

Jonathan Chan

+447453417448 | jonathan.chan0@protonmail.com | <https://www.linkedin.com/in/jchan0/> | <https://github.com/JonChan0/>

EDUCATION

University of Oxford, Merton College DPhil in Medical Sciences (Bioinformatics/Cardiovascular Genomics)	Oxford, United Kingdom 2022 – Present (Oct 2026)
University of Oxford, St Hilda's College MBiochem in Molecular and Cellular Biochemistry – 1 st Class (Rank: 2 nd of 97)	Oxford, United Kingdom 2018 – 2022

HONOURS

- Radcliffe Department of Medicine & Clarendon Fund DPhil Scholarship (~£175k), 2022
- Gibbs Prize for Proxime Accessit in Biochemistry (2nd in Cohort), 2022
- Department of Biochemistry Project Prize for Master's Research (3rd in Cohort), 2022

RESEARCH EXPERIENCE

Dart Biosciences Ltd, London, United Kingdom

Computational Biologist (Part-Time), Oct 2024 – Present

- Built MVP for at-scale cell-specific marker gene identification via *cellxgene*, *scanpy*, *scVI* and *cellPLM*.
- Conducted project feasibility analysis on single-cell transcriptome → surfaceome prediction via processing of CITE-seq datasets (*muon*) and benchmarking of SOTA model (*SPIDER*).
- Co-authored NSF SBIR and NIH SBIR Omnibus grant applications.

University of Oxford Radcliffe Department of Medicine, Oxford, United Kingdom

Doctoral Student (Prof. Hugh Watkins & Prof. Anuj Goel), Sep 2022 – Present

- Applying bioinformatic & ML approaches to integrate genomic, proteomic, clinical, and imaging data in large patient/population cohorts.
- Building multifactorial models for prediction of hypertrophic cardiomyopathy risk and severity.
- Applying statistical genetic and population-scale analyses to identify novel biomarkers of disease risk and progression.

University of Oxford Ludwig Institute for Cancer Research, Oxford, United Kingdom

Master's Student (Prof. Yang Shi), Sep 2021 – Jun 2022

- Performed genome-wide CRISPR-cas9 knockout screening of cancer cell lines + NGS analysis
- Discovered novel vulnerabilities with top hit *ASCL1* progressing to validation via mouse models.

SKILLS

Tech

- R: *tidyverse*; *ggplot2*; *markdown*
- Python: *pandas*; *NumPy*; *seaborn*; *scikit-learn*; *scikit-survival*
- HPC: *SLURM*
- Cloud Computing: *DNAexus*; *GCP*

Bioinformatics

- GWAS (*REGENIE*; *PLINK*; *SNPTTEST*)
- Post-GWAS analyses (*LDSC*; *FINEMAP*; *coloc*)
- Polygenic risk score modelling (*PRS-CS*; *SBayesRC*)
- Rare-variant association analysis (*REGENIE*; *SAIGE-GENE+*; *VEP*)
- Mendelian randomisation (*TwoSampleMR*)
- Pipelining (*snakemake*; *Bash*; *Docker*; *WDL*)

- Single-cell transcriptomic analysis (*scanpy*, *scVI*, *cellxgene*, *DESeq2*)
- Multimodal -omic (CITE-seq) data analysis (*muon*)

Population-Scale Data Analysis

- Data analysis in patient & population datasets (*HCMR*; *UK Biobank*; *All of Us*)
- Systematic review (*PRISMA*) and meta-analysis (*meta*)
- Survival/TTE analysis (*Kaplan-Meier*; *Cox regression*)

PUBLICATIONS/PRESENTATIONS

Chan, J.H., Grace, C., Mahidi, M., Clarke, R., Ho, C., Neubauer, S., Kramer, C., Watkins, H., Goel, A.
Biobank-Scale Plasma Proteomics Identifies Novel Biomarkers in Hypertrophic Cardiomyopathy,
Circulation: Precision & Genomic Medicine (*Under Review*)

Jiao, A.L., Maghrouni, A., Velazquez, A.G., Annett, A., Wen, T., Chan, J., Nguyen, S., Tayeh, B.B., Le Dily, F., Kleinman, C., di Croce, L., Shi, Y.
H3K27M co-opts ASCL1 to maintain progenitor states and drive gliomagenesis, Nature Communications (*Under Review*)

Chakraborty, A., Kobzev, E., Chan, J., de Zoysa, G.H., Sarojini, V., Piggot, T.J., Allison, J.R. (2021)
Molecular Dynamics Simulation of the Interaction of Two Linear Battacin Analogue with Model Gram Positive and Gram Negative Bacterial Cell Membranes, ACS Omega

Prioritising modifiable risk factors and biomarkers for hypertrophic cardiomyopathy: a Mendelian randomization approach

American Society of Human Genetics Annual Meeting (Boston, US), Oct 2025

Uncovering how Sarcomeric Variants affect Disease Heterogeneity in Hypertrophic Cardiomyopathy: A Cardiac Magnetic Resonance Imaging Study in the HCM Registry

International Society of Heart Research XXV World Congress (Nara, Japan), May 2025

Integrating Rare and Common Genetics for Risk Prediction in Hypertrophic Cardiomyopathy

Genomics England Research Summit (London, UK), Jul 2024

EXTRACURRICULAR

Peer Review Experience

- Nature Cardiovascular Research
 - NCVR-2025-03-0348 (Statistical genetics, Mendelian randomisation), Apr 2025

Bio x AI Hackathon – 3rd Place

Entrepreneur First (London), Nov 2024

- Leveraged scRNA-seq foundation model (*CellPLM*) to harmonise lung adenocarcinoma datasets and applied optimal transport to transcriptomic embeddings to model cancer evolution.

Oxford University Biotech Society, Oxford, United Kingdom

President, Jun 2023 – Jun 2024

- Managed team of 11 across all society facets e.g operations, finance, communications etc.
- Spearheaded inaugural OxBioHack hackathon in collaboration with Oxford CompSoc and OPMS.