

# Maxwell Murphy

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## EDUCATION

### University of California, Berkeley

M.A. Biostatistics

**Coursework:** Theoretical Statistics and Probability, Causal Inference, Infectious Disease Modeling, Statistical and Computational Genomics, Computational Immunology

B.A. Molecular and Cellular Biology - Developmental Genetics

Berkeley, CA

Expected May 2019

May 2013

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## SKILLS

### Computer/Programming:

- Languages: Python, R, Typescript, Javascript, SQL, Java, C++, C, VBA
- Frameworks/Libraries/Tools: Tidyverse, SQLAlchemy, Flask, NumPy, SciPy, Matplotlib, Pandas, D3.js, TensorFlow, Angular, Git, Docker, Bash
- Github: <https://github.com/m-murphy>
- Parallel programming/algorithm implementation, and cloud computing

### Statistics:

- Experience working with large -omics and sequencing datasets such as scRNAseq and microarray data
  - Experience working with large data sets in epidemiological contexts
  - Experience applying causal inference techniques and ensemble machine learning to estimate effects of longitudinal, static, and dynamic interventions
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## RESEARCH EXPERIENCE

### University of California, Berkeley

#### Graduate Student

Berkeley, CA

Aug 2017 - Current

Analyzed scRNAseq data to explore changes in gene expression during mouse embryogenesis. Analyzed DNA methylation array data to identify regions of differential methylation associated with spina bifida. Applied causal inference methods to estimate the impact of different intermittent preventative treatment protocols on malaria incidence in the context of a birth cohort in Eastern Africa.

### University of California, San Francisco

#### Graduate Student Researcher - Principle Investigator: Bryan Greenhouse (Biohub)

San Francisco, CA

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.

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## INDUSTRY EXPERIENCE

### 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.

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## SOFTWARE DEVELOPMENT

### 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](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.

### Sketch to Diagram (<https://github.com/m-murphy/sketch-to-diagram>)

Sketch to Diagram was built in a hackathon type event applying modern machine learning methods. SKtD is a proof of concept web app that uses a convolutional neural network based model to identify user drawings which are then converted into rendered objects. The goal of SKtD was to demonstrate how a non-trivial problem such as gesture recognition could be tackled in a flexible manner using modern machine learning in a user application. The application runs completely within the web browser at <http://sketch-to-diagram.surge.sh>.

# Publications

1. 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. *Malar J* **17**. doi:10.1186/s12936-018-2626-5 (Dec. 2018).
2. 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 Negl Trop Dis* **12**. doi:10.1371/journal.pntd.0006924 (Nov. 2018).
3. 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. *Malar J* **17**. doi:10.1186/s12936-018-2545-5 (Nov. 2018).
4. 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 CRP in Asymptomatic Individuals with Confirmed Malaria Using a Novel Multiplex Immunoassay. *J Clin Microbiol*. doi:10.1128/JCM.00948-18 (Nov. 2018).
5. 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. *J Infect Dis*. doi:10.1093/infdis/jiy640 (Nov. 2018).
6. Quan, J., Langelier, C., Kuchta, A., Batson, J., Teyssier, N., Lyden, A., Caldera, S., McGeever, A., Dimitrov, B., King, R., Wilhelm, J., **Murphy, M.**, Pesce Ares, L., Travisano, K. A., *et al.* FLASH: A next-generation CRISPR diagnostic for multiplexed detection of antimicrobial resistance sequences. *BioRxiv*. doi:10.1101/426338 (Sept. 2018).
7. 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. *J Infect Dis* **217**. doi:10.1093/infdis/jiy014 (Mar. 2018).
8. 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**. doi:10.1002/pmic.201700277 (Jan. 2018).
9. 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 Naive Human Challenge Infections. *Am J Trop Med Hyg* **97**. doi:10.4269/ajtmh.17-0245 (Nov. 2017).
10. Katrak, S., **Murphy, M.**, Nayebare, P., Rek, J., Smith, M., Arinaitwe, E., Nankabirwa, J. I., Kamya, M., Dorsey, G., Rosenthal, P. J. & Greenhouse, B. Performance of Loop-Mediated Isothermal Amplification for the Identification of Submicroscopic Plasmodium falciparum Infection in Uganda. *Am J Trop Med Hyg* **97**. doi:10.4269/ajtmh.17-0225 (Oct. 2017).
11. 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. *Clin Infect Dis* **64**. doi:10.1093/cid/cix131 (May 2017).
12. Chang, H.-H., Worby, C. J., Yeka, A., Nankabirwa, J., Kamya, M. R., Staedke, S. G., Dorsey, G., **Murphy, M.**, Neafsey, D. E., Jeffreys, A. E., Hubbard, 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 Comput Biol* **13**. doi:10.1371/journal.pcbi.1005348 (Jan. 2017).

## Posters

13. **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).
14. 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).
15. 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).
16. Kuchta, A., **Murphy, M.**, Arinaitwe, E., Rek, J., Chen, A., Wilhelm, J., Tessema, S. K., Bousema, T., Kamya, M., Staedke, S., et al. *Population Structure of Plasmodium Falciparum is Detectable at Small Spatial Scales in Kihhihi, Uganda in American Journal of Tropical Medicine and Hygiene* (2017).
17. 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).
18. 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).
19. 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).
20. 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).
21. 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).
22. **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).