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Sean Lawrence Wu

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   2014 - 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   2008 - 2013
Bachelor of Arts *cum laude* in International Studies, Minor in Statistics

Experience

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

- Developed novel stochastic simulation algorithms for systems with state-dependent delays.
- Applied GAMs to fit unspecified functional relationships in mechanistic models.

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

- 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
August 2016 – Present   UC Berkeley

- Developing **C++**/**R** software to simulate gene drive dynamics in mosquito populations. Preform survival analyses of laboratory data to parameterize specific simulation parameters.
- Designed individual-based simulation models to evaluate reactive *Plasmodium falciparum* case detection strategies in near elimination settings.

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

- Helped develop differential-equation based mathematical model and associated **R Shiny** user interface for investigating effect of mosquito-control tools on malaria transmission. Analyzed field trial data of vector control interventions with statistical models.

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

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

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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 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**, Sánchez HM, Henry JM, Citron DT, Zhang Q, Compton K, Liang B, Verma A, Cummings DAT, Le Menach A, Scott TW, Wilson AL, Lindsay SW, Moyes CL, Hancock PA, Russell TL, Burkot TR, Marshall JM, Kiware SS, Reiner RC, Smith DL. 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 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 HM, **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 HM, Kiware SS, Ndhlovu M, Ouédraogo AL, Touré MB, Sturrock HJ, Ghani AC, Ferguson NM. Mathematical models of human mobility of relevance to malaria transmission in Africa. *Scientific Reports*, *8*(1), 7713 (2018). 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. 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. **Wu SL**, Bennett JB, Sánchez HM, León TM, Dolgert AJ, Marshall JM (2020). MGDrivE2: Mosquito Gene Drive Explorer 2. R package version 1.0.1. https://CRAN.R-project.org/package=MGDrivE2

2. Sánchez HM, Bennett JB, **Wu** SL, Marshall JM (2019). MGDrivE: Mosquito Gene Drive Explorer. R package version 1.6.0. https://CRAN.R-project.org/package=MGDrivE

Pre-Prints

1. **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 PNAS*)
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. 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, Equitorial Guinea. bioRxiv doi: https://doi.org/10.1101/2020.06.18.160101

5. (*Under review at Frontiers in Public Health*)
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.

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Presentations & Proceedings

1. **Wu SL**, Sánchez HM, Liang B, Citron DT, Henry JM, Smith DL: *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, USA.

2. **Wu SL**, Sánchez HM, Bennett JB, Marshall JM: *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.

3. **Wu SL**, Sánchez HM, Liang B, Citron DT, Henry JM, Zhang Q, Smith DL: *MBITES: Mosquito Bout-based Individual-based Transmission Simulator*. Presented at IDDConf 2018; September 2018; Ambleside, Cumbia, UK.

4. Marshall JM, Bennett JB, **Wu SL**, Sánchez HM: *CRISPR-Cas9-based gene drive architecture for control of agricultural pests*. Presented at Innovative Genomics Institute Open House; October 2017; UC Berkeley, CA, USA.

5. **Wu SL**, Sánchez HM, Liang B, Citron DT, Henry JM, Zhang Q, Marshall JM, Smith DL: *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, USA.

6. Sánchez HM, Bennett JB, **Wu SL**, Marshall JM: *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, USA.

7. Sánchez HM, **Wu SL**, Bennett JB, Marshall JM: *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, USA.

8. Zhou Y, Park D, **Wu SL**: *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, USA: https://api.semanticscholar.org/CorpusID:30964549

9. Jurgens AM, Kraay A, Weissman JL, Dong J, Pangallo M, **Wu SL**, Stopnitzky S, Zhan SH, Gurevich Y, Liu Y: *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, USA: https://wiki.santafe.edu/images/9/95/2017_CSSS_Proceedings_Book.pdf

10. Kiware SS, Tatarsky A, **Wu SL**, Sánchez HM, Chitnis N, Marshall JM: *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. **Wu SL**, Marshall JM, Sawadogo SP, Etienne B, Diabaté A: *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. Kiware SS, Tatarsky A, **Wu AL**, Sánchez HM, Chitnis N, Marshall JM: *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, USA.

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Fellowships & Awards

- 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

- 2017 Complex Systems Summer School at Santa Fe Institute (Santa Fe, NM, USA)
- New England Complex Systems Institute Winter School 2016 (MIT, Boston, MA, USA)
- 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