Mid-Atlantic Microbiome Meet-up (M³)

CAMI/M³ joint meeting May 7-8, 2017



Organizers: Todd Treangen, Mihai Pop (University of Maryland, College Park) Alice McHardy (Helmholtz Centre for Infectious Disease, Braunschweig, Germany), Alex Sczyrba (Bielefeld University, Germany)

Talk selection committee: Alice McHardy(Helmholtz Centre for Infectious Disease), Mihai Pop (UMD), Alex Sczyrba (Bielefeld University), Todd Treangen (UMD)

Meeting administration: Elizabeth Hontz, Barbara Lewis (University of Maryland, College Park)

Media outreach: Tom Ventsias (University of Maryland, College Park)

M³ advisory committee:

Andrea Ottesen (US FDA) Rita Colwell (U. of Maryland, CosmosID) Jocelyne DiRuggiero (JHU) Nick Bergman (NBACC) Jacques Ravel (U. of Maryland School of Medicine/Inst. for Genome Sciences) Jason Kralj (NIST) Jennifer Biddle (U. of Delaware)

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web: <u>http://blog.umd.edu/m3</u> discussion forum: <u>http://groups.io/g/m3</u> 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. To help formalize this consortium we created a website, discussion forum, and twitter handle (see above). As of May 2017, the discussion forum included 130 registrants from over 20 different institutions.

The Critical Assessment of Metagenomic Interpretation (CAMI, http://www.cami-challenge.org) group is an international community of scientists led by Alice McHardy (Helmholtz Centre for Infectious Disease), Alex Sczyrba (Bielefeld University), and Thomas Rattei (University of Vienna). The goal of CAMI is to independently evaluate bioinformatics analysis methods used in metagenomics applications.

M³ and CAMI co-organized a workshop in May 2017 in order to further strengthen the ties between our two communities, and to help engage in the CAMI effort local federal agencies such as NIST and the FDA, agencies that have within their core mission the evaluation of analytical methods.

The first day of the workshop was focused on CAMI and software validation, while the second day of the workshop focused on the broader M³ community (see agenda at: http://blog.umd.edu/m3/upcoming-events/2017-spring-M3/workshop-agenda/). For the week prior to the workshop, researchers and students from the Helmholtz Centre for Infectious Disease, Bielefeld University, Pittsburgh Supercomputing Center, DOE Joint Genome Institute and UMD participated in a joint hackathon focusing on visualization techniques for metagenomic validation, bioboxes for reproducible analytic workflows, and frameworks for evaluating metagenomic binning techniques.

Day 1 – CAMI workshop on metagenomic software validation

The first day of the workshop was focused on topics related to the CAMI challenge. Participants in the prior week's hackathon presented their results, and Alice McHardy introduced the second round of the CAMI challenge and started a group discussions about CAMI, the relevant challenges to be addressed by CAMI2, and performance metrics to be evaluated.

Fiona Brinkman from Simon Fraser University gave a keynote presentation on "*Perspectives on prediction – keeping the goals in sight*".

The day ended with a presentation by Phil Blood from the Pittsburgh Supercomputing Center on the resources provided by the PSC to the bioinformatics community community, followed by a poster session.

Day 2 – M3 workshop

The second day focused on the broader activities of the Mid-Atlantic Microbiome Meet-up. The day started with a keynote presentation by Nikos Kyrpides from the DOE Joint Genome Institute. Dr. Kyrpides presented a broad overview of microbiome science and highlighted recent research conducted by the JGI in this field.

As in prior M³ meetings, a series of "lightning talks" allowed members of our community to highlight their latest research results.

The afternoon was devoted to hands-on training on metagenomic assembly (led by Todd Treangen and Mihai Pop from UMD) and phylogenetic analysis for taxonomic annotation (led by Siavash Mirarab from UCSD).

The meeting ended with a talk by Thomas Rattei from the University of Vienna on challenges in viral metagenomics.

Special acknowledgments

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Special thanks to Markus Fedarko, Jay Ghurye, and Nate Olson, as well as other students from the Pop Lab for helping with meeting logistics.

Participants

The CAMI/M3 workshop had 132 registered participants affiliated with the following institutions:

- Aperiomics, Inc.
- American Society for Biochemistry and Molecular Biology

- Bielefeld University
- BNBI/NBACC
- Center for Algorithmic Biotechnology, St. Petersburg, Russia
- Cosmos ID
- DNA4 Tech
- DOE Joint Genome Institute
- FedCentric Technologies
- George Mason University
- George Washington University
- Georgetown University
- Harris
- Helmholtz Centre for Infectious Disease Research
- Johns Hopkins University
 - Applied Physics Laboratory
 - Homewood
 - School of Medicine
- MRI Global
- 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)
- Pittsburgh Supercomputing Center
- RIKEN

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- Simon Fraser University
- Smithsonian Institution
- SUNY Binghampton
- University of California, San Diego
- University of Delaware
- University of Illinois, Urbana Champaign
- University of Maryland School of Medicine
- University of Maryland, College Park
- University of Pennsylvania
- University of Virginia
- US Food and Drug Administration (FDA)
- US Naval Research Laboratory (NRL)
- Walter Reed Army Institute of Research