

Mackenzie Noon

New Haven, CT • 909-488-1101 • me@mackenzienoon.com • GitHub • LinkedIn

DEGREES

Yale University — PhD Candidate, Genetics (September 2022 – Present)

University of California, Berkeley — B.A., Biology, GPA 3.888 (August 2019 – May 2021)

AWARDS

AIxBiosecurity Research Fellowship • 1st place overall, AIxBio Hackathon • Boehringer Emerging Scientist Talent (BEST) Program • NSF Graduate Research Fellowship, Honorable Mention • Gruber Science Fellowship

PUBLICATIONS

- Bypassing current biosecurity screens with AI-designed proteins, and closing the gap with edge-AI functional screening — *Apart Research AIxBio Hackathon* (2026). *1st place overall*
- Global Evaluation of Congenital Heart Disease-Associated Non-Coding Variants — in review at Nature Communications, available on bioRxiv
- Identifying non-coding variant effects at scale via machine learning models of cis-regulatory reporter assays — in review at Nature, available on bioRxiv
- Histone Variant H2A.J Regulates Trophoblast Development Through Ribosome Biogenesis in Early Human Development — in review at Nature
- Taming the transposon: H3K9me3 turns foe to friend in human development — *Cell Stem Cell* (2022)
- A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development — *Cell* (2021)

SOFTWARE

- **scMPRAforge** — Python package for simulating, designing, and testing single-cell massively parallel reporter assays. Manuscript in preparation; release pending.
- **tensorzinb-plusplus** — Fork of TensorZINB adding current TensorFlow support, sparse input matrices, and sample-weighted zero-inflated negative binomial regression.
- **commec-gui** / **commec-in-a-box** — offline DNA-synthesis screening for IBBIS's Common Mechanism: upstream-merged kiosk and LAN interface, and a pre-imaged appliance that keeps sequences on site. Funded by a BlueDot Impact Rapid Grant.

RESEARCH EXPERIENCE

Cambridge Boston Alignment Initiative, with IBBIS — AIxBiosecurity Research Fellow (June 2026 – August 2026)

- Built commec-in-a-box, an offline DNA-synthesis screening appliance: a pre-imaged mini-PC running IBBIS's Common Mechanism behind a local web interface, so no sequence leaves the synthesis provider.

Reilly Lab, Yale — PhD Candidate (September 2022 – Present)

- Developing high-throughput single-cell assays and supporting software for assessing the function of noncoding human genetic variation.
- Developing deep learning models to predict transcriptional regulatory activity.

Xiao Lab, Yale — Post-baccalaureate Research Associate (June 2021 – September 2022)

He Lab, UC Berkeley — Undergraduate Researcher (September 2019 – June 2021)

Kaplan Lab, UC Davis — Undergraduate Researcher (January 2018 – March 2019)

TEACHING & LEADERSHIP

- Teaching Assistant, Genomic Methods for Genetic Analysis – Yale (2025).
- Bioinformatics Bootcamp Instructor/TA – Yale (2024-2025).
- Community Biology Instructor, Yale Pathways to Science (2024).
- Graduate Student Instructor, Developmental Biology – UC Berkeley (2021).
- Earlier experience teaching programming, robotics, and animation.

SKILLS

Programming & Computing: Python (extensive), C++ (extensive), R, Rust (intermediate); Linux and bioinformatics utilities; software development; machine learning (PyTorch, TensorFlow); statistical learning.

Experimental Biology: Molecular cloning, gel electrophoresis, transformation; MPRA; custom Illumina library design and sequencing (NextSeq 2000); Oxford Nanopore assay design; tissue culture, embryo manipulation, fluorescence microscopy; mouse colony management.