

## JONATHAN PATSENKER

(339)-221-4136 | [jonathan.patsenker@yale.edu](mailto:jonathan.patsenker@yale.edu) | [jon.patsenker.com](http://jon.patsenker.com) | [www.linkedin.com/in/jonathan-patsenker](https://www.linkedin.com/in/jonathan-patsenker)

## EDUCATION

**Yale University**, New Haven, CT

May 2019 – Present

*PhD Applied Mathematics*

Research focus: Machine learning, optimization, and stochastic modeling, with focus on generative modeling, diffusion models, and diffusion geometry

**Rensselaer Polytechnic Institute**, Troy, NY

May 2018

*B.S. Computer Science and Mathematics (Concentration in Operations Research)*

## PROFESSIONAL EXPERIENCE

**Moderna TX.**, Norwood, MA

June 2023 – August 2023

*Technical Development Intern*

- Designed a novel technique, leveraging deep transfer learning methods with approaches based in diffusion geometry to automate analysis of CryoEM image data containing lipid nanoparticles
- Implemented a custom pipeline and codebase to run the novel technique on CryoEM data in an industrial research environment to handle high throughput data
- Designed and implemented a novel method to model the kinetics of relevant reactions for high throughput industrial processing

## TECHNICAL SKILLS

- Languages: Python, R, C/C++, Julia, Matlab, Java
- ML Frameworks: PyTorch, TensorFlow, NumPy, SciPy
- Expertise: Deep Learning, Generative Modeling, Computer Vision, NLP, Optimization, Inverse Problems, Stochastic Processes, Numerical Analysis, Statistics, Big Data

## RESEARCH EXPERIENCE

*PhD Researcher, Kluger Lab*, Yale University

May 2019 – Present

*Applied Mathematics Program, Advisor: Yuval Kluger, PhD*

- Developing theoretical frameworks for understanding and controlling biases of large generative models
- Developed fast and noise-robust solvers for inverse problems, leveraging diffusion models with strong theoretical guarantees
- Designed novel LLM and manifold learning approaches for analyzing both high resolution multi-channel images and protein data
- Contributed to theoretical analyses of word2vec and links between stochastic optimization and physical dynamics
- Collaborated with pathologists to design data-driven solutions to drug survivability, cancer identification problems
- Published 8+ peer-reviewed publications in top ML, computational biology, and applied mathematics venues

*Undergraduate Researcher, Computer Science Department*, Rensselaer Polytechnic Institute

Sept 2017 – May 2018

*Supervisor: Malik Magdon-Ismail, PhD*

- Developed, implemented and tested a statistically informed method for network routing on large graphs
- Analyzed network routing algorithms to develop average-case guarantees for path length

*Research Intern, Department of Systems Biology*, Harvard Medical School

May 2015 – Sept 2017

*Supervisor: Leonid Peshkin, PhD*

- Developed a statistical method for assessing the quality of genomes and proteomes
- Deployed a tool for proteome research for annotating and cleaning proteomes

## LEADERSHIP EXPERIENCE

---

### *Teaching Fellow, Yale Department of Mathematics*

Jan 2021 – Present

- Collaborated with faculty to design curriculum in the Discrete Mathematics (MATH 244) course.
- Tutoring undergraduate students in both the Discrete Mathematics (MATH 244) and Structure of Networks (AMTH 160) courses
- Designing, building, and maintaining an automated homework server for the Structure of Networks (AMTH 160) course

### *Mentor, Yale Biotech Club Datathon*

Dec 2022

- Assisted undergraduate, graduate, and professional students in datathon in partnership with Boehringer Ingelheim and Code Ocean for tackling problems in healthcare informatics

### *Project Leader/External Mentor, Rensselaer Center for Open Source*

Sept 2014 – May 2018

- Founded and led a student-based research group in computational music generation and analysis
- Collaborated with students and professors to build style-specific rhythm generators, and chord progression generators
- Worked on feature based and deep learning based approaches for music generation

## SELECTED PUBLICATIONS

---

Jonathan Patsenker, Henry Li, Myeongseob Ko, Ruoxi Jia, and Yuval Kluger. "Injecting Measurement Information Yields a Fast and Noise-Robust Diffusion-Based Inverse Problem Solver." *arXiv preprint arXiv:2508.02964* (2025).

Myeongseob Ko, Henry Li, Zhun Wang, Jonathan Patsenker, Jiachen Tianhao Wang, Qinbin Li, Ming Jin, Dawn Song, and Ruoxi Jia. "Boosting alignment for post-unlearning text-to-image generative models." *Advances in Neural Information Processing Systems* 37 (2024): 85131-85154.

Jonathan Patsenker, Henry Li, Yuval Kluger. "Exponential Weight Averaging as Damped Harmonic Motion." *ICML 2023 Frontiers4LCD Workshop*, 25 July 2023.

Wang, Meng, Jonathan Patsenker, Henry Li, Yuval Kluger, and Steven H. Kleinstein. "Supervised fine-tuning of pre-trained antibody language models improves antigen specificity prediction." *PLOS Computational Biology* 21, no. 3 (2025): e1012153.

Wang, Meng, Jonathan Patsenker, Henry Li, Yuval Kluger, and Steven H. Kleinstein. "Language model-based B cell receptor sequence embeddings can effectively encode receptor specificity." *Nucleic acids research* 52, no. 2 (2024): 548-557.

Daniel E. Carvajal-Hausdorf, Jonathan Patsenker, Kelly P. Stanton, Franz Villarroel-Espindola, Amanda Esch, Ruth R. Montgomery, Amanda Psyrri et al. "Multiplexed (18-Plex) Measurement of Signaling Targets and Cytotoxic T Cells in Trastuzumab-Treated Patients using Imaging Mass Cytometry." *Clinical Cancer Research* 25, no. 10 (2019): 3054-3062.

Ariel Jaffe, Yuval Kluger, Ofir Lindenbaum, Jonathan Patsenker, Erez Peterfreund, and Stefan Steinerberger. "The spectral underpinning of word2vec." *Frontiers in applied mathematics and statistics* 6 (2020): 593406.

Lina Irshaid, Jonathan Bleiberg, Ethan Weinberger, James Garritano, Rory M. Shallis, Jonathan Patsenker, Ofir Lindenbaum, Yuval Kluger, Samuel G. Katz, and Mina L. Xu. "Histopathologic and machine deep learning criteria to predict lymphoma transformation in bone marrow biopsies." *Archives of Pathology & Laboratory Medicine* 146, no. 2 (2022): 182-193.

Virginia Savova, Jon Patsenker, Sébastien Vigneau, and Alexander A. Gimelbrant. "dbMAE: the database of autosomal monoallelic expression." *Nucleic acids research* 44, no. D1 (2016): D753-D756.

## PROFESSIONAL SERVICE

---

### **Reviewing**

- AISTATS 2026, AAAI 2026, ICML 2023 (Frontiers4LCD Workshop)