

# 邹 鉴

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## 研究方向

基于临床和高维组学数据的统计学习与机器学习方法的开发和应用

## 教育经历

生物统计学博士 2019 年 9 月 – 2023 年 5 月 (预计)

美国匹兹堡大学 (University of Pittsburgh) 公共卫生学院

- GPA: 3.93/4.00
- 导师: George C. Tseng; 合作导师: Steffi Oesterreich & Adrian Lee
- 毕业论文: “Various Statistical Modeling and Learning Issues in Omics Data Analysis”

生物统计学硕士 (理论与方法方向) 2017 年 9 月 – 2019 年 5 月

美国纽约哥伦比亚大学 (Columbia University in the City of New York) Mailman 公共卫生学院

- GPA: 4.00/4.33
- 导师: Bin Cheng & Ying Wei
- 实践项目: “Statistical Evaluation and Selection of Normalization Methods for microRNA Sequencing Data in Cancer Biomarker Studies”

生物技术与应用化学学士 (双学位) 2013 年 9 月 – 2017 年 5 月

华中师范大学生命科学学院

- GPA: 3.85/4.00
- 导师: 杨旭 & 李睿
- 毕业论文: “茶多酚对小鼠神经毒性的影响”

## 工作经历

研究助理/生物统计师 (Graduate Student Researcher) 2019 年 9 月至今

UPMC Magee-Womens 研究所 (导师: Steffi Oesterreich & Adrian Lee) 美国匹兹堡

统计咨询与癌症生物学的临床和组学数据分析

当前工作: 激素治疗前后的多组学数据比较; 原位乳腺癌与脑转移的微环境分析

完成工作: 前哨淋巴结活检与放疗对老年乳腺癌患者的预后影响; 乳腺癌回顾性队列研究

研究助理 (Graduate Student Researcher) 2019 年 9 月至今

匹兹堡大学生物统计系 (导师: George C. Tseng) 美国匹兹堡

机器学习方法及其在癌症生物学中的应用

当前工作: 癌症模型的多组学与单细胞测序评估

完成工作: 约束性聚类方法 (constrained clustering); 癌症模型的转录组相似性评估; 荟萃分析中的生物标志物探测

研究实习 (Research Intern) 2019 年 1 月 – 2019 年 5 月

纪念斯隆-凯特琳癌症中心 (Memorial Sloan Kettering Cancer Center) (导师: Li-Xuan Qin) 美国纽约

小分子 RNA(microRNA) 测序数据的归一化方法 (normalization) 的统计评估与选择

研究助理 (Research Assistant) 2018 年 5 月 – 2019 年 5 月

哥伦比亚大学生物统计系 (导师: Ying Wei) 美国纽约

美国国家执业医师数据库 (National Practitioner Data Bank) 的牙科事故数据分析

用潜变量 (latent variable) 进行多维变量计数数据 (multi-variable count data) 的建模

## 论文发表

注: †: 共同第一作者; \*: 通讯/资深作者

1. Steffi Oesterreich†\*, Azadeh Nasrazadani†, Jian Zou†, Neil Carleton, Tiffany Onger, Matthew D Wright, Yujia Li, Kathryn Demanelis, Bhuvaneswari Ramaswamy, George Tseng, Adrian V. Lee, Nicole Williams\*, Megan Kruse\*. Clinicopathological Features and Outcomes Comparing Patients with Invasive Ductal and Lobular Breast Cancer, accepted by *Journal of the National Cancer Institute*. (IF: 11.816; JCR: Q1)
2. Jian Zou†, Yannick Düren†, and Li-Xuan Qin\* (2022). PRECISION.seq: An R Package for Benchmarking Depth Normalization in microRNA Sequencing. *Frontiers in Genetics* 12. (IF: 4.772; JCR: Q1)
3. Neil Carleton, Jian Zou, Yusi Fang, ..., George C. Tseng, Oscar C. Marroquin, Adrian V. Lee\*, Priscilla F. McAuliffe\* (2021). Outcomes After Sentinel Lymph Node Biopsy and Radiotherapy in Older Women With Early-Stage, Estrogen Receptor-Positive Breast Cancer, *JAMA Network Open* 4(4): e216322-e216322.
4. Terrell E. Jones, Jian Zou, George C. Tseng, Somak Roy, Rohit Bhargava\* (2021). The Utility of Next-Generation Sequencing in Advanced Breast and Gynecologic Cancers: Experience of a Large Tertiary Care Women's Hospital, *American Journal of Clinical Pathology* 156(3): 455-460.
5. Li-Xuan Qin\*, Jian Zou, Jiejun Shi, Ann Lee, Aleksandra Mihailovic, Thalia A. Farazi, Thomas Tuschl, Samuel Singer (2020). Statistical Assessment of Depth Normalization for Small RNA Sequencing, *JCO Clinical Cancer Informatics* 4 (June): 567-582.
6. Peng Liu, Silvia Liu, Yusi Fang, Xiangning Xue, Jian Zou, George C. Tseng\*, Liza Konnikova\* (2020). Recent Advances in Computer-assisted Algorithms for Cell Subtype Identification of Cytometry Data, *Frontiers in Cell and Developmental Biology* 8 (April): 234.

## 待发表工作

7. Jian Zou, George C. Tseng\*. Mutual Information for Multi-Study Multi-Class Concordant Biomarker Detection.
8. Jian Zou, Yujia Li, George C. Tseng\*. CGMM: A Novel Algorithm for Constrained Model-Based Clustering.
9. Jian Zou, George C. Tseng\*. Genomics Congruence Framework to Optimally Select Representative Cancer Models for Specific Tumor Subtypes.
10. Wei Zong, Tanbin Rahman, Li Zhu, Xiangrui Zeng, Yingjin Zhang, Jian Zou, Song Liu, Zhao Ren, Jingyi Jessica Li, Steffi Oesterreich, Tianzhou Ma, George C. Tseng\*. CAMO: A Molecular Congruence Analysis Framework for Evaluating Model Organisms.
11. Sayali Onkar, Jian Cui, Jian Zou, Carly Cardello, Anthony R Cillo, Mostofa Rafid Uddin, April Sagan, Marion Joy, Hatice U Osmanbeyoglu, Katherine Pogue-Geile, Priscilla F. McAuliffe, Peter C. Lucas, George C. Tseng, Adrian V Lee, Tullia C Bruno, Steffi Oesterreich\*, Dario A.A. Vignali\*. Immune Landscape in Estrogen Receptor Positive Breast Cancer Reveals a Divergent Macrophage-Driven Microenvironment, under second review in *Nature Cancer*.

学术报告

1. CGMM: an algorithm for constrained model-based clustering (poster)  
*ICSA Applied Statistics Symposium, Florida, June 2022; Symposium on Data Science & Statistics, Pittsburgh, June 2022; ASA Pittsburgh Spring Banquet, Pittsburgh, April 2022*
2. Congruence analysis to optimally select representative cell lines for breast cancer histological subtypes (poster)  
*NISS Graduate Student Research Conference, May 2022*
3. Congruence analysis between cell lines and tumors (talk)  
*Pitt Biostatistics Research Day, March 2022*
4. Outcomes after sentinel lymph node biopsy and radiation therapy in elderly women with ER+, early stage breast cancer (poster)  
*Pitt GSPH Dean's Day, April 2021*
5. Abstract PS11-02: Comprehensive comparative analysis of invasive ductal and lobular breast cancer cases in great lakes breast cancer consortium (3rd author) (poster)  
*San Antonio Breast Cancer Symposium, December 2020*
6. Abstract PS1-10: Outcomes after sentinel lymph node biopsy and radiation therapy in women over 70 years old with ER+, HER2-, clinically node negative breast cancer (3rd author) (poster)  
*San Antonio Breast Cancer Symposium, December 2020*
7. Statistical assessment of depth normalization methods for microRNA sequencing (talk)  
*11th ICSA International Conference, Hangzhou, December 2019*

获奖情况

• Student & Early Career Travel Award, <i>2022 Symposium on Data Science &amp; Statistics</i>	2022 年 4 月
• The 2022 Mihaela Serban Award for Best Poster Presentation, <i>ASA Pittsburgh Chapter</i>	2022 年 4 月
• 优秀毕业生, 华中师范大学	2017 年 6 月
• 全国大学生生命科学创新实验大赛二等奖, 高等学校国家级实验示范中心联席会	2016 年 8 月

统计软件

• MSCC: An R package for Multi-Study Multi-Class Concordance Analysis, available on <a href="#">GitHub</a>	
• CASCAM: An R package of Congruence Analysis and Selector of Cancer Models, available on <a href="#">GitHub</a>	
• PRECISION.seq: An R Package for Performance Assessment of Depth Normalization Methods in microRNA Sequencing, available on <a href="#">GitHub</a>	

教学经历

• 讲师, Mathematical Methods for Statistics, 匹兹堡大学生物统计系	2021 年秋
• 助教, Analysis of Categorical Data, 哥伦比亚大学生物统计系	2018 年夏

学会会员

• 会员, 泛华统计协会 ( <i>International Chinese Statistical Association, ICSA</i> )	2021 年至今
• 会员, 美国统计协会 ( <i>American Statistical Association, ASA</i> )	2020 年至今

学术服务

• 学生代表, 匹兹堡大学生物统计系	2020 年至今
• 学生代表, 美国统计协会匹兹堡分会	2020 年至今
• 成员, 美国统计协会基因组学和遗传统计学分会 ( <i>SSGG</i> ) 成员参与委员会	2020 年至今