

Mid-Atlantic Microbiome Meet-up (M³)

Inaugural Workshop and Conference

November 1-2, 2016



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web: <http://blog.umd.edu/m3>

discussion forum: <http://groups.io/g/m3>

twitter: @join_M3

Introduction

The M³ consortium was created as a way to catalyze interactions between microbiome researchers within the broadly defined Mid-Atlantic geographic region. At an initial kick-off meeting in July 2016 we had identified strong interest in bringing this community together in order to achieve several goals: (i) create bridges between academia, government, and industry; (ii) provide opportunities for cross-pollinating ideas across communities; (iii) develop best practices and standards for microbiome research; (iv) match data generators with analysts; (v) create career-development and educational opportunities; and (vi) provide networking opportunities to help match local employers with potential job applicants.

To help formalize this consortium we created a website, discussion forum, and twitter handle (see above). As of November 28, 2016, the discussion forum included 114 registrants from about 20 different institutions.

On November 1-2, 2016 we organized a first formal conference under the aegis of the M³ consortium, the summary of which is presented in this document. The conference comprised an initial workshop focused on technical presentations¹ followed by a broader scientific conference².

Day 1 – Workshop

Our meeting started with a workshop targeted specifically at the more junior members of our community. The workshop was restricted to 55 participants due to space limitations. The slots were filled quickly and we received multiple requests to over-subscribe the event, highlighting the strong need for similar events in the future.

The morning was focused on presentations on best practices for microbiome analysis, presented by Emmanuel Mongodin (University of Maryland Institute for Genome Sciences), Nate Olson (NIST & UMD), Brian Brubach (UMD), Mathieu Almeida (UMD), Senthil Muthiah (UMD), and Jay Ghurye (UMD).

The afternoon focused on presentations and demos of analytical software tools:

- Mash – Brian Ondov (NBACC)
- Canu – Sergey Koren (NIH/NHGRI)
- PathoScope & PathoStat – Matthew Bendall (George Washington University)
- VIROME – Daniel Nasko (University of Delaware)
- MetaViz – Jayram Kancherla & Justin Wagner (UMD)
- Pavian – Florian Breitweieser (JHU)

Day 2 – Conference

The second day of our meeting was organized at the Riggs Alumni Center on the University of Maryland Campus and attracted 83 participants from ~20 different institutions.

The meeting started with a keynote by Dr. Maria Giovanni (NIH/NIAID), NIAID Associate Director for Genomics and Bioinformatics, and Director, Office of Genomics and Advanced Technologies, who provided an overview of the broad range of microbiome research projects supported by NIAID, and highlighted future challenges and opportunities in this field.

A second keynote was presented by Dr. Julie Segré (NIH/NHGRI), Chief of the Translational and Functional Genomics Branch and Head of the Microbial Genomics Section of NHGRI. Dr. Segré highlighted recent research from her lab focused on the human skin microbiome as well as on tracking the spread of hospital acquired infections.

Two sets of lightning talk sessions included presentations selected from the 27 poster submissions to the conference. The first session was focused on methods, and included talks from Tandy Warnow (UIUC & Smithsonian), Jeremy Selengut (UMD), Johanna Holm (UM IGS), Sharon Bewick (UMD), and Jason Kralj (NIST). A second lightning talk session focused on applications and included talks on pathogen detection by Kelly Moffat (Cosmos ID), hospital acquired infections by Sean Conlan (NIH/NHGRI), deep-water microbiota by Rosa León-Zayas (University of Delaware), desert microbiota by German Urtskiy (JHU), and the role of microbiota in the success of organ transplantation by Lauren Hittle (UM IGS).

The afternoon session was kicked off by Amy Sapkota (UMD), who presented the CONSERVE project, a recently funded multi-institutional study aimed at identifying safe non-traditional irrigation water sources for agriculture, project within which metagenomic tools are used to understand the environmental context, as well

1 <http://blog.umd.edu/m3/upcoming-events/2016-fall-mid-atlantic-microbiome-meetup/workshop-agenda>

2 <http://blog.umd.edu/m3/upcoming-events/2016-fall-mid-atlantic-microbiome-meetup/conference-agenda>

as to evaluate the quality of water pre- and post-treatment, and the health risks posed to the eventual consumers of agricultural products.

To promote participant interactions, the rest of the afternoon session consisted of a breakout session. Participants were randomly assigned to different tables and, as an ice breaking exercise, worked together on a puzzle – placing a series of events related to microbiome research in chronological order³. The rest of the breakout session was kicked off by a thought-provoking presentation by Adam Phillippy, head of the Genome Informatics Section at NHGRI. Adam proposed the creation of a "digital immune system" – using sequencing and informatics to gather real-time data about the environmental microbiome to understand, detect, and respond to health threats.

The discussions from the breakout session are summarized below.

The workshop concluded with a poster session and a reception, and ~30 participants continued discussions over dinner at Adele's restaurant in the Adele H. Stamp student union.

Summary of breakout session

The breakout session spurred active discussions on a number of themes. Several of the topics discussed were:

- Microbiome studies are leading to a dramatic increase in database sizes. How can we design databases and search methods that can effectively scale with the data?
- Is there a scalable alternative to traditional species-level taxonomies? Traditional taxonomies are based on phenotypic characteristics which cannot be easily inferred from marker genes or even from draft genome sequences. How do we "name" organisms found in metagenomic mixtures? How do we tie any new naming schemes to the traditional taxonomies? How do we deal with lateral gene transfer?
- Current databases still lack many of the microbes found on earth. How can we expand this body of knowledge?
- Is it OK to skip culture and the information we can glean from isolate organisms and simply trust the information inferred from assembled genomes?
- How can we enable and incentivize data sharing? MG-RAST, for example, provides standardized analyses in return for data deposition. Are there other possible models?
- Who would be the potential clients (market) for a new start-up company focused on bio-surveillance.
- What guidelines can we enact/enforce for the quality of the data being deposited in databases? What meta-data can be automatically recorded (such as geotagging, meta-data from sequencing instruments, etc.)

Special acknowledgments

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Logistical support was provided by the University of Maryland Institute for Advanced Computer Studies (UMIACS)

3 <http://www.slideshare.net/MihaiPop20/m3-game-download>

Participating institutions

The participants to the meeting were affiliated with the following institutions:

- Cosmos ID
- George Mason University
- George Washington University
- Georgetown University
- Johns Hopkins School of Medicine
- Johns Hopkins University
- Johns Hopkins University Applied Physics Laboratory
- National Biodefense Analysis and Countermeasures Center
- National Institutes of Health (NIH)
 - National Cancer Institute (NCI)
 - National Human Genome Research Institute (NHGRI)
 - National Institute for Allergy and Infectious Disease (NIAID)
- National Institute for Standards and Technology (NIST)
- Smithsonian Institution
- SUNY Binghamton
- University of Delaware
- University of Illinois
- University of Maryland School of Medicine
- University of Maryland, College Park
- University of Virginia
- US Food and Drug Administration (FDA)
- US Naval Research Laboratory (NRL)

