian Mueller (Simons Center for Data Analysis, Simons Foundation)

Presentations in the Auditorium   9:30-12:15pm

Keynote Address

Bonnie Berger - Massachusetts Institute of Technology
"Compressive Metagenomics: Scaling Faster than Light"

Coffee Break in the Broad Lobby   10:30-10:45am

Technical Presentations

Susan Holmes- Stanford University, Holmes Lab
"Longitudinal Analyses for the Human Microbiome: Statistical Challenges"

Georg Gerber and Elijah Bogart – Harvard Medical School, Gerber Lab
"Predictive and Interpretable Bayesian Models for Analyzing Microbiome Mime-series Data"

Juan José Egozcue – U. Politécnica de Cataluña (UPC)
"Measuring and Testing Linear Compositional Association"

Lunch for all attendees in the Broad Lobby   12:15-1:30pm

Technical Presentations   1:30-5:15pm

Amy Willis – Cornell University, Bunge Lab
"Visualizing uncertainty in phylogenetic trees"

Emma Schwager – Harvard School of Public Health, Huttenhower Lab
"A Bayesian Method for Detecting Pairwise Associations in Compositional Data"

Pixu Shi – University of Pennsylvania, Hongzhe Li Lab
"Regression Analysis for Microbiome Compositional Data"

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Coffee Break in the Broad Lobby   3-3:45pm

Edoardo Pasolli – University of Trento- Italy, Segata Lab
"Tools and challenges for Large-scale and Accessible Metagenomic Meta-analyses"

Sebastien Raguideau – French National Institute for Agricultural Research, Laroche Lab
"Inferring Aggregated Functional Traits from Metagenomic Data Using Constrained Non-negative Matrix
Factorization: Application to Fiber Degeneration in the Human Gut Microbiota"

Alon Shaiber – University of Chicago, Meren Lab
"A Metagenome-Driven, Gene-Centric Classification Approach to Investigate What Makes a Genome Tick"

Breakout Sessions; locations noted below   5:30-7pm

Mini-Workshop I in the Board Room
led by Tandy Warnow and Siavash Mirarab
Algorithmic ideas and techniques in TIPP and SEPP (and also HIPPI): methods in metagenomic sequence analysis

Mini-Workshop II in Olympus Conference Room
led by Ali Rahnavard
HAllA tutorial

Mini-Workshop III in the Auditorium
led by Meren
Metagenomic Binning

Reception in the Broad Lobby   5pm – 8:00pm
    Hors D'oeuvres   5pm
    Buffet Dinner   6:45pm

Poster Viewing in the Broad Lobby   7 – 8:00pm

Friday, February 17, 2017

8-9am

Registration Open
Breakfast for all attendees in the Broad Lobby

Poster Primer   9am
Christian Mueller , Simons Center for Data Analysis, Simons Foundation

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Presentations in the Auditorium   9:10-12:15pm

Keynote Address

Wolfgang Huber– European Molecular Biology Laboratory
"Covariate-powered weighted multiple testing with false discovery rate control"

Technical Presentations

Patrick Bradley – University of California San Francisco, Pollard Lab
"Identifying Gene Families under Selection in the Human Gut Microbiome

Coffee Break   10:40-11am

Siavash Mirarab – University of Illinois at Urbana- Champaign, Warnow Lab
"Taxonomic Profiling using Scalable Phylogenetic Placement"

Justin Wagner – University of Maryland, Corrada Bravo Lab
"Metaviz: Interactive Statistical and Visual Analysis of Metagenomic Data"

Elmar Pruesse – University of Colorado Denver, Lozupone Lab
"Coverage vs Abundance -- Linking Genetic Elements within Metagenome Assemblies"

Lunch for attendees in the Broad Lobby   12:15-1:30pm

Technical Presentations   1:30-5:15pm

Matt Dillon and Evan Bolyen – Northern Arizona University, Caporaso Lab
"QIIME 2: Decentralized, Extensible, and Reproducible Microbiome Analysis"

Alexander Dilthey – NIH National Human Genome Research Institute, Phillippy Lab
"Fast Approximate Mapping and Identity Estimation of Nanopore Reads"

Eva Yiwen Wang – University of Queensland Diamantina Institute, Le Coa Lab
"Adjusting for Batch Effects in Microbiome Experiments: A Multivariate Perspective"

Coffee Break   3:30-3:45pm

Shannon Ellis – Johns Hopkins School of Public Health, Leek Lab
"Increasing the Value of Public Data with In-silico Phenotyping"

Hyunwook Koh – New York University School of Medicine, Huilin Li Lab

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"A Robust and Powerful Microbiome-based Association Test"

Dan Schlatter and Zewei Song – University of Minnesota, Kinkel Lab
"Sympatric Interaction Networks Shed Light on the Ecology and Evolution of Soil Microbiomes"

Poster Session   5pm – 6pm
Poster presentations throughout