John Peter ZINNO IV

Personal Information

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Relevant Work Experience

SEP 2022 – PRESENT

New York Genome Center & Weill Cornell Medicine, New York, NY
Senior Genomics Data Scientist (Jan 2024 – Present)
Genomics Data Scientist (Sep 2022 – Dec 2023)

Working on development of tools and pipelines for the processing and analysis of diverse genomics projects. Projects include high-throughput, GPU accelerated, distributed, multiomic pipeline development and data analysis for single cell whole genome and whole trancriptome in the same cells at unprecedented scale, phylogenetic reconstruction of somatic mosaicism from whole genome single cell DNA. Development of generative models for single cell "omics" analysis. Developed and optimized frameworks for state of the art deep learning based *de novo* cell free DNA cancer detection. Led computational collaborations with external teams such as Oracle and NVIDIA.

DEC 2021 – FEB 2023

NYU Langone Health, Perlmutter Cancer Center, New York, NY
Bioinformatician

Worked on developing pipelines for the processing of high volumes of genomic data, including patient matched 30x WGS, ATAC-seq and RNA-seq. This work is part of a study to identify novel germline genetic markers for improved clinical strategies to tailor the prediction of melanoma prognosis to individual patients. Additionally, we aim to identify markers indicative of response to novel immunotherapies. Aside from just identifying biomarkers, I also worked to identify more complex genetic signatures and integrated the various types of data we had to address the aims of the project.

JAN 2018 – SEP 2022

NYU Center for Genomics and Systems Biology, New York, NY
Assistant Research Scientist

Studied the genetic and evolutionary mechanisms underlying early embryonic development. My job responsibilities included performing and providing bioinformatic support for ongoing projects in the lab, such as 3D structural modeling, phylogenetic analysis, NGS analysis, and machine learning/deep learning methods. I additionally performed most of the labs training, CRISPR gene editing, superresolution microscopy, and image processing/quantification.

JUL 2017 – DEC 2017

Stony Brook Univeristy, Stony Brook, NY
Teaching Assistant

Teaching Biochemistry Laboratory (Bio 365). Responsibilities included lecturing on and guiding students in carrying out various methods in biochemistry, such as protein purification, sequencing, western blotting, DNA and RNA extraction and quantification, and enzyme kinetics.

AUG 2014 - MAY 2016

Florida Southern College, Lakeland, FL
Teaching Assistant

Conducted weekly tutoring group sessions for chemistry students and prepared students for their exams by working on practice problems

Laboratory Assistant

Prepared the labs weekly for the General Chemistry courses and maintained a safe laboratory environment

Education

Aug 2020 – May 2022	**New York University**, New York, NY Masters of Science in Bioinformatics
Aug 2016 – Dec 2017	**Stony Brook University**, Stony Brook, NY Masters of Science in Biochemistry & Cell Biology
Aug 2012 – May 2016	**Florida Southern College**, Lakeland, FL Bachelor of Science in Chemistry Bachelor of Science in Biology Minor in Physics concentrating in Quantum and Statistical Mechanics

Skills

Computational	Python, PyTorch/JAX, Javascript/Typescript, Rust, R, Nextflow, Git, Docker, High Performance Computing, Cloud Computing, Linux/Unix, Multivariate Analysis, Image processing/quantification, Machine Learning Classification and Regression, MCMC, Bayesian Modeling, Approximate Bayesian Computation, Deep Learning, Reinforcement Learning, Computer Vision, Generative models (LLM/Diffusion), Agentic Workflows, LaTeX
Biology	Super-resolution Microscopy, CRISPR, Protein Structure and Complex Prediction, Structural Biology, PyMOL, Molecular Dynamics, Liquid Biopsy, Next Genereation Sequencing (NGS), Single Cell Sequencing (RNA/DNA/ATAC - Multiomic)

Publications

2025	Tamara Prieto, Dennis J Yuan, **John Zinno**, Clayton Hughes, Nicholas Midler, Sheng Kao, Jani Huuhtanen, Ramya Raviram, Fenia Fotopoulou, Neil Ruthen, Srinivas Rajagopalan, Joshua S Schiffman, Andrew R D Avino, Sang-Ho Yoon, Jesus Sotelo, Nathaniel D Omans, Noelle Wheeler, Alejandro Garces, Barun Pradhan, Alexandre Pellan Cheng, Nicolas Robine, Catherine Potenski, Katharine Godfrey, Nobuyuki Kakiuchi, Akira Yokoyama, Seishi Ogawa, Julian Abrams, Ivan Raimondi, Dan A Landau. Large-scale single-cell phylogenetic mapping of clonal evolution in the human aging esophagus. *bioRxiv*. doi: 10.1101/2025.10.11.681805
	Wei-Yu Chi, Sang-Ho Yoon, Evrim Goksel, Levan Mekerishvili, Joe Pelt, Yiyun Lin, Tamara Prieto, **John Zinno**, Saravanan Ganesan, Catherine Potenski, Franco Izzo, Dan A. Landau, Ivan Raimondi. Single-cell mapping of regulatory DNA:Protein interactions. *bioRxiv*. doi: 10.1101/2024.12.31.630903
	Yakun Pang, Tamara Prieto, Veronica Gonzalez-Pena, Athena Aragon, Yuntao Xia, Sheng Kao, Sri Rajagopalan, **John Zinno**, Jean Quentin, Julien Laval, Dennis Yuan, Nathaniel Omans, David Klein, Matthew MacKay, Iwijn De Vlaminck, John Easton, William Evans, Dan A. Landau, Charles Gawad. Measuring Longitudinal Genome-wide Clonal Evolution of Pediatric Acute Lymphoblastic Leukemia at Single-Cell Resolution. *bioRxiv*. doi: 10.1101/2025.03.19.644196

Publications (continued)

2024 | Dennis J Yuan, **John Zinno**, Theo Botella, Dalia Dhingra, Shu Wang, Allegra Hawkins, Ariel Swett, Jesus Sotelo, Ramya Raviram, Clayton Hughes, Catherine Potenski, Akira Yokoyama, Nobuyuki Kakiuchi, Seishi Ogawa, Dan A Landau. Genotype-to-phenotype mapping of somatic clonal mosaicism via single-cell co-capture of DNA mutations and mRNA transcripts. *Cancer Discovery*. doi: 10.1158/2159-8290.CD-24-0853

2022 | Hin Hark Gan, **John Zinno**, Fabio Piano, Kristin C Gunsalus. Omicron Spike protein has a positive electrostatic surface that promotes ACE2 recognition and antibody escape. *Frontiers in Virology*. doi: 10.3389/fviro.2022.894531

2021 | Elisabeth A. Marnik, Miguel V. Almeida, P. Giselle Cipriani, George Chung, Edoardo Caspani, Emil Karaulanov, Falk Butter, Catherine S. Sharp, **John Zinno**, Hin Hark Gan, Fabio Piano, René F Ketting, Kristin C. Gunsalus, Dustin L. Updike. The Caenorhabditis elegans TDRD5/7-like protein, LOTR-1, interacts with the helicase ZNFX-1 to balance epigenetic signals in the germline. *PLOS Genetics*. doi:10.1371/journal.pgen.1010245

Patricia Giselle Cipriani, Olivia Bay, **John Zinno**, Michelle Gutwein, Hin Hark Gan, Vinay K Mayya, George Chung, Jia-Xuan Chen, Hala Fahs, Yu Guan, Thomas F Duchaine, Matthias Selbach, Fabio Piano, Kristin C Gunsalus. Novel LOTUS-domain proteins are organizational hubs that recruit C. elegans Vasa to germ granules. *eLife*. doi: 10.7554/eLife.60833