

EDUCATION

Ph.D in Physics, University of Illinois at Urbana-Champaign (Champaign, IL) *Aug 2018 - Aug 2023*

- Center for Physics of Living Cells Fellow (2018 - 2020)

B.S in Green Energy Science, Hong Kong Baptist University (Hong Kong) *Sep 2014 – July 2018*

- Hong Kong Special Administrative Region Government Scholarship (2015 - 2018)
- Scholastic Award (2018)

RESEARCH AND PROFESSIONAL EXPERIENCE

BillionToOne, Senior Bioinformatics Scientist, Oncology (CA) *Aug 2023 - Present*

- Joined as the first bioinformatic scientist in BillionToOne oncology and built the bioinformatics roadmap for BillionToOne liquid biopsy assays, Northstar Select and Northstar Response
- Coordinated a 30+ people cross-functional CLIA laboratory to process 2000+ clinical samples. Regularly conducted custom NGS data analysis, performed quality control, and troubleshooted wet-lab processes
- Launched Northstar Response V1.1, a bioinformatic enhancement that boosted performance by 5x
- Launched Northstar Select Nextflow pipeline (3x faster) and reduced turnaround-time by 1 day
- Launched a full-stack oncology data dashboard web-app (NiceGUI, AWS)
- Led continuous algorithm development for the Northstar products (MSI caller, CNV caller, QC metrics)
- Led continuous software development to scale-up sample processing capacity by >100X
- Grew the bioinformatics team by 6X. Facilitated hiring of 15+ full-time roles in BillionToOne.
- Worked with executive team in decision-making, facilitated commercial growth, and delivered accurate results to 2000+ cancer patients

Seppie Kuehn lab (University of Chicago / UIUC), Research Assistant (IL) *July 2019 - July 2023*

- Designed and conducted end-to-end genotyping (shotgun whole-genome sequencing) and phenotyping (carbon utilization assay) experiments on 100+ novel environmental microbes
- Used machine learning to achieve state-of-the-art prediction of microbial carbon utilization, combining experimental data and large-scale web-scraped datasets with over 4000 bacterial genomes
- Built custom bioinformatic pipelines (Snakemake) on high-performance computing clusters to analyze over 10TBs of multi-omics NGS data spanning more than 1000 samples
- Created accurate mathematical models for two systems (microbial respiration/photosynthesis and buffering capacity of complex biological media) and validated the models in experiments
- Constructed microcontroller-based (Raspberry Pi) experimental devices and troubleshoot Python-based software to interface sensors, PID controllers, and other electronic components

Upward Farms, Microbial Research Associate (Brooklyn, NY) *May 2022 - Aug 2022*

- Led end-to-end experiment to improve hydroponic crop yields by plant microbiome manipulation. Used statistical modeling and 16S sequencing to identify potential plant growth-promoting bacteria
- Prototyped two production software in AWS: a NGS annotation pipeline (Snakemake) and a R&D experiment management web portal
- Performed Nanopore long-read sequencing with the R&D team to profile hydroponic metagenome
- Contributed to other R&D experiments in crop phenotyping and sample collection

Hong Kong Baptist University, Research Assistant (Hong Kong) *July 2015 - June 2018*

- Built novel machine learning models based on biological neural networks and non-equilibrium statistical physics to conduct signal computation
- Implemented novel optimization algorithms in C++ and Python to model *C. elegans* neurons
- Collaborated in three data-driven projects with interdisciplinary teams spanning four research labs

SKILLS

Full-stack bioinformatics: Nextflow, NGS (amplicon, target enrichment, whole-genome sequencing, UMI); extraction, library prep, common wet lab; microcontrollers (Arduino, Raspberry Pi)

Full-stack data science: machine learning, statistics, high-dimensional data analysis; data engineering, dashboards (NiceGUI/Dash), databases (Postgresql); AWS, Django, REST APIs, CI/CD, Git; Python, Rust, SQL, R, Bash, Java, Groovy, JavaScript, C/C++, \LaTeX ; project management

Computational biology: cancer biology, liquid biopsy, statistical physics

OTHER EXPERIENCE

The Abdus Salam International Centre for Theoretical Physics *Mar 2018*
Spring College on the Physics of Complex Systems (Trieste, Italy)

- Completed graduate-level courses with the highest grade in reinforcement learning, statistical physics, protein biophysics, and computational neuroscience

Iowa State University, Exchange Student (Ames, Iowa, United States) *August 2016 - December 2016*

Hong Kong Baptist University, Teaching Assistant (Hong Kong) *July 2016 - June 2018*

PUBLICATIONS

Xavier Bower, Jan Wignall, Joyce Zhu, Michael O'Sullivan, Naomi E. Searle, Lenny K. Hong, Matthew G. Varga, Tiffany E. Farmer, Emilio Rosas-Linhard, **Zeqian Li**, Jason Luong, Esther Lin, Marie Erica Simon, David S. Tsao, John R. ten Bosch, Gary Palmer MD, Ajeet Gajra MD, Chanh Huynh MD, Wen Zhou
"Validation of a liquid biopsy assay with increased sensitivity for clinical comprehensive genomic profiling." *Manuscript submitted for publication.* (2024)

Angela Hsiao, Brian Woodward, Patrick Ye, Matthew G Varga, Ghaith Altaie, Kevin Lu, Naomi Searle, Robb Viens, Sydne Langpap, **Zeqian Li**, Gary Palmer, Hatim Husain. "Brief Report: Methylation-Based ctDNA Serial Monitoring Correlates with Therapeutic Response in Lung Cancer." *Manuscript submitted for publication.* (2024)

Zeqian Li, Ahmed Selim, Seppe Kuehn. "Statistical prediction of microbial metabolic traits from genomes." *PLOS Computational Biology* 19.12 (2023): e1011705.

Kyle Crocker, Milena Chakraverti-Wuerthwein, **Zeqian Li**, Madhav Mani, Karna Gowda, Seppe Kuehn. "Genomics patterns in the global soil microbiome emerge from microbial interactions." *Nature Microbiology* (2024): 838-853.

Chandana Gopalakrishnappa, **Zeqian Li**, Seppe Kuehn. "Environmental modulators of algae-bacteria interactions at scale." *Cell Systems* 15.9 (2024): 838-853.

Zeqian Li, Vaibhhav Sinha, and Seppe Kuehn. "Constraints on microbial metabolic complexity." *Nature Microbiology* 8.10 (2023): 1756-1757.

Luis Miguel de Jesús Astacio*, Kaumudi H. Prabhakara*, **Zeqian Li**, Harry Mickalide, Seppe Kuehn. "Closed microbial communities self-organize to persistently cycle carbon." *Proceedings of the National Academy of Sciences* 118, no. 45 (2021): e2013564118.

SELECTED CONFERENCE PRESENTATIONS

Speaker: Microbiome Research Symposium, The University of Chicago, "Machine learning predicts microbial metabolic traits from genomes." (2023)

Speaker: The American Physical Society March Meeting, "Unique functional structure of the Yellowstone hot spring microbial mats revealed by multi-omics studies." (2022)

Speaker: The Yellowstone Hot Spring Microbial Mats Symposium, Carnegie Institution for Science,
“Co-expression constrains genome organization in an extensively recombined microbial population.”
(2022)