

# David Pattinson

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## Summary

*I am a computational scientist with a strong background in evolutionary biology and have worked at the intersection of virology, immunology and disease informatics since I began my Ph.D. in 2014. My current research focuses on assessing and predicting seasonal influenza virus antigenic evolution as well as tracking population immune responses to SARS-CoV-2. I*

*use a wide range of methods including Bayesian data analysis, antigenic cartography, antibody landscapes, phylogenetics and computational structural biology. I enjoy creating custom data visualisations to gain deep insights into patterns in data, underlying processes and how models function.*

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## Experience

Influenza Research Institute, [University of Wisconsin–Madison](#)

MADISON WI, USA

### Scientist I

Mar '22 – present

I was promoted to Scientist two years after joining Prof. Kawaoka's lab having provided expertise in antigenic cartography, antibody landscapes, phylogenetics, computational structural biology, next-generation sequencing analysis to the group. I teach in small groups, write bespoke analysis pipelines, and continue my own research projects.

### 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, for instance by estimating important epidemiological parameters such as [antibody decay rates](#). I helped plan, design experiments for, and conduct analyses for a prospective serosurveillance cohort in collaboration with [Marshfield Clinic Research Institute](#) and the [U.S. CDC](#).

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## 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.

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## Skills

**Computational:** I have used **python** daily 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*).

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## References

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- 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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