

KATHRYN (KATE) H. BRIDGES

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EDUCATION

Yale University, New Haven, CT, 2018 – present

Ph.D. in Biomedical Engineering, expected Spring/Summer 2023

- Thesis: Improved cell classification and inference of cellular communication from single-cell immunological data
- Thesis Committee: Kathryn Miller-Jensen, Ph.D. (chair), Valerie Horsley, Ph.D., Yuval Kluger, Ph.D., and Andre Levchenko, Eng.Sc.D.
- Certificate from the Integrated Graduate Program in Physical and Engineering Biology, expected 2023

M.Phil. in Biomedical Engineering, May 2021

M.S. in Biomedical Engineering, December 2019

University of Virginia, Charlottesville, VA, 2014 – 2018

B.S. in Biomedical Engineering, minor in Engineering Business, with Highest Distinction, May 2018

B.A. in Mathematics, May 2018

RESEARCH EXPERIENCE

Department of Biomedical Engineering, Yale University, New Haven, CT

Doctoral Research

August 2018 – present

Research advisor: Kathryn Miller-Jensen, Ph.D.

- Developed computational pipelines to connect and extract biological insight about cellular communication from single-cell data with primary application to melanoma and wound healing.
- Led all single-cell RNA-seq data analysis for \$2.8M National Cancer Institute grant exploring mechanisms of combinatorial immunotherapies in mouse models of melanoma.
- Presented findings in multiple peer-reviewed publications and in 5+ internal and national symposia.
- Mentored three undergraduate students and one graduate rotation student in single-cell RNA-sequencing data analysis.

Barron Associates, Charlottesville, VA

Undergraduate Capstone Research

August 2017 – May 2018

Research advisors: Alec Bateman, Ph.D. and Michael DeVore, Ph.D.

- Integrated an established deterministic pharmacokinetic model of propofol transport into a novel Simulink-based stochastic framework to aid predictions of optimal anesthetic dose.
- Presented findings in an undergraduate thesis in partial fulfillment of B.S.

Department of Biomedical Engineering, University of Virginia, Charlottesville, VA

Undergraduate Research

February 2016 – October 2017

Research advisor: Jeffrey Saucerman, Ph.D.

- Integrated novel gene expression data into a logic-based ODE model of the cardiomyocyte hypertrophy signaling network to investigate the role of genetic variability of network species in hypertrophic response and implicate specific signaling network constituents as therapeutic targets.
- Presented findings at two national conferences (BMES Annual Meeting 2016 and 2017).

SKILLS

- Experienced in single-cell data analysis, statistical analysis, genomics and proteomics, including analysis of single-cell and bulk RNA-sequencing data, single-cell and bulk protein secretion data, and T cell receptor sequencing data.
- Highly skilled in Python and R, with experience in Matlab, Linux, Java, and Mathematica, and in version control (GitHub).

TEACHING EXPERIENCE

Yale University, 2019 – 2021

Responsible Conduct of Research (Spring 2020 and Spring 2021)

- Collaborated with the instructor and co-teaching fellow to develop interactive lesson plans on technologically relevant ethical topics (e.g., the use of neuroimaging in the court system)
- Invited speakers to give guest lectures on relevant topics, including 2004 Nobel Laureate in Chemistry Aaron Ciechanover, M.D., D.Sc., whose Spring 2021 talk was titled “COVID-19: The road between patients and curative medical technologies is strewn with bioethical bumps.”

Discovery and Design (Fall 2019)

- Held weekly discussion sections to cover additional skills pertinent to students’ success in the course, including but not limited to grant writing, effective presenting, and literature review
- Graded assignments and exams

University of Virginia, 2016 – 2017

- *Integrated Design and Experimental Analysis Laboratory* (Fall 2017)
- *Ordinary Differential Equations* (Spring 2017 and Fall 2017)
- *Computational Biomedical Engineering* (Fall 2016)

UNIVERSITY SERVICE

Graduate Society of Women Engineers: Treasurer, 2019 – 2021; Conference Planning Committee, 2019 – 2021

Peer Advisor: University Link Peer Advising Service, University of Virginia, 2016 – 2018

Alpha Omega Epsilon Sorority: Membership Educator, 2016

Tour Guide: School of Engineering and Applied Science, University of Virginia, 2015 – 2018

PUBLICATIONS

Bridges K*, Krykbaeva I*, Damsky W, Alexander AF, McGeary M, Pizzurro GA, Turner N, Weiss SA, Olino K, Kaech S, Kluger H, Miller-Jensen K, and Bosenberg MW. Combinatorial immunotherapy with agonistic CD40 activates dendritic cells to overcome PD-1 resistance. *In preparation.*

Bridges K*, Kunte M*, Chen M, Kellman LN, Alexander AF, Pizzurro GA, Muñoz-Rojas AR, Bass V, and Miller-Jensen K. M-CSF-differentiated murine bone marrow-derived macrophages contain a small dendritic-cell-like subpopulation of high IL-12p40-secreting cells. *In preparation.*

Justynski O, **Bridges K**, Forni MF, Wasko RR, Ting Y, Miller-Jensen K, and Horsley V. The Gas6/Axl axis coordinates cell death signaling among myeloid cells in the transition between phases of the wound healing response. *In preparation*.

Pizzurro GA, **Bridges K**, Wang M, Miller-Jensen K, and Colegio OR. F4/80 expression separates functionally distinct subsets of tumor-associated macrophages with differing contributions to immunosuppression. *In preparation*.

Wasko RR, **Bridges K**, Pannone R, Sidhu I, Xing Y, Naik S, Miller-Jensen K, and Horsley V. Langerhans cells are an essential component of the angiogenic niche during skin repair. *Under review at Developmental Cell*.

Bridges K and Miller-Jensen K. Mapping and validation of scRNA-seq-derived cell-cell communication networks in the tumor microenvironment. *Frontiers in Immunology*. April 2022.

Pizzurro GA*, Liu C*, **Bridges K**, Alexander AF, Huang A, Baskaran JP, Ramseier J, Bosenberg MW, Mak M, and Miller-Jensen K. 3D model of the early melanoma microenvironment captures macrophage transition into a tumor-promoting phenotype. *Cancers*. September 2021.

Wasko R, Xing Y, Sidhu I, **Bridges K**, Miller-Jensen K, Naik S, and Horsley V. Langerhans cells promote revascularization and repair during skin wound healing. Abstract published in the *Journal of Investigative Dermatology*. May 2021.

Bridges K and Baritaud C. A Modeler's Responsibility: The Importance of Transparency in Computational Modeling. Undergraduate Thesis/Dissertation. University of Virginia Library. Charlottesville, VA. May 2018.

Bridges KH*, Brennan CE*, DeVore MD, and Bateman AJ. Integrating Stochasticity into an Established Pharmacokinetic Model to Maximize the Probability of Successful Anesthetic Dosage. Undergraduate Thesis/Dissertation. University of Virginia Library. Charlottesville, VA. May 2018.

* Denotes equal contribution.

PRESENTATIONS (Invited Talks and Posters)

Bridges K*, Krykbaeva I*, Alexander AF, McGeary M, Damsky W, Djureinovic D, Kluger H, Miller-Jensen K, and Bosenberg MW. Triple immunotherapy mobilizes myeloid-mediated, T cell-dependent antitumor response in a murine melanoma model. Virtual talk at the 2021 National Cancer Institute Cancer Systems Biology Consortium Annual Meeting.

Bridges K*, Krykbaeva I*, Alexander AF, McGeary M, Damsky W, Miller-Jensen K, and Bosenberg MW. Novel triple therapy mobilizes myeloid-mediated, T cell-dependent antitumor response in a murine melanoma model. Poster presented virtually at the 2021 National Cancer Institute Cancer Systems Biology Consortium Junior Investigator's Meeting and the 2021 Yale Systems Biology and Cancer Systems Biology Symposium (additional flash talk given).

Bridges KH, Pizzurro G, Damsky W, Du V, Brickman Raredon MS, Greaney A, Niklason L, Kaech S, Bosenberg M, and Miller-Jensen K. Cell type classification of scRNA-seq data using a neural network-based approach. Poster intended for presentation at the 2020 Cell Symposia: The Conceptual Power of Single-Cell Biology Conference, San Francisco, CA. Postponed to 2022 due to COVID-19.

Bridges KH, Pizzurro G, Damsky W, Du V, Kaech S, Bosenberg M, and Miller-Jensen K. Constructing Cell-Cell Communication Networks in the Melanoma Tumor Microenvironment from scRNA-seq Data. Poster presented at the 2019 Advances in Systems Analysis of Aggressive Cancers Symposium, New Haven, CT, and the 2019 Physics of Living Systems Conference, Munich, Germany (additional flash talk given).

Bridges KH, Damsky W, Bosenberg M, and Miller-Jensen K. Developing a Computational Pipeline to Elucidate Cell-Cell Communication in the Melanoma Tumor Microenvironment from scRNA-seq Data. Poster presented at the 2019 Yale Cancer Center Retreat, New Haven, CT, and the 2019 Gruber Science Fellowship Symposium, New Haven, CT.

Bridges K, Chun B, and Saucerman J. Inclusion of Fold Change Genes into a Computational Model to Identify Novel Regulators of Cardiomyocyte Hypertrophy. Poster presented at the 2017 BMES Annual Meeting, Phoenix, AZ.

Bridges K, Chun B, and Saucerman J. Integrating Gene Expression Data into a Computational Model to Ascertain the Role of Genetic Background in Cardiomyocyte Hypertrophy. Oral presentation at the 2016 BMES Annual Meeting, Minneapolis, MN.

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