Noah Olsman

noah_olsman@hms.harvard.edu
+1 (323) 445-1789
nolsman.com

Experimental synthetic biologist | High-throughput cellular platforms | AI-facing biological data

Control-theoretic and experimental synthetic biologist building end-to-end platforms that connect molecular design to dynamic cellular behavior. I combine synthetic circuit libraries, single-cell microfluidics, automated fluid handling, live-cell imaging, sequencing/bioinformatics, distributed image analysis, and quantitative modeling to produce analysis-ready datasets for biological engineering and AI-enabled protein/circuit design.

Research highlights

- Built **BARRACUDA** (Barcoded ARRAys of Circuits Under Dynamic Actuation), an end-to-end screening platform that captures single-cell, time-resolved dynamics for up to **1M circuit variants per experiment** — breaking the throughput/resolution tradeoff between pooled sequencing screens and live-cell imaging.
- Produced the **first comprehensive design landscape of a biomolecular feedback controller in living cells** (>25,000 variants across a 5D parameter space) and discovered a hidden host–circuit coupling that destabilizes otherwise-stable controllers — a failure mode absent from idealized models.
- Ran an end-to-end **de novo regulator design-and-test cycle**: generative models proposed candidate binders, screened in a 10,692-variant *in vivo* library; top designs matched or exceeded native function while inducing lower host stress.
- **Bridge theory and experiment**: control-theory Ph.D. plus hands-on molecular biology, instrumentation, microfluidics, and multi-terabyte data infrastructure.

Research experience

Harvard Medical School, Department of Systems Biology 2019-present
Paulsson Lab: Research Associate (2024-present); Postdoctoral Fellow (2019-2024) *Boston, MA*

- Developed **BARRACUDA**, combining combinatorial genetic libraries, microfluidic mother-machine time-lapse imaging, dynamic chemical inputs, fluorescent reporters, sequencing, and optical pooled screening for barcode-resolved dynamic phenotyping of synthetic circuits.
- Built experimental automation infrastructure for large live-cell screens, including custom fluid-handling/flow-control hardware, fluidics, PCB design, microscope control workflows, and reproducible dynamic stimulation protocols.
- Created computational infrastructure to convert multi-terabyte microscopy runs (2–4 TB per run) into analysis-ready biological data: a custom distributed **Dask** pipeline for image processing, single-cell tracking/segmentation, time-series extraction, barcode decoding, library-sequencing analysis, QC, and genotype-to-phenotype integration.
- Produced the first comprehensive design landscape of an antithetic integral feedback controller in *E. coli*: >25,000 variants across a five-dimensional parameter space; identified hidden host-circuit coupling that drove otherwise stable circuits into over-adaptation and cryptic oscillatory behavior.
- Developed cloning and library QC protocols for high-fidelity construction of **1M+ combinatorial circuit libraries**, supporting systematic variation of regulatory topology, expression strength, protein identity, environmental perturbation, and host response.
- Screened de novo regulatory proteins designed with a generative model (BoltzGen): 30,000 generated binders against three sigma-factor targets; 60 synthesized candidates; 10,692-variant *in vivo* library spanning target, binder, expression strength, and host-stress reporters.
- Found designed regulators that matched or exceeded native antisigma performance *in vivo* while inducing lower host stress, demonstrating cellular-context evaluation beyond molecular binding alone.
- Provided platform and methods support for a collaborative **ARPA-H** program, enabling multiple researchers' high-throughput imaging experiments through shared infrastructure, protocols, and instrumentation.

California Institute of Technology 2013-2018
Ph.D. Candidate, Control and Dynamical Systems *Pasadena, CA*

- Developed control-theoretic analyses of biomolecular feedback networks, including stability, fragility, speed/robustness tradeoffs, noise, and steady-state error in antithetic integral feedback systems.
- Translated idealized control models into architectural design rules relating molecular parameterization to system-level biological performance.

Technical skills

Wet lab	Synthetic gene-regulatory circuits; combinatorial library design and cloning; bacterial genetics; nanopore sequencing; microfluidic experiments; fluorescence time-lapse microscopy; optical pooled screening
Platform	Automated fluid handling and flow control; microfluidic experimental setup; PCB design for experimental automation; microscope configuration and maintenance; high-throughput imaging workflows; shared laboratory infrastructure.
Computation	Python; Dask/distributed computing; image and time-series analysis; sequencing analysis for library QC and barcode/genotype mapping; data pipelines for multi-terabyte microscopy screens; statistical analysis of high-throughput phenotypes.
Modeling	ODE/stochastic modeling; nonlinear dynamics; control theory; optimal experiment design; design-space mapping; performance tradeoff analysis for biological control systems.
AI biology	Applied generative protein design (BoltzGen) and evaluated candidates in living cells; designed screens that yield analysis-ready training data and quantified *in vivo* failure modes; model-driven hypothesis generation; builds AI-agent tooling (e.g., Claude Code) into research workflows.

Education

Ph.D., Control and Dynamical Systems, California Institute of Technology 2018
Co-advised by John C. Doyle and Lea Goentoro. Thesis: *Architecture, Design, and Tradeoffs in Biomolecular Feedback Systems.*

B.S., Electrical Engineering, minor in Mathematics, University of Southern California 2012
Magna cum laude.

Selected publications

- **A Scalable Framework for the Design and Analysis of Complex Synthetic Gene-Regulatory Networks**. N. Olsman, J. Shenker, D. Choudhary, J. Paulsson. In preparation (2026).
- **Hard limits and performance tradeoffs in a class of antithetic integral feedback networks**. N. Olsman, A.-A. Baetica, F. Xiao, Y. P. Leong, R. M. Murray, J. C. Doyle. *Cell Systems* 9, 49-63 (2019).
- **Architectural principles for characterizing the performance of antithetic integral feedback networks**. N. Olsman, F. Xiao, J. C. Doyle. *iScience* 14, 277-291 (2019).
- **Allosteric proteins as logarithmic sensors**. N. Olsman, L. Goentoro. *PNAS* 113, E4423-E4430 (2016).
- **Cybernetics, systems biology, and the phenomenological gap**. N. Olsman. *IEEE Control Systems Magazine* (2021).
- **Efficient Bayesian learning in social networks with Gaussian estimators**. E. Mossel, N. Olsman, O. Tamuz. *Allerton Conference on Communication, Control, and Computing* (2016).

Teaching and leadership

- Teaching Fellow, SB200: Systems Biology, Harvard University (2024-2025): graduate course covering ODE modeling, kinetic proofreading, bifurcation analysis, and stochastic processes in cells.
- Coordinator, Harvard Systems Biology Diversity, Equity, and Inclusion working group (2020-2023): supported summer research access and graduate application assistance programs.
- Chief Analytics Officer, Seed Consulting Group (2014-2018): leadership role in pro bono environmental consultancy; fundraising, management, outreach, and data-oriented projects.