

# JACK GISBY

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## RESEARCH INTERESTS

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PhD candidate at Imperial College London with a keen interest 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.

## EDUCATION

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### 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

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### **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**

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- **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**

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### **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**

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- **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**

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<b>Operating Systems</b>	Windows, Ubuntu
<b>Programming Languages</b>	Python, R, SQLite, Bash, working knowledge of C++
<b>Packages</b>	Bioconductor, ggplot2, scikit-learn, tensorflow
<b>Other Tools</b>	Git, Linux HPC
<b>General Software</b>	MS Office, Latex

## ADDITIONAL COURSES

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- 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