

## David Joseph Pattinson — Ph.D. MRes BA

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<https://github.com/davipatti>

Influenza Research Institute  
Science Dr.

Madison, WI 53711

USA

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, Bayesian inference and data visualisation.

### Employment

**University of Wisconsin–Madison**, Madison WI, USA

*Scientist*. Influenza Research Institute, Mar 2022–present

*Postdoctoral Research Associate*. Influenza Research Institute, Nov 2019–Mar 2022

### Education

**University of Cambridge**, Cambridge, UK

*Ph.D. Infectious disease informatics*. Department of Zoology, 2014–2019

Pass

*BA Natural Science*. Queens' College, 2009–2012

1<sup>st</sup> class

**Imperial College London**, London, UK

*MRes Biosystematics*. Natural History Museum, 2012–2013

Distinction

**Aylesbury Grammar School**, Aylesbury, UK

*A level Maths, Further Maths, Biology, Chemistry, Physics*. 2000–2008

5×A

### Computational skills

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 familiar with **R** and **Javascript**. — I use the unix command line daily. — Scientific 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.

### Research

[Link to my publications](#).

**Predicting the antigenic evolution of seasonal influenza viruses with application to vaccination strategy**. Quantifying the relationship between VE and mismatch. — Developing linear mixed models for association testing and genotype to phenotype mapping with antigenic phenotypes. — A framework to rank substitutions by similarity to cluster transition substitutions. — [Link to thesis](#).

*Ph.D.*

Supervised by Prof. Derek Smith

Pass

**Endogenous retrovirus screening in catarrhine primates**

*MRes*

Supervised by Dr. Michael Tristem

Distinction

**Novel methods in mitochondrial DNA enrichment**

*MRes*

Supervised by Dr. Martijn Timmermans

Distinction

**A morphometric assessment of species delimitation in *Canarian Pericallis***

*MRes*

Supervised by Dr. Mark Carine

Distinction

**Combining molecular and morphological data in phylogenetic analyses**

*BA*

Supervised by Dr. Robert Asher

1<sup>st</sup> class.

This won the Palaeontological Association Undergraduate Prize and John Ray Trust Science Prize.

### Additional experience

**Research assistant**

Oct 2013 - Apr 2014

Natural History Museum

London, UK

Developed Hypericum online: <http://hypericum.myspecies.info/>.

**Research internships**

Jun–Aug 2011 and 2012

University Museum of Zoology

Cambridge, UK

Phylogenetic analyses using combined morphological and molecular data. — Artificial extinction experiments. — Characterised prenatal dental eruption sequences using  $\mu$ CT imagery. — Funded by the Weis-Fogh and the J. Arthur Ramsay funds.