

# Evan E. Seitz

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## 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](#)   March 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 SQUID 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 unbiased discovery of mutations poised to reprogram cis-regulatory mechanisms and function, illuminating evolutionary trajectories and supporting the rational design of synthetic regulatory sequences.
- Distinguished sequence features that are robust to mutation from those that are readily reprogrammable, enabling visual separation of motif-driven signals from biologically important background patterns.
- Demonstrated SEAM reduces noise and better highlights regulatory features than other attribution methods.

**Columbia University**, PhD Researcher with Nobel laureate Dr. [Joachim Frank](#)  
[Departments of Biological Sciences & Biochemistry and Molecular Biophysics](#)   May 2017 – February 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** — awarded to the most promising PhD student, Columbia University, 2022

**PhD with Distinction** — awarded for dissertation excellence by faculty committee, Columbia University, 2022

**BS with Highest Honors** — top distinction for academic excellence in physics (GPA 3.74/4), Georgia Tech, 2017  
**Sigma Pi Sigma** — National Physics Honor Society

## Skills

- **Supervised learning:** Deep neural networks, convolutional neural networks, nonlinear regression
- **Unsupervised learning:** Dimensionality reduction, spectral methods, manifold learning, latent space analysis
- **Model interpretability:** Explainable AI (XAI), attribution analysis, surrogate modeling, meta-explainability, global importance analysis, high-dimensional data visualization
- **Computational tools:**
  - Languages and frameworks* — Python, Bash, LaTeX, TensorFlow, PyTorch, NumPy, SciPy, Pandas, Conda
  - Development and reproducibility* — GitHub, ReadTheDocs, HPC environments
  - Molecular modeling* — UCSF Chimera, PyMOL, VMD, RELION, Phenix
  - Visualization and media* — Adobe Creative Suite, Cinema4D, Final Cut Pro, 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)

**Research Advisor**, Cold Spring Harbor Laboratory 2023–2025  
Nika Chuzhoy (Computer Science, Caltech) — Research on surrogate modeling for interpreting genomic DNNs  
Tina Yu (Syosset High School, NY) — Research on surrogate modeling for interpreting genomic DNNs  
Sophia Chen (Syosset High School, NY) — Research focused on meta-interpretability of genomic DNNs

## Referee Service

**2025:** ICML GenBio Workshop

**2024:** Nature (×2), Nature Genetics (×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