Madeleine S. Gastonguay

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Education

University of Connecticut, Storrs, CT   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

La Sorbonne University, Paris, France   Jan. 2018-May 2018
    Course de Civilisation Française

Research Experience

The Jackson Laboratory (JAX), Bar Harbor, ME   June 2020 - present
Research Data Analyst I
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

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

Metrum Research Group, Simsbury, CT   June 2018 – Aug. 2018
Summer Intern
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

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

Children's Hospital of Philadelphia, Philadelphia, PA and **Metrum Research Group,** Simsbury, CT   Sept. 2015 – Aug. 2016
High School Independent Study
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

Gastonguay, M. S., Keele, G. R., & Churchill, G. A. (2021). The impact of measurement noise in mediation analysis.

Publications and Preprints

Crouse, W. L., Keele, G. R., Gastonguay, M. S., Churchill, G. A., & Valdar, W. (2021). A Bayesian model selection approach to mediation analysis. *BioRxiv*, 2021.07.19.452969. https://doi.org/10.1101/2021.07.19.452969

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

Selected Oral Presentations

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

Poster Presentations

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 2019

Fellowships and Grants

Summer Undergraduate Research Fund, University of Connecticut Office of Undergraduate Research — May 2019
- Awarded funding for a 9-week summer research project

Holster Scholar, University of Connecticut Honors Program — May 2017
- 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

Honors and Awards

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; basic Matlab, SQL, Julia, and bash shell; Git; LaTeX; OpenRefine; High Performance Computing with SLURM; *mrgsolve*; *shiny*; *tidyverse; plotly;* JAGS; Bayesian Data Analysis

Wet Lab: Polymerase Chain Reactions, Gel Electrophoresis, Gel Extraction, Sanger sequencing

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 (* indicates upcoming)

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