

Dr. Hongmei Zhang's **statistical methodology research interest** is in Bayesian inferences and includes (with a brief mentioning of their applied areas)

(1) Clustering and joint clustering: Use probability models to (jointly) group subjects and variables such that those variables have a similar association with an external variable of interest, e.g., age or time. This research was supported by NIAID/NIH aiming to improve the homogeneity in clusters with respect to the association of allergic sensitization over time, as well as DNA methylation patterns at different loci (see **Areas that the above methods applied to** for its layman definition).

(2) Variable selections with and without measurement errors: Develop variable selection methods with the ability to select variables in linear regressions via improvement of Zellner's g-prior. Data collected in various studies are sometimes accompanied by measurement errors or misclassifications, e.g., gene expression data or self-reported smoking status. Incorporating the errors into the analytical model has the potential to improve the analysis quality. This study was supported by NHLBI/NIH for the purpose of identify genetic markers via gene expressions related to lung function.

(3) Variable selections in clustering: The goal of this study is to select dependent variables and in the meantime cluster those variables showing similar patterns with external variables of interest. This is part of an NIAID/NIH funded project and aims to detect stable and dynamic DNA methylation.

(4) Graphical modeling: Develop methods to construct Bayesian network and compare Bayesian networks from multiple populations. The concert work of genetic variants and of epigenomic features on health outcomes and its connection to the identification of genetic/epigenetic markers motivated this project.

Areas that the above methods applied to: (1) Allergic diseases including eczema, asthma, and rhinitis, lung function, and their related risk factors. (2) Obesity and related risk factors. (3) DNA methylation patterns and its change over time (in layman language, DNA methylation is basically an addition of a methyl group, a chemical group, to a DNA molecule). (4) single nucleotide polymorphisms, DNA methylation, and gene expressions with respect to their joint effects.

All the projects could not succeed without tremendous contribution from the great graduate students and post-doctoral fellows.