

JACK GISBY

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RESEARCH INTERESTS

PhD candidate at Imperial College London interested in data-driven research and the -Omics technologies. I have the aspiration to pursue a career in biological research, exploiting the vast datasets produced by modern biology to answer fundamental research questions. My core project involves combining genomic, transcriptomic and proteomic datasets to identify molecular pathways that play a driving role in inflammatory disease. I am also interested in developing data processing and mining methods to facilitate the extraction of biological insights from -Omics datasets.

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 and Dr Jacques Behmoaras
- 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

SELECTED PUBLICATIONS

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

First author

Manuscript in progress

- 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.

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

- 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

- Developed a pipeline to apply two sample Mendelian Randomisation comparing COVID-19 GWAS to Olink pQTLs.
- Used fine mapping and colocalisation tools in tandem with public data repositories to investigate causal variants of disease.

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

- Provided statistical support for the analysis of a repeated measures study design.
- Generated data visualisations to investigate biological hypotheses.

CONFERENCES AND PRESENTATIONS

- **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
- **Presentation - Centre for Inflammatory Disease, Imperial College London** - 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.

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

- **Code Club Volunteer** - 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++
Packages	Bioconductor, ggplot2, scikit-learn, tensorflow
Other Tools	Git, Linux HPC
General Software	MS Office, Latex

ADDITIONAL COURSES

- Systems biology: From large datasets to biological insight (1 week) by Wellcome Connecting Science and 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++ (1 week) 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