

# Ruoyi Cai

Department of Biostatistics, University of Washington  
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## EDUCATION

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### 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

## SKILLS

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- 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

## PUBLICATIONS

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- **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

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**Department of Biostatistics, University of Washington** Sep 2019 – Present

*Research assistant and independent study project advised by Professor Sharon Browning and Professor Brian Browning*

- Developed a method for understanding gender-specific demographic history by comparing the historical effective population sizes estimated from human X chromosomes with results from human autosomes
- Analyzed both simulated data and real human genomics data; prepared reproducible pipelines for inferring gender-specific demographic history using the proposed method
- Prepared manuscript

**Fred Hutchinson Cancer Research Center**

June 2020 – Present

*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 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

**WORK EXPERIENCE**

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**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
- Clarified example problems and summarized concepts for students to enhance their understanding of course materials; successfully built up students' skills to solve problems via statistical tools