**OVERALL RESPONSIBILITY**

The successful candidate will work with Dr. Leigh Greathouse on biostatistical research on a recently funded DoD project examining the interaction between diet and the human gut microbiome in colon cancer. This project is designed to identify gut microbiota, microbial metabolites, immune markers, and dietary factors that affect treatment response (e.g. chemotherapy-induced diarrhea), recurrence, and survival. As such, analysis will include microbial community multi-omics (metagenomes, metabolomes, etc.) to identify species, strains, microbial gene products, and metabolites with immunomodulatory functions. He or she will be responsible for bioinformatic and biostatistical methods development for microbiome quantitative, metagenomic, and multi-omic data on the project, with a focus on bacterial small RNAs in human gut microbiome that can modulate inflammation.

**PRINCIPAL DUTIES AND RESPONSIBILITIES** (\*Essential Functions)

* \* Development of biostatistical methods for microbiome data analysis, particularly models for population epidemiology of longitudinal, zero-inflated, and compositional measurements of microbial taxa and functional features, with a focus on machine learning methods for building risk predictors.
* \* Development, publication, and implementation of novel quantitative methods for microbiome multi-omics, with a focus on better methods for modeling shifts in microbial states, including Dynamic Bayesian network analysis.
* \* Presentation of results to collaborators, local, national, and international scientific audiences encompassing diverse fields (dietary, computational, and biological).
* Optional mentoring and/or teaching opportunities in the context of Ph.D. students from Biology, undergraduates, and public guest lectures and workshops.
* Regular interaction with internal and external contacts, including scientists from Mayo Clinic and Baylor College of Medicine, collaborators, students, postdocs, and external clinicians.

**MINIMUM QUALIFICATIONS**

* PhD in Biostatistics, Bioinformatics, Computational Biology, or related fields. Some experience with microbiome, microbiological, or molecular 'omics preferred.
* Familiarity with statistics for high-throughput sequencing, ideally microbial community metagenomics, and/or microbial genetics, or RNA-seq.
* Excellent record of scientific contributions, publications, and presentations; primary or key author on one or more major presentations and papers.
* Must be able to handle a variety of tasks, to effectively solve problems with numerous and complex variables, and to shift priorities rapidly.
* Demonstrated success in working on complex, novel research problems.
* Creativity, curiosity, and the desire, persistence and ability to create scientific advances in human microbiome science.