

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 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 visual or quantitative representations of data drive scientific inquiry. Data visualization is a core component of my work. I often iterate 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. Quantitatively, I have used antigenic cartography, antibody landscapes and custom Bayesian models to resolve antigenic variation of viruses, infer the effects of mutations, and uncover predictable patterns in evolution.

Experience

Influenza Research Institute, University of Wisconsin—Madison

MADISON WI, USA

Scientist II

Mar 24–present

Scientist I

Mar 22–Mar 24

I lead computational investigations for the group which comprise antigenic cartography, antibody landscapes, phylogenetics, computational structural biology, next-generation sequencing analyses and constructing bespoke Bayesian models.

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 Mosterin, 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

Banerjee, **Pattinson**, Wincek, Bunk, Chapin, Navlakha, and Meyer (2024). “BATMAN: Improved T cell receptor cross-reactivity prediction benchmarked on a comprehensive mutational scan database”. *bioRxiv*. doi: [10.1101/2024.01.22.576714](https://doi.org/10.1101/2024.01.22.576714).

Fan, Kong, Babujee, Presler, Jester, Burke, **Pattinson**, Barr, Smith, Neumann, and Kawaoka (2024). “Assessment of the antigenic evolution of a clade 6B.1 human H1N1pdm influenza virus revealed differences between ferret and human convalescent sera”. *eBioMedicine* 101, p. 105013. issn: 2352-3964. doi: [10.1016/j.ebiom.2024.105013](https://doi.org/10.1016/j.ebiom.2024.105013).

Guan, Babujee, Presler, **Pattinson**, Nguyen, Hoang, Le, van Bakel, Kawaoka, and Neumann (2024). “Avian H6 Influenza Viruses in Vietnamese Live Bird Markets during 2018–2021”. *Viruses* 16.3. doi: [10.3390/v16030367](https://doi.org/10.3390/v16030367).

Guan, Eisfeld, **Pattinson**, Gu, Biswas, Maemura, Trifkovic, Babuje, Presler, Randall Dahn, Halfmann, Barnhardt, Neumann, Thompson, Swinford, Dimitrov, Poulsen, and Kawaoka (2024). “Cow’s Milk Containing Avian Influenza A(H5N1) Virus — Heat Inactivation and Infectivity in Mice”. *New England Journal of Medicine* 391.1, pp. 87–90. issn: 0028-4793. doi: [10.1056/nejmc2405495](https://doi.org/10.1056/nejmc2405495).

Kok, Wilks, Tureli, James, Bestebroer, Burke, Funk, van der Vliet, Spronken, Rijnink, **Pattinson**, Meulder, Rosu, Lexmond, van den Brand, Herfst, Smith, Fouchier, and Richard (2024). “A vaccine antigen central in influenza A(H5) virus antigenic space confers subtype-wide immunity”. doi: [10.1101/2024.08.06.606696](https://doi.org/10.1101/2024.08.06.606696).

Kovaleva, **Pattinson**, Barton, Chapin, Minervina, Richards, Sant, Thomas, Pogorelyy, and Meyer (2024). “copepodTCR: Identification of Antigen-Specific T Cell Receptors with combinatorial peptide pooling”. *bioRxiv*. doi: [10.1101/2023.11.28.569052](https://doi.org/10.1101/2023.11.28.569052).

Pattinson, Jester, Gu, Guan, Armbrust, Petrie, King, Nguyen, Belongia, Halfmann, Neumann, and Kawaoka (2024). “Ipsilateral and contralateral coadministration of influenza and COVID-19 vaccines produce similar antibody responses”. *eBioMedicine* 103, p. 105103. issn: 2352-3964. doi: <https://doi.org/10.1016/j.ebiom.2024.105103>.

Petrie, **Pattinson**, King, Neumann, Guan, Jester, Rolfes, Meece, Kieke, Belongia, Kawaoka, and Nguyen (2024). “SARS-CoV-2 incidence, seroprevalence, and antibody dynamics in a rural, population-based cohort: March 2020 – July 2022”. *American Journal of Epidemiology*, kwae125. issn: 0002-9262. doi: [10.1093/aje/kwae125](https://doi.org/10.1093/aje/kwae125).

Belongia, Petrie, Feldstein, Guan, Halfmann, King, Neumann, **Pattinson**, Rolfes, McLean, and Kawaoka (2023). “Neutralizing Immunity Against Antigenically Advanced Omicron BA.5 in Children After SARS-CoV-2 Infection”. *Journal of the Pediatric Infectious Diseases Society* 13.1, pp. 100–104. doi: [10.1093/jpids/piad109](https://doi.org/10.1093/jpids/piad109).

Chiba, Hatta, **Pattinson**, Yasuhara, Neumann, and Kawaoka (2023). “Ferret model to mimic the sequential exposure of humans to historical H3N2 influenza viruses”. *Vaccine* 41.2, pp. 590–597. doi: [10.1016/j.vaccine.2022.12.005](https://doi.org/10.1016/j.vaccine.2022.12.005).

- Guan, Babujee, Browning, Presler, **Pattinson**, Nguyen, Hoang, Le, Bakel, Neumann, and Kawaoka (2023). "Continued Circulation of Highly Pathogenic H5 Influenza Viruses in Vietnamese Live Bird Markets in 2018–2021". *Viruses* 15.7, p. 1596. doi: [10.3390/v15071596](https://doi.org/10.3390/v15071596).
- Guan, Zhong, Fan, Plisch, Presler, Gu, Babujee, **Pattinson**, Nguyen, Hoang, Le, Bakel, Neumann, and Kawaoka (2023). "Highly Pathogenic H5 Influenza Viruses Isolated between 2016 and 2017 in Vietnamese Live Bird Markets". *Viruses* 15.5, p. 1093. doi: [10.3390/v15051093](https://doi.org/10.3390/v15051093).
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- Petrie, King, McClure, Rolfes, Meece, **Pattinson**, Neumann, Kawaoka, Belongia, and McLean (2023). "Effectiveness of first and second COVID-19 mRNA vaccine monovalent booster doses during a period of circulation of Omicron variant sublineages: December 2021–July 2022". *Influenza and Other Respiratory Viruses* 17.3. doi: [10.1111/irv.13104](https://doi.org/10.1111/irv.13104).
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- Pattinson**, Jester, Guan, Yamayoshi, Chiba, Presler, Rao, Iwatsuki-Horimoto, Ikeda, Hagihara, et al. (2022). "A novel method to reduce ELISA serial dilution assay workload applied to SARS-CoV-2 and seasonal HCoVs". *Viruses* 14.3, p. 562. doi: [10.3390/v14030562](https://doi.org/10.3390/v14030562).
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