

# Abhishek Mallela, PhD

(972) 951-9004 • [abhishek.mallela@gmail.com](mailto:abhishek.mallela@gmail.com) • <https://www.linkedin.com/in/abhishek-mallela> • [dynova.github.io](https://github.com/dynova)

## EDUCATION

*Applied Mathematics, PhD, Mar '22*

*Applied Statistics and Analytics, MS, May '17*

*Mathematics and Statistics, MS, May '15; BS, Dec '11*

University of California at Davis (UC-DAVIS), Davis, CA

University of Kansas Medical Center (KUMC), Kansas City, KS

University of Missouri at Kansas City (UMKC), Kansas City, MO

## SUMMARY

Applied mathematician with over 10 years of experience in modeling and computation across various biological subfields. Expert in TensorFlow, JAX, and Python, with a strong background in deep learning and mathematical modeling. Eager to contribute to innovative projects in modeling and machine learning.

## SKILLS

- Programming: Python, MATLAB, R, Julia, LaTeX, Mathematica, basic C++, and shell scripting
- AI/ML: Automatic differentiation; Completed Deep Learning, Natural Language Processing, and Foundations of Algorithms and Data Structures specializations (Coursera)
- Data: Pre- and post-processing of COVID-19 surveillance data across all US counties and county equivalents
- Communication: 14 publications in peer-reviewed journals, 5 invited talks, 9 contributed talks and posters, cross-disciplinary expertise, and proficiency in technical writing

## EXPERIENCE

- *Postdoctoral Fellow (Lab of Santiago Schnell at University of Notre Dame and Dartmouth College; Feb '25 to present)*
  - **Modeling:** Designing and estimating the parameters of enzyme-catalyzed experiments and designing a mathematical model of a minimal mechanism for hormesis in protein aggregation.
  - **AI/ML:** Collaborating with researchers at Harvard University on an effort involving repeated games with LLMs.
- *Postdoctoral Fellow (Center for Nonlinear Studies at Los Alamos National Laboratory; May '22 to Jan '25)*
  - **Modeling:** Estimated the basic reproduction number for COVID-19 in 50 US states and 280 urban areas, identifying regions at risk of high disease transmission and aiding future pandemic preparedness. *Techniques used: Bayesian inference, Adaptive MCMC algorithm, and convergence diagnostics.*
  - **Collaboration:** Contributed significantly to the collective efforts of a large consortium of COVID-19 researchers.
  - **Software:** Python (NumPy, SciPy, Jax, Diffrax, Pandas, Jupyter Notebook, Keras, TensorFlow, Numba); Julia
  - **AI/ML:** Designed a framework comparing methods of local sensitivity analysis for gradient evaluation in ML, optimization, and statistical inference applications involving ODEs. *Techniques used: Automatic differentiation, methods of adjoint, forward, and finite-differencing, scaling analyses, and cluster computing.*
  - **Achievements:** 8 peer-reviewed publications (3 as first-author), 2 international conference talks, 3 invited talks, 1 local poster presentation.
- *PhD Candidate, Graduate Teaching Assistant, and Tutor (UC-DAVIS; Sep '17 to Mar '22)*
  - **Modeling:** Explored the stochastic aspects of coupled bistable systems arising from the Allee effect in ecology. Found that changing one parameter in multi-dimensional systems can result in tipping point cascades, common in many fields and across spatial scales. *Techniques used: Stochastic Differential Equations, Individual-Based Models, Fourier transforms, Partially Observable Markov Decision Processes*
  - **Achievements:** PhD degree with 3 first-author publications, TA and tutor for several math courses.
- *Graduate Research Associate (University of Kansas; Oct '15 to Sep '17)*
  - **Modeling:** Developed mathematical models to analyze a) post-translational modification cycles subject to synthesis and degradation, and b) length control of bacterial structure assembly. Used an agent-based framework based on the stochastic Doob-Gillespie algorithm to efficiently simulate the models numerically on a computer cluster. Achieved a 100x speedup by switching from MATLAB to Python and then C++.
  - **Software:** MATLAB, Python, C++, Kappa, BNGL, R, Mathematica
  - **Achievements:** 2 peer-reviewed publications (1 as first-author), 2 local poster presentations.
- *Graduate Student Researcher and Course Instructor (UMKC; Aug '13 to May '15)*
  - **Modeling:** Designed, analyzed, and simulated an ODE model of HIV-TB co-infection. Formulated and solved an optimal control problem to simultaneously minimize disease burden and implementation cost.
  - **Collaboration:** Led project with research supervisor and external collaborator, a world-class expert in optimal control theory, to design an optimal treatment protocol for HIV-TB co-infected populations.
  - **Achievements:** 1 first-author publication, 1 first-place poster prize (500 USD), 2 international conference talks, 3 invited talks, Adjunct Instructor of Record (Trigonometry and College Algebra).

## PUBLICATIONS AND PRESENTATIONS

### • Publications (15)

- *Evaluation of FluSight influenza forecasting in the 2021-22 and 2022-23 seasons with a new target laboratory-confirmed influenza hospitalizations.* Mathis, S.M., Webber, A.E., Basu, A., **et al.** ('24), *Nature Communications*, 15:6289
- *Impacts of vaccination and Severe Acute Respiratory Syndrome Coronavirus 2 variants Alpha and Delta on Coronavirus Disease 2019 transmission dynamics in four metropolitan areas of the United States.* **Mallela, A.**, Chen, Y., Lin, Y.T., Miller, E.F., Neumann, J., He, Z., Nelson, K.E., Posner, R.G., and Hlavacek, W.S. ('24), *Bulletin of Mathematical Biology*, 86(3):31
- *Differential contagiousness of respiratory disease across the United States.* **Mallela, A.**, Lin, Y.T., and Hlavacek, W.S. ('23), *Epidemics*, 45:100718
- *Quantification of early nonpharmaceutical interventions aimed at slowing transmission of Coronavirus Disease 2019 in the Navajo Nation and surrounding states.* Miller, E.F., Neumann, J., Chen, Y., **Mallela, A.**, Lin, Y.T., Hlavacek, W.S., and Posner, R.G. ('23), *PLOS Global Public Health*, 3(6):e0001490
- *The United States COVID-19 Forecast Hub dataset.* Cramer, E.Y., Huang, Y., Wang, Y., **et al.** ('22), *Scientific Data*, 9(462):1-15
- *Optimal management of stochastic invasion in a metapopulation with Allee effects.* **Mallela, A.** and Hastings, A. ('22), *Journal of Theoretical Biology*, 549:111221
- *Bayesian inference of state-level COVID-19 basic reproduction numbers across the United States.* **Mallela, A.**, Neumann, J., Miller, E.F., Chen, Y., Posner, R.G., Lin, Y.T., and Hlavacek, W.S. ('22), *Viruses*, 14(1):157
- *Implementation of a practical Markov chain Monte Carlo sampling algorithm in PyBioNetFit.* Neumann, J., Lin, Y.T., **Mallela, A.**, Miller, E.F., Colvin, J., Duprat, A.T., Chen, Y., Hlavacek, W.S., and Posner, R.G. ('22), *Bioinformatics*, 38(6):1770-1772
- *Tipping cascades in a multi-patch system with noise and spatial coupling.* **Mallela, A.** and Hastings, A. ('21), *Bulletin of Mathematical Biology*, 83(11):1-27
- *Robustness and the evolution of length control strategies in the T3SS and flagellar hook.* Nariya, M.K., **Mallela, A.**, Shi, J.J., and Deeds, E.J. ('21), *Biophysical Journal*, 120(17):3820-3830
- *The role of stochasticity in noise-induced tipping cascades: A master equation approach.* **Mallela, A.** and Hastings, A. ('21), *Bulletin of Mathematical Biology*, 83(5):1-20
- *Daily forecasting of regional epidemics of Coronavirus disease with Bayesian uncertainty quantification.* Lin, Y.T., Neumann, J., Miller, E.F., Posner, R.G., **Mallela, A.**, Safta, C., Ray, J., Thakur, G., Chinthavali, S., and Hlavacek, W.S. ('21), *Emerging Infectious Diseases*, 27(3):767
- *Crosstalk and ultrasensitivity in protein degradation pathways.* **Mallela, A.**, Nariya, M.K., and Deeds, E.J. ('20), *PLOS Computational Biology*, 16(12):e1008492
- *Optimal control applied to a SEIR model of 2019-nCoV with social distancing.* **Mallela, A.** ('20), medRxiv
- *HIV-TB co-infection treatment: modeling and optimal control theory perspectives.* **Mallela, A.**, Lenhart, S., and Vaidya, N.K. ('16), *Journal of Computational and Applied Mathematics*, 307:143-161

### • Invited talks (5)

- Joint Mathematics Meetings, San Francisco, CA (Jan '24)
  - Title: *Differential contagiousness of respiratory disease across the United States*
- CNLS at LANL, Los Alamos, NM
  - Title: *Impacts of vaccination and SARS-CoV-2 variants Alpha and Delta on COVID-19 transmission dynamics in four metropolitan areas of the US* (Jun '23)
  - Title: *Differential contagiousness of respiratory disease across the United States* (Sep '22)
  - Title: *Crosstalk and ultrasensitivity in protein degradation pathways* (Dec '21)
- SIAM Central States Sectional Meeting, Rolla, MO (Apr '15)
  - Title: *Ideal treatments for HIV-TB co-infected populations: modeling and optimal control theory perspectives*

### • Contributed talks and posters (9)

- SIAM Conference on Uncertainty Quantification, Trieste, Italy (Mar '24)
  - Talk: *Differential contagiousness of respiratory disease across the United States*
- Quantitative and Systems Biology (q-bio) conference
  - Poster: *Bayesian inference with PyBioNetFit of state-level  $R_0$  values for COVID-19 across the US*; Fort Collins, CO (Jun '22)
  - Poster: *Protein turnover impacts dynamics of post-translational modifications*; Nashville, TN (Jul '16)
- Conference on Modeling Protein Interactions, Lawrence, KS (Oct '16)
  - Poster: *Protein turnover impacts dynamics of post-translational modifications*
- SIAM Conference on Applications of Dynamical Systems, Snowbird, UT (May '15)
  - Talk: *Optimal treatment strategies for HIV-TB co-infected individuals*
- UMKC Mathematics and Statistics Research Day, Kansas City, MO (Apr '15)
  - Talk: *Ideal treatments for HIV-TB co-infected populations: modeling and optimal control theory perspectives*
- UMKC Community of Scholars Symposium, Kansas City, MO
  - Talk: *Optimal treatment strategies for HIV-TB co-infected populations* (Apr '15)
  - Poster: *Optimal treatment strategies for HIV-TB co-infected populations* (May '14)
- Joint Mathematics Meetings, San Antonio, TX (Jan '15)
  - Talk: *Optimal treatment strategies for HIV-TB co-infected populations*