Masayuki “Moon” Nagai

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PROFESSIONAL SUMMARY

Ph.D. candidate in Quantitative Biology at Cold Spring Harbor Laboratory (Peter Koo lab), developing **AI methods for regulatory genomics** with an emphasis on generalization across diverse genetic variation and cellular contexts. My work focuses on designing and integrating causally informative perturbations to bridge wet-lab experimentation and computational modeling, extracting mechanistic biological insights, and characterizing model failure modes, with a key application in programmable regulatory sequence design.

EXPERTISE & SKILLS

- Deep learning and bioinformatics for genomics (PyTorch, TensorFlow, JAX)
- Model interpretability and failure modes (attribution, surrogates, virtual experiments)
- Continual integration of perturbational and multi-modal data into genomic models
- Optimal experimental design for sequence design and model improvement

EDUCATION

Cold Spring Harbor Laboratory Aug 2023 – Current
Ph.D. Candidate, School of Biological Sciences *NY, USA*

DePauw University Aug 2018 – May 2022
B.A. in Computer Science & Biochemistry (GPA: 4.0/4.0) *IN, USA*

University of Oxford Sept 2021 – Dec 2021
Visiting Student, Deep Learning & Genomics *Oxford, UK*

EXPERIENCE

PhD candidate Aug 2023 – Current
Advisor: Dr. Peter Koo *Cold Spring Harbor Laboratory, NY*

- Developed **continual learning** methods for genomic sequence-to-function models with perturbation data to refine model’s causal understanding.
- Built a fine-tuning framework for AlphaGenome (with Kundaje lab, Stanford). [Link]
- Fine-tuned Borzoi and applied interpretability methods to study *cis*-regulatory code in pancreatic ductal adenocarcinoma (with Vakoc lab, CSHL).
- Designed regulatory DNA sequences for (i) stimulus-dependent activity (with Ahituv lab, UCSF) and (ii) high-activity, out-of-distribution sequences.
- Applied ESM2 to identify conserved and coevolved residues in an uncharacterized Argonaute protein (with Joshua-Tor lab, CSHL). [Link]

Research Assistant Aug 2021 – Jun 2023
Advisor: Dr. Itoshi Nikaido *RIKEN (National Research Institute), Tokyo*

Investigated chimeric reads in single-cell RNA-seq data using machine learning to filter out artificial chimeric reads.

Bioinformatics Software Developer Dec 2019 - Jun 2023
ANPLAT Inc. (2021 – 2023) & Amelieff Inc. (2019 – 2021) *Tokyo, Japan*

Developed bioinformatics tools, including RNA-seq pipelines, a SARS-CoV-2 classifier, off-target detection, FASTQ simulation, and domain-specific databases (e.g., Variant Reflector).

Undergraduate Researcher – Variant Classification Sept 2019 – May 2022
Advisor: Dr. Daniel Gurnon & Dr. Chad Byers *DePauw University, IN*

Integrated heterogeneous data sources (ClinVar, gnomAD, BLAST, AlphaFold, CADD) to build a web-accessible platform for effective classification of variants of uncertain significance.

Undergraduate Researcher – Decision-Making System Summer 2020
Advisor: Dr. Steven Bogaerts & Dr. Chad Byers *DePauw University, IN*

Developed a high-performing decision-making system for the Gin Rummy card game using ensemble methods with hyperparameter optimization (genetic algorithms, grid search). [Link]

Undergraduate Researcher - Chemistry Learning Modules Summer 2019
Advisor: Dr. David Harvey *DePauw University, IN*
Developed two interactive learning modules in R that simulate chemical kinetics and enzyme kinetics process.

PUBLICATIONS (*co-first author)

[1] Murphy, A.E.*, **Nagai, M.*** & Koo, P.K. *Predicting non-coding variant effects with AlphaGenome.* Cell Research, Research Highlight (2025) [Link]

[2] **Nagai, M.***, Murphy, A.E.*, Rizzo, K. & Koo, P.K. *Toward Interpretable and Generalizable AI in Regulatory Genomics.* arXiv, Review/Perspective (2026) (in review, Nature Genetics) [Link]

[3] Sarkar, A., ..., **Nagai, M.**, ..., Koo, P.K. *Designing DNA With Tunable Regulatory Activity Using Score-Entropy Discrete Diffusion.* bioRxiv (2024) [Link]

[4] **Nagai, M.**, Shrivastava, K., Ta, K., Bogaerts, S. & Byers, C. *A Highly-Parameterized Ensemble to Play Gin Rummy.* Proceedings of the AAAI Conference on Artificial Intelligence (2021) [Link]

CONTRIBUTED TALKS

[1] Improving Genomic Deep Learning Models with Perturbation Data through Continual Learning. CSHL Systems Biology, NY. March 2026.

[2] Mitigating Catastrophic Forgetting in Genomic Foundation Models with Contiual Learning. Machine Learning in Computational Biology, NY. March 2025. [Link]

HONORS & AWARDS

Ph.D. Fellowship Nakajima Foundation, 2023–2027
Awarded 18,000,000 JPY (approx. 130,000 USD) for Ph.D. study [Link]

Research Fellow AI Alignment Network, 2025 – Current
Awarded for AI safety workshop organization and outreach, including an invited talk [Link]

Scholar-Athlete Award North Coast Athletic Conference, 2022
Recognizes student-athletes with outstanding academic achievement [Link]

John A. Ricketts Prize DePauw University, 2019
Awarded for outstanding performance in physical chemistry [Link]

Rector Scholar (Four-Year Full-Tuition) DePauw University, 2018 – 2022
The university's oldest and preeminent merit-based scholarship [Link]

Grew Bancroft Scholarship The Grew Bancroft Foundation, 2018 – 2022
Selective scholarship for Japanese students at leading U.S. liberal arts colleges [Link]

PROFESSIONAL ACTIVITIES

Referee Service

- Journals: Science (2025), Nature Machine Intelligence (2025), Cell Genomics (2024)
- Conferences: RECOMB (2024), ISMB (2025), AAAI (2025), MLCB (2025)

Mentorship

- Mentoring an undergraduate student (UC Berkeley) on "mutagenesis library design for inferring higher-order sequence–function relationships" (Summer 2025–current)
- Mentored a high school student on regulatory DNA sequence design (Summer 2025)

Organization

- Workshop committee member, "The First Workshop on Post-Singularity Symbiosis," AAAI (2025) [Link]
- Organized journal clubs on "Interpretability & Explainable AI" (2025), "Genomic Deep Learning Models" (2025), and "AI Agents" (2026)
- Organized hackathons on "Sparse Autoencoders for Life Science" (2025) and "AI Agents for Biology" (2026)