

Ruoyi Cai

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EDUCATION

University of Washington

Ph.D., Department of Biostatistics September 2019 – Present
• School of Public Health Award 2019

University of Wisconsin-Madison

Bachelor of Science in *Statistics (Honors)* and *Mathematics* May 2019
• Dean's List (All Semesters)
• Hilldale Undergraduate/Faculty Research Fellowship 2018
• University Book Store Academic Excellence Award 2019

PUBLICATIONS

- **Cai R**, Ané C. Assessing the fit of the multi-species network coalescent to multi-locus data. *Bioinformatics*. 2020 Oct 7;btAA863. doi: 10.1093/bioinformatics/btaa863.
- Zhang H, **Cai R**, Dai J, Sun W. EMeth: An EM algorithm for cell type decomposition based on DNA methylation data. *Sci Rep*. 2021 Mar 11;11(1):5717. doi: 10.1038/s41598-021-84864-9.

RESEARCH EXPERIENCES

Department of Biostatistics, University of Washington Sep 2019 – Present

Independent study project and research assistant advised by Professor Sharon Browning

- Developed a method for inferring effective population size using identical-by-descent segments in human X chromosome with application to estimate gender-specific demographic history by combining the X chromosome effective population sizes with autosomal effective size
- Conducted data simulation; analyzed real human genotype data; coded scripts for the proposed method in shell script, R and Julia; prepared manuscript

Fred Hutchinson Cancer Research Center

June 2020 – March 2021

Independent study project advised by Professor Wei Sun

- Worked on an independent study project to investigate the association between cell-type proportions in bulk tumor tissues and the outcome of immunotherapy
- Analyzed large-scale scRNA-seq data; prepared cell type-specific reference gene expression matrix; inferred cell-type proportions in bulk tumor tissues

Department of Biostatistics, University of Washington

July 2020 – Aug 2020

Research assistant advised by Professor Brian Browning

- Evaluated accuracy of genotype phasing and imputation performed by the Michigan Imputation Server (MIS) as compared to BEAGLE

- Coded shell scripts for formatting unphased input genotype data, conducting genotype phasing and imputation using both BEAGLE and MIS, and computing the phasing and imputation accuracy

Department of Statistics, University of Wisconsin-Madison

Spring 2018 – June 2019

Senior Honors Thesis advised by Professor Cecile Ane

- Developed a goodness-of-fit test to identify the population structure and reticulation complexity sufficiently explaining the evolutionary relationships reflected in genomic data
- Coded functions and scripts in Julia for the application of the test and for doing simulations on empirical examples to evaluate the precision and efficiency of the test; prepared manuscript

Department of Genetics, University of Wisconsin-Madison

Aug 2017 – June 2019

Undergraduate Research advised by Professor Audrey Gasch

- Conducted independent research to study the effect of strain backgrounds and gene expression levels on the stress sensitivity of the budding yeast *Saccharomyces cerevisiae*
- Discovered research questions, wrote research proposal, designed experiments, applied benchwork and computational techniques of genetics research, drew conclusions from research data using statistical analysis, and presented research findings in lab meeting

PRESENTATIONS

- **Cai R**, Browning BL, and Browning SR. “Sex-specific effective population size inference in recent history.” American Society of Human Genetics 2021 Annual Meeting. *Oral presentation.*
- **Cai R**, Ané C. “A goodness-of-fit test to study the history of a group of species based on genome sequences.” 2019 Undergraduate Symposium, University of Wisconsin-Madison. *Poster presentation.*
- **Cai R**, Gasch A. “Elucidating genotype-phenotype relationship in *Saccharomyces cerevisiae* via the effect of strain background and gene expression on stress sensitivity.” 2019 Undergraduate Symposium, University of Wisconsin-Madison. *Poster presentation.*

TEACHING EXPERIENCE

Department of Biostatistics, University of Washington

Sep 2021 – Dec 2021

Teaching Assistant for BOST 514/517: Biostatistics I

- Held two 50-minute discussion sessions and a 90-minute office hour each week; graded weekly homework and two exams for 100 students; replied to students’ questions through email and Canvas discussion board

Undergraduate Learning Center, University of Wisconsin-Madison

Sep 2017 – May 2019

Paid Tutor in Statistics

- Assisted with statistics courses and programming in R for around 20 students by one 3-hour drop-in session and by appointment every week

SKILLS

- R, Julia, Unix shell script, Java, C++, and LaTeX
- Techniques for genetics research: growing and collecting cells; extracting and purifying RNA; running gels; using microscope; gene annotation; functional enrichment