Evan E. Seitz

evanseitz.com   evan.e.seitz@gmail.com   github.com/evanseitz   linkedin.com/in/eeseitz

New York, NY 11001   +1 (404) 964-9821

Summary

Computational biologist with expertise in interpretable machine learning for regulatory genomics and structural biology, seeking research-focused roles that bridge deep learning and biology.

Education

PhD in Biological Sciences, with Distinction – Columbia University
Departments of Biological Sciences & Biochemistry and Molecular Biophysics

MPhil and MA – Columbia University
BS in Physics, with Highest Honors – Georgia Institute of Technology
BA in Mass Communication – Georgia College

Experience

Cold Spring Harbor Laboratory, Postdoctoral Fellow with Drs. Peter Koo and Justin Kinney
Simons Center for Quantitative Biology   Mar 2022 – Present

Developed a surrogate modeling framework—SQUID—to mechanistically interpret deep neural networks trained on genomic data, enabling robust dissection of cis-regulatory logic in high-throughput functional assays.

- Modeled additive and higher-order interactions between sequence features while removing confounding effects from nonlinearities and experimental noise using shallow neural networks as interpretable surrogates.
- Demonstrated that this framework identifies more consistent motifs across genomic loci and improves single-nucleotide variant effect prediction, outperforming established attribution methods like DeepSHAP.

Invented a meta-explainability framework—SEAM—that systematically investigates how mutations reshape regulatory mechanisms, enabling interpretable insights into mutational effects on gene regulation.

- Enabled systematic and unbiased exploration of the reprogrammability of cis-regulatory mechanisms
- Revealed the remarkable evolvability of human regulatory elements, disentangled transcription factor-specific effects from broader sequence context, and advanced decoding of the cis-regulatory code
- Illuminated evolutionary trajectories and supported the rational design of synthetic regulatory sequences

Columbia University, PhD Researcher with Nobel laureate Dr. Joachim Frank
Departments of Biological Sciences & Biochemistry and Molecular Biophysics   2017 – 2022

Invented a geometric machine learning method—ESPER—to interpret latent manifolds derived from cryo-EM ensembles of macromolecular complexes, enabling accurate reconstruction of 3D structures across the free-energy landscape.

- Improved the interpretability of spectral embeddings by introducing a novel eigenbasis realignment procedure that extracts conformational degrees of freedom along eigenfunctions of the Laplace–Beltrami operator.
- Enabled reconstruction of conformational continua and free-energy landscapes in key biomolecular systems, including the 80S ribosome, V-ATPase, and SARS-CoV-2 Spike protein.

Awards

NIH F32 Postdoctoral Fellowship, National Human Genome Research Institute (F32HG013265), 2024–2027
John S. Newberry Prize, Columbia University, 2022 — most promising PhD student by faculty nomination
PhD with Distinction, Columbia University, 2022 — dissertation excellence by thesis committee nomination

BS with Highest Honors, Georgia Institute of Technology, 2017 — awarded for minimum GPA of 3.55 (3.74)
Sigma Pi Sigma, National Physics Honor Society

Skills

- Supervised and unsupervised learning, deep neural networks, convolutional neural networks, surrogate modeling, attribution analysis, global interpretability, explainable AI (XAI), meta-explainability, data visualization, dimensionality reduction, manifold learning, data wrangling/munging
- Python, Tensorflow, PyTorch, Bash, High Performance Computing, LaTeX, NumPy, SciPy, Pandas, Conda, GitHub, ReadTheDocs, UCSF Chimera, PyMOL, VMD, RELION, Phenix, Adobe Illustrator, Adobe After Effects, Adobe Photoshop, Cinema4D, Matplotlib, Mayavi

Select Publications

Seitz et al., ICLR GEM Workshop, 2025 — Decoding the mechanistic impact of genetic variation with deep learning.
Seitz et al., *Nat Mach Intell*, 2024 — Interpreting genomic deep neural networks using surrogate models.
Seitz et al., *RSC Digital Discovery*, 2023 — Geometric relationships between manifolds of cryo-EM conformers.
Seitz et al., *IEEE Trans Comput Imaging*, 2022 — Recovery of cryo-EM conformations using manifold embedding.
Sztain et al., *Nat Chem*, 2021 — Conformational mapping of the SARS-CoV-2 spike protein receptor binding domain.

A complete publication list is available on my Google Scholar profile.

Presentations

Talks: ICLR GEM Workshop (2025), Quantitative Biology and AI In-house Seminar Series (2023–2025), Bioinformatics and Computational Neuroscience Lecture Series (2023, 2024), Cryo-EM Microscopy Center Fall Workshop (2021)
Posters: CSHL Biology of Genomes (2023, 2025), Genome Informatics (2023), Biological Data Science (2024), Probabilistic Modeling in Genomics (2025) and In-House Symposium (2024, 2025)

Teaching and Mentoring

Teaching Assistant, Columbia University   2018–2019
BCHM GU4323: Biophysical Chemistry — Recitation instructor (Prof. John Hunt and Prof. Art Palmer)

Learning Assistant, Georgia State University   Spring 2015
PHYS 1111K: Introductory Physics — Lab instructor (Prof. Joshua Von Korff)

Educational Media and Animation
Georgia Institute of Technology — Creative Director for physics MOOCs (Prof. Michael Schatz, 2016–2017)
Stanford University — Creative Director for behavioral science education (Prof. Jennifer Aaker, 2013–2015)

Undergraduate Research Advisor   2023
Nika Chuzhoy (Computer Science, Caltech) — Research on surrogate modeling for interpreting genomic DNNs

High School Research Mentor   2024
Tinu Yu (Syosset High School, NY) — Research on surrogate modeling for interpreting genomic DNNs

Referee Service

2024: Nature ($\times 2$), Nature Genetics ($\times 2$), American Journal of Human Genetics, RECOMB, ICML AI4Science
2023: Nature, Nature Machine Intelligence, Genome Research, Cold Spring Harbor Perspectives in Biology, NeurIPS AI4Science Workshop, NeurIPS Generative AI and Biology Workshop, ICML Workshop on Computational Biology
2020: Journal of Chemical Information and Modeling