

# Siyi Chen, Ph.D.

## RESEARCH INTERESTS

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My research addresses Mendelian randomization/TWAS, causal inference, structural equation modeling, stochastic modeling, species problem, approximate Bayesian computation, Bayesian statistics.

## EDUCATION

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<b>Peking University</b> <i>Bachelor of Science, Chemistry</i>	Beijing, China <i>July 2013</i>
<b>Rice University</b> <i>Master of Science, Statistics</i>	Houston, TX <i>May 2015</i>
<b>Rice University</b> <i>Doctor of Philosophy, Statistics</i>	Houston, TX <i>Dec 2020</i>

## POSITIONS AND EMPLOYMENT

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<b>Department of Statistics, Rice University</b> <i>Graduate Research Assistant</i>	2016-2020 <i>Houston, TX</i>
<b>Division of Biostatistics, School of Public Health, University of Minnesota</b> <i>Post-Doctoral Associate</i>	2021-2023 <i>Minneapolis, MN</i>
<b>Department of Neurological Sciences, Rush University Medical Center</b> <i>Instructor</i>	2023-2024 <i>Chicago, IL</i>
<b>RUSH Alzheimer's Disease Center, Rush University</b> <i>Biostatistician</i>	2023-2024 <i>Chicago, IL</i>
<b>Biostatistics &amp; Data Science (BSDS), LSU School of Public Health</b> <i>Assistant Professor</i>	2024-present <i>New Orleans, LA</i>

## RESEARCH EXPERIENCE

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<b>Postdoctoral research associate</b> <i>Department of Biostatistics, University of Minnesota</i> <ul style="list-style-type: none"><li>• Supervisor: Dr. Wei Pan</li></ul>	2021-2023 <i>Minneapolis, MN</i>
<b>Research Assistant</b> <i>Department of Statistics, Rice University</i> <ul style="list-style-type: none"><li>• Supervisor: Dr. Marek Kimmel</li><li>• Developed a sequential truncated-population approximate Bayesian computation (ABC) algorithm and applied the ABC methods to symmetric Dirichlet-multinomial model and the proposed asymmetric Dirichlet-multinomial model to estimate hematopoietic stem cells count</li></ul>	2017-2020 <i>Houston, TX</i>
<b>Research Assistant</b> <i>Department of Statistics, Rice University</i> <ul style="list-style-type: none"><li>• Simulated barcoding experiments and empirical distributions of the estimators of barcodes number in mice blood cell samples</li><li>• Developed a multi-type Markov age-dependent branching process for modeling hematopoietic stem cell expansion</li></ul>	2016-2017 <i>Houston, TX</i>

## PUBLICATIONS & MANUSCRIPTS

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Katie A Matatall, Mira Jeong, **Siyi Chen**, Deqiang Sun, Fengju Chen, Qianxing Mo, Marek Kimmel, Katherine King (2016) “Chronic infection depletes hematopoietic stem cells through stress-induced terminal differentiation”, *Cell Reports*, 17, 2584–2595.

**Siyi Chen**, Zhaotong Lin, Xiaotong Shen, Ling Li, and Wei Pan “Inference of causal metabolite networks in the presence of invalid instrumental variables with GWAS summary data,” *Genetic Epidemiology* (2023)

**Siyi Chen** “Statistical modeling for species count data with heterogeneity,”  
<https://scholarship.rice.edu/handle/1911/109642>

**Siyi Chen**, Katherine King, Marek Kimmel “Statistical inference from stem cell barcoding data using adaptive approximate Bayesian computation”, *Submitted*.  
[https://assets.researchsquare.com/files/rs-187743/v1\\_covered.pdf?c=1631853488](https://assets.researchsquare.com/files/rs-187743/v1_covered.pdf?c=1631853488)

## PRESENTATIONS

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### **2023 IGES Annual Meeting**

*Presentation*

Nashville, TN

2023

### **STATGEN 2024**

*Presentation*

Pittsburgh, PA

2024

## TEACHING EXPERIENCE

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### **Teaching Assistant**

*Department of Statistics*

Rice University

*Houston, TX*

- **Mathematical Probability I**, Fall 2015
- **Probability**, Fall 2015 & Fall 2016
- **Probability in Bioinformatics and Genetics**, Spring 2016