Joshua Chiou, Ph.D.

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SUMMARY

- Computational scientist with industry experience in early drug development for cardiometabolic diseases.
- Expertise in summarizing findings from large-scale human genetics and single-cell 'omics datasets to identify new targets, guide biomarker strategy, and support indication expansion with cross-functional teams.
- Dedicated to leveraging cloud infrastructure to scale analytical platforms and enhance visualization tools.

PROFESSIONAL EXPERIENCE

- **Pfizer** Cambridge, MA
  ***Senior Principal Computational Geneticist**, Internal Medicine Research Unit* *Oct. 2023 – Present*
  - Led cross-functional target discovery for cardiovascular disease, modernizing human genetics-based approaches through LLMs and CRISPR screens with functional genomics teams.
  - Drove strategic planning and roadmap for genetics infrastructure, resulting in a scalable cloud-based framework for storage, analysis, and interactive visualization of summary level data.
  - Represented Pfizer in external collaborations with academic and industry partners, driving impactful research from investments and communicating project updates to internal stakeholders.
  - Managed a postdoctoral fellow and intern to advance cutting-edge research in applied statistical genetics and single-cell genomics.

- **Pfizer** Cambridge, MA
  ***Senior Computational Geneticist**, Internal Medicine Research Unit* *Apr. 2021 – Sep. 2023*
  - Supported biologists on target discovery for renal disease through integrative analyses of human genetics and 'omics, resulting in 10+ novel targets and impacting key portfolio decisions.
  - Guided clinical teams on biomarker strategies and commercial teams on indication expansion using epidemiological evidence from large-scale biobanks with longitudinal electronic health records.
  - Collaborated with machine learning experts to develop state-of-the-art deep learning models trained on genomic datasets, accelerating target evaluation efforts by providing therapeutic directionality.
  - Developed Nextflow pipelines for statistical genetics analyses with data engineers, enabling cross-department benchmarking and selection of optimal methods for fine-mapping and colocalization.

- **University of California, San Diego** La Jolla, CA
  ***Graduate Student Researcher**, Advisor: Dr. Kyle Gaulton* *Sep. 2016 – Mar. 2021*
  - Conducted the largest GWAS study for type 1 diabetes, demonstrating how to integrate genetics and single-cell epigenomics to uncover novel disease mechanisms, published in *Nature*.
  - Partnered with cross-functional research teams to provide biological insights from large-scale genomics datasets, resulting in 25 high-impact publications in less than 5 years.

- **IncellDx** Menlo Park, CA
  Development Scientist *Sep. 2015 – Aug. 2016*
  - Optimized a cell-based companion diagnostic assay for HIV that was acquired by ViiV Healthcare.

- **National Aeronautics and Space Administration** Houston, TX
  Microbiology Intern *Jun. 2015 – Aug. 2015*
  - Prototyped a rapid assay to improve detection of infectious herpesviruses for astronauts in space.

TECHNICAL SKILLS

- **Programming & AI/ML:** Python (pandas, dask, scikit-learn, PyTorch), Machine learning, Predictive modeling, Data mining, Data visualization, Web applications, APIs, LLMs.
- **Statistical Genetics:** GWAS, ExWAS, Plink, Regenie, Population cohorts (UK Biobank, FinnGen, Biobank Japan), Meta-analysis, Fine-mapping, Colocalization, Mendelian randomization, Electronic health records, Survival analysis.
- **Genomics:** Single-cell (Transcriptomics, Epigenomics), Proteomics, Multi-omic data integration.
- **Infrastructure:** Cloud computing (AWS), HPC, Nextflow pipelines, Version control (Git), Containers (Docker, Singularity), Environment management (Conda, Pixi), FAIR data principles, Databases (SQL).

EDUCATION

- **University of California, San Diego** — La Jolla, CA
  Ph.D. in Biomedical Sciences — *Sep. 2016 – Mar. 2021*
- **University of California, Los Angeles** — Los Angeles, CA
  B.S. in Microbiology, Immunology, and Molecular Genetics — *Sep. 2011 – Jun. 2015*

SELECTED PUBLICATIONS (10 OF 40)

1. Retel JS, Poehlmann A, **Chiou J**, et al. A fast machine learning dataloader for epigenetic tracks from BigWig files. *Bioinformatics* 40 (1), btad767. (2024).
2. Sun BB, **Chiou J**, et al. Plasma proteomic associations with genetics and health in the UK Biobank. *Nature* 622, 329-338 (2023).
3. **Chiou J**, et al. Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. *Nature* 594, 398-402 (2021).
4. **Chiou J***, Zeng C*, et al. Single-cell chromatin accessibility identifies pancreatic islet cell type- and state-specific regulatory programs of diabetes risk. *Nature Genetics* 53, 455-466 (2021).
5. Wang G*, **Chiou J***, et al. Integrating genetics with single-cell multiomic measurements across disease states identifies mechanisms of beta cell dysfunction in type 2 diabetes. *Nature Genetics* 55, 984-994 (2023).
6. Geusz RJ*, Wang A*, **Chiou J***, et al. Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. *eLife* 10:e59067 (2021).
7. Wang A*, **Chiou J***, et al. Single cell multiomic profiling of human lung reveals cell type-specific and age-dynamic control of SARS-CoV2 host genes. *eLife* 9:e62522 (2020).
8. Greenwald WW*, **Chiou J***, et al. Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. *Nature Communications* 10, 2078 (2019).
9. Zhang K, Hocker JD, Miller M, Hou X, **Chiou J**, et al. A single-cell atlas of chromatin accessibility in the human genome. *Cell* 184 (24), 5985-6001. (2021).
10. Yan J, [et al. including **Chiou J**]. Systematic analysis of binding of transcription factors to noncoding variants. *Nature* 591, 147-151 (2021).

Full publication history available at: Google Scholar and ORCID. (*denotes co-first authorship).