



Maxwell Murphy

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EDUCATION

University of California, Berkeley

Ph.D. Biostatistics

M.A. Biostatistics

B.A. Molecular and Cellular Biology - Developmental Genetics

Berkeley, CA

Expected May 2022

May 2019

May 2013

SKILLS

Computer/Programming:

- Languages: Python, R, Typescript, Javascript, SQL, Java, C++, C, Bash
- Frameworks/Libraries/Tools: Tidyverse, Flask, NumPy, SciPy, Matplotlib, Pandas, D3.js, TensorFlow, Angular, Git, Docker
- Parallel programming/algorithm implementation, and cloud computing

Statistics:

- Applying causal inference techniques and ensemble machine learning to estimate effects of longitudinal, static, and dynamic interventions
 - Developing and applying Bayesian Modeling methodology and using probabilistic programming languages
 - Working with large -omics and sequencing datasets such as scRNAseq and microarray data
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RESEARCH EXPERIENCE

University of California, Berkeley

Berkeley, CA

Center for Targeted Machine Learning and Causal Inference

Accenture Targeted Learning and Causal Inference Fellow

Jan 2020 - Current

Developing software for applying targeted learning and causal inference methodology with a focus on real industry use-cases and "big data" sets.

University of California, San Francisco

San Francisco, CA

Graduate Student Researcher – Principle Investigator: Bryan Greenhouse (Biohub)

Aug 2017 - Current

Currently developing statistical models to infer underlying complexity of malaria infections using mixed genetic data and spatial models of population structure to infer origin of clinically detected infections. Providing support to lab members in developing statistical models for various bioinformatics pipelines.

Staff Research Associate II / Lab Manager – Greenhouse Lab/Malaria Elimination Initiative

Apr 2014 - Aug 2017

Conducted large scale multiplex and nested PCR experiments to generate genetic data for malaria transmission mapping. Developed data analysis pipeline and graphical user interface for high-throughput analysis of genetic data from malaria causing parasites. Developed applications for tracking clinical samples used in lab, and data visualization tools for analyzing transmission network based data. Carried out administrative duties of lab, managed other members of the lab, conducted PCR experiments on clinical samples, liaised with foreign clinical labs and provided technical support for protocols.

INDUSTRY EXPERIENCE

Verily Life Sciences - Project Debug

South San Francisco, CA

Data Science Intern

May 2019 - Aug 2019

Developed statistical pipelines to provide realtime estimates of and inference around mosquito abatement techniques using. Developed probabilistic spatial models of mosquito dispersal to inform and optimize adaptive mosquito release scheduling. Provided statistical guidance in developing experimental trial design.

CytomX Therapeutics

South San Francisco, CA

Database Developer

Oct 2013 - Apr 2014

Developed SQL database to organize and make accessible in-vivo data generated by the Pharmacology group. Used VBA to develop an Excel/VBA based front-end to access and upload data for non-technical users. Carried out data analysis on publicly available gene expression data (The Cancer Genome Atlas) and built internal tools for data exploration and use by other members of company.

Pharmacology/Bioinformatics Intern

May 2013 - Aug 2013

Performed data analysis on publicly available gene expression data to identify potential targets for cancer therapeutics, then carried out cell cytotoxicity experiments at the bench to validate predictions. Carried out day-to-day tasks in the pharmacology group tasked with characterizing efficacy of novel cancer therapeutics, including maintaining cancerous mammalian cell lines and basic animal husbandry in a BSL 2 lab.

SOFTWARE DEVELOPMENT

moiR (<https://github.com/m-murphy/moiR>)

R package for joint Bayesian estimation of allele frequencies and multiplicity of infection from potentially multiply infected malaria samples using genotyping of multi-allelic loci.

MicroSPAT: Microsatellite Parameterized Analysis Tools (<https://github.com/Greenhouse-Lab/MicroSPAT>)

MicroSPAT is a collection of tools for semi-automated analysis of raw capillary electrophoresis (CE) data output by the ABI 3730. MicroSPAT integrates several features including a plate view for quality checking, automated ladder identification, sample based association of FSA data to keep data organized in a logical manner, automated allele identification using a clustering algorithm, automated artifact correction, automated quantification bias correction, and automated genotyping of samples with the option of manual curation.

SampleDB (https://github.com/Greenhouse-Lab/sample_db)

SampleDB is an open source database implementation with graphical user interface to track clinical lab samples and their usage. SampleDB supports tracking of sample specimens by barcoded tubes, for example the Matrix™ barcoded tube system.

Publications

1. Hsiang, M. S., Ntshalintshali, N., Kang Dufour, M.-S., Dlamini, N., Nhlabathi, N., Vilakati, S., Malambe, C., Zulu, Z., Maphalala, G., Novotny, J., **Murphy, M.**, Schwartz, A., Sturrock, H., Gosling, R., *et al.* Active Case Finding for Malaria: A 3-Year National Evaluation of Optimal Approaches to Detect Infections and Hotspots Through Reactive Case Detection in the Low-transmission Setting of Eswatini. *Clinical Infectious Diseases* **70**, 1316–1325. ISSN: 1058-4838. <https://doi.org/10.1093/cid/ciz403> (May 2019).
2. Tessema, S. K., Hathaway, N. J., Teyssier, N. B., **Murphy, M.**, Chen, A., Aydemir, O., Duarte, E. M., Simone, W., Colborn, J., Saute, F., Crawford, E., Aide, P., Bailey, J. A. & Greenhouse, B. Sensitive, highly multiplexed sequencing of microhaplotypes from the *Plasmodium falciparum* heterozygome. *bioRxiv*. <https://www.biorxiv.org/content/early/2020/02/26/2020.02.25.964536> (2020).
3. Jang, I. K., Tyler, A., Lyman, C., Rek, J. C., Arinaitwe, E., Adrama, H., **Murphy, M.**, Imwong, M., Proux, S., Haohankhunnatham, W., Barney, R., Rashid, A., Kalnoky, M., Kahn, M., *et al.* Multiplex Human Malaria Array: Quantifying Antigens for Malaria Rapid Diagnostics. *The American Journal of Tropical Medicine and Hygiene*. ISSN: 0002-9637. <https://www.ajtmh.org/content/journals/10.4269/ajtmh.19-0763> (2020).
4. Roh, M. E., Tessema, S. K., **Murphy, M.**, Nhlabathi, N., Mkhonta, N., Vilakati, S., Ntshalintshali, N., Saini, M., Maphalala, G., Chen, A., Wilhelm, J., Prach, L., Gosling, R., Kunene, S., *et al.* High Genetic Diversity of *Plasmodium falciparum* in the Low-Transmission Setting of the Kingdom of Eswatini. *J Infect Dis* **220**, 1346–1354. <http://dx.doi.org/10.1093/infdis/jiz305> (2019) (Sept. 2019).
5. Tessema, S. K., Wesolowski, A., Chen, A., **Murphy, M.**, Wilhelm, J., Mupiri, A.-R., Ruktanonchai, N. W., Alegana, V. A., Tatem, A. J., Tambo, M., Didier, B., Cohen, J. M., Bennett, A., Sturrock, H. J., *et al.* Using parasite genetic and human mobility data to infer local and cross-border malaria connectivity in Southern Africa. *eLife* **8**. <http://dx.doi.org/10.7554/eLife.43510> (Apr. 2019).
6. McCreesh, P., Mumbengegwi, D., Roberts, K., Tambo, M., Smith, J., Whittemore, B., Kelly, G., Moe, C., **Murphy, M.**, Chisenga, M., Greenhouse, B., Ntuku, H., Kleinschmidt, I., Sturrock, H., *et al.* Subpatent malaria in a low transmission African setting: a cross-sectional study using rapid diagnostic testing (RDT) and loop-mediated isothermal amplification (LAMP) from Zambezi region, Namibia. *Malaria Journal* **17**. <http://dx.doi.org/10.1186/s12936-018-2626-5> (Dec. 2018).
7. Coutrier, F. N., Tirta, Y. K., Cotter, C., Zarlinda, I., González, I. J., Schwartz, A., Maneh, C., Marfurt, J., **Murphy, M.**, Herdiana, H., Anstey, N. M., Greenhouse, B., Hsiang, M. S. & Noviyanti, R. Laboratory challenges of *Plasmodium* species identification in Aceh Province, Indonesia, a malaria elimination setting with newly discovered *P. knowlesi*. *PLoS Neglected Tropical Diseases* **12**. <http://dx.doi.org/10.1371/journal.pntd.0006924> (Nov. 2018).
8. Jang, I. K., Das, S., Barney, R. S., Peck, R. B., Rashid, A., Proux, S., Arinaitwe, E., Rek, J., **Murphy, M.**, Bowers, K., Boadi, S., Watson, J., Nosten, F., Greenhouse, B., *et al.* A new highly sensitive enzyme-linked immunosorbent assay for the detection of *Plasmodium falciparum* histidine-rich protein 2 in whole blood. *Malaria Journal* **17**. <http://dx.doi.org/10.1186/s12936-018-2545-5> (Nov. 2018).
9. Jang, I. K., Tyler, A., Lyman, C., Kahn, M., Kalnoky, M., Rek, J. C., Arinaitwe, E., Adrama, H., **Murphy, M.**, Imwong, M., Ling, C. L., Proux, S., Haohankhunnatham, W., Rist, M., *et al.* Simultaneous Quantification of *Plasmodium* Antigens and Host Factor C-Reactive Protein in Asymptomatic Individuals with Confirmed Malaria by Use of a Novel Multiplex Immunoassay. *Journal of Clinical Microbiology* **57** (ed Loeffelholz, M. J.) ISSN: 0095-1137. <https://jcm.asm.org/content/57/1/e00948-18> (2019).
10. Pringle, J. C., Tessema, S., Wesolowski, A., Chen, A., **Murphy, M.**, Carpi, G., Shields, T. M., Hamapumbu, H., Searle, K. M., Kobayashi, T., Katowa, B., Musonda, M., Stevenson, J. C., Thuma, P. E., *et al.* Genetic Evidence of Focal *Plasmodium falciparum* Transmission in a Pre-elimination Setting in Southern Province, Zambia. *The Journal of Infectious Diseases* **219**, 1254–1263. ISSN: 0022-1899. <https://doi.org/10.1093/infdis/jiy640> (Nov. 2018).
11. Quan, J., Langelier, C., Kuchta, A., Batson, J., Teyssier, N., Lyden, A., Caldera, S., McGeever, A., Dimitrov, B., King, R., Wilhelm, J., **Murphy, M.**, Ares, L. P., Travisano, K. A., *et al.* FLASH: a next-generation CRISPR diagnostic for multiplexed detection of antimicrobial resistance sequences. *Nucleic Acids Research* **47**, e83–e83. ISSN: 0305-1048. <https://doi.org/10.1093/nar/gkz418> (May 2019).
12. Chen, I., Diawara, H., Mahamar, A., Sanogo, K., Keita, S., Kone, D., Diarra, K., Djimde, M., Keita, M., Brown, J., Roh, M. E., Hwang, J., Pett, H., **Murphy, M.**, *et al.* Safety of Single-Dose Primaquine in G6PD-Deficient and G6PD-Normal Males in Mali Without Malaria: An Open-Label, Phase 1, Dose-Adjustment Trial. *The Journal of Infectious Diseases* **217**, 1298–1308. ISSN: 0022-1899. <https://doi.org/10.1093/infdis/jiy014> (Jan. 2018).
13. Taghavian, O., Jain, A., Joyner, C. J., Ketchum, S., Nakajima, R., Jasinskas, A., Liang, L., Fong, R., King, C., Greenhouse, B., **Murphy, M.**, Bailey, J., Galinski, M. R., Barnwell, J. W., *et al.* Antibody Profiling by Proteome Microarray with Multiplex Isotype Detection Reveals Overlap between Human and *Aotus nancymae* Controlled Malaria Infections. *PROTEOMICS* **18**, 1700277. <https://onlinelibrary.wiley.com/doi/abs/10.1002/pmic.201700277> (2018).
14. Das, S., Jang, I. K., Barney, B., Peck, R., Rek, J. C., Arinaitwe, E., Adrama, H., **Murphy, M.**, Imwong, M., Ling, C. L., Proux, S., Haohankhunnatham, W., Rist, M., Seilie, A. M., *et al.* Performance of a High-Sensitivity Rapid Diagnostic Test for *Plasmodium falciparum* Malaria in Asymptomatic Individuals from Uganda and Myanmar and Naïve Human Challenge Infections. *The American Journal of Tropical Medicine and Hygiene* **97**, 1540–1550. ISSN: 0002-9637. <http://www.ajtmh.org/content/journals/10.4269/ajtmh.17-0245> (2017).

15. Katrak, S., **Murphy, M.**, Nayebare, P., Rek, J., Smith, M., Arinaitwe, E., Nankabirwa, J. I., Kanya, M., Dorsey, G., Rosenthal, P. J. & Greenhouse, B. Performance of Loop-Mediated Isothermal Amplification for the Identification of Submicroscopic Plasmodium falciparum Infection in Uganda. *The American Journal of Tropical Medicine and Hygiene* **97**, 1777–1781. ISSN: 0002-9637. <http://www.ajtmh.org/content/journals/10.4269/ajtmh.17-0225> (2017).
16. Ranadive, N., Kunene, S., Darteh, S., Ntshalintshali, N., Nhlabathi, N., Dlamini, N., Chitundu, S., Saini, M., **Murphy, M.**, Soble, A., Schwartz, A., Greenhouse, B. & Hsiang, M. S. Limitations of Rapid Diagnostic Testing in Patients with Suspected Malaria: A Diagnostic Accuracy Evaluation from Swaziland, a Low-Endemicity Country Aiming for Malaria Elimination. *Clinical Infectious Diseases* **64**, 1221–1227. ISSN: 1058-4838. <https://doi.org/10.1093/cid/cix131> (Mar. 2017).
17. Chang, H.-H., Worby, C. J., Yeka, A., Nankabirwa, J., Kanya, M. R., Staedke, S. G., Dorsey, G., **Murphy, M.**, Neafsey, D. E., Jeffreys, A. E., Hubbart, C., Rockett, K. A., Amato, R., Kwiatkowski, D. P., *et al.* THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. *PLOS Computational Biology* **13**, 1–18. <https://doi.org/10.1371/journal.pcbi.1005348> (Jan. 2017).

Posters

18. **Murphy, M.**, Tessema, S., Mupiri, A.-R., Tambo, M., Smith, J. L., Bennett, A., Sturrock, H. J., Gosling, R., Mumbengegwi, D., Hsiang, M. S., Noviyanti, R., Trimarsanto, H., Price, R., Rodríguez-Barraquer, I., *et al.* Geographic assignment of *P. falciparum* and *P. vivax* infections using genetic data in *American Journal of Tropical Medicine and Hygiene* (2018).
19. Jang, I. K. E., Kahn, M., Barney, B., Kalnoky, M., Das, S., Peck, R., Tyler, A., Lyman, C., Rek, J., **Murphy, M.**, *et al.* Development of a Multiplex Assay for Simultaneous Quantification of Plasmodium Vivax and P. Falciparum Infection in *American Journal of Tropical Medicine and Hygiene* (2017).
20. Kuchta, A., Crawford, E., Quan, J., Wilhelm, J., **Murphy, M.**, Tessema, S. K., Derisi, J. & Greenhouse, B. Cas-9 Based Sequencing Enrichment for Malaria Genotyping in *American Journal of Tropical Medicine and Hygiene* (2017).
21. Kuchta, A., **Murphy, M.**, Arinaitwe, E., Rek, J., Chen, A., Wilhelm, J., Tessema, S. K., Bousema, T., Kanya, M., Staedke, S., *et al.* Population Structure of Plasmodium Falciparum is Detectable at Small Spatial Scales in Kihhi, Uganda in *American Journal of Tropical Medicine and Hygiene* (2017).
22. Sudathip, P., Cotter, C., Kitchikarn, S., Rattanapairoj, O., Zelman, B., Maneesiri, R., Sugaram, R., Schwartz, A., **Murphy, M.**, Greenhouse, B., Gonzalez, I. J., Vorster, L., Imwong, M., Gosling, R. D., *et al.* Malaria elimination in Thailand: Using LAMP in reactive case detection to increase infection detection. in *American Journal of Tropical Medicine and Hygiene* (2017).
23. Tessema, S., **Murphy, M.**, Mupiri, A.-R., Smith, J. L., Chen, A., Wilhelm, J., Hsiang, M. S., Sturrock, H. J., Mumbengegwi, D. & Greenhouse, B. Fine-Scale Population Genetics of Plasmodium Falciparum in Northern Namibia in *American Journal of Tropical Medicine and Hygiene* (2017).
24. Hamre, K. E., Tessema, S. K., **Murphy, M.**, Ayodo, G., Tran, T. M., Schwartz, A., John, C. C. & Greenhouse, B. Changes in population genetic parameters of Plasmodium falciparum before and after a period of low or interrupted malaria transmission in Kenyan highlands in *American Journal of Tropical Medicine and Hygiene* (2016).
25. Roh, M., **Murphy, M.**, Tessema, S., Ntshalintshali, N., Saini, M., Prach, L., Maphalala, G., Nhlabathi, N., Mkonta, N., Kunene, S., Hsiang, M. & Greenhouse, B. Influence of Malaria Importation on P. falciparum Population Genetic Diversity: A Study from Pre-elimination Setting of Swaziland in *American Journal of Tropical Medicine and Hygiene* (2016).
26. McCreesh, P., Roberts, K., Tambo, M., Bennett, A., Smith, J., Kelly, G., Cueto, C., Moe, C., Haindongo, E. U., Chisenga, M., **Murphy, M.**, Kleinschmidt, I., Sturrock, H., Uusiku, P., *et al.* Identifying risk factors for malaria in the Zambezi region of Namibia: A cross-sectional study using rapid diagnostic testing (RDT) and loop mediated isothermal amplification (LAMP) in *American Journal of Tropical Medicine and Hygiene* (2015).
27. **Murphy, M.**, Schwartz, A., Liu, Y., Kemere, J., Hsiang, M. & Greenhouse, B. Automated Methods for High-Throughput Analysis of Plasmodium Microsatellite Genotyping Data in *American Journal of Tropical Medicine and Hygiene* (2015).