Leke Lyu

Curriculum vitae

I. Background

Professional Experience

2025-present, *Emory University*, *Atlanta, GA, USA* Postdoctoral Fellow Mentor: Max Lau

Education

2019-2025, *University of Georgia*, *Athens, GA, USA*Ph.D. in Bioinformatics
Thesis title: "Tracking Local-Scale Viral Transmission Using Genomic Data"
Mentor: Justin Bahl

2014-2018, *Sichuan University*, *Chengdu*, *China* B.S. in Biological Science B.Eng. in Software Engineering

II. Research Accomplishments

* indicates first author

Peer-reviewed publications

- Leke Lyu*, Mandev Gill, Guppy Stott, Sachin Subedi, Cody Dailey, Gabriella Veytsel, Magdy Alabady, Kayo Fujimoto, Ryker Penn, Pamela Brown, Roger Sealy, Justin Bahl. (2025).
 Tracing SARS-CoV-2 Clusters Across Local Scales Using Genomic Data. (<u>Proceedings of the National Academy of Sciences of the United States of America)</u>
- 2) Sihua Peng*, <u>Leke Lyu</u>, Ludy Registre Carmola, Sachin Subedi, M H M Mubassir, Mohamed Bakheet, Justin Bahl. (2025). **Evolving fitness and immune escape: A retrospective analysis of SARS-CoV-2 spike protein (2020-2024) using protein language model.** (<u>Frontiers in Immunology</u>)
- 3) <u>Leke Lyu</u>*, Gabriella Veytsel, Guppy Stott, Spencer Fox, Cody Dailey, Lambodhar Damodaran, Kayo Fujimoto, Pamela Brown, Roger Sealy, Armand Brown, Magdy Alabady, Justin Bahl. (2025). **Characterizing spatial epidemiology in a heterogeneous transmission landscape using the spatial transmission count statistic.** (*Communications Medicine*)
- 4) Kayo Fujimoto*, Jacky Kuo, Guppy Stott, Ryan Lewis, Hei Kit Chan, <u>Leke Lyu</u>, Gabriella Veytsel, Michelle Carr, Tristan Broussard, Kirstin Short, Pamela Brown, Roger Sealy, Armand Brown, Justin Bahl. (2023). **Beyond scale-free networks: integrating multilayer**

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social networks with molecular clusters in the local spread of COVID-19. ($\underline{Scientific}$ $\underline{Reports}$)

- 5) Jialin Yang*, Michael Skaro, Jiani Chen, Duna Zhan, <u>Leke Lyu</u>, Skylar Gay, Ahmed Kandeil, Mohamed A. Ali, Ghazi Kayali, Kateryna Stoianova, Pensheng Ji, Magdy Alabady, Justin Bahl, Liang Liu, Jonathan Arnold. (2023). The species coalescent indicates possible bat and pangolin origins of the COVID-19 pandemic. (*Scientific Reports*)
- 6) <u>Le-Ke Lyu</u>*, Dong-Lei Wang*, Long Li*, Ying-Ying Zhu, De-Chun Jiang, Jian-Quan Liu, and Xiao-Ting Xu. (2021). Polyphyly and species delimitation of *Picea brachytyla* (Pinaceae) based on population genetic data. (*Journal of Systematics and Evolution*)
- 7) Yongzhi Yang*, Pengchuan Sun*, <u>Leke Lv</u>, Donglei Wang, Dafu Ru, Ying Li, Tao Ma, Lei Zhang, Xingxing Shen, Fanbo Meng, Beibei Jiao, Lanxing Shan, Man Liu, Qingfeng Wang, Zhiji Qin, Zhenxiang Xi, Xiyin Wang, Charles C. Davis, Jianquan Liu. (2020). **Prickly waterlily and rigid hornwort genomes shed light on early angiosperm evolution**. (*Nature Plants*)

Under preparation

- 8) <u>Leke Lyu</u>*, Justin Bahl. (2025). Viral Genomic Epidemiology at the Local Scale: Key Insights, Ongoing Progress, and Remaining Challenge. (<u>this is a review paper</u>)
- 9) Guppy Stott*, <u>Leke Lyu</u>, Gabriella Veytsel, Justin Bahl. (2025). **Phylogenetic Analysis**Subsampling Tool (PAST): A Novel Tool to Address Sequencing Bias in Phylodynamic Analysis.
- 10) Sachin Subedi*, M H M Mubassir, Tanin Rajamand, <u>Leke Lyu</u>, Mohamed Bakheet, Justin Bahl. (2025). **Investigating the Ecological and Evolutionary Drivers of H5Nx HPAI Spread Across Species and Geographic Regions in Europe**.
- 11) Garrick Stott*, <u>Leke Lyu</u>, Gabriella Veytsel, Jacky Kuo, Ryan Lewis, Armand Brown, Kayo Fujimoto, Justin Bahl. (2022). **Phylogeny and Metadata Network Database for Epidemiologic Surveillance**. (*bioRxiv*)

Oral research presentations

2024, MIDAS Network Annual Meeting, Atlanta, GA, USA

Title: Phylogeographic Inference of SARS-CoV-2 Delta Wave in Texas, USA using a Novel Spatial Transmission Count Statistic.

2023, CEIRR Annual Network Meeting, Baltimore, MD, USA

Title: Geographic Diffusion Patterns of SARS-CoV-2 in Texas During the Delta Wave.

Poster presentations

2025, **Ecology and Evolution of Infectious Diseases Conference**, University of Notre Dame, South Bend, IN, USA

Title: Tracing SARS-CoV-2 Clusters Across Local Scales Using Genomic Data.

2024, **Ecology and Evolution of Infectious Diseases Conference**, Stanford University, Palo Alto, CA, USA

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Title: Optimizing Targeted Interventions: Identifying and Tracing Imported SARS-CoV-2 Lineages.

III. Teaching Experience

Classroom

2021, BINF 8500: Bioinformatics Algorithms

BINF 8500 is a core course in the Ph.D. Bioinformatics curriculum. It covers a range of modules, from introductory sorting algorithms to advanced topics such as Gibbs sampling and MCMC. As the teaching assistant, I prepared lecture materials, developed exam questions, and handled exam administration and grading.

Outreach

2024, *Molecular Epidemiology Training:* Nextstrain Build and Nextstrain Narratives
This training event was organized by the Center for Applied Pathogen Epidemiology and
Outbreak Response (CAPE) network. The workshop was designed for bioinformatics staff from
the Georgia Department of Public Health and focused on using the Nextstrain workflow to study
viral dispersal. As an instructor, I co-developed and delivered lecture materials with Tanin
Rajamand.

IV. Workshops and Professional Development

2025, The Summer Institute in Statistics and Modeling in Infectious Diseases, Emory

University, Atlanta, GA, USA

Module: Introduction to Machine Learning for Infectious Disease Modeling

Instructors: Max Lau, Wei Jin

Module: MCMC for Infectious Diseases Modeling

Instructors: Phil O'Neill, Theo Kypraios

2021, The Summer Institute in Statistics and Modeling in Infectious Diseases, Online

Module: Reconstructing Transmission with Genomic Data

Instructors: Caroline Colijn, Jessica Stockdale

Module: Infectious Diseases, Immunology and Within-Host Models

Instructors: Andreas Handel, Paul Thomas

Module: Evolutionary Dynamics and Molecular Epidemiology of Viruses

Instructors: Julia Palacios, Nicola Mueller