# Xiaohan Chi

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## EDUCATION

**The University of Texas MD Anderson Cancer Center UTHealth Graduate School of Biomedical Sciences**
*Ph.D. in Quantitative Sciences - Biostatistics* *Sep. 2022 – Present*

**Shanghai Jiao Tong University** | School of Life Sciences and Biotechnology
*M.S. in Biology (Bioinformatics and Biostatistics)* *Sep. 2019 – Jun. 2022*

- Overall GPA: 3.73/4.0
- Courses: Clinical Trial Design (A+), Survival Analysis (A), Causal Inference Methods in Data Science (A+)

*B.S. in Biotechnology (Bioinformatics and Biostatistics)* *Sep. 2015 – Jun. 2019*

- Overall GPA: 3.55/4.0; Major GPA: 3.88/4.0
- Courses: Probability and Statistics (A+), Calculus II (A), Biostatistical Models (A+)

## RESEARCH EXPERIENCE

**A Seamless 2-in-1 Bayesian Design Combining Dose Optimization and Proof of Concept for Drug Combination Therapy (1st Rotation)** *Sep. 2022 – Present*
*Department of Biostatistics, MD Anderson Cancer Center* *Supervisor: Prof. Ying Yuan*

- Propose a phase II adaptive design with dose optimization to drop ineffective combination doses and reduce the number of required arms and patients
- Adaptively make go/no-go decisions and establish the proof of concept for the combination drug based on the logistic regression model with information borrowing

**A Generalized Calibrated Bayesian Hierarchical Modeling Approach to Basket Trials** *Sep. 2021 – Aug. 2022*
*Department of Biostatistics, MD Anderson Cancer Center* *Supervisor: Prof. Ruitao Lin*

- Extended the calibrated Bayesian hierarchical modeling (BHM) approach to monitor phase II basket trials with multiple endpoints
- Proposed two generalizations, one based on the latent variable approach and the other based on the multinomial-normal hierarchical model, to accommodate different types of endpoints and dependence assumptions regarding information sharing
- Introduced shrinkage parameters as functions of statistics measuring homogeneity among subtypes, and proposed a general calibration approach to determine the functional forms
- Investigated theoretical properties of the generalized hierarchical models
- Used simulation studies to demonstrate that the monitoring procedure based on the generalized approach yields desirable operating characteristics

**BOB: Bayesian Optimal Design for Biosimilar Trials with Co-Primary Endpoints** *Jan. 2021 – Aug. 2021*
*Department of Biostatistics, MD Anderson Cancer Center* *Supervisor: Prof. Ruitao Lin*

- Developed a Bayesian optimal design for biosimilar trials by incorporating both safety and efficacy endpoints in a uniform framework and built a Bayesian joint safety and efficacy model
- Employed a so-called Bayesian biosimilar probability to make go/no-go decisions
- Optimized the Bayesian design to maximize the statistical power while maintaining the frequentist type I error rate at the nominal level
- Carried out extensive simulation studies to show that the design has desirable performance in terms of the false positive rate and the average sample size
- Applied the proposed design to a biosimilar trial evaluating a ranibizumab product

**A Bayesian-based Method in Evaluating Bioequivalence of Highly Variable Drugs** *Sep. 2019 – Sep. 2020*

*Department of Bioinformatics and Biostatistics, SJTU* *Supervisor: Prof. Zhangsheng Yu*

- Innovatively considered the prior as a "weighting function" to give a better explanation of the prior in the bioequivalence evaluation of highly variable drugs
- Constructed elastic priors combining multiple distributions to place higher weight on complex test regions with respect to the feature of bioequivalence tests
- Conducted simulations to prove that the proposed procedure has increased efficacy in comparison to alternative methods recommended by the FDA and EMA and sufficiently controls the type I error rate

**Statistical Methods of Drug Consistency Evaluation in Non-lognormal Distribution** *Sep. 2018 – Jun. 2019*

*Department of Bioinformatics and Biostatistics, SJTU* *Supervisor: Prof. Zhangsheng Yu*

- Proposed a novel non-parametric hypothesis testing procedure based on the Delta Method with asymptotic type I error rate guaranteed regardless of normality assumption
- Applied the Box-Cox transformation to enhance the robustness of bioequivalence tests
- Carried out extensive simulations to show that the proposed procedure yields power improvements in finite samples and performs stronger robustness under different types of distributions

## PUBLICATIONS

1. **Chi, X.**, Yuan, Y., Lin, R.*, and Yu, Z. (2022+). A Generalized Calibrated Bayesian Hierarchical Modeling Approach to Basket Trials with Multiple Endpoints. Under Review *in Biostatistics*.
2. **Chi, X.**, Yu, Z., and Lin, R.* (2022). BOB: Bayesian Optimal Design for Biosimilar Trials with Co-Primary Endpoints. *Statistics in Medicine*. 41(26): 5319 – 5334.
3. **Chi, X.**, Chen, S., Cui, Y., and Yu, Z.* (2022). Two Approaches to Improve the Robustness of Average Bioequivalence Evaluation – under Non-lognormal Distribution. *Chinese Journal of Health Statistics*. In Press

## PRESENTATIONS

**A Generalized Calibrated Bayesian Hierarchical Modeling Approach to Basket Trials with Multiple Endpoints**

- NESS Symposium 2022 Invited Student Paper Session. Oral presentation. *May. 2022*

**BOB: Bayesian Optimal Design for Biosimilar Trials with Co-Primary Endpoints.**

- 2021 China Biostatistics Conference (CBC2021). Beijing, China. Poster. *Nov. 2021*
- 2021 International Youth Biostatistics Forum. Shanghai, China. Oral presentation. *Apr. 2021*

## HONORS & AWARDS

- Honorable Mention Winner of 2022 JSM Biopharmaceutical Student Paper Awards *2022*
- Third Prize of Best Poster at the CBC2021 *2021*
- Second Prize of Excellent Reporter at the 2021 International Youth Biostatistics Forum *2021*
- First-level Academic Scholarship for Graduate Students, SJTU *2021*
- Outstanding Graduate, SJTU (15%) *2019*
- Kwang-Hua Scholarship, SJTU (5%) *2018*

## TECHNICAL SKILLS

- **Programming Languages:** Proficient in R, Python, Shell, Stan, JAGS, LaTeX
- **Languages:** English (TOEFL:100), Mandarin (Native)