Thesis Defense - Samantha Sevilla Chill, PhD, Bioinformatics and Computational Biology
November 10, 2021 3:30 - 5:00 PM
VIEW EVENT
All are invited to attend the defense. For more information please contact Graduate Coordinator at kharrism@gmu.edu.

Candidate: Samantha Sevilla Chill

Program: PhD, Bioinformatics and Computational Biology

Date: Wednesday, November 10, 2021

Time: 3:30 PM

Place: https://gmu.zoom.us/j/92443783368?pwd=YXFNVk50Q1ltYnJKenJQU3daVEZxQT09

Title: Microbiome Analysis: Technical Considerations and Practical Applications

Committee Chair: Dr. Iosif Vaisman

Committee Members: Dr. Ancha Baranova, Dr. Patrick Gillevet

ABSTRACT:

Continued advances in high-throughput sequencing have created new opportunities to discern microbiome composition from a variety of samples and to develop applications in ecological recycling efforts and health and disease exploration. In this work, the study of Tenebrio molitor Linnaeus's microbiome elucidated how these mealworms adapt to consuming biodegradable-resistant materials, including polystyrene (PS), on a varied diet. With 14 million US tons generated yearly, PS is a considerable environmental contaminant. Determining the mechanism behind the digestion of PS into biodegradable components would have significant ecological implications. Additionally, this work seeks to add to the understanding of the gut-brain axis through microbiome profile examination, recently implicated in mental health disorders. The dysbiosis observed between healthy patients and those afflicted with mental health disorders highlights the potential of differential microbial composition and functional predictive modeling. However, for either of these applications to be most meaningful, the implicit technical bias in microbiome research must be understood. Previous studies have attempted to assess these variations with simplistic and unreliable models, failing to reflect a complexity seen in either human or environmental samples. Along with the practical ecological and health-related findings, this study highlights that the careful designing of microbiome-related comparisons, and matching data processing pipelines, are necessary to ensure the reproducibility and reliability of results.