

Introduction

I am a mathematical epidemiologist who is investigating stochastic processes through analytic and numerical methods to help infectious disease researchers better understand and describe disease transmission systems. 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 am developing software to model malaria at the national scale. 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

Experience

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

- Developed novel stochastic simulation algorithms for systems with state-dependent delays.
- Applying GAMs 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 national-scale stochastic simulation of malaria transmission. Multi-scale models incorporate mechanisms including within-host immunological response, human movement patterns, mosquito ecology and transmission dynamics.

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

- Developing **C++/R** software to simulate gene drive dynamics in mosquito populations.
- Preform survival analyses of laboratory data to parameterize specific simulation parameters.

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 and analyzed field trial data.

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

1. Adams CJ, **Wu SL**, Shao XR, Bradshaw PT, Gonzales E, Smith JB, Xiang AH, Bellesis KH, Chinn T, Bos SD, Wendel-Haga MW, Olsson T, Kockum I, Langer-Gould AM, Schaefer C, Alfredsson L, Barcellos LF. Pregnancy does not modify the risk of MS in genetically susceptible women. *Neurology Neuroimmunology & Neuroinflammation* Nov 2020, 7 (6) <https://nn.neurology.org/content/7/6/e898>
2. **Wu SL**, Mertens AN, Crider YS, Nguyen A, Pokpongkiat NN, Djajadi S, Seth A, Hsiang MS, Colford JM, Reingold A, Arnold BF, Hubbard A, Benjamin-Chung J. Substantial underestimation of SARS-CoV-2 infection in the United States. *Nature Communications* 11 (2020) <https://doi.org/10.1038/s41467-020-18272-4>
3. 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>
4. **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>
5. 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>
6. 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>
7. 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>

8. 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>
9. 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

1. Héctor Manuel Sánchez Castellanos, Jared Bennett, **Sean L. Wu**, John M. Marshall (2019). MGDriVE: Mosquito Gene Drive Explorer. R package version 1.6.0.
<https://cran.r-project.org/web/packages/MGDriVE/index.html>

Pre-Prints

1. (*Submitted to Methods in Ecology and Evolution*)
Wu SL, Bennett JB, Sánchez C HM, Dolgert AJ, León TM, Marshall JM. MGDriVE 2: A simulation framework for gene drive systems incorporating seasonality and epidemiological dynamics. bioRxiv doi: <https://doi.org/10.1101/2020.10.16.343376>
2. (*Under review at The Lancet: Public Health*)
Head JR, Andrejko K, Cheng Q, Collender PA, Phillips S, Boser A, Heaney AK, Hoover CM, **Wu SL**, Northrup GR, Click K, Harrison R, Lewnard JA, Remais JV. The effect of school closures and reopening strategies on COVID-19 infection dynamics in the San Francisco Bay Area: a cross-sectional survey and modeling analysis. medRxiv doi: <https://doi.org/10.1101/2020.08.06.20169797>
3. (*Under review at PNAS*)
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>
4. (*Under review at International Journal of Health Geographics*)
Fries B, Smith DL, **Wu SL**, Dolgert AJ, Guerra CA, Hay SI, García GA, Smith JM, Oyono JN, Donfack OT, Nfumu JO. (2020) Measuring the accuracy of gridded human population density surfaces: a case study in Bioko Island, Equatorial Guinea. bioRxiv doi: <https://doi.org/10.1101/2020.06.18.160101>
5. 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>.
6. 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

1. **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.
2. **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 Satellite Workshop on Genome Evolution in Pathogen Transmission and Disease; November 2018; Kyoto, Japan.
3. **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 IDDCong 2018; September 2018; Ambleside, Cumbria, UK.
4. 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.
5. **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.
6. 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.
7. 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.
8. 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>
9. Alexandra Jurgens, Alicia Kraay, Jake L. Weissman, Jingnuo Dong, Marco Pangallo, **Sean Wu**, Shanee Stopnitzky, Shing Hei Zhan, Yael Gurevich, Yao Liu: *Quantifying and comparing “memory” in biological, ecological, physical, and socio-economic systems*. Research paper written at 2017 Santa Fe Institute Complex Systems Summer School; June 2017; Santa Fe Institute, Santa Fe, NM: https://wiki.santafe.edu/images/9/95/2017_CSSS_Proceedings_Book.pdf
10. 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.
11. **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.

12. 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.

Fellowships

- UC Berkeley Center for Computational Biology Student Travel Grant (November 2018): Presented at conference hosted by the Society for Molecular Biology and Evolution in Kyoto, Japan.
- Summer Institute in Statistics and Modeling in Infectious Diseases Scholarship (July 2016)
- Center for Emerging & Neglected Diseases Kathleen L. Miller Graduate Fellowship: *Searching for a Biomarker of Susceptibility to Schistosomiasis Reinfection* (February 2015)

Workshops

- 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, Parasites & Vectors, Malaria Journal