David J. Pattinson *September 19, 1989*

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Summary

I am a computational biologist with a background in evolutionary biology and infectious diseases. My research spans inferring infection histories from messy serological data, elucidating the antigenic effect of mutations and testing the predictability of seasonal influenza viruses. I am a Senior Scientist at the Influenza Research Institute, University of Wisconsin—Madison, where I lead computational investigations in the group, teach, and run my own projects. In my career I have developed strong skills in Bayesian inference, high throughput computing, data visualization and phylogenetics.

Fundamentally, I am interested in how different aesthetic or mathematical representations of data enable scientific inquiry. Aesthetically, I use data visualization as a core component of my work, iterating to generate custom visualizations that provide detailed insight into datasets and the workings of statistical models while empowering the viewer to see patterns they did not know they were looking for. Mathematically, I have made heavy use of antigenic cartography and antibody landscapes to elucidate antigenic variation of viruses and infer the effects of mutations.

Experience

Influenza Research Institute, University of Wisconsin—Madison   Madison WI, USA

Scientist I   *Mar '22–present*

I was promoted to Senior Scientist after two years to lead computational investigations in the group including antigenic cartography, antibody landscapes, phylogenetics, Bayesian statistics, computational structural biology and next-generation sequencing analyses.

Postdoctoral Research Associate   *Nov '19–Mar '22*

I joined Prof. Yoshihiro Kawaoka's lab to research mechanisms of influenza virus antigenic change using computational structural biology. During the COVID-19 pandemic I helped run a COVID-19 serosurveillance cohort in collaboration with the U.S. CDC and the Marshfield Clinic Research Institute.

Education

University of Cambridge   Cambridge, UK

Ph.D. Infectious Disease Informatics, Department of Zoology   *2014–2019*

Supervised by Prof. Derek Smith • Quantifying the relationship between vaccine effectiveness and antigenic mismatch • GWAS linear mixed models for association testing and genotype-phenotype mapping applied to influenza virus antigenicity • A framework to predict influenza virus antigenic cluster transition substitutions.

Imperial College London   London, UK

M.Res. Biosystematics, Natural History Museum   *2012–2013*

Endogenous retrovirus screening in catarrhine primates (Dr. Michael Tristem) • Novel methods in mitochondrial DNA enrichment (Dr. Martijn Timmermans) • A morphometric assessment of species delimitation in Canarian Pericallis (Dr. Mark Carine).

University of Cambridge   Cambridge, UK

B.A. Natural Science, Queens' College   *2009–2012*

Part II Zoology. Research Project: Combining molecular and morphological data in phylogenetic analyses (Dr. Robert Asher) • Part IB Biochemistry, Animal Biology, Plant Biology • Part IA Evolution and Behaviour, Biology of Cells, Chemistry, Mathematics for Biologists.

Skills

Computational: I have used **Python** on a daily basis since 2013; developing (e.g. ititer, pymds) and using scientific research packages (e.g. **PyMC**, **NumPy**, **MDAnalysis**, **SciPy**, **scikit-learn**, **matplotlib**, **pandas**, **Bambi**) • I develop interactive visualization dashboards with **dash** • I am a proponent of **unit testing** and **reproducible research practices** • I am familiar with **R** and **JavaScript**, and am learning **Rust** • I use the **UNIX** command line and **git** daily • Bioinformatics software I have used includes: **MrBayes**, **RAxML** and **MAFFT** for phylogenetics and **GROMACS** and **Amber** for structural biology • I have used **Snakemake** in several projects • I have used the **SLURM** and **HTCondor** cluster scheduling systems.

Languages: English (*mother tongue*), German (*elementary*).

Current Projects

Pattinson, Neumann, and Kawaoka (in prep). "The molecular basis of influenza virus antigenic change".

> I developed a Bayesian model to predict immune assay measurements between viruses and antisera that has state-of-the-art performance and is easily interpretable. It has applications as diverse as early detection of novel antigenic variants in sequence data and testing biophysical hypotheses related to antigen-antibody binding. Colleagues are currently preparing three other manuscripts that use this model.

Pattinson, Petrie, Jester, Guan, King, Nguyen, Belongia, Rolfes, Feldstein, Neumann, and Kawaoka (in prep). "Evaluating protection against SARS-CoV-2 infection using antibody dynamics".

> Since mid-2021 I have been helping run a COVID-19 serosurveillance cohort based in Wisconsin, USA. In this paper I developed a large scale custom Bayesian model that reconstructs antibody titers through time whilst incorporating effects from known vaccinations and PCR+ records. We then use these inferences to recover protection curves for different antigens and show how these changed as novel antigenic variants emerged.

Pattinson, Wilks, Fan, Mögling, James, Aban, Höpping Mosterín, Turner, Tureli, Skepner, Jones, Hurt, de Graaf, Barr, Neumann, Fouchier, Kawaoka, and Smith (in prep). "Predicting the antigenic evolution of seasonal influenza".

> During my Ph.D., I joined an ongoing project to evaluate the predictability of seasonal influenza antigenic evolution. This paper is the culmination of that work and reframes the goal of seasonal influenza vaccination to that of optimizing population immune responses in antigenic space ahead of likely evolutionary paths. This project has already impacted WHO influenza vaccine strain selection choices administered to 100s of millions of people annually.

Publications

Pattinson, Jester, Gu, Guan, Armbrust, Petrie, King, Nguyen, Belongia, Halfmann, Neumann, and Kawaoka (in review). "Choosing sides: comparing ipsilateral and contralateral coadministration of influenza and COVID-19 vaccines". *eBioMedicine*.

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