

Manuel Razo-Mejia

Scientist II, Computational Biology · Altos Labs

Mountain View, CA

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Computational biologist with a PhD in biophysics from Caltech and postdoctoral training at Stanford. Develops hybrid models combining biophysical principles, deep learning, and scalable Bayesian inference for noisy biological data. Research spans single-cell genomics, evolutionary dynamics, and gene regulation, with hands-on experimental experience and a strong commitment to reproducible scientific software.

Professional Experience

Scientist II, Computational Biology

Altos Labs

August 2025 — Present

Recruited to develop hybrid models combining biophysical principles with deep learning for biological research.

- Developed a framework for training geometry-aware variational autoencoders, supporting representation learning informed by the geometry of biological data.
- Developed SCRIBE, a framework for single-cell RNA-seq analysis using scalable Bayesian inference to account explicitly for measurement noise and uncertainty. Manuscript in preparation.
- Building a new approach to single-cell analysis at Altos, with emphasis on high-dimensional inference, interpretable assumptions, and reproducible, maintainable scientific code.

Visiting Researcher

SoftMax AI

May 2025 — June 2025 (6 weeks)

Contributed to the open-source Metta AI multi-agent reinforcement learning platform.

- Designed exploration curricula and reward structures for multi-agent policy learning, drawing on biological models to formulate learning objectives and evaluation metrics.

Postdoctoral Scholar & Schmidt Science Fellow

Stanford University

October 2021 — August 2025

Department of Biology | Dmitri Petrov Lab

- Developed Bayesian methods for inferring relative fitness from high-throughput DNA barcode competition assays, propagating measurement uncertainty and scaling inference with variational methods (PLoS Computational Biology, 2024).
- Used geometry-aware variational autoencoders to study phenotype-to-fitness landscapes and evolutionary dynamics (PRX Life, 2026).
- Authored BarBay.jl and AutoEncoderToolkit.jl, reusable scientific software for Bayesian analysis and representation learning.

Statistical Consultant

Superfluid Dx, Inc.

February 2024 — April 2024

Statistical modeling of high-dimensional sequencing data for medical diagnostics.

- Proposed a normalization method for clinical bulk RNA-seq data that accounts for sequencing depth and batch effects, with a scalable variational inference algorithm.

PhD Researcher

California Institute of Technology

September 2014 — August 2021

Division of Biology and Biological Engineering | Rob Phillips Lab

- Combined statistical physics and information theory to predict the information-processing capacity of genetic circuits from biophysical principles.
- Performed fluorescence microscopy experiments and compared model predictions with experimental measurements of gene regulation.

Technical Skills

Programming	Python , Julia, Linux , Git & GitHub , Docker, bash, GitHub Actions, GPU Kernel Programming
ML Libraries	JAX , NumPyro , PyTorch , Pyro, NumPy, SciPy, Pandas, Matplotlib, Seaborn, Jupyter
Math & Statistics	Bayesian Inference , Variational Inference , Deep Learning , Statistical Physics, Differential Geometry, Stochastic Processes, Differential Equations, Linear Algebra, Probability Theory
Biological Data	Bulk & Single-Cell RNA Sequencing , DNA Barcode Technologies, Quantitative Microscopy, Flow Cytometry

Scientific Software

SCRIBE

A Python package for analyzing single-cell RNA sequencing (scRNA-seq) data using GPU-accelerated Bayesian inference in NumPyro, including variational inference and MCMC. Private repository; manuscript in preparation. Technical walkthrough available upon request.

AutoEncoderToolkit.jl

A Julia package for training variational autoencoders and their extensions. Includes utilities for geometric analysis of the latent spaces. [GitHub](#) | [Docs](#)

BarBay.jl

A Julia package for statistical analysis of high-throughput pooled assays in experimental evolution using variational Bayesian inference. [GitHub](#) | [Docs](#)

Education

PhD Biochemistry & Molecular Biophysics

California Institute of Technology

2014 - 2021 | Pasadena, CA | Advisor: [Rob Phillips](#)

BSc Biotechnological Engineering

Instituto Politecnico Nacional

2009 - 2014 | Silao, Gto, MX

Selected Publications

A full list is available via [Google Scholar](#) and my [personal website](#).

Razo-Mejia, M., Mani, M., Petrov, D. (2026). *Learning the Shape of Evolutionary Landscapes: Geometric Deep Learning Reveals Hidden Structure in Phenotype-to-Fitness Maps*. PRX Life , 4, 013030 . [DOI](#)

[Paper website](#) | [GitHub repository](#)

Razo-Mejia, M. (2024). *AutoEncoderToolkit.jl: A Julia package for training (Variational) Autoencoders*. JOSS . [DOI](#)

Razo-Mejia, M., Mani, M., Petrov, D. (2024). *Bayesian inference of relative fitness on high-throughput pooled competition assays*. PLoS Comput Biol , 20, e1011937 . [DOI](#)

[Paper website](#) | [GitHub repository](#)

Razo-Mejia, M., et al. (2020). *First-principles prediction of the information processing capacity of a simple genetic circuit*. Physical Review E , 102, 022404 . [DOI](#)