David Pattinson *September 19, 1989*

Last update on November 16, 2022

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Summary

I am a computational scientist interested in understanding and predicting the antigenic evolution of seasonal influenza viruses and tracking population immune responses to SARS-CoV-2. I use antigenic cartography, antibody landscapes, phylogenetics, computational structural biology and Bayesian inference. I enjoy creating custom data visualisations to guide the methods I develop, leverage the information content of data, and empower novel insights.

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 laboratory having provided expertise in computational analyses to the group (antigenic cartography, antibody landscapes, phylogenetics, computational structural biology, next-generation sequencing analysis). I teach to 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 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 epidemioloical parameters such as antibody deccay 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.

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. **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**. • 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 analysis pipelines in several projects. • I have used the **slurm** and **HTCondor** cluster submission systems.

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.