

David Pattinson September 19, 1989

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davipatti@protonmail.com • +1 (516) 413-4078 • github.com/davipatti
1 Bungtown Rd, Cold Spring Harbor, NY 11724

Summary

I am a computational biologist with a background in evolutionary biology. My infectious disease research spans inferring infection histories from messy serological data, elucidating the antigenic effect of mutations and testing the predictability of seasonal influenza viruses. I was promoted to Senior Scientist after two years as a postdoc at the Influenza Research Institute (UW—Madison) and currently lead computational investigations in the group, teach, and run my own projects. In my career I have developed strong skills in Bayesian statistics, high throughput computing, data visualisation and phylogenetics.

Fundamentally, I am interested in how different aesthetic or mathematical representations of data can enable scientific inquiry. Aesthetically, I use data visualisation as a core component of my work, iterating to generate custom visualisations that provide detailed insight into datasets and the workings of statistical models whilst empowering the viewer to see patterns they didn't know they were looking for. Mathematically, I have used antigenic cartography and antibody landscapes heavily 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 at the IRI and now lead computational investigations in the group comprising antigenic cartography, antibody landscapes, phylogenetics, Bayesian statistics, computational structural biology and next-generation sequencing analysis.

Postdoctoral Research Associate

Nov '19–Mar '22

I joined Prof. Yoshihiro Kawaoka's lab to research mechanisms of antigenic change using computational structural biology. The COVID-19 pandemic prompted a switch to studying SARS-CoV-2 serology involving running a COVID-19 serosurveillance cohort in collaboration with MCRI and the U.S. CDC.

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. • LMMs for association testing and GP-mapping with influenza antigenic phenotypes. • A framework to rank substitutions by similarity to those that have caused antigenic cluster transitions.

Imperial College London

LONDON, UK

MRes 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

BA 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** virtually every day since 2013; developing (e.g. **ititer**, **pymds**) and using scientific research packages (e.g. **pymc**, **numpy**, **MDAnalysis**, **scipy**, **scikit-learn**, **matplotlib**, **pandas**, **bambi**). I make interactive visualisation 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, among many others. • I have used **snakemake** to automate pipelines in several projects. • I have used the **slurm** and **HTCondor** cluster submission systems.

Natural languages: English (*mother tongue*) and German(*elementary*).

References

- Fan, Kong, Babujee, Presler, Jester, Burke, **Pattinson**, Barr, Smith, Neumann, and Kawaoka (in press). "Assessment of the Antigenic Evolution of a Clade 6B.1 Human H1N1pdm Influenza Virus Revealed Differences Between Ferret and Human Convalescent Sera". *eBioMedicine*.
- Guan, Babujee, Presler, **Pattinson**, Nguyen, Hoang, Le, van Bakel, Kawaoka, and Neumann (in press). "Avian H6 Influenza Viruses in Vietnamese Live Bird Markets in 2018-2021". *Viruses*.
- Pattinson**, Jester, Gu, Guan, Armbrust, Petrie, King, Nguyen, Belongia, Halfmann, Neumann, and Kawaoka (in press). "Choosing sides: comparing ipsilateral and contralateral coadministration of influenza and COVID-19 vaccines". *eBioMedicine*.
- Pattinson**, Neumann, and Kawaoka (in prep). "The molecular basis of 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.
- Pattinson**, Petrie, Jester, Guan, King, Nguyen, Belongia, Rolfes, Feldstein, Neumann, and Kawaoka (in prep). "Evaluating protection against SARS-CoV-2 infection based on antibody dynamics timeseries and infection histories".
- 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 change 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.
- 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).
- 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).
- 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.
- 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.
- 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.
- 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.
- Soga, Duong, **Pattinson**, Sakai-Tagawa, Tokita, Izumida, Nishino, Hagiwara, Wada, Miyamoto, Kuroki, Hayashi, Seki, Kasuya, Koga, and Adachi M (2023). "Characterization of Influenza A(H1N1)pdm09 Viruses Isolated in the 2018–2019 and 2019–2020 Influenza Seasons in Japan". *K* 15.2, p. 535.
- McLean, McClure, King, Meece, **Pattinson**, Neumann, Kawaoka, Rolfes, and Belongia (2022). "mRNA COVID-19 vaccine effectiveness against SARS-CoV-2 infection in a prospective community cohort, rural Wisconsin, November 2020 to December 2021". *Influenza and Other Respiratory Viruses* 16.4, pp. 607–612.

- 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.
- McLean, McClure, King, Meece, **Pattinson**, Neumann, Kawaoka, Rolfes, and Belongia (2021). "mRNA COVID-19 vaccine effectiveness against SARS-CoV-2 infection in a prospective community cohort, rural Wisconsin, November 2020-December 2021". *medRxiv*.
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