

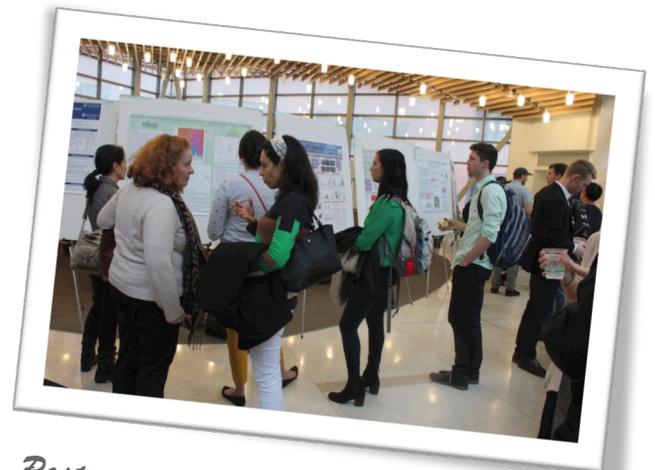


January 9th, 2019
Mudd Hall Auditorium, Johns Hopkins University, Baltimore, MD

Mid-Atlantic Microbiome Meetup

Predictions and the Microbiome

The 2019 Mid-Atlantic Microbiome Meet-up on Predictions and the Microbiome showcased microbiome research at Johns Hopkins and mid-Atlantic region advancing the field in quantitative microbiome analysis and prediction. The conference consisted of a full day of scientific talks, posters and discussion. Talks included both invited speakers and accepted abstracts spanning the spectrum of microbiomes studies. Talks were organized into three sessions and two invited talks. Research from around the region was also showcased during the poster session. A breakout session challenged participants to identify major barriers to applying predictions in their field of study. Participants also mingled and networked over food and drinks.



Poster session and networking with other researcher encourages collaborations.

Summary

This year's meeting, held on Weds. January 9th at Johns Hopkins University, was organized by Jocelyne DiRuggiero and Sarah Preheim. It was attended by 130 researchers and students from multiple institutions around Maryland and Washington DC but also as far as New Jersey, Pennsylvania, Virginia, Illinois, North Carolina, and Florida.



Alvaro Sanchez (Yale University) got the conference off to a great start with his talk “Predictive metabolic models of microbial community assembly”. He highlighted the importance of bridging observational and basic theoretical research drawing on examples from the field of astronomy and how it could relate to predictive microbiome research. When theory and observation come together, major advances can be made. Research in his lab advances a theoretical framework of community assembly on various carbon sources that will eventually be used to interpret observations of environmental or clinical microbial communities. Another invited lecture from Joseph Zackular (University of Pennsylvania) on “Pathogen-microbiota interactions during *Clostridium difficile* Infection” highlighted how detailed microbiome analysis and interactions can help clinicians fight a deadly infectious disease. He presented work about the influence of dietary metals, specifically zinc, on *C. difficile* infections. He also presented work on the interactions between the pathogen and other microbes during infection.



Breakout session

The breakout session allowed participants to provide their opinion about the state of predictions in their field. Participants could choose to engage in one of three targeted discussions. Section 1: Goals and state of the field for microbiome predictions which asked questions such as "How would your field benefit from accurate microbiome predictions?" Section 2: Tools development: Simplifications and model systems which included questions such as "What are some of the considerations for simplifications necessary for predictive models?" Section 3: Applications: Practical issues facing implementation of predictive models including questions like "What are some requirements for predictive models to be accepted/used in your field?"



Alvaro Sanchez during the breakout report

Breakout report

After discussing specific questions within small groups, each breakout section was asked to summarize their findings to all participants. Major themes included the need to brake "silos" between fields and between experimenters and modelers, the need for more data and metadata and the lack of standardized methods. Participants also highlighted the need to develop models that can be tested by the community and a proper framework to understand risk before implementation of predictions, especially in the medical fields.



This meeting would not be possible without the generous support of our sponsors:



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Abstract talks

Abstract talks consisted of ten talks across from different fields of microbiome research. This allowed participants to be exposed to a range of topics, unified under the umbrella of analyzing complex microbial communities with innovative tools or techniques. Speakers were from labs from various academic and government agencies in the region.

Human-associated microbiome and computational methods

1.

Talks on human microbiome studies and computational tool development.

Model systems

2.

Talks from researchers using various host-associated systems for studying fundamental microbiome questions.

Unique environments and metabolism

3.

Extreme environments and non-standard metabolisms.

Attendees contributed substantially to the content and quality of the meeting. We are grateful to everyone for their participation.

The benefits of a regional meeting

Although there are many national and international microbiology and microbiome conferences, there are many benefits to organizing an annual regional meeting including, networking, identification of local resources and getting to know research labs in the area. It also provides students with the ability to attend and present at a scientific meeting without the expense of traveling. Many of the participants enjoyed this experience, saying that it was like a Gordon Research conference and that they enjoyed both the scientific content and the social interactions that this provided. Overall, the community support and interest in this regional conference suggests that it has been a successful endeavor that we will push for years to come.

