Matthew G. Durrant, Ph.D

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Education

Stanford University – School of Medicine   *Sep 2016 – Dec 2020*

PhD in Genetics – National Science Foundation Graduate Research Fellow

- Doctoral Dissertation – "Mobile genetic elements: mechanisms of microbial evolution and reservoirs of genome engineering tools"
- Advised by Dr. Ami Bhatt and Dr. Stephen Montgomery
- Courses of Study: Foundations in Experimental Biology, Frontiers in Biological Research, Advanced Genetics, Genomics, Statistical and Machine Learning Methods for Genomics, Deep Learning, Economics of

Brigham Young University

Bachelor of Science – Summa cum laude – Provo, Utah   *Sep 2016*

- Double Major: Bioinformatics and Neuroscience, Minor: Mathematics
- Cumulative GPA: 4.0
- Courses of Study: Computational Biology, Bioinformatics, Algorithm Design and Analysis, Advanced Programming, Statistics for Engineers and Scientists, Multivariable Calculus, Linear Algebra, Ordinary Differential Equations, Molecular Biology, Genetics, Advanced Neuroscience, Bioinnovation and Entrepreneurship

Research Experience

Arc Institute   *Jan 2022 – Present*

Senior Scientist

- Working in the lab of Dr. Patrick Hsu
- Working with computational and experimental scientists to build a platform for the discovery of new genome engineering systems
- Discovered a family of programmable recombinases that encode a bridge RNA and was co-inventor on several related patents
- Worked on building and evaluating Evo, a cutting-edge large DNA language model
- Directly mentoring graduate students attending UC Berkeley and Stanford
- Gaining experience with directly managing full-time employees, currently building a small team

Stylus Medicine   *Jan 2022 – Present*

Co-founding Scientist

- Developed target product profiles, pitch decks, scientific resources
- Helped to recruit and build the computational biology team
- Implemented the first year of the computational biology research plan for the company
- Performed work that produced new intellectual property for the company
- Primarily using Google Cloud resources and cloud native tools such as Bigtable, BigQuery, Batch, Dataflow, Pub/Sub, etc.

Pragma Bio (Formerly VastBiome)   *Dec 2021 – July 2022*

Computational Biology Consultant

- Worked on a team of computational biologists

- Developed data analysis pipelines and software packages for mining biological sequence data for new enzymes
- Operated through AWS batch for high-throughput computing

UC Berkeley – Department of Bioengineering $\hfill$ *Jan 2021 – Dec 2021*
Postdoctoral Fellow
- Worked in the lab of Dr. Patrick Hsu
- Led several projects to discover new molecular tools for genome engineering
- Gained extensive experience using cloud computing to store and analyze massive biological datasets

Bhatt & Montgomery Labs – Stanford School of Medicine $\hfill$ *June 2017 – Dec 2020*
Genetics PhD Candidate
- Advisors: Dr. Ami Bhatt and Dr. Stephen Montgomery
- Research Focuses:
  - Structural variation in microbial genomes
  - Mining bacterial genomes to identify novel tools for genome editing
  - Deep learning to annotate small open reading frames (smORFs) in bacterial genomes.
  - Computational methods development
  - Human RNA-seq, ATAC-seq, allele-specific expression, gene-environment interaction discovery
- Stanford SPARK Scholar – A program to assist scholars as they develop new biotechnology products.
- Other interests:
  - Statistical genetics
  - Machine learning and Deep Learning in genomics

NorthShore Bio
Computational Biologist $\hfill$ *July 2017 – Oct 2017*
- Worked remotely on contract as a computational biologist
- Developed analytical software to accompany molecular analysis technology

Yale University and the Rothberg Institute $\hfill$ *June 2015 – Dec 2015*
Bioinformatics Research Intern – New Haven, CT
- Programmed an application to store millions of genetic variants and perform quality control analysis
- MongoDB, Python, R experience
- Wrote a manuscript documenting quality control procedure and drafting results of a rare variant analysis of an ADHD patient NGS dataset.
- Next Generation Sequencing (whole exome) data experience

Tute Genomics $\hfill$ *Nov 2014 - Feb 2015*
Bioinformatics Research Intern – Provo, UT
- Programmed at Tute Genomics, a bioinformatics company which has developed a comprehensive cloud-based genome annotation platform for clinicians and researchers
- Advised by Bryce Daines, Ph.D. in Human Genetics
- Developed pharmacogenomics platform to be used for commercial purposes in team of 5 interns
- Project development, python programming, database curation, and MongoDB experience

Max Planck Institute for Chemical Ecology $\hfill$ *May 2014 – Aug 2014*
Bioinformatics Research Fellow – Jena, Germany
- Experience with Python, UNIX command line, R, and Adobe Illustrator
- Analyzed microarray and RNA-seq transcriptome data

- Published manuscript entitled *Evidence of an evolutionary hourglass pattern in herbivory-induced transcriptomic responses* in the journal *New Phytologist*

Brigham Young University   *May 2013 – August 2016*
Undergraduate Research Assistant – Provo, Utah
- Researched under the guidance of Dr. David Busath and Dr. Mary Davis
- Published in BMC Genetics, *Investigation into a recent rise of dual-amantadine resistant mutations in the Influenza A M2 Sequence*. Presented article at The 11th Annual Biotechnology and Bioinformatics Symposium.
- Presented an abstract at the American Society of Human Genetics conference in October 2015 entitled *Analysis of pathways associated with Body Mass Index in individuals with multiple sclerosis*
- Contributed as a member of the YGen Consortium, a group investigating the relationship between human Y chromosome variation, complex traits, and clinical metadata.
- Molecular Dynamics Simulations experience with VMD, NAMD, CHARMM

Other Work and Volunteer Experience

Utah Science and Engineering Fair   *Feb 2024 – March 2024*
Project Mentor and Competition Judge
- Mentored a high school student in preparation for their competition.
- Judged science projects presented by high school students in Utah.
- Focused on machine learning, molecular biology, bioinformatics, and biomedical engineering projects.

January, Inc.   *June 2019 – Sep 2019*
Machine Learning / Science Team
- Worked directly with both experimental biologists and machine learning engineers
- Collaborated with team members to develop features of a direct-to-consumer digital health product
- Clustered and typed users based on behavioral patterns collected from the company's app

Stanford University – Department of Genetics   *Jan 2019 – Apr 2019*
Genomics Teaching Assistant – Stanford, CA
- Tutored for 2 hours per week
- Taught weekly Python programming lecture to graduate students.
- Evaluated students' code and project proposals.

Software / Data Carpentry   *Jan 2017 – Dec 2019*
Volunteer Instructor – Stanford, CA
- Certified instructor trained in evidence-based teaching methods.
- Experience teaching graduate students to utilize Python, Jupyter Notebooks, R, and Unix in their research.
- Volunteering regularly as an instructor on a continual basis.

Vykon Technologies   *Jan 2015 – 2017*
Co-founder – Provo, Utah
- Development of low-cost movement disorder monitoring software application that couples with commercially available 3D motion-capture cameras
- Developed the initial prototype of the leading product DextraSense
- Managed the development of the technology with co-founder Jacob Durrant, PhD
- Market survey development, deployment, and data analysis
- FDA medical device compliance experience

Publications

1) *Nguyen, E., *Poli, M., *<u>Durrant, M.</u>, *Kang, B., *Katrekar, D., *Li, D., Bartie, L., Thomas, A., King, S., Brixi, G., Sullivan, J., Ng, M., Lewis, A., Patel, A., Lou, A., Ermon, A., Baccus, S., Hernandez-Boussard, T., Ré, C., Hsu, P., Hie, B. (2024), Sequence modeling and design from molecular to genome scale with Evo. *Science,* DOI: https://doi.org/10.1126/science.ado9336. *Authors contributed equally

2) *<u>Durrant, M.</u>, *Perry, N., Pai, J., Jangid, A., Athukoralage, J., Hiraizumi, M., McSpedon, J., Pawluk, A., Nishimasu, H., Konermann, S., Hsu, P. (2024), Bridge RNAs direct programmable recombination of target and donor DNA. *Nature*, DOI: https://doi.org/10.1038/s41586-024-07552-4. *Authors contributed equally

3) Hiraizumi, M., Perry, N., <u>Durrant, M.</u>, Soma, T., Nagahata, N., Okazaki, S., Athukoralage, J., Isayama, Y., Pai, J., Pawlkuk, A., Konermann, S., Yamashita, K., Hsu, P., Nishimasu, H. (2024), Structural mechanism of bridge RNA-guided recombination. *Nature*, DOI: https://www.nature.com/articles/s41586-024-07570-2

4) Wei, J., Lotfy, P.m Faizi, K., Baungaard, S., Gibson, E., Wang, E., Slabodkin, H., Kinnaman, E., Chandrasekaran, S., Kitano, H., <u>Durrant, M.</u>, Duffy, C., Pawluk, A., Hsu, P., Konermann, S. (2023), Deep learning and CRISPR-Cas13d ortholog discovery for optimized RNA targeting. *Cell Systems*, DOI: https://www.cell.com/cell-systems/pdf/S2405-4712(23)00329-0.pdf

5) *<u>Durrant, M.</u>, *Fanton, A., *Tycko, J., Hinks, M., Chandrasekaran, S., Perry, N., Schaepe, J., Du, P., Lotfy, P., Bassik, M., Bintu, L., Bhatt, A., Hsu, P. (2022), Systematic discovery of recombinases for efficient integration of large DNA sequences into the human genome. *Nature Biotechnology*, DOI: https://doi.org/10.1038/s41587-022-01494-w, *Authors contributed equally

6) Smail, C., Ferraro, N., Hui, Q., <u>Durrant, M</u>., Aguirre, M., Tanigawa, Y., Keever-Keigher, M., Rao, A., Justesen, J., Li, X., Gloudemans, M., Assimes, T., Koopergerg, C., Reiner, A., Huang, J., O'Donnel, C., Sun, Y., Million Veteran program, Rivas, M., Montgomery, S. (2022), Integration of rare expression outlier-associated variants improves polygenic risk prediction. *The American Journal of Human Genetics*, DOI: https://doi.org/10.1016/j.ajhg.2022.04.015

7) Gloudemans, M., Balliu, B., Nachun, D., Schnurr, T., <u>Durrant, M.</u>, Ingelsson, E., Wabitsch, M., Quertermous, T., Montgomery, S., Knowles, J., Carcamo-Orive I. (2022), Integration of genetic colocalizations with physiological and pharmacological perturbations identifies cardiometabolic disease genes. *Genome Medicine*, DOI: https://doi.org/10.1186/s13073-022-01036-8

8) Balliu, B., Carcamo-Orive, I., Gloudemans, M., Nachun, D., <u>Durrant, M.</u>, Gazal, S., Park, C., Knowles, D., Wabitsch, M., Quertermous, T., Knowles, J., Montgomery, S. (2021), An integrated approach to identify environmental modulators of genetic risk factors for complex traits. *The American Journal of Human Genetics*, DOI:https://doi.org/10.1016/j.ajhg.2021.08.014

9) *<u>Durrant, M.</u>, *Fremin, B., Rao, A., Cribas, E., Montgomery, S., Bhatt, A. (preprint, 2021), Chromatin accessibility changes induced by the microbial metabolite butyrate reveal possible mechanisms of anti-cancer effects. *biorXiv*, DOI:https://doi.org/10.1101/2021.03.30.437582, *Authors contributed equally

10) <u>Durrant, M.</u>, Bhatt, A. (2021), Automated Prediction and Annotation of Small Open Reading Frames in Microbial Genomes. *Cell Host & Microbe*, DOI:https://doi.org/10.1016/j.chom.2020.11.002

11) Contrepois, K., Wu, S., Moneghetti, K., Hornburg, D., Ahadi, S., Tsai, M., Metwally, A., Wei, E., Lee, B., Quijada, J., Chen, S., Christle, J., Ellenberger, M., Balliu, B., Taylor, S., <u>Durrant, M.</u>, Knowles, D., Choudhry, H., Ashland, M., Bahmani, A., Enslen, B., Amsallem, M., Kobayashi, Y., Avina, M.,

Perelman, D., Miryam, S., Zhou, W., Ashley, E., Montgomery, S., Chaib, H., Haddad, F., Snyder, M. (2020), Molecular Choreography of Acute Exercise. *Cell*, DOI:https://doi.org/10.1016/j.cell.2020.04.043

12) <u>Durrant, M.</u>, Li, M., Siranosian, B., Bhatt, A. (2020), A Bioinformatic Analysis of Integrative Mobile Genetic Elements Highlights Their Role in Bacterial Adaptation. *Cell Host & Microbe*, DOI:https://doi-org.stanford.idm.oclc.org/10.1016/j.chom.2019.10.022

13) Balliu, B., <u>Durrant, M.</u>, de Goede, O., Abell, N., Li, X., Liu, B., Gloudemans, M., Cook, N., Smith, K., Pala, M., Cucca, F., Schlessinger, D., Jaiswal, S., Sabatti, C., Lind, L., Ingelsson, E., Montgomery, S. B. (2019), Genetic dysregulation of gene expression and splicing during a ten-year period of human aging. *Genome Biology*. 519520; doi: 10.1186/s13059-019-1840-y.

14) <u>Durrant, M.</u>, Bhatt, A. (2019), Microbiome genome structure drives function. *Nature Microbiology*, News & Views. doi: 10.1038/s41564-019-0473-yx

15) <u>Durrant, M.</u>, Boyer, J., Zhou, W., Baldwin, I., Xu, S. (2017), Evidence of an evolutionary hourglass pattern in herbivory-induced transcriptomic responses. *New Phytologist*. doi:10.1111/nph.14644

16) <u>Durrant, M.</u>, Eggett, D., & Busath, D. (2015). Investigation of a recent rise of dual amantadine-resistance mutations in the influenza A M2 sequence. *BMC genetics*, 16(2), S3.

Abstracts, Posters, and Presentations

1) <u>Durrant, M.</u>, (2024), Mobile genetic elements, programmable recombination, and the future of genomic discovery. *University of Utah Department of Biomedical Informatics Department Seminar Series*.

2) *<u>Durrant, M.</u>, *Perry, N. (2024), Bridge RNAs direct modular and programmable recombination of target and donor DNA. Talk given at *Harvard Medical School Genome Engineering Seminar Series.* *Presented jointly.

3) <u>Durrant, M.</u>, (2024), Bridge RNAs direct modular and programmable recombination of target and donor DNA. Guest Lecture for UC Berkeley Course *Advanced Topics in Bioengineering* (BIOE 190/290).

4) *<u>Durrant, M.</u>, *Perry, N., Pai, J., Jangid, A., Athukoralage, J., Hiraizumi, M., McSpedon, J., Pawluk, A., Nishimasu, H., Konermann, S., Hsu, P. (2024), Bridge RNAs direct modular and programmable recombination of target and donor DNA. Poster presented at *Keystone Symposia Precision Genome Engineering.* *Presented jointly.

5) *<u>Durrant, M.</u>, *Fanton, A., *Tycko, J. (2022), Systematic discovery of recombinases for efficient integration of large DNA sequences into the human genome. Talk given at *Harvard Medical School Genome Engineering Seminar Series.* *Presented jointly.

6) <u>Durrant, M.</u>, Fanton, A., Tycko, J., Hinks, M., Chandrasekaran, S., Perry, N., Schaepe, J., Du, P., Lotfy, P., Bassik, M., Bintu, L., Bhatt, A., Hsu, P. (2022), Systematic discovery of recombinases for efficient integration of large DNA sequences into the human genome. Talk and poster presented at *Keystone Symposia Precision Genome Engineering.*

7) <u>Durrant M.</u>, Tycko J., Bintu L., Bassik M., Bhatt A. (2019), Mining bacterial genomes to identify thousands of novel recombinases for genome editing. Poster abstract presented at *Stanford Medicine Genetics Retreat.*

8) <u>Durrant MG</u>, Fremin B., Montgomery S., Bhatt A. (2018), Microbial metabolite butyrate affects allele-specific expression and disrupts chromatin architecture in a colon cancer cell line. Reviewers' choice poster abstract presented at *American Society of Human Genetics Annual Meeting.*

9) <u>Durrant MG</u>, Fremin B., Greenside P., Kundaje A., Montgomery S., Bhatt A. (2017) The impact of butyrate, a microbial metabolite, on allele-specific expression and chromatin accessibility in colon cancer cells. Poster abstract presented at *Stanford Medicine Genetics Retreat*.

10) <u>Durrant M.</u>, Denny J., Davis M. (2015) Analysis of pathways associated with Body Mass Index in individuals with multiple sclerosis. Poster abstract presented at *American Society of Human Genetics Annual Meeting*.

11) <u>Durrant M.</u>, Eggett D., Busath D. (2014) Investigation of a recent rise of dual amantadine-resistance mutations in the influenza A M2 sequence. Talk and poster presented at the *11th Annual Biotechnology and Bioinformatics Symposium*.

Intellectual Property

1) <u>Durrant, M.</u>, Perry, N., Hsu, P. (2024), Programmable DNA Transposases for Nucleic Acid Manipulation (WO2024119163A1). Patent application.
2) <u>Durrant, M.</u>, Konermann, S., Hsu, P. (2024), Systems, Methods, and Compositions for Identifying Nucleic Acid-Guided Systems (WO2024119154A1). Patent application.
3) <u>Durrant, M.</u>, Hsu, P., Fanton, A., Moon, C. (2023), Integration of large nucleic acids into genomes (WO2023177424A1). Patent application.
4) <u>Durrant, M.</u>, Bhatt, A., Tycko, J., Hsu, P., Fanton, A., Bassik, M., Bintu, L. (2023), Serine recombinases (WO2023081762A2). Patent application.

Code Portfolio

1) *BridgeRNADesigner* - Python package for designing bridge RNA guides for genome engineering experiments.
2) *BridgeRNA2024* - Code to accompany Durrant & Perry et al. (2023).
3) *SystematicDiscoveryRecombinases2022* - Code to accompany Durrant, Fanton & Tycko et al. (2022). Includes a custom pipeline for identifying engineered recombinase plasmid insertions in the human genome.
4) *SmORFinder* - A command line tool to identify and annotate small proteins in genomes and metagenomes. https://github.com/bhattlab/SmORFinder
5) *MGEFinder* - A toolbox for identifying mobile genetic element (MGE) insertions from short-read sequencing data of bacterial isolates. https://github.com/bhattlab/MGEfinder
6) Github: https://github.com/durrantmm

Awards and Distinctions

- National Science Foundation Graduate Research Fellow
- Stanford SPARK Scholar
- College of Life Sciences Dean's List - 2010, 2011, 2013, 2014, 2015. (Deferred enrollment 2012)
- Brigham Young University Full Ride Scholarship
- Regent's Scholar - Utah System of Higher Education
- LFSCI 399R Internship Grant - Helped cover the cost of my internship at the Max Planck Institute
- Miller New Venture Challenge Prize Winner - Cofounder of Winning Company Vykon Technologies

Other Skills and Accomplishments

- Proficient in Bash, Python, and R
- Extensive experience with cloud computing, SQL, workflow automation tools, anaconda, shiny web applications
- Speaks Slovak and Czech Languages

- Eagle Scout