

MICHAEL OVERTON

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Curious and driven PhD-trained biologist with expertise in evolutionary and molecular biology, bioinformatics, and microbiology. Five years of experience developing custom pipelines for short-read sequencing analysis, paired with extensive wet lab background in genetic engineering, sequencing, and microbial physiology. Skilled at integrating experimental and computational workflows to deliver high-quality, actionable data.

PROFICIENCIES

Molecular biology techniques Cell culturing and growth assays NGS and transcriptomics
Statistical analyses and modeling Data visualization and communication Leadership and collaboration

EXPERIENCE

GRADUATE RESEARCH ASSISTANT

2021 – 2024

Kryazhimskiy Lab, University of California San Diego

Genetic Engineering | Experimental Evolution | Bioinformatics

- Implemented cloning, mating, barcoding, and CRISPR methods to construct a diverse array of 30+ yeast strains
- Conducted high-precision physiological and growth measurements to link genetic variants with fitness effects
- Prepared and analyzed whole-genome sequencing data for 295 yeast clones from a massive evolution experiment
- Designed and implemented custom genotyping, filtering, error detection, and analysis pipelines in Linux HPC (Torque/Slurm) environments using R and shell scripting
- Leveraged tools such as BLAST and Genome Browser to detect, validate, and annotate genomic variants
- Developed quantitative models, including ANCOVAs and GLMMs, to reveal genetic factors influencing mutation rates and physiology in yeast
- Generated publication-quality static and interactive visualizations using ggplot2, RMarkdown, and RShiny to communicate findings to diverse audiences
- Managed lab activities, including training, supervision, inventory, data curation, and biosafety compliance

RESEARCH ASSOCIATE

2015 – 2019

Snyder Lab, Cal Poly Pomona

Molecular Techniques | Viral Genetics and Evolution

- Created a genetic system for the extremophilic virus STIV3 using Gibson assembly and cloning techniques to facilitate mutagenesis and host range experiments
- Developed protocols for viral propagation, mutagenesis, genome extraction, southern blotting, and qPCR, increasing reproducibility and throughput
- Purified and characterized proteins using HPLC, ELISA, and western blotting
- Applied BLAST, Geneious, and custom R scripts to characterize viral genotypes and host–virus relationships, informing subsequent experimental design

EDUCATION

DOCTOR OF PHILOSOPHY, Biology

2025

University of California San Diego

Revealing the genetic variation that drives loss of heterozygosity rates in yeast

Advisor: Dr. Sergey Kryazhimskiy

MASTER OF SCIENCE, Environmental Biology

2019

Cal Poly Pomona

Genetic and Bioinformatic Characterization of Sulfolobus Turreted Icosahedral Virus 3

Advisor: Dr. Jamie Snyder

PUBLICATIONS

- Overton, M.S.**, Kryazhimskiy, S. (2025). Improved Genotype Inference Reveals Cis- and Trans-Driven Variation in the Loss-of-Heterozygosity Rates in Yeast. *bioRxiv*. DOI:10.1101/2025.06.26.661874v1 and *in review*
- Overton, M.S.**, Guy, S.E., Chen, X., Martsul, A., Carolino, K., Akbari, O.A., Meyer, J.R., Kryazhimskiy, S. (2023). Upper Bound on the Mutational Burden Imposed by a CRISPR-Cas9 Gene-Drive Element. *bioRxiv*. DOI:10.1101/2023.11.28.569142 and *in review*
- Overton, M.S.**, Manual, R.D., Lawrence, C.M., Snyder, J.C. (2023) Viruses of the Turriviridae: an emerging model system for studying archaeal virus-host interactions, *Frontiers in Microbiology*, 14, p. 1258997. DOI: 10.3389/fmicb.2023.1258997

References provided on request