PI profile

## Daniel Wilson

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|  | **Dr Daniel J Wilson**  **Titles**: Group Leader / PI / Professor  **Location**: Big Data Institute  **Department**: Oxford Population Health  **Group**: Infectious Disease Genomics  **Webpage**: www.danielwilson.me.uk  **Email**: daniel.wilson@bdi.ox.ac.uk  **PA**: faye.mellis@ndph.ox.ac.uk |

### GMS themes:

* Genomics of (infectious) disease
* Genomic analysis (bioinformatics and statistical genetics)
* Genome biology (genomes and genetic variation)

### Research Overview

Danny is Professor of Infectious Disease Genomics at the University of Oxford. He holds a Robertson Fellowship at the Big Data Institute, and serves as Director of Studies in Data Science at the Department for Continuing Education.

His group’s research interests are in the genetic risk of infectious disease and the evolution of pathogen populations, which they study through comparative genome analysis. People in the group come from biology, statistics, medicine and machine learning backgrounds. Their research focuses on the analysis of bacterial diseases and populations, but covers viruses, non-pathogenic microorganisms and host genetics.

Motivating themes in their work are (i) understanding the genomics of virulence and susceptibility and (ii) the effects of transmission, natural selection and recombination on shaping pathogen diversity. They have investigated the evolution of pathogen populations from the colonization of individual hosts and transmission between hosts, through to the whole-species and phylogenetics levels.

The group’s research is supported by the Wellcome Trust and Robertson Foundation. They collaborate with the Modernising Medical Microbiology consortium based at the John Radcliffe Hospital, Oxford, and the Department of Statistics. Their work has been published in the top field-specific and general science journals.

Project areas: Infectious disease genomics, GWAS, host-pathogen interactions, transcriptomics and proteomics, population genetics, evolution, epidemiology, statistical methods development

### Specific project proposals:

* Developing analysis methods to detect human-pathogen interactions
* Open to other projects in infectious disease genomics and statistical genetics, such as bacterial genome-wide association studies.

Please contact directly for further information.

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Project proposal

# **Title**: Developing analysis methods to detect human-pathogen interactions

Supervisors: Associate Professor Daniel Wilson

Wet/dry lab mix (approx): 100% dry lab

### Description:

Infection is fundamentally an interaction between the human and pathogen. Consequently there is long-standing interest in the role of human-pathogen genetic interactions in infection traits, including disease severity and clinical outcome. While the biological questions are readily framed, logistic and analytic challenges have held back progress in this area. The chief difficulties are genotyping and whole genome sequencing large cohorts of humans and pathogens, and devising sensitive analyses that do not generate large numbers of false positives. Research groups around the world are now pursuing such cohorts in earnest. The focus of this project therefore is on the development and application of tools for performing trillions of tests of association between the millions of human genetic variants and millions of pathogen genetic variants, while controlling the false positive rate without loss of statistical power. This is critical for the emerging field of human-pathogen genome-wide association studies. Focusing on published data or new data generated in-house (subject to the project's progress by the commencement of this internship), we will develop and apply the harmonic mean *p*-value method to this problem. Depending on the student, there will be opportunity to focus more on the applied or theoretical side of the project, and to apply the approach to related problems such as epistasis. Subject to satisfactory progress, there may be opportunity to publish the results of the internship.

### Training Opportunities:

The students will learn about genome-wide association studies and statistical genetics with the help of the supervisor and other group members. Students are welcome to attend other training courses at the university or elsewhere.

### Background reading / references:

* The COVID-19 Host Genetics Initiative (2021)  
  Mapping the human genetic architecture of COVID-19  
  *Nature* doi:10.1038/s41586-021-03767-x ([abstract](http://www.danielwilson.me.uk/abstracts/covid19hgi_2021.html) [pdf](https://www.nature.com/articles/s41586-021-03767-x))
* D. J. Wilson (2019)  
  The harmonic mean *p*-value for combining dependent tests.  
  *Proceedings of the National Academy of Sciences USA* 116: 1195-1200. ([abstract](http://www.danielwilson.me.uk/abstracts/wilson_2019.html) [pdf](https://www.pnas.org/content/116/4/1195))
* Young, B. C., et al. (2019)  
  Panton-Valentine leukocidin is the key determinant of *Staphylococcus aureus* pyomyositis in a bacterial genome-wide association study.  
  *eLife* 8: e42486 ([abstract](http://www.danielwilson.me.uk/abstracts/young_etal_2019.html) [preprint](https://www.biorxiv.org/content/early/2018/09/29/430538) [pdf](https://elifesciences.org/articles/42486))

See [www.danielwilson.me.uk](http://www.danielwilson.me.uk) for further group information.