

Summary

I am a computational scientist interested in understanding and predicting the antigenic evolution of seasonal influenza viruses, tracking population immune responses to SARS-CoV-2, Bayesian inference, and clean, reproducible research software practices. I use antigenic cartography, antibody landscapes, phylogenetics, computational structural biology, Bayesian inference and data visualisation.

Experience

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

MADISON WI, USA

Scientist

Mar '22 – present

I was promoted to Scientist two years after joining Prof. Kawaoka's laboratory having provided expertise in computational analyses to the group (including antigenic cartography, antibody landscapes, phylogenetics, computational structural biology, next-generation sequencing analysis). 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 laboratory to primarily work on using computational structural biology to understand mechanisms of antigenic change. The COVID-19 pandemic prompted a switch to studying SARS-CoV-2 serology. I help plan, design experiments, and conduct analyses for a prospective serosurveillance project in collaboration with [Marshfield Clinic Research Institute](#) and the [U.S. CDC](#). I also conducted [Bayesian analyses](#) to estimate antibody decay rates after SARS-CoV-2 infection.

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. Developing linear mixed models for association testing and genotype to phenotype mapping with influenza virus antigenic phenotypes. Developing and testing a framework to rank substitutions by their similarity to substitutions that have caused antigenic cluster transitions.

Imperial College London

LONDON, UK

MRes Biosystematics, Natural History Museum

2012 – 2013

I conducted three independent research projects

- Endogenous retrovirus screening in catarrhine primates. Supervised by Dr. Michael Tristem.
- Novel methods in mitochondrial DNA enrichment. Supervised by Dr. Martijn Timmermans.
- A morphometric assessment of species delimitation in Canarian Pericallis. Supervised by 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. Supervised by Dr. Robert Asher.
- Part IB Biochemistry, Animal Biology, Plant Biology.
- Part IA Evolution and Behaviour, Biology of Cells, Chemistry, Mathematics for Biologists.

Aylesbury Grammar School

AYLESBURY, UK

A level Maths, Further Maths, Biology, Chemistry, Physics

2000 – 2008

Skills

Computational: I have used **python** daily for 9 years; developing (e.g. [ititer](#), [pymds](#)) and using scientific research packages (e.g. [pymc3](#), [numpy](#), [scipy](#), [scikit-learn](#), [matplotlib](#), [pandas](#), [bambi](#)). I make apps with **dash** and have some experience with **django**. • I am a big proponent of **unit testing** for code I write and datasets I curate. • I am familiar with **R** and **Javascript**. • 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** in several projects.

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

Publications

(See this list on [Google scholar](#).)

- [1] R. Asher, **D. Pattinson**, R. Tabuce, E. Gheerbrant, and L. Hautier. Patterns of dental eruption and variability in mammals. In *Journal Of Vertebrate Paleontology*, volume 32, pages 58–58. Taylor & Francis Inc 325 Chestnut St, Suite 800, Philadelphia, Pa 19106 Usa, 2012.
 - [2] R. Asher, G. Gunnell, E. Seiffert, **D. Pattinson**, R. Tabuce, L. Hautier, and H. Sallam. Dental eruption and growth in hyracoidea (mammalia, afrotheria). *Journal of Vertebrate Paleontology*, 37(3):e1317638, 2017.
 - [3] T. Janowitz, E. Gablenz, **D. Pattinson**, T. Wang, J. Conigliaro, K. Tracey, and D. Tuveson. Famotidine use and quantitative symptom tracking for covid-19 in non-hospitalised patients: a case series. *Gut*, 69(9):1592–1597, 2020.
 - [4] K. E. Jones, S. Pérez-Espona, **D. Pattinson**, Caujapé-Castells, S. Hiscock, and M. Carine. Why do different oceanic archipelagos harbour contrasting levels of species diversity? the macaronesian endemic genus *pericallis* (asteraceae) provides insight into explaining the ‘azores diversity enigma’. *BMC evolutionary biology*, 16(1):1–15, 2016.
 - [5] C. Kawakami, S. Yamayoshi, M. Akimoto, K. Nakamura, H. Miura, S. Fujisaki, **D. Pattinson**, K. Shimizu, H. Ozawa, T. Momoki, et al. Genetic and antigenic characterisation of influenza a (h3n2) viruses isolated in yokohama during the 2016/17 and 2017/18 influenza seasons. *Eurosurveillance*, 24(6):1800467, 2019.
 - [6] H. McLean, D. McClure, J. King, J. Meece, **D. Pattinson**, G. Neumann, Y. Kawaoka, M. Rolfes, and E. Belongia. mrna covid-19 vaccine effectiveness against sars-cov-2 infection in a prospective community cohort, rural wisconsin, november 2020-december 2021. *medRxiv*, 2021.
 - [7] **D. Pattinson**. *Predicting the Antigenic Evolution of Influenza Viruses with Application to Vaccination Strategy*. PhD thesis, University of Cambridge, 2020.
 - [8] **D. Pattinson**, R. Thompson, A. Piotrowski, and R. Asher. Phylogeny, paleontology, and primates: do incomplete fossils bias the tree of life? *Systematic Biology*, 64(2):169–186, 2015.
 - [9] **D. Pattinson**, P. Jester, L. Guan, S. Yamayoshi, S. Chiba, R. Presler, H. Rao, K. Iwatsuki-Horimoto, N. Ikeda, M. Hagihara, et al. A novel method to reduce elisa serial dilution assay workload applied to sars-cov-2 and seasonal hcovs. *Viruses*, 14(3):562, 2022.
 - [10] S. Yamayoshi, A. Yasuhara, M. Ito, O. Akasaka, M. Nakamura, I. Nakachi, M. Koga, K. Mitamura, K. Yagi, K. Maeda, K. Hideaki, N. Masanori, **D. Pattinson**, et al. Antibody titers against sars-cov-2 decline, but do not disappear for several months. *EClinicalMedicine*, 32:100734, 2021.
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