



**2019 Annual Report for the Richard and Elizabeth Henes Endowed
Professorship in Mathematical Sciences**

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During the past year, I used the endowment funds to support a PhD student. Below I summarize the research progress I have made over the year.

Publications: I co-authored eight publications in peer-reviewed journals. One of the papers was published in *Bioinformatics* that is one of the best journals in statistical genetics. These publications are listed below (* denotes corresponding author; graduate students' names are underlined).

1. Li X, **Zhang S**, Sha Q. Joint analysis of multiple phenotypes using a clustering linear combination method based on hierarchical clustering. *Genet Epidemiol.* 2019 Sep 20. doi: 10.1002/gepi.22263. [Epub ahead of print]
2. Zhang J, Wu B, Sha Q, **Zhang S**, Wang X. A general statistic to test an optimally weighted combination of common and/or rare variants. *Genetic Epidemiol.* 2019 Sep 09. doi: 10.1002/gepi.22255. [Epub ahead of print]
3. Yang X, **Zhang S**, Sha Q (2019). Joint analysis of multiple phenotypes in association studies based on cross-validation prediction error. *Sci. Rep.*, 9 (1): 1073. <https://www.nature.com/articles/s41598-018-37538-y.epdf>
4. Sha Q, Wang Z, Zhang X, **Zhang S*** (2019) A clustering linear combination approach to jointly analyze multiple phenotypes for GWASs. *Bioinformatics*, 35 (8): 1373–1379.
5. Wang Z, Sha Q, Fang S, Zhang K, **Zhang S*** (2018) A novel test by testing an optimally weighted combination of common and rare variants with multiple traits. *PLoS ONE*, 13(7): e0201186. Doi: 10.1371/journal.pone.0201186.
6. Liang X, Sha Q, **Zhang S*** (2018) Joint analysis of multiple phenotypes in association studies using allele-based K-means clustering approach for non-normal distributions. *Ann Hum Genet*, 82(6): 389-395.
7. Liang X, Sha Q, Rho Y, **Zhang S*** (2018) A hierarchical clustering method for dimension reduction in joint analysis of multiple phenotypes. *Genet Epidemiol*, 42:344-353.
8. Zhu H, **Zhang S**, Sha Q (2018) A novel method to test associations between a weighted combination of phenotypes and genetic variants. *PLoS One*, 13(1): e0190788. doi: 10.1371/journal.pone.0190788

Advising graduate students: I advised three PhD students, Steve Yan, Joy Hu, and Lirong Zhu. Joy is doing an internship at the Food and Drug Administration (FDA) this year. She is expected to graduate in spring or summer of 2020. Steve gave his first presentation at an international conference, the American Society of Human Genetics (ASHG), in Oct 2019. This is the best and largest conference in statistical genetics. The title of the presentation is “Gene-based analysis using gene expression data and polygenic risk score”. Lirong just enrolled in the PhD program this fall.

External funding: Dr. Qiuying Sha and I have an ongoing NIH R15 project. This project is going well and will be completed in April 2020. Collaborated with Dr. Qiuying Sha and Dr. Scott Hebring in Marshfield Clinic, we submitted a R01 proposal to the NIH in Feb 2019. Although this proposal was not funded, we are working on revising the proposal and plan to resubmit it in 2020.

Collaborations: As I mentioned above, I have been collaborating with Dr. Hebring at Marshfield Clinic for over a year. Dr. Hebring just visited Michigan Tech for the second time in Nov 2019. During his visit, we discussed a new project based on the family data collected in Marshfield Clinic. We plan to develop network methods to estimate disease heritability based on the family structure and the Electronic Health Record (EHR) of the members in the families. I am very excited on this project and looking forward to moving this project forward.