slwu89@berkeley.edu
slwu89.github.io

Sean Lawrence Wu

Short Bio

I am a mathematical epidemiologist interested in investigating stochastic processes through analytic and numerical methods to help infectious disease epidemiology better understand and describe disease transmission systems. In my current research at UC Berkeley I work on stochastic simulation for novel gene-drive based methods of mosquito control. At the Institute for Health Metrics and Evaluation I work on developing software for modeling malaria as well as more basic research into stochastic simulation techniques. In addition, I deeply enjoy teaching, both formal and informal mentoring, as well as learning from those around me.

Education

University of California, Berkeley   Expected Graduation December 2020
PhD Candidate (Epidemiology), Designated Emphasis in Computational Biology

University of California, Berkeley   May 2016
Master of Public Health (Epidemiology & Biostatistics)
Thesis: Mathematical Modelling of a Novel Vector Control Intervention for Malaria in Burkina Faso

University of California, Irvine   June 2013
Bachelor of Arts *cum laude* in International Studies, Minor in Statistics

Research Experience

Intern at Microsoft Research   Redmond, Washington
June 2020 – September 2020

- Developing piecewise deterministic stochastic models of mosquito ecology in the **Julia** programming language.
- Applying GAM techniques to fit unspecified functional relationships in mechanistic models.

Graduate Student Researcher at Institute for Health Metrics and Evaluation   Seattle, Washington
August 2016 – Present

- Developing **C++/C** and **R** packages for continuous time stochastic simulation of malaria transmission.
- Assisting development of mathematical models of human movement for malaria elimination planning in Equatorial Guinea.

Graduate Student Researcher at Divisions of Epidemiology & Biostatistics   UC Berkeley
August 2016 – Present

- Developing **C++** and **R** software to simulate population dynamics of gene drives in mosquitoes.
- Creating stochastic and deterministic models of human infection dynamics for evaluation of possible effect sizes of genetics-based control strategies on malaria and arboviruses.

Graduate Student Researcher at Malaria Elimination Initiative   UC San Francisco
August 2015 – November 2017

- Helped develop mathematical model and associated **R Shiny** user interface for investigating effect of mosquito-control tools on malaria transmission.
- Analyzed mosquito intervention trial data with differential equation models in Bayesian framework.

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Berkeley Schistosomiasis Group   UC Berkeley/Sichuan Province CDC, China
January 2015 – September 2015

- Worked at Sichuan Province CDC to develop case-control study of differential miRNA expression to investigate genetic basis of susceptibility to schistosomiasis infection.

Teaching

Graduate Student Instructor: PH252B Modelling the Dynamics of Infectious Disease Processes
UC Berkeley (Spring 2016)
Instructor: John M. Marshall

- *Content:* ordinary & delay differential equations modelling of infectious and vector-borne diseases, discrete time stochastic models, Bayesian model fitting (Metropolis-Hastings MCMC, Sequential Monte Carlo, Approximate Bayesian Computation)

Statistical Mentoring: ESPM290 Statistical Methods for Species Distribution and Abundance Models
UC Berkeley (Fall 2019)
Instructors: Alan Hubbard, Perry de Valpine, Steve Beissinger, William Fithian

- *Responsibilities:* provided office hours to explain statistical methods to students; topics included Gaussian processes, Markov random field models, point process models, stochastic compartmental models, and generalized linear (mixed) models

Publications

- Sánchez C HM, Bennett JB, **Wu SL**, Rašić G, Akbari O, Marshall JM. Modeling confinement and reversibility of threshold-dependent gene drive systems in spatially-explicit Aedes aegypti populations. *BMC Biology*. 18 (2020) https://doi.org/10.1186/s12915-020-0759-9

- **Wu SL**, et al. Vector bionomics and vectorial capacity as emergent properties of mosquito behaviors and ecology. *PLoS Computational Biology*. 16**.**4 (2020) https://doi.org/10.1371/journal.pcbi.1007446

- Spear RC, Cheng Q, **Wu SL**. An Example of Augmenting Regional Sensitivity Analysis Using Machine Learning Software. *Water Resources Research* 56.4 (2020) https://doi.org/10.1029/2019WR026379

- Sánchez C HM, **Wu SL**, Bennett JB, Marshall JM. MGDrivE: A modular simulation framework for the spread of gene drives through spatially explicit mosquito populations. *Methods in Ecology and Evolution*. 2019 https://doi.org/10.1111/2041-210X.13318

- Kandul NP, Liu J, Sánchez C. H. M., **Wu SL**, Marshall JM, Akbari O. (2019). Transforming insect population control with precision guided sterile males with demonstration in flies. *Nature Communications*, 10(1), 84 https://doi.org/10.1038/s41467-018-07964-7

- Marshall JM, **Wu SL**, Sánchez C. H. M., Kiware S. S., Ndhlovu M., Ouédraogo A. L., … Ferguson N. M. (2018). Mathematical models of human mobility of relevance to malaria transmission in Africa. *Scientific Reports*, 8(1), 7713. https://doi.org/10.1038/s41598-018-26023-1

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- Kiware SS, Chitnis N, Tatarsky A, **Wu SL**, Sánchez HM, Gosling R, Smith DL, Marshall JM (2017) Attacking the mosquito on multiple fronts: Insights from the Vector Control Optimization Model (VCOM) for malaria elimination. PLoS One. 2017 Dec 1;12(12):e0187680 https://doi.org/10.1371/journal.pone.0187680

Software

- Héctor Manuel Sánchez Castellanos, Jared Bennett, **Sean L. Wu**, John M. Marshall (2019). MGDrivE: Mosquito Gene Drive Explorer. R package version 1.5.0. https://cran.r-project.org/web/packages/MGDrivE/index.html

Pre-Prints

- Citron DT, Guerra CA, Dolgert AJ, **Wu SL**, Henry JM, Sánchez C HM, Smith DL. (2020) Comparing Metapopulation Dynamics of Infectious Diseases under Different Models of Human Movement. medRxiv doi: https://doi.org/10.1101/2020.04.05.20054304 *Under review at PNAS*

- **Wu SL**, et al. (2020) Substantial underestimation of SARS-Cov-2 infection in the United States due to incomplete testing and imperfect test accuracy. medRxiv doi: https://doi.org/10.1101/2020.05.12.20091744 *Under review at Nature Comunications*

- Jing Q, **Wu SL**, He Z, Yuan L, Ma M, Bai Z, Jiang L, Marshall J, Lu J, Yang Z (2019) New genotype invasion of dengue virus serotype 1 drove massive outbreak in Guangzhou, China. BioRxiv doi: https://doi.org/10.1101/697052. *Under review at Frontiers in Public Health*

- Sánchez HM, Marshall JM, **Wu SL**, Vallejo EE (2017) Effects of spatial heterogeneity on transmission potential in vectorial-contact networks: A comparison of three *Aedes aegypti* control strategies. bioRxiv doi: https://doi.org/10.1101/210450.

Presentations & Proceedings

- **Sean Wu**, Héctor Manuel Sánchez Castellanos, Biyonka Liang, Daniel T. Citron, John M. Henry, David L. Smith: *MBITES: A modelling framework for the study of mosquito bionomics and vectorial capacity as emergent patterns*. Presented at American Society of Tropical Medicine & Hygiene; November 2019; National Harbor, MD.

- **Sean Wu**, Héctor Manuel Sánchez Castellanos, Jared Bennett, John M. Marshall: *Spatio-temporal Force of Infection Modelling: with applications to mosquito-borne pathogens*. Presented at SMBE Satellie Workshop on Genome Evolution in Pathogen Transmission and Disease; November 2018; Kyoto, Japan.

- **Sean Wu**, Héctor Manuel Sánchez Castellanos, Biyonka Liang, Daniel T. Citron, John M. Henry, Qian Zhang, David L. Smith: *MBITES: Mosquito Bout-based Individual-based Transmission Simulator*. Presented at IDDConf 2018; September 2018; Ambleside, Cumbia, UK.

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- John M. Marshall, Jared Bennett, **Sean Wu**, Héctor Manuel Sánchez Castellanos: *CRISPR-Cas9-based gene drive architecture for control of agricultural pests*. Presented at Innovative Genomics Institute Open House; October 2017; UC Berkeley, CA.

- **Sean Wu**, Héctor Manuel Sánchez Castellanos, Biyonka Liang, Daniel T. Citron, John M. Henry, Qian Zhang, John M Marshall, David Smith: *MICRO: An Eco-epidemiological Agent Based Framework for the Modeling of Mosquito-borne Pathogens*. Presented at UC Berkeley Computational Biology Retreat; November 2017; EarthRise Conference Center, Petaluma, CA.

- Héctor Manuel Sánchez Castellanos, Jared Bennett, **Sean Wu**, John M Marshall: *A Tale of Two Cities: Confinability and Remediation Potential of UDmel and Translocation Gene-Drives in Spatially Explicit Aedes aegypti Populations*. Presented at UC Berkeley Computational Biology Retreat; November 2017; EarthRise Conference Center, Petaluma, CA.

- Héctor Manuel Sánchez Castellanos, **Sean Wu**, Jared Bennett, John M Marshall: *MGDrivE: A Mosquito Population Framework to Evaluate and Optimize Gene-Drive Releases for Vector-Borne Disease Control*. Presented at NorCal CompBio Symposium; October 2017; University of California, Santa Cruz, CA.

- Yimin Zhou, Doheum Park, **Sean Wu**: *Organic urban boundaries and clusters – analyzing Singapore as an example*. Research paper written at 2017 Santa Fe Institute Complex Systems Summer School; June 2017; Santa Fe Institute, Santa Fe, NM: https://api.semanticscholar.org/CorpusID:30964549

- Samson Kiware, Allison Tatarsky, **Sean Wu**, Héctor Manuel Sánchez Castellanos, Nakul Chitnis, John M Marshall: *Attacking the Mosquito on Multiple Fronts: Insights on Optimal Combinations of Vector Control Interventions for Malaria Elimination from a Mathematical Model*. Presented at Annual Malaria Research Conference II; July 2016; South Africa.

- **Sean Wu**, John M Marshall, Sawadogo P. Simon, Bilogo Etienne, Abdoulaye Diabaté: *Spraying of Male Mating Swarms as a Novel Vector Control Intervention: Insights from a Mathematica Model*. Poster presented at: American Society of Tropical Medicine & Hygiene; November 2016; Atlanta, GA.

- Samson Kiware, Allison Tatarsky, **Sean Wu**, Héctor Manuel Sánchez Castellanos, Nakul Chitnis, John M Marshall: *Attacking the Mosquito on Multiple Fronts: Insights on Optimal Combinations of Vector Control Interventions for Malaria Elimination from a Mathematical Model*. Poster presented at: American Society of Tropical Medicine & Hygiene; November 2016; Atlanta, GA.

Awards & Fellowships

- Center for Emerging & Neglected Diseases Kathleen Miller Fellow: *Searching for a Biomarker of Susceptibility to Schistosomiasis Reinfection* (Spring 2015)
- Member of Phi Beta Kappa National Honor Society (Spring 2013)

Workshops

Sean Lawrence Wu

- Alumni of 2017 Complex Systems Summer School at Santa Fe Institute (Santa Fe, NM, USA)
- Attended New England Complex Systems Institute Winter School 2016 (MIT, Boston, MA, USA)
- Attended Summer Institute in Statistics and Modeling in Infectious Diseases (SISMID) 2016 (University of Washington, Seattle, WA, USA)

Professional Service

- Reviewer for: Mathematical Biosciences, Journal of Theoretical Biology