Jongmin Sung, PhD

AI Research Scientist

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PROFESSIONAL SUMMARY

AI Research Scientist with 15+ years of experience spanning industry and academia. Combines expertise in Physics, Biology, and Computation to develop **AI-driven solutions for complex biological challenges**. Specializes in statistical modeling, multi-omics, and machine learning for human health, longevity, and drug discovery. Key contributor to the development and launch of Roche's **SBX** high-throughput single-molecule nanopore sequencing technology, enabling ultra-rapid genomic analysis for personalized medicine. **Core competencies** include:

Data Science | Data Engineering | Cloud Computing | Statistical Modeling | Signal Processing
Artificial Intelligence (AI) | Deep Learning | Machine Learning | Computer Vision | Natural Language Processing (NLP)
Large Language Models (LLM) | Computational Biology | Bioinformatics | Molecular & Cellular Biology

PROFESSIONAL EXPERIENCE

SCALE AI | Human Frontier Collective Specialist - GenAI (Part-time), Remote 03/2025 – Present

- Contribute to training and evaluating state-of-the-art generative AI LLM reasoning models using domain expertise.

ROCHE SEQUENCING SOLUTIONS | Principal Data Scientist, Santa Clara, CA 10/2019 – Present

Computational Science & Informatics | Statistical Modeling team

Applied biophysics principles, data science, and deep learning to advance SBX single-molecule sequencing technology.

- Implemented primary and secondary data analysis pipelines for SBX sequence data analysis, focusing on raw read accuracy, read length, and overall throughput.
- Developed SBX raw sequencing signal simulators using stochastic biophysical and electrochemical circuit models.
- Created a simulation data pipeline generating ground truth sequence information to validate production base-calling software and optimize GPU throughput at maximum sequencing speeds.
- Developed Brownian dynamics simulation of molecular transport via fluid flow, Brownian motion and electric fields.
- Identified performance limitations through root-cause analysis of abnormal sequencing signals.
- Implemented Bayesian inference with Hamiltonian Monte Carlo to extract predictive sequencing features.

KITECH & KEIT | Consultant (Part-time), Remote 03/2020 – 08/2021

- KITECH: Advised Korean healthcare startups on market entry and R&D strategies for the US.
- KEIT: Evaluated RFPs for emerging digital therapeutics, contributing strategic insights to drive innovation.

UCSF | Postdoctoral Research Fellow, San Francisco, CA (Advisor: Ron Vale) 06/2014 – 10/2019

- Developed an automated pipeline to elucidate the molecular mechanism of APC cell cycle regulation.
- Characterized human axonemal dynein motility through DNA origami-based reconstitution.
- Established an analytical method for nanometer-scale distance measurements at the single-molecule level.
- Investigated immune cell signaling in T-cells and macrophages using advanced microscopy.

STANFORD UNIVERSITY | Research Assistant, Stanford, CA (Advisor: James Spudich) 04/2008 – 05/2014

- Invented harmonic force spectroscopy to reveal the force-velocity relationship in muscle contraction.
- Conducted single-molecule studies on human β-cardiac myosin to investigate hypertrophic cardiomyopathy.
- Validated correlated X-ray scattering method for atomic-level structural determination of particles in solution.
- Developed nanometer-precision method for measuring intramolecular fluorophore distances and orientations.
- Built a state-of-the-art dual-beam laser trap instrument (hardware and software) from scratch.

EDUCATION

- **PhD / MS in Applied Physics** | Stanford University, Stanford, CA
- **BS in Physics** | POSTECH, Pohang, South Korea

TECHNICAL SKILLS

- **Machine Learning & AI**: PyTorch, TensorFlow, TensorFlow Probability, Transformers, NLP/LLM, Graph Neural Networks, Self-Supervised Learning, Multiple Instance Learning, Digital Pathology with Clinical Data
- **Computational Biology & Bioinformatics**: Genomics & Transcriptomics Analysis, PyMOL, AlphaFold, BioPython
- **Statistical Modeling & Simulation**: Monte Carlo Simulation, Brownian Dynamics Simulation, Bayesian Inference (including Hamiltonian Monte Carlo), Time-Series Analysis
- **Programming & Data Engineering**: Python (NumPy, Pandas, Scikit-learn, Matplotlib), SQL, Git, Linux/Bash, C
- **Cloud & Infrastructure**: GCP/GKE, AWS, Docker, Airflow
- **Biotechnology**: Biophysics, Biochemistry, Molecular Biology, Protein Engineering, Spectroscopy, Microscopy

SELECTED PROJECTS

- **Pancreatic Cancer Survival Prediction**: Predicted patient outcomes using self-supervised learning and multiple instance learning frameworks, integrating TCGA and external datasets. (2025) Link
- **Anti-Aging Drug Discovery with GNNs**: Leveraged Siamese graph neural networks to analyze gene knockout and drug perturbation data, integrating multi-omics insights. (2024) Link
- **Stenosis Segmentation in Coronary Angiograms**: Developed a deep learning pipeline with F-CNN and U-Net architectures to enhance detection accuracy for clinical diagnostics. (2023) Link

SELECTED PUBLICATIONS

- Hartooni, N., **Sung, J.**, Jain, A., & Morgan, D. O. (2022). Single-molecule analysis of specificity and multivalency in binding of short linear substrate motifs to the APC/C. *Nature Communications*, 13(1), 1–13.
- Niekamp, S., **Sung, J.**, Huynh, W., Bhabha, G., Vale, R., & Stuurman, N. (2019). Nanometer-accuracy distance measurements between fluorophores at the single-molecule level. *PNAS*, 116(10), 4275–4284.
- **Sung, J.**, Nag, S., Mortensen, K. I., Vestergaard, C. L., Sutton, S., Ruppel, K., et al. (2015). Harmonic force spectroscopy measures load-dependent kinetics of individual human β-cardiac myosin molecules. *Nature Communications*, 6(1), 7931.
- Mortensen, K. I.*, **Sung, J.***, Flyvbjerg, H., & Spudich, J. A. (2015). Optimized measurements of separations and angles between intra-molecular fluorescent markers. *Nature Communications*, 6(1), 8621. **(* equal contributions)**
- Mendez, D., Lane, T. J., **Sung, J.**, Sellberg, J., Levard, C., Watkins, H., Cohen, A. E., Soltis, M., Sutton, S., Spudich, J., Pande, V., Ratner, D., & Doniach, S. (2014). Observation of correlated X-ray scattering at atomic resolution. *Philos. Trans. R. Soc. B: Biological Sciences*, 369(1647), 20130315.
- Sommese, R. F.*, **Sung, J.***, Nag, S.*, Sutton, S., Deacon, J. C., Choe, E., et al. (2013). Molecular consequences of the R453C hypertrophic cardiomyopathy mutation on human β-cardiac myosin motor function. *PNAS*, 110(31), 12607–12612. **(* equal contributions)**

AWARDS & HONORS

1st place for innovation (among 45 teams from 21 countries), Rochehack Hackathon	2020
NRSA/F32 Postdoctoral Fellowship, National Institutes of Health	2015 - 2018
Bio-X Graduate Student Fellowship, Stanford University	2009 - 2012

SELECTED PRESENTATIONS

- “Sequencing by Expansion (SBX): a novel single-molecule sequencing technology.”, Invited talk at BAKG (2025)
- “Deciphering mechanobiological pathways: single-molecule and nanoparticle approaches to dynein motility and immune receptor activation.”, Invited seminars at KAIST, SNU, POSTECH (2017)
- “Harmonic Force Spectroscopy reveals a force-velocity curve from a single human β-cardiac myosin motor.”, International conference talks at APS Meeting, Denver and BPS Meeting, San Francisco (2014)

TEACHING EXPERIENCE

Teaching Assistant, Stanford University – BIOS 207 (2013), BIOE 41 (2013), BIOC 226 (2011), MED 223 (2010)