The gut microbiota has emerged as an integral component of organism well-being, influencing the most basic of functions, such as metabolism, to more specialized systems e.g., immunological function.

While work has been done to understand the interactions of host, microbiota, and environment in one dimension, few have attempted to integrate all three of these aspects. This gap is largely due to a lack of computational tools that have the capability to integrate and build models from the large multi-omic datasets that arise from each component.

Viewing the combined data as high dimensional tensors allows us to use techniques such as factor analysis and latent feature representations to find multi-way correlations across the three components. The increased dimensionality also necessitates the need for being able to perform such analyses in a scalable fashion using modern supercomputers, (e.g., NSF-funded Frontera).

We will collect preliminary microbiome data and begin to design new computing approaches. This effort will be translated into a proposal to the NSF solicitation “URoL: Microbiome Theory and Mechanisms.”