



Winter 2018 Mid-Atlantic Microbiome Meetup Biodefense and pathogen detection



Wednesday, January, 10th 2018

**Colony Ballroom, Adele H. Stamp Student Union
University of Maryland College Park**

- 8:00: **Registration and breakfast**
- 8:45: **Kick-off: Welcome to Winter M3**
Todd J. Treangen
Center for Health-related Informatics and Bioimaging (CHIB)
University of Maryland College Park
- 9:00: **M3 Opening Keynote**
Tara O'Toole
Executive Vice President, In-Q-Tel
- 10:00: **Coffee break**
- 10:20: **Data-driven session**
Chair: *Stephanie Rogers*
- 10:20: **"Bridging technology, venture, and national security"**
Stephanie Rogers
B.Next (In-Q-Tel)
- 10:45: **"Tragedy of the commons: RefSeq database growth influences the accuracy and sensitivity of species identification from metagenomic samples"**
Dan Nasko
Center for Bioinformatics and Computational Biology (CBCB)
University of Maryland College Park
- 11:00: **"Comparison of sequencing and culture-based methods for the detection of foodborne pathogens in non-traditional irrigation water in the Mid-Atlantic United States: A CONSERVE study "**
Sarah Allard
School of Public Health
University of Maryland College Park

- 11:15: **"Tracking Antibiotic Resistance Across Space and Time"**
Sean Conlan
National Human Genome Research Institute (NHGRI)
National Institutes of Health (NIH)
- 11:30: **"Longitudinal analysis of microbiomes"**
Greg Caporaso
National Cancer Institute (NCI)
National Institutes of Health (NIH)
- 11:45: **M3 invited seminar**
"College Dorms as a Laboratory for Studying Respiratory Infection"
Don Milton
School of Public Health
University of Maryland College Park
- 12:10: **Lunch**
- 13:00: **M3 game**
- 13:30: **Methods-driven session**
Chair: Nicholas Bergman
- 13:30: **"Metagenomics in bioforensics"**
Nicholas Bergman
National Biodefense Analysis and Countermeasures Center (NBACC)
- 14:00: **"Mash Screen: Fast sequence containment estimation using MinHash"**
Brian Ondov
National Human Genome Research Institute (NHGRI)
National Institutes of Health (NIH)
- 14:15: **"A Sample Mixture Experiment to Assess 16S rRNA Metagenomic Methods"**
Nathan Olson
National Institute of Standards and Technology (NIST)

14:30: **"MetaCompass: Reference-guided Assembly of Metagenomes"**

Victoria Cepeda

Center for Bioinformatics and Computational Biology (CBCB)

University of Maryland College Park

14:45: **"Metaviz: Interactive Statistical and Visual Analysis of Human Microbiome Project Data"**

Héctor Corrada-Bravo

Center for Bioinformatics and Computational Biology (CBCB)

University of Maryland College Park

15:00: **Coffee Break**

15:30: **Breakout session**

- **Group 1: Viral and fungal pathogens: off the beaten path.** Chairs: Jacquelyn Meisel, Dan Nasko
 - *While many studies survey the bacterial microbiome of different environments, few have explored the role of fungi or viruses in these microbial communities. This is in large part due to limitations in laboratory procedures and, in the case of viruses, the lack of a universally distributed marker gene. This session will discuss the technical and computational challenges in collecting, sequencing, and analyzing mycobiome and virome datasets. We will consider the strengths and limitations of existing pipelines and databases, as well as the potential applications of these tools in the biodefense field.*
- **Group 2: Crowdsourcing biodefense: data sharing, data standards, data security, and data visualization.** Chairs: Héctor Corrada-Bravo, Brian Ondov
 - *Large studies profiling microbial communities and their association with healthy or disease phenotypes are now commonplace. Data from many of these studies are publicly available but significant effort is required for users to effectively organize, explore and integrate it with their own data, limiting the utility of these rich data resources. Effective integrative and interactive visual and statistical tools to analyze multiple metagenomic samples can greatly increase the value of these data for researchers. Furthermore, sharing metagenomic data in sensitive applications, clinical or security, for instance, raises privacy and security concerns that are presently difficult to address. This session will explore four topics critical to data democratization in the genomics era: data sharing, data security, data visualization and data standards.*
- **Group 3: Need for speed: Navigating the trade-off between analysis accuracy and speed.** Chairs: Adam Bazinet, Todd Treangen
 - *In this session, we will consider various types of metagenomic analyses that could be time-critical in a bioforensic or biodefense scenario, and we will explore ways of speeding up those analyses while simultaneously assessing any potential impact on analysis accuracy. Examples of such analyses might include taxonomic abundance profiling, functional profiling, taxonomic sequence classification, metagenomic assembly, and sequence annotation (e.g., annotation of antibiotic resistance and virulence genes or*

identification of synthetic, bioengineered, or otherwise non-natural sequences). Considerations for improving analysis speed might include choice of hardware, software, or algorithms used for analysis; “approximate” analyses that may only analyze part of the data; and analysis paradigms that analyze subsets of data in parallel. We will also discuss emerging sequencing technologies that have the potential to radically accelerate the speed with which data can be generated. By the end of the session, we hope to have sketched out a number of different possible analysis workflows that exhibit favorable characteristics regarding the tradeoff between accuracy and speed.

- 16:45: **Break**
- 17:00: **Ecology-driven session**
Chair: Jocelyne DiRuggiero
- 17:00: **"Dynamic Response of Atacama Desert Extremophiles to Weather Perturbations "**
German Uritskiy
Johns Hopkins University
- 17:15: **"Frequency and impact of transitions between microbial populations mediating biogeochemical cycling in a freshwater lake"**
Sarah Preheim
Johns Hopkins University
- 17:30: **"Cloud based bioinformatics platform for cross-disciplinary microbiome research"**
Nur A. Hasan
CosmosID
- 17:45: **Winter M3 closing remarks**
Mihai Pop
Center for Health-related Informatics and Bioimaging (CHIB)
University of Maryland College Park
- 18:00: **Poster session and reception**
- 19:30: **M3 Dinner (Adele's, STAMP)**