Georgia Doing

Postdoctoral Fellow, The Oh Lab
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Career Goals

Postdoctoral fellow intending to establish her own laboratory at a leading research and teaching institution to pursue the computational and molecular characterization of dynamic microbial communities.

Education

2022	**Ph.D. Microbiology**. Geisel School of Medicine at Dartmouth, Hanover, NH. Deborah A. Hogan, Ph.D., advisor
2015	**B.A**. Biology and Computer Science. Bard College, Annandale-on-Hudson, NY. GPA 3.94

Publications

Doing G., A.J. Lee, S.L. Neff, T. Reiter, J.D. Holt, B.A. Stanton, C.S. Greene, D.A. Hogan "Computationally efficient assembly of a *Pseudomonas aeruginosa* gene expression compendium." Msystems, Dec 2022. DOI: 10.1128/msystems.00341-22.

Lee, A.J., **Doing G**., S.L. Neff, T. Reiter, C.S. Greene, D.A. Hogan "Compendium-wide analysis of P. aeruginosa ore and accessory genes reveal nuanced transcriptional patterns." Msystems, Dec 2022. DOI: 10.1128/msystems.00342-22

Lee, A.J., D.L. Mould, J. Crawford, D. Hu, R.K. Powers, **G. Doing**, J.C. Costello, D.A. Hogan, C.S. Greene "SOPHIE: Generative neural networks separate common and specific transcriptional responses." Genomics, Proteomics and Bioinformatics, Oct 2022. DOI: 10.1016/j.gpb.2022.09.011

Lee, A.J., T. Reiter, **G. Doing**, J. Oh, D.A. Hogan, C.S. Greene "Using genome-wide expression compendia to study microorganisms." Computational and Structural Biotechnology Journal, Aug 2022. DOI: 10.1016/j.csbj.2022.08.012

Neff, S.L., T.H. Hampton, C. Puerner, L. Cengher, **G. Doing**, A.J. Lee, K. Koeppen, A.L. Cheung, D.A. Hogan, R.A. Cramer, B.A. Stanton "CF-Seq, An Accessible Web Application for Rapid Re-Analysis of Cystic Fibrosis Pathogen RNA Sequencing Studies." Scientific Data, Jun 2022. DOI: 10.1101/2022.03.07.483313

Lee, A.J., Y. Park, **G. Doing**, D.A. Hogan, C.S. Greene "Correcting for experiment-specific variability in expression compendia can remove underlying signals." GigaScience, Nov 2020, 9(11): giaa117

Doing G., K. Koeppen, P. Occhipinti, C.E. Harty, D.A. Hogan "Conditional antagonism in co-cultures of *Pseudomonas aeruginosa* and *Candida albicans*: an intersection of ethanol and phosphate signaling distilled from dual-seq transcriptomics." PLOS Genetics. Aug 2020, 16(8): e1008783.

Harty, C., D. Martins, **G. Doing**, D.L. Mould, M. Clay, D. Nguyen, D.A. Hogan "Ethanol stimulates trehalose production through a SpoT-DksA-AlgU dependent pathway in *Pseudomonas aeruginosa.*" Journal of Bacteriology. Mar 2018, 200 (8) e00703-17.

Chen K.M., J. Tan, G.P. Way, **G. Doing**, D.A. Hogan, C.S. Greene "PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia." BioData Mining. Jul 2018 **11**(14).

Dahlstrom,K.M., A.J. Collins, **G. Doing**, J.N. Taroni, T.J. Gauvin, C.S.Greene, D.A. Hogan, G.A. O'Toole "A Multimodal Strategy Used by a Large c-di-GMP Network." Journal of Bacteriology. Mar 2018, 200 (8) e00703-17

Doing   G., G.G. Perron, B.A.   Jude   "Draft   Genome   Sequence   of   a   Violacein-Producing *Iodobacter* sp. from the Hudson Valley Watershed." Genome Announcements. Jan 2018, 6 (1) e01428-17

Bettina A.M., **G. Doing**, K. O'Brien, G.G. Perron, B.A. Jude "Draft Genome Sequences of Phenotypically   Distinct *Janthinobacterium* sp.   Isolates   Cultured   from   the   Hudson   Valley Watershed." Genome Announcements. Jan 2018, 6 (3) e01426-17

Tan, J.*, **G. Doing***, K. A. Lewis, C. E. Price, K. M. Chen, K. C. Cady, B. Perchuk, M. T. Laub, D. A. Hogan and C. S. Greene "Unsupervised Extraction of Stable Expression Signatures from Public Compendia with an Ensemble of Neural Networks." Cell Systems. July 2017, 5(1): 63-71.e66. [* authors contributed equally]

Presentations

Doing, G. "Wrangling Microbial Diversity." Bio Seminar, Bard College, Annandale-on-Hudson NY 2022.

Doing, G. "Wrangling strain diversity in staphylococci contextualizes skin microbiomes." UConn/JAX Postdoc Flash Talks, 2022.

Doing, G. "Strain-aware pipelines for microbial 'omics data." JAX Computational Community Midyear Retreat, Virtual, 2022.

Doing, G. "Measuring Microbial Mingling." Thomas Jefferson High School Microbial Genomics and Bioinformatics Lecture, Virtual, 2022.

Doing, G. "A reductionist approach to transcriptomics: a focus on *Pseudomonas aeruginosa*." Public Thesis Defense, Dartmouth College, 2021.

Doing, G. "The hidden life of *Pseudomonas aeruginosa*: transcriptional patterns latent during microbial interactions." Postdoc Candidate Seminar, JAX-GM, Virtual, 2021.

Doing, G. "Well-spoken killer whales: should we believe what we hear?" Science on Tap, Dartmouth College, Virtual, 2020.

Doing, G. "*P. aeruginosa* and *C. albicans* interactions as told by dual RNAseq." Bio Seminar, Bard College, Virtual, 2020.

Doing, G. "Illuminating the black box of Neural Networks in R: visualizing the learned for the visual learner." R Club, Dartmouth College, Hanover NH, 2020.

Doing, G., C. Greene, D. Hogan, "Deconvolving *Pseudomonas aeruginosa* Gene Expression in Co-Culture with *Candida albicans*: a Machine Learning Approach.", New England Microbiology, Physiology, Ecology and Taxonomy, Blue Mountain Lake, NY, 2019.

Doing, G. "Exploratory plotting with heterogeneous data." R Club, Dartmouth College, Hanover NH. 2019.

Doing, G., D. Hogan, "Gradients: nuances in microbial interactions." Microbiology and Molecular Pathogenesis Program Annual Retreat, Fairlee VT, 2018.

Doing, G., J. Tan, C. Greene, D. Hogan, "Integrating diverse *Pseudomonas aeruginosa* transcriptional profiles." Computational, Systems and Integrative Genomics, Princeton NJ, 2017.

Doing, G., R. Thomas, B. Jude, "Machine Learning on Images of a Microbial Mutant Library." Elect Senior Project Presentations, Bard College, 2015.

Posters

Doing, G. J. Riera, M. Spoto, J. Oh, "Developing omics pipelines to wrangle strain diversity in staphylococci contextualizes skin microbiomes." Dartmouth Immunology Retreat, Woodstock VT, 2022.

Doing, G., A. Lee, A. Crocker, D. Vermilyea, C. Greene, D. Hogan, "Denoising autoencoder-derived gene expression signatures of *Pseudomonas aeruginosa* grown in *ex vivo* sputum." Cold Spring Harbor Laboratories Biological Data Science Meeting, Virtual, 2020.

Doing, G., D. Hogan, "Red Oxidative Toxin: how phosphate and metabolism color *Pseudomonas aeruginosa ~ Candida albicans* interactions." Microbiology and Molecular Pathogenesis Program Annual Retreat Poster Session, Fairlee VT, 2020.

Doing, G., D. Mould, C. Greene, D. Hogan, "Iron influences microbial interactions." Dartmouth Molecular and Cellular Biology Retreat Poster Session, Whitefield NH, 2019.

Doing, G., C. Greene, D. Hogan, "'Duel'-RNAseq highlights a role for ethanol in the fight for phosphate and iron in *Pseudomonas aeruginosa ~ Candida albicans* interactions." Microbiology and Molecular Pathogenesis Program Annual Retreat Poster Session, Fairlee VT, 2019.

Doing, G., J. Tan, C. Greene, D. Hogan, "Ethanol stimulates PhoB: non-canonical signaling in *Pseudomonas aeruginosa ~ Candida albicans* interactions." Dartmouth Molecular and Cellular Biology Retreat Poster Session, Whitefield NH, 2018.

Doing, G., J. Tan, C.S. Greene, D.A. Hogan, "Using denoising autoencoders to elucidate functional signatures connecting quorum sensing and environmental responses in *Pseudomonas aeruginosa*." Computational, Systems and Integrative Genomics Poster Session, Princeton NJ, 2017.

Doing, G., J. Tan, K. Lewis, C. Price, C. Greene, D. Hogan, "Denoising Autoencoders reveal a role for KinB in the *Pseudomonas aeruginosa* response to phosphate starvation." Dartmouth Molecular and Cellular Biology Retreat Poster Session, Whitefield NH, 2016.

Doing, G., B. Jude, "Construction of Genetic Knockouts in Violacein-producing Microbes." Regional ASM conference poster session, Albany NY, 2013.

Doing, G., T. Delaney, D. Ruggiero, S. Anderson, R. Thomas, "Feature-Based Estimates of Sentence Readability." Bard Summer Research Institute Poster Session, Annandale-on-Hudson NY, 2012.

Scholarships and Awards

2022	Postdoc Flash Talk Competition, 3rd place, JAX-GM and UConn Health
2020	JXTX James P. Taylor Foundation for Open Science Scholarship
2017 - 2020	Molecular and Cellular Biology Training Grant at Dartmouth
2015	Undergraduate Award in Science, Mathematics and Computing
2014	John Bard Scholar
2013 – 2014	Distinguished Science Scholar
2013	Stanley and Elaine Reichel Science Scholarship

Teaching and Mentoring

Spring 2023	**Leader of the Postbacc Journal Club.**	The Jackson Laboratory.
Winter 2023	**Citizen Science Faculty.**	Bard College.
Winter 2020	**Citizen Science Faculty.**	Bard College.
Fall 2020	**Mentor to a 1st year PhD rotation student.**	Dartmouth College.
Summer 2020	**TA for RNA-Seq Workshop**.	Dartmouth Center for Quantitative Biology.
Winter 2020	**Mentor to a Masters student.**	Dartmouth College.
Fall 2019	**Mentor to a 2nd year PhD student.**	Dartmouth College.
Fall 2018	**Mentor to a 1st year PhD rotation student.**	Dartmouth College.
Winter 2017	**Teaching Assistant and Laboratory Instructor.**	Genetics, Dartmouth College.
Fall 2017	**Tutor for MCB core class.**	Biochemistry, Dartmouth College.

Research Experience

1. **Undergraduate Research:** I conducted a summer research project in the natural language processing and machine learning laboratory of Dr. Rebecca Thomas at Bard College that aimed to automate text simplification. The project combined sentence parsing, features determined by unsupervised machine learning and classification schemes using supervised machine learning to reduce the complexity of text while maintaining its semantic content, a process which could greatly aid in the development of speech-assistance devices and increase the accessibility of text-based information.

2. **Undergraduate Research:** My second summer research experience at Bard College was in the lab of Dr. Brooke Jude during which I assembled the genome of an environmentally isolated strain of a violacein-producing bacterium and used genetic manipulation to determine the operon responsible for violacein production and genes that contributed to biofilm formation. This project resulted in a poster presented at the regional ASM conference, published genome announcements and provided the foundation for my senior project in which I mutagenized the same organism and developed automatic image processing techniques to assess biofilm formation across the mutant library.

3. **Graduate Research:** As a graduate student in the lab of Dr. Deborah Hogan I investigated gene expression in *Pseudomonas aeruginosa* and *Candida albicans* in order to better understand the interactions between the two microbes that may extrapolate to consequences of infection. In a first author publication, I published the first dual-RNA-seq of *P. aeruginosa* and C. *albicans* in co-culture. I took part in a collaboration with the lab of Dr. Casey Greene at the University of Colorado-Anschutz that resulted in a publication of a machine learning based model of gene expression for *Pseudomonas aeruginosa*. I used this model to answer multiple questions of gene expression in analyses and validation experiments as a contributing author to publications out of the Hogan, Greene, O'Toole and Stanton labs. I continued to expand this project to more deeply analyze *Pseudomonas aeruginosa* gene expression by leveraging thousands of public *P. aeruginosa* RNA-seq datasets to aid in the interpretation of *P. aeruginosa* gene expression profiles when cultured in expectorated sputum, a state-of-the-art move toward comprehensive meta-transcriptomic techniques.

4. **Postdoctoral Research:** In the lab of Dr. Julia Oh at the Jackson Laboratory for Genomic Medicine, I am investigating the role of commensal and pathogenic keystone members of the skin microbiome. I am deploying machine learning methods to explore public omics data from *Staphylococcus aureus* and *Staphylococcus epidermidis* and developing pipelines to integrate gene expression and essentiality from multi-omics data generated by the Oh lab with the aim of developing and testing hypotheses regarding skin microbiome ecology, microbial interactions and effects on human health.