Michael Wasney
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EDUCATION

PhD Candidate in Human Genetics September 2021-present
UCLA, Los Angeles, CA

BA in Biological Sciences, BA in English Language and Literature 2018
University of Chicago, Chicago, IL

TEACHING EXPERIENCE

Teaching Assistant, Population Genetics, UCLA Spring 2025

- Lectured students on principles of population genetics
- Created homework and exam materials related to course content

Teaching Assistant, Advanced Research Analysis in Microbiome, UCLA Fall 2024

- Lectured students on principles of microbial ecology and evolution
- Taught students how to use various softwares to analysis microbiome sequencing data
- Edited manuscripts and posters presenting students' final projects

Direct Mentor, Bruins-In-Genomics Summer Program Summer 2023, Summer 2024

- Trained mentees in bioinformatics approaches employed by the Garud Lab
- Taught mentees basic coding skills in Python, R, and BASH
- Showed mentees key aspects of the scientific method (forming hypotheses, testing them, etc.)

Writing Tutor, Bioscience Scholar Program Summer 2022, Summer 2023

- Helped BSP students draft their graduate school admission essays
- Provided BSP students with edits on their scientific writing (abstracts, presentations, etc.)
- Held office hours to help BSP students workshop their writing

RESEARCH EXPERIENCE

Graduate Student Researcher January 2022-Present
Garud Lab, UCLA, Los Angeles, CA

- Characterized the spatial dynamics of strain colonization and adaptation in the gut microbiome
- Detected evolution in the context of fecal microbiota transplants (FMTs)
- Developed a statistic to estimate genetic linkage in unphased microbiome data
- Mentored multiple undergraduate students

Rotation Student March 2022-June 2022
Lohmueller Lab, UCLA, Los Angeles, CA
- Estimated mutation rate variation across the human genome using trio studies
- Modeled the effect mutation rate variation on estimates of background selection

Rotation Student September 2021-December 2021
Kruglyak Lab, UCLA, Los Angeles, CA
- Measured and analyzed aging phenotypes in 20 strains of *Saccharomyces cerevisiae*
- Performed bulk segregant linkage analysis on 4 strains of yeast to identify genetic loci associated with aging and quiescence phenotype

Research Technician October 2019-July 2021
Pott Lab, University of Chicago, Chicago, IL
- Developed and applied single-cell –omics tools, including Drop-seq and scNOMe-seq
- Assayed human heart tissue with scRNA-seq, scATAC-seq, and scNOMe-seq as part of a project to generate a cellular atlas of the heart
- Analyzed scRNA-seq, scATAC-seq, and scBS-seq data using python- and R-based software

Research Assistant October 2015-January 2018
Coleman Lab, University of Chicago, Chicago, IL
- Analyzed the spatial and temporal distribution patterns of freshwater viruses in the Great Lakes
- Cultivated and isolated freshwater bacteria

SULI Intern June 2016-August 2016
Argonne National Laboratory
- Modeled the nitrous oxide emissions associated with growing various biofuels for GREET, a life-cycle analysis tool developed by Argonne to calculate cradle-to-grave greenhouse gas emissions of transportation systems
- Conducted a literature review of GREET's usage in academic studies

GRANTS & FELLOWSHIPS

Goodman-Luskin Microbiome Center Seed Fellowship January 2024-December 2024

PUBLICATIONS

First author
Wasney, M. *et al.* Uniform bacterial genetic diversity along the. 2025.01.28.635365 Preprint at https://doi.org/10.1101/2025.01.28.635365 (2026). **[Accepted in principle, Nature Communications]**

Co-author
Selewa, A. *et al.* Single-cell genomics improves the discovery of risk variants and genes of atrial fibrillation. *Nat Commun* **14**, 4999 (2023).

Methods
Pott, S., Wasney, M. & Khan, N. Multiplexed scNOMe-seq protocol based on isolated single nuclei. *protocols.io* https://www.protocols.io/view/multiplexed-scnome-seq-protocol-based-on-isolated-bb7iirke (2020).

POSTERS & PRESENTATIONS

Bacterial genetic diversity is uniform along the gut of humanized mice
- *MVIF 40 (2025), virtual (Best MicroTalk of MVIF.40 recipient) –* ***5-minute talk***
- *ASM Microbe 2025, Los Angeles, CA –* ***15-minute talk***
- *CSHL Microbiome 2024, Cold Spring Harbor, NY –* ***poster***
- *Southern California Microbiome Symposium 2024, Irvine, CA –* ***poster***
- *ASM Microbe 2024, Atlanta, GA –* ***15-minute talk***
- *GLMC Symposium 2024, Los Angeles, CA –* ***15-minute talk, poster***
- *SCalE Meeting 2024, Irvine, CA –* ***poster, lightning presentation***

Toward an Epigenetic Atlas of the Heart
- *CZI Seed Network 2020 Annual meeting, Remote Conference –* ***poster***

REVIEWS

2023
- Reviewed an article submitted to the ISME Journal

2024
- Reviewed an article submitted to Cell Host & Microbe
- Reviewed an article submitted to PLOS Genetics

HONORS AND AWARDS

Best MicroTalk of MVIF.40, MVIF 40, virtual	2025
Fellow, Lawrence A. Kimpton Fellows Program, University of Chicago	2018
Dean's List, University of Chicago	2015, 2016, 2017, 2018

TECHNICAL COMPETENCIES

Computational

- Python
- R
- Linux/bash scripting
- SAS
- Processing sequencing data
- Working on a server (hoffman2 and others)

Wet Lab

- Assays: scRNA-seq (10X Genomics), scATAC-seq (10X Genomics), scNOMe-seq, Drop-seq/DroNc-seq
- Assay development/design (involved in the development of Drop-seq and scNOMe-seq)
- DNA/RNA extraction
- Fluorescence microscopy
- Yeast husbandry

PROFESSIONAL EXPERIENCE

Editorial Assistant November 2018-June 2019
Imagination Publishing, Chicago, IL

Editorial Intern June 2018-September 2018
Encyclopædia Britannica, Chicago, IL

Staff Writer and Contributing Editor January 2018-March 2019
South Side Weekly, Chicago, IL

LANGUAGES

English (Fluent)

Italian (Conversational)