

# Shiying Liu

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## EDUCATION

<b>Case Western Reserve University</b> , Cleveland, OH <i>Doctor of Philosophy, Epidemiology &amp; Biostatistics</i>	08/2019 – present
<b>Carnegie Mellon University</b> , Pittsburgh, PA <i>Master of Science, Biomedical Engineering</i>	08/2016 – 12/2017
<b>Fudan University</b> , Shanghai, China <i>Bachelor of Science, Biological Sciences</i>	09/2012 – 07/2016
<b>The University of Hong Kong</b> , Hong Kong, China <i>Exchange Study, Biological Sciences</i>	09/2014 – 12/2014

## RESEARCH EXPERIENCE

<b>Case Western Reserve University</b> , Cleveland, OH <i>Research Assistant for Dr. Dana Crawford</i> <b>Longitudinal Changes in T-Cell Receptor Sequence Diversity in Minimal Change Disease</b> <ul style="list-style-type: none"><li>Characterized and compared the T-cell receptor repertoire metrics, including clonality and overlap, for patients with minimal change disease both during active disease and complete remission</li><li>Identified T-cell receptor beta-chain amino acid sequences unique to the active disease status</li><li>Characterize the major histocompatibility complex (MHC) region and estimate human leukocyte antigen (HLA) alleles from whole-genome sequencing data</li></ul>	12/2019 – present
<i>Rotation with Dr. Jonathan Haines</i> <b>Practice with Genome-Wide Association Study (GWAS) and Command Line Programs</b> <ul style="list-style-type: none"><li>Performed quality control, population stratification, and association analysis using PLINK and compared the characteristics of different versions of PLINK, including 1.07, 1.9 and 2.00 beta</li><li>Practiced working with command lines, high-performance computing, and the LINUX system</li></ul>	03/2020 – 05/2020
<i>Rotation with Dr. Hao Harry Feng</i> <b>Analysis of Single-cell RNA Sequencing Data of Fragile X Syndrome (FXS) Forebrain Organoids</b> <ul style="list-style-type: none"><li>Analyzed the gene expression of the FXS forebrain organoids at the single-cell level, in which the differentially expressed genes and the conservative marker genes were obtained for each cluster, and the single-cell pseudo-time trajectories were constructed to show the altered developmental trajectory in a cell type-specific manner</li></ul>	09/2019 – 12/2019
<b>University of Pittsburgh</b> , Pittsburgh, PA <i>Research Assistant for Dr. (Joyce) Chung-Chou H. Chang</i> <b>Statistical Approaches in Analyzing Medical Data</b> <ul style="list-style-type: none"><li>Identified the association between care fragmentation and mortality, adjusting for covariates and clustering effects</li><li>Explored surrogate marker in depth through literature research of causal inference and propensity score analysis</li><li>Inspected the data analytic strategies involved in the analysis of electronic health records using machine learning algorithms</li></ul>	04/2018 – 04/2019
<b>Center for Neuroscience research, Allegheny General Hospital</b> , Pittsburgh, PA <i>Research Assistant for Dr. Kevin M. Kelly</i> <b>Changes of Hippocampal Neuropeptide Y (NPY) Protein Expression after Controlled Cortical Impact (CCI)</b> <ul style="list-style-type: none"><li>Identified the associations among long-term alterations of NPY expression in three targeting subfields of hippocampi, CCI treatment, and posttraumatic epileptogenesis adjusting for injury severity</li></ul>	08/2017 – 07/2018

**Fudan University**, Shanghai, China

**Undergraduate Thesis Project (Mentor: Dr. Juan Lin)**

11/2015 – 07/2016

**Role of Ca<sup>2+</sup>/Cation Antiporters (CAX) Gene Family in *Arabidopsis Thaliana***

- Constructed overexpression vectors for *CAX1-11* to elucidate their function of salt/drought resistance and analyzed the gene expression after treated with a range of concentrations of cations with qPCR.

**Research Intern for Dr. Feng Zhang**

01/2015 – 10/2015

**Identification of Single-Nucleotide Polymorphisms (SNPs) in *TBX6* Associated with Infertility in Mice**

- Identified SNPs from the experimental CRISPR mice cohort with spermatogenic impairment and verified the findings in the human study groups.

## **PUBLICATIONS**

Sun, Z., **Liu, S.**, Kharlamov, E. A., Miller, E. R., & Kelly, K. M. (2018). Hippocampal neuropeptide Y protein expression following controlled cortical impact and posttraumatic epilepsy. *Epilepsy & Behavior*.

Zheng, Y., Wang, L. B., Sun, S. F., **Liu, S. Y.**, Liu, M. J., & Lin, J. (2020). Phylogenetic and ion-response analyses reveal a relationship between gene expansion and functional divergence in the Ca<sup>2+</sup>/cation antiporter family in Angiosperms. *Plant Molecular Biology*, 1-18.

Kang, Y., Zhou, Y., Li, Y., Han, Y., Xu, J., Niu, W., **Liu, S. Y.**, ... & Wen, Z. (2021). A human forebrain organoid model of fragile X syndrome exhibits altered neurogenesis and highlights new treatment strategies. *Nature Neuroscience*, 24(10), 1377-1391.

## **PRESENTATIONS**

**Liu, S.**, Longitudinal changes in T-cell receptor sequence diversity in minimal change disease. *American Society of Human Genetics (ASHG) 2020*.

## **AWARDS & HONORS**

Summer Institute in Statistical Genetics (SISG) scholarship at the University of Washington (2020)

Diana Jacobs Kalman/AFAR Scholarships for Research in the Biology of Aging (2021)

## **TEACHING**

Department of Population and Quantitative Health Sciences (PQHS), Case Western Reserve University

PQHS 431: Introduction to Statistical Methods I

Teaching Assistant

2021

## **SOFTWARE SKILLS**

- R, SQL, Stata, Python, MATLAB, SAS, Java, etc.
- PLINK, MERLIN