**Madeleine S. Gastonguay**

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**Education**

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| **Johns Hopkins School of Medicine,** Baltimore, MD  PhD in Biomedical Engineering  GPA: 4.0/4.0  Advisor: Dr. Alison L. Hill | August 2022 - present |
| **University of Connecticut,** Storrs, CT | August 2016 - May 2020 |
| Bachelor of Science, Applied Mathematics  Summa Cum Laude with Honors; GPA: 3.98/4.00  Minor: Bioinformatics  Thesis: A Quantitative Pipeline for The Identification of Combinations of Targets for Claudin-Low Triple Negative Breast Cancer Reversion  Advisor: Dr. Paola Vera-Licona |  |

**Research Experience**

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| **Johns Hopkins Institute for Computational Medicine,** Baltimore, MD  *Biomedical Engineering PhD Candidate* | August 2022 – present |

Topic: Integrating mathematical models and statistical methods for within-host viral dynamics with quantitative systems pharmacology models of novel immunotherapies

* Building mathematical models and evaluating their dynamic properties
* Developing Bayesian methods for parameter estimation and uncertainty quantification
* Implementing nonlinear-mixed effects modeling to quantify interindividual variability and understand therapeutic mechanisms of action
* Designing stochastic simulations to predict long-term behavior of the system and evaluate therapeutic interventions
* Collaborating with experimentalists in the field of infectious diseases

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| **The Jackson Laboratory (JAX)**, Bar Harbor, ME  *Research Data Analyst I* | June 2020 – July 2022 |

Topic: A Bayesian approach to mediation analysis of complex traits with measurement noise

* Contributed to the development and validation of an R package implementation of a Bayesian model selection approach to mediation analysis that is flexible in both data inputs and potential inferences, and extended it to moderated mediation
* Diagnosed the effect of measurement noise on the inference of mediation
* Applied these tools to better understand the mechanisms underlying the effects of sex and diet on protein and gene expression in the livers of genetically diverse mice

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| **UConn Health Center for Quantitative Medicine,** Farmington, CT  *Undergraduate Research Assistant* | Sept. 2018 - May 2020 |

Topic: A quantitative pipeline for cancer reversion analysis in triple negative breast cancer

* Constructed a static intracellular signaling network for a claudin-low triple negative breast cancer (CL TNBC) cell line with multi-omics data using bioinformatics techniques
* Applied a structure-based control method for nonlinear systems, implemented in python, to identify putative targets that steer the system to any desired attractor
* Conducted virtual screenings using a network-based approach and a signal propagation algorithm to estimate long term behaviors to identify concerted perturbations of control nodes resulting in reversion of the CL TNBC phenotype

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| **Metrum Research Group**, Simsbury, CT  *Summer Intern* | June 2018 - Aug. 2018 |

Topic: A maternal-fetal physiologically based pharmacokinetic model for drugs metabolized by cytochrome P450 isoenzymes

* Modeled maternal and fetal drug exposures at varying gestational ages by incorporating anatomical, biochemical, and physiological changes associated with pregnancy as a system of ordinary differential equations using R and *mrgsolve*
* Performed local sensitivity analysis, optimized model parameters, and validated the model by comparing model predictions to external published data

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| **University of Connecticut,** Department of Molecular and Cellular Biology, Storrs, CT  *Undergraduate Research Assistant/Holster Scholar* | Jan. 2017 - Sept. 2017 |

Topic: The effect of host genetic variability on Epstein Barr Virus (EBV)-associated cancer susceptibility

* Reviewed relevant literature to identify genes that may impact EBV-associated cancer susceptibility
* Used wet lab techniques such as Polymerase Chain Reactions, Gel Electrophoresis, and Sanger Sequencing to sequence the genes of interest in several EBV-associated cancer cell lines and a non-cancerous EBV+ control cell line
* Aligned the genetic sequence of target genes to identify common and distinct single nucleotide polymorphisms (SNPs) across EBV-associated cancer cell lines using the software Geneious and BLAST

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| **Children’s Hospital of Philadelphia,** Philadelphia, PA, **Metrum Research Group,** Simsbury, CT  *High School Independent Study* | Sept. 2015 - Aug. 2016 |

Topic: A pharmacogenomic study of midazolam and morphine clearance in critically ill pediatric patients

* Analyzed variability of SNPs in the sample dataset for inclusion in the analysis
* Estimated the effect of pediatric risk of mortality score on drug clearance using population pharmacokinetic modeling
* Identified a SNP in UGT2B7 whose minor allele frequency is associated with increased midazolam clearance

**Manuscripts in Preparation**

Juillard, F.+, Gastonguay, M. S. +, Szymula, A.+, Gerold, J., Li, S., Lomonte, P., Simas, J.P., Hill, A. L., Kaye, & K. M. (2025+). KSHV episomal DNA replicates and partitions to progeny cell nuclei at similar, imperfect efficiencies.

*+ These authors contributed equally to the work*

**Publications and Preprints**

Liu, T. Y. A., Liu, Y., Gastonguay, M. S., Midgett, D., Kuo, N., Zhao, Y., Ullah, K., Alexander, G. Hartman, T., Koseoglu, N., Jones,   
C. (2025). Predicting imminent conversion to exudative age-related macular degeneration using multimodal data and ensemble   
machine learning. Ophthalmology Science, https://doi.org/10.1016/j.xops.2025.100785.

Gastonguay, M. S., Keele, G. R., & Churchill, G. A. (2023). The trouble with triples: Examining the impact of measurement error in mediation analysis. Genetics, 224(1), iyad045. https://doi.org/10.1093/genetics/iyad045

Crouse, W. L., Keele, G. R., Gastonguay, M. S., Churchill, G. A., & Valdar, W. (2022). A Bayesian model selection approach to mediation analysis. PLOS Genetics, 18(5), e1010184. https://doi.org/10.1371/journal.pgen.1010184

Utsey, K., Gastonguay, M. S., Russell, S., Freling, R., Riggs, M. M., & Elmokadem, A. (2020). Quantification of the Impact of Partition Coefficient Prediction Methods on Physiologically Based Pharmacokinetic Model Output Using a Standardized Tissue Composition. *Drug Metabolism and Disposition*, *48*(10), 903 LP – 916. https://doi.org/10.1124/dmd.120.090498

Zuppa, A. F., Benitez, G. R., Zane, N. R., Curley, M. A. Q., Bradfield, J., Hakonarson, H., Gastonguay, M. S., Moorthy, G., Prodell, J., & Gastonguay, M. R. (2019). Morphine Dose Optimization in Critically Ill Pediatric Patients With Acute Respiratory Failure. *Critical Care Medicine*, *47*(6), e485–e494. https://doi.org/10.1097/CCM.0000000000003741

Zuppa, A. F., Conrado, D. J., Zane, N. R., Curley, M. A. Q., Bradfield, J., Hakonarson, H., Gastonguay, M. S., Moorthy, G., Prodell, J., & Gastonguay, M. R. (2019). Midazolam Dose Optimization in Critically Ill Pediatric Patients With Acute Respiratory Failure. *Critical Care Medicine*, *47*(4), e301–e309. https://doi.org/10.1097/CCM.0000000000003638

**Oral Presentations**

Gastonguay MS, Gerold J, Juillard F, Szymula A, Hill AL, Kaye K, *Quantifying the dynamics of Kaposi’s sarcoma-associated herpesvirus persistence*, Dynamics & Evolution of Human Viruses, Paris, France, May 9th, 2025

Gastonguay MS, Gerold J, Juillard F, Szymula A, Hill AL, Kaye K, *Quantifying the dynamics of Kaposi’s sarcoma-associated herpesvirus persistence*, Epidemics, Bologne, Italy, November 27th, 2023

Gastonguay MS, Russell S, Freling R, Utsey K, and Elmokadem A, *Prediction of maternal-fetal exposures of CYP450-metabolized drugs using physiologic pharmacokinetic modeling implemented in R and mrgsolve.,* R/Pharma Conference, Cambridge, MA, August 23rd, 2019

Gastonguay MS, Marazzi L, Vera-Licona P, *Identification of Combinations of Targets for Claudin-Low Triple Negative Breast Cancer Reversion,* UConn Center for Cell Analysis and Modeling Summer Seminar, July 26th, 2019

Gastonguay MS, Russell S, Freling R, Utsey K, and Elmokadem A, *Development of an Open and General Physiologically Based Pharmacokinetic Model to Predict Maternal-Fetal Exposures for Drugs Metabolized by CYP Isoenzymes,* R/Medicine Conference, New Haven, CT, September 8th, 2018

Gastonguay MS, *The Effect of Host Genetic Variability on Epstein Barr Virus-associated cancer susceptibility,* UConn Holster Scholar Symposium, October 2017

**Poster Presentations**

Gastonguay MS, Gerold J, Juillard F, Szymula A, Hill AL, Kaye K, *Quantifying the dynamics of Kaposi’s sarcoma-associated herpesvirus persistence*, MIDAS Network Annual Meeting, Bethesda, MD, November 18th, 2024

Gastonguay MS, Gerold J, Juillard F, Szymula A, Hill AL, Kaye K, *Quantifying the dynamics of Kaposi’s sarcoma-associated herpesvirus persistence*, International Workshop on Kaposi's Sarcoma Herpesvirus (KSHV) & Related Agents, Boston, MA, July 7th, 2024

Gastonguay MS, Marazzi L, Vera-Licona P, *Identification of Combinations of Pharmacologic Targets for Claudin-Low Triple Negative Breast Cancer Reversion,* International Society of Pharmacometrics Quantitative Systems Pharmacology Student Symposium, Virtual, April 28th, 2021

Gastonguay MS, Marazzi L, Vera-Licona P, *Identification of Combinations of Targets for Claudin-Low Triple Negative Breast Cancer Reversion,* Joint Meeting in Mathematics, Denver, CO, January 15th – 18th, 2020

Gastonguay MS, Russell S, Freling R, Utsey K, and Elmokadem A, *Development of an Open-source Physiologically-Based Pharmacokinetic Model to Predict Maternal-Fetal Exposures of CYP450-Metabolized Drugs,* International Society of Pharmacometrics Regional Quantitative Systems Pharmacology Day, Princeton, NJ, July 16th, 2019

Gastonguay MS, Russell S, Freling R, Utsey K, and Elmokadem A, *Development of an Open-source Physiologically-Based Pharmacokinetic Model to Predict Maternal-Fetal Exposures of CYP450-Metabolized Drugs,* University of Connecticut Frontiers in Undergraduate Research, April 12th, 2019

**Open-Source Contributions**

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| **bmediatR,** an open-source R package implementing a Bayesian model selection approach to mediation analysis. Available to install from github https://github.com/wesleycrouse/bmediatR.   * Contributed to methods development and package validation in both synthetic and real data * Designed and built package Vignettes | May 2022 |

**Fellowships and Grants**

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| **Summer Undergraduate Research Fund,** University of Connecticut Office of Undergraduate Research   * Awarded funding for a 9-week summer research project | May 2019 |
| **Holster Scholar**, University of Connecticut Honors Program   * Offered enrollment in a semester-long course to learn how to develop and write a project proposal * Selected as one of 8 students awarded funding for a 10-week summer research project | May 2017 |

**Honors and Awards**

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| **Blue Ribbon Poster Award,**ISoP Quantitative Systems Pharmacology Student Symposium | April 2021 |
| **Dean’s List**, The University of Connecticut | Sept. 2016 - May 2020 |
| **Academic Excellence Scholarship**, The University of Connecticut | Sept. 2016 - May 2020 |
| **Babbidge Scholar**, The University of Connecticut | Dec. 2017, 2019 |
| **New England Scholar**, The University of Connecticut | Dec. 2018 |

**Skills & Certifications**

**Technical:** R; Python; Matlab, SQL, Julia, and bash shell; Git; LaTeX; High Performance Computing with SLURM; Nonlinear mixed-effects modeling with Monolix; *mrgsolve*; *shiny*; *tidyverse; plotly;* JAGS;Bayesian Data Analysis

**Language:** Proficient in French conversation, reading, and writing; Certified in French level B1.2 by La Sorbonne in Paris

**Teaching:** Certified Instructor with The Carpentries

**Teaching Experience**

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| **Dynamic modeling of infectious diseases in patients and populations,** Johns Hopkins University (TA) | Oct. - Dec. 2024 |
| **Systems pharmacology and personalized medicine,** Johns Hopkins University (TA) | Feb. - May 2024 |
| **Data carpentry ecology with R workshop**, Bioinformatics Training Program at JAX (Instructor) | Dec. 2021 |
| **Data carpentry genomics workshop**, Bioinformatics Training Program at JAX (Instructor) | Nov. 2021 |
| **Introductory statistics with R,** Bioinformatics Training Program at JAX (TA) | Sept. 2021 |
| **Introduction to R and RStudio,** Bioinformatics Training Program at JAX (TA) | June 2021 |

**Professional Development and Continuing Education**

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| **Summer Institute in Statistics and Modeling in Infectious Diseases**, Emory University | July 2024 |
| **Building Tidy R Packages**, R/pharma 2021 | Oct. 2021 |
| **Julia Language for R Programmers,** R/pharma 2021 | Oct. 2021 |
| **Advanced Shiny,** RStudio | Sept. 2021 |
| **Introduction to Bayesian Data Analysis**, Juliacon | July 2021 |
| **Carpentries Instructor Training,** The Carpentries | Mar. 2021 |
| **Shiny, RMarkdown, and RStudio Connect,** RStudio | Mar. 2021 |
| **Quantitative Trait Mapping in the Diversity Outbred,** University of Wisconsin-Madison | Dec. 2020 |
| **Containerization with Singularity,** JAX | Oct. 2020 |
| **Introduction to HPC,** JAX | Sept. 2020 |
| **Human and Mammalian Genetics and Genomics: The 61st McKusick Short Course,** JAX | July 2020 |
| **Shiny Reproducibility**, R/pharma 2019 | Aug. 2019 |
| **Machine Learning**, R/pharma 2019 | Aug. 2019 |

**Volunteer Work and Extra‐Curricular Activities**

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| **Student Mentor,** Johns Hopkins University Women Mentoring Women Program   * Served as a mentor for an undergraduate student with similar research interests | Jan. 2025 - present |
| **BME Application Assistance Program,** Johns Hopkins University | Sept. 2022 - present |

* Provided prospective students personalized feedback on graduate program applications

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| **Math Motivators,** The University of Connecticut | Oct. 2017 - May 2019 |

* Tutored high school freshmen enrolled in public school in Hartford, CT

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| **iGEM Genetic Engineering Team,** The University of Connecticut | Sept. 2016 - Dec. 2017 |

* Developed and presented a project proposal for the iGEM jamboree with a team of students