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| **Madeleine S. Gastonguay**  [Madeleine.Gastonguay@uconn.edu](mailto:Madeleine.Gastonguay@uconn.edu)  <https://madeleine-gastonguay.netlify.app/> | I am an aspiring systems biologist looking for a graduate program where I can develop my skills as an independent researcher and thinker. |

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| **Education**  **BS in Applied Mathematics, University of Connecticut, May 2020**   * Summa Cum Laude with Honors in the Major * Bioinformatics Minor * Thesis: A Quantitative Pipeline for The Identification of Combinations of Targets for Claudin-Low Triple Negative Breast Cancer Reversion   **Grants and Awards**   * Summer Undergraduate Research Fund Trimble Family Award, University of Connecticut * Holster Scholar, University of Connecticut * Academic Excellence Scholarship, University of Connecticut * Dean’s List, University of Connecticut   **Skills & Certifications**   * R, Python, Matlab, Unix, LaTeX * Carpentries Instructor Certification, in progress * Certified in French level B1.2 by La Sorbonne * Certified in Cecchetti Ballet Grades 2-7   **Research Experience**  **The Jackson Laboratory Churchill Lab,** Bar Harbor, ME  **Research Data Analyst I** (June 2020 – present)  Topic: A Bayesian approach to mediation analysis of complex traits with measurement noise   * Contributing to construction and validation of an R package for Bayesian model selection * Extending current methods for mediation analysis to include moderated mediation * Uncovering the effect of measurement noise on mediation analysis * Building a Bayesian model to incorporate prior knowledge of measurement noise to increase the accuracy of mediation analysis | **Research Experience Con’t**  **Center for Quantitative Medicine, UConn Health Center,** Farmington, CT  **Undergraduate Research Assistant** (September 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 Cytoscape and GeneXplain * Applied a structure-based control method for nonlinear systems to identify putative control targets * Approximated the attractor landscape of the static network and conducted virtual screenings of concerted perturbations of control targets using a topological estimation of signal flow * Identified perturbations resulting in reversion of the CL TNBC phenotype though machine learning clustering and classification methods   **Metrum Research Group,** Simsbury, CT  **Summer Intern** (June 2018-August 2018)  Topic: Developing an open and general maternal-fetal physiologically based pharmacokinetic model for drugs metabolized by cytochromes P450 isoenzymes   * Described the physiological pharmacokinetics of midazolam, metoprolol, and caffeine in nonpregnant women with a system of differential equations with *mrgsolve* * Extended the model for nonpregnant women to predict maternal and fetal drug exposures at different gestational ages by incorporating anatomical, biochemical, and physiological changes a woman undergoes throughout pregnancy * Calibrated the model with local sensitivity analysis and optimization of model parameters * Validated the model by comparing predicted concentration profiles to published data for several other drugs metabolized by cytochrome P450 isoenzymes   **Activities & Hobbies**   * Singing with my a cappella group * Hiking and fishing in Acadia National Park |