

1154-00-1964 **X Wang*** (xwang@tougalo.edu), **WA Pruett** and **J Wilson**. *Uncovering and Understanding Population Difference with Topological Method*. Preliminary report.

In this project, we use topological data analysis and our analytic tool suite to generate information for pathway analysis to better describe the mechanisms of disease in the study population. We begin with the hypothesis that obesity, hypertension, renal disease, and combinations of the three are the result of distinct etiologies within the study participants. Further, we hypothesize that by analyzing aptamer, metabolic, and clinical data alone or in tandem, then differences between populations will explain these etiologies. The primary output of TDA is a dissection of a study population into subpopulations that are internally consistent across all monitored variables. In diseases like hypertension and metabolic syndrome, the same "disease" may come from many different mechanisms. The mechanisms underlying the disease determine the best treatment. The goal of this analysis is to break populations with complex diseases into mechanistically consistent subpopulations and propose treatments based on the mechanism. The value of this technique is that it allows the structure of a space to be studied without reducing its dimensionality. This means that we can ostensibly study panels with tens of thousands of genes, metabolites, or other data points. (Received September 16, 2019)