

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