

# Jesse R. Ames

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## EDUCATION

**Columbia University, Mailman School of Public Health**, New York, NY Expected May 2023  
*Master of Science in Biostatistics Theory and Methods*

**Williams College**, Williamstown, MA June 2019  
*Bachelor of Arts in Biology and Statistics* GPA: 3.49  
Awards: Dean's List (Fall 2015, Spring 2016, Spring 2019)

## RESEARCH EXPERIENCE

**Rutgers University Center for Advanced Biotechnology and Medicine**, Piscataway, NJ Jul 2019 – Aug 2021  
*Laboratory Researcher, Lab of Dr. Martin J. Blaser*

- Conducted original scientific research concerning the gut microbiome's role in host estrogen metabolism by reviewing relevant literature; designing experiments; collecting, organizing, and cataloguing several hundred biological samples from C57BL6 mice; performing dozens of laboratory assays; wrangling, visualizing, and analyzing data using R, Excel, and QIIME2; and drawing conclusions to inform future experiments
- Assisted colleagues by designing bacterial PCR primers and helping with various assays including DNA extraction, plasmid extraction, PCR, electrophoresis, qPCR, and mouse sacrifice and dissection
- Presented research findings at lab meetings and virtual poster sessions and received constructive feedback

**Williams College**, Williamstown, MA Jul – Aug 2017  
*Student Research Assistant, Lab of Dr. David W. Loehlin*

- Collected critical data for a study on the evolution of Alcohol dehydrogenase (Adh) in *Drosophila*
- Researched application of generalized linear mixed-effect models

**New York University Langone Medical Center**, New York, NY Summer 2015, 2016  
*Student Research Intern, Lab of Dr. Martin J. Blaser* (Summer 2016)

- Extracted and amplified DNA from samples for murine microbiome STAT (Sub-Therapeutic Antibiotic Treatment) study
- Used QIIME and LEfSe to analyze 16s-rRNA  $\alpha$  and  $\beta$  diversity and taxonomic abundance in murine microbiome STAT study with HDAC6 knockouts

*Volunteer Intern, Lab of Dr. Martin J. Blaser* (Summer 2015)

- Used QIIME and LEfSe to analyze 16s-rRNA  $\alpha$  and  $\beta$  diversity and taxonomic abundance in 13-lined ground squirrel cecal microbiota in STAT study
- Used R to help incorporate new features into the SpiecEasi package developed by Zachary Kurtz

## LEADERSHIP EXPERIENCE

**Williams College Jewish Association** (Board Member) Jan 2016 – Apr 2019

- Supervised volunteers to help prepare and serve weekly community Shabbat dinners; attended board meetings

## PUBLICATIONS & SPEAKING ENGAGEMENTS

Aline C. Fenneman, Elena Rampanelli, Yue S. Yin, Jesse Ames, Martin J. Blaser, Eric Fliers, and Max Nieuwdorp (2020). Gut microbiota and metabolites in the pathogenesis of endocrine disease. *Biochemical Society Transactions* 48 915-931.

David W. Loehlin, Jesse R. Ames, Kathy Vaccaro, Sean B. Carroll. (2019). A major role for noncoding regulatory mutations in the evolution of enzyme activity. *PNAS* 116 (25) 12383-12389.

"Genetic Recombination, Poisson Processes, and Human History" (Senior Colloquium), Williams College, Williamstown, MA, February 2019.

## SKILLS

**Programming Experience:** Data wrangling, visualization, and analysis in R; data structures in Java; data visualization and machine learning in JMP; computational biology in Python; modeling in MATLAB; basics of UNIX terminal