

# Shang-Kuan (Steven) Lin

## Contact

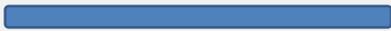
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## Coding Skills

R Advanced, 5 years



Python Experienced, 6 years



Bash Experienced, 6 years



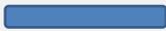
SQL Intermediate, 2 years



C++ Intermediate, 2 years



Perl Basic, 1 year



## Languages

English Professional



Mandarin Native



German Basic



## Summary

I like using computational approaches to address biological problems. I am particularly experienced in using established as well as novel statistical approaches to investigate genomics data in infectious disease from both the sides of the human and the pathogen.

## Research Experience

### PhD student, University of Oxford, UK

- Discovered novel genetic risk factors for human infectious diseases through incorporating national scale databases (UK biobank, Second Generation Surveillance System)
- Conducted genome-wide association studies with Covid-19 Host Genetics Initiative that uncovered the human genetic basis for Covid-19 susceptibility and clinical outcome
- Reconstructed Hepatitis C virus epidemiological history through host-pathogen genomic data integration
- Developed a novel method that identified novel signals of coevolution in the Hepatitis B virus genome with implications on its drug resistance mutations.

### MSc student, Imperial College London, UK

- Developed statistical methods to investigate competition between viral strains using their genomic data
- Developed a machine learning approach to incorporate protein function information into protein structure prediction
- Processed raw gene expression data to improve diagnosing

## Public Engagement

- Tutored for multiple graduate courses in evolutionary biology. Demonstrated programming fundamentals and basic evolution models
- Co-organized public engagement event of Royal Society Summer Science Exhibition
- Served as mentor in Project Access to help university application process for underprivileged students

## Publications

**Lin, Shang-Kuan**, et al. "Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a." *Virus evolution* (2021): veab065.

As a member of COVID-19 HGI published in top journals including Nature and the New England Journal of Medicine.