

JACK GISBY

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EDUCATION

Imperial College London

July 2020 - August 2023

PhD Candidate - Department of Immunology and Inflammation

- Thesis: Using Multi-Omics to Understand Inflammatory Disease
- Supervised by Dr James Peters
- Assessed by Professor Marc Chadeau and Dr Jessica Strid

University of Birmingham

September 2016 - June 2020

Biochemistry with Professional Placement (MSci) - First Class

- Dissertation: A Prior Knowledge-Based Computational Workflow for *de novo* Structural Elucidation of Small Molecules in Mass Spectrometry Metabolomics

PUBLICATIONS

Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death

First author

eLife 2021 - [doi:10.7554/eLife.64827](https://doi.org/10.7554/eLife.64827)

- Lead the analysis of a high-dimensional proteomics (Olink) dataset with a complex cohort consisting of repeated measurements at inconsistent time points.
- Applied linear mixed models and joint models to identify key proteins that changed over time following COVID-19 symptom onset.
- Utilised supervised learning algorithms to identify biomarkers of severe disease.

Mendelian randomisation identifies alternative splicing of the FAS death receptor as a mediator of severe COVID-19

Equal first contributor

medRxiv 2021 - [doi:10.1101/2021.04.01.21254789](https://doi.org/10.1101/2021.04.01.21254789)

- Developed a parallelised [pipeline for two sample Mendelian Randomisation](#) and subsequently investigated COVID-19 susceptibility and severity using Olink & SOMA pQTLs.
- Used fine mapping and colocalisation tools in tandem with public data repositories to investigate causal variants of disease.

The widespread nature of Pack-TYPE transposons reveals their importance for plant genome evolution

First author

bioRxiv 2021 - [doi:10.1101/2021.06.18.448592](https://doi.org/10.1101/2021.06.18.448592)

- Designed an algorithm for the specific annotation of repetitive elements that capture chromosomal DNA; implemented this as an [R package available as part of the Bioconductor project](#).
- Mined open source genetic data to demonstrate the abundance of these elements for multiple superfamilies and genomes. Found that recent insertions of these elements have impacted the evolution of genes.

Plasma Lectin Pathway Complement Proteins in Patients With COVID-19 and Renal Disease

Equal first contributor

Frontiers in Immunology 2021 - [doi:10.3389/fimmu.2021.671052](https://doi.org/10.3389/fimmu.2021.671052)

- Provided statistical support for the analysis of a repeated measures study design.

- Generated data visualisations to investigate biological hypotheses.

CONFERENCES AND PRESENTATIONS

- **Presentation - Biomarkers of the Future 2021** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death
- **Poster - HUPO Reconnect 2021** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death
- **Poster - UK-CIC Immunology 2021** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death
- **Presentation - Longitudinal Studies 2021, Wellcome Genome Campus** - Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death

ADDITIONAL RESEARCH EXPERIENCE

A Prior Knowledge-Based Computational Workflow for *de novo* Structural Elucidation of Small Molecules in Mass Spectrometry Metabolomics

Dissertation project, Dr Ralf Weber

October 2019 - June 2020

- Developed and optimised a Python package, *MetaboBlend*, to propose candidate molecules using tandem mass spectra.
- Processed large, high-dimensional mass-spectrometry datasets for the validation of *MetaboBlend*.
- Used Python, SQLite and Bash to implement the *MetaboBlend* workflow on a Linux high-performance computing cluster for the generation of large structure databases.
- Created a "metabolite-likeness" model based on a deep learning implementation of the one-class support vector data description algorithm, adapted to model metabolites with a transformer architecture.

Development of an Immunoturbidimetric Assay for Serum Amyloid A for an Automated Clinical Analyser

Industrial Placement, The Binding Site

August 2018 - August 2019

- Developed assays for inflammatory biomarkers, such as Serum Amyloid A, for use in clinical laboratories.
- Interacted with, and regularly delivered presentations to, researchers from diverse fields and non-scientific staff to ensure the timely completion of my development project.
- Took responsibility for planning and carrying out experiments and statistical analyses in a research environment.

TEACHING EXPERIENCE

- **Lecture:** RNA-seq in Molecular Epidemiology - Developed a two-part lecture explaining the basics of RNA sequencing and its application to investigate genetic variants. Set homework and final exam questions for the module.
- **Supervision:** Co-supervisor of a medical undergraduate - On-going project using Olink proteomics to investigate Lupus.
- **Volunteer:** Code Club - Developed my teaching abilities and provided help with coding skills to 9-13 year-olds as part of the Code Club voluntary initiative.

SPECIFIC COMPUTATIONAL SKILLS

Operating Systems	Windows, Ubuntu
Programming Languages	Python, R, SQLite, Bash, working knowledge of C++ & Julia
Other Tools	Git, Linux HPC, Conda, Docker, Nextflow
General Software	MS Office, L ^A T _E X
Data types	Olink & SOMA proteomics, RNA-seq, MS metabolomics, whole genome sequences, GWAS
Bioinformatics/Statistics	Package development in R and Python, Linear and mixed models, Mendelian randomisation & colocalisation, Joint models, Supervised learning (scikit-learn, tensorflow, pytorch), WGCNA

ADDITIONAL COURSES

- From large datasets to biological insight by Wellcome Connecting Science & EMBL-EBI
- Introduction to Assessment and Feedback by Imperial College London
- Introduction to Teaching and Learning by Imperial College London
- Profiling and optimisation in Python by Imperial College London
- Computational Systems Biology: Deep Learning in the Life Sciences by MITx
- Software Development with C++ by University of Birmingham Research Computing
- The Biostars Handbook: Bioinformatics Data Analysis by Istvan Albert
- Introduction to Computer Science and Programming Using Python by MITx
- Introduction to Computational Thinking and Data Science by MITx
- Data Analysis for Life Sciences and Genomics Data Analysis by HarvardX