

# Matthew G. Durrant, Ph.D

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## Education

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### 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 Biotechnology

### 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

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### 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
- Directly mentoring graduate students attending UC Berkeley and Stanford.

### 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**

*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**

*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*

*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**

*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**

*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**

*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

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### 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 – Present

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

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- 1) \*Durrant, M., \*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. *bioRxiv*, DOI: <https://www.biorxiv.org/content/10.1101/2024.01.24.577089v1>. \*Authors contributed equally
- 2) Wei, J., Lotfy, P.m Faizi, K., Baungaard, S., Gibson, E., Wang, E., Slabodkin, H., Kinnaman, E., Chandrasekaran, S., Kitano, H., Durrant, M., 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](https://www.cell.com/cell-systems/pdf/S2405-4712(23)00329-0.pdf)

- 3) \*Durrant, M., \*Fantom, 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
- 4) Smail, C., Ferraro, N., Hui, Q., Durrant, M., Aguirre, M., Tanigawa, Y., Keever-Keigher, M., Rao, A., Justesen, J., Li, X., Gloudemans, M., Assimes, T., Kooperger, 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>
- 5) Gloudemans, M., Balliu, B., Nachun, D., Schnurr, T., Durrant, M., 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>
- 6) Balliu, B., Carcamo-Orive, I., Gloudemans, M., Nachun, D., Durrant, M., 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>
- 7) \*Durrant, M., \*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
- 8) Durrant, M., Bhatt, A. S. (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>
- 9) 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., Durrant, M., Knowles, D., Choudhry, H., Ashland, M., Bahmani, A., Ensen, B., Amsellem, 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>
- 10) Durrant, M., Li, M., Siranosian, B., Bhatt, A. S. (2020), A Bioinformatic Analysis of Integrative Mobile Genetic Elements Highlights Their Role in Bacterial Adaptation. *Cell Host & Microbe*, DOI: <https://doi.org/10.1016/j.chom.2019.10.022>
- 11) Balliu, B., Durrant, M., 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.
- 12) Durrant, M., Bhatt, A. S. (2019), Microbiome genome structure drives function. *Nature Microbiology*, News & Views. doi: 10.1038/s41564-019-0473-yx
- 13) Durrant, M., Boyer, J., Zhou, W., Baldwin, I. T. and Xu, S. (2017), Evidence of an evolutionary hourglass pattern in herbivory-induced transcriptomic responses. *New Phytologist*. doi:10.1111/nph.14644
- 14) Durrant, M., Eggett, D. L., & Busath, D. 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

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- 1) \*Durrant, M., \*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*. \*Authors contributed equally.
- 2) \*Durrant, M., \*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*. \*Authors contributed equally.
- 3) \*Durrant MG, \*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*. \*Authors contributed equally.
- 4) \*Durrant MG, \*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*. \*Authors contributed equally.
- 5) \*Durrant MG, \*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*. \*Authors contributed equally.
- 6) Durrant MG, Denny JC, Davis MF. (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*.
- 7) Durrant MG, Eggett DL, Busath DD. (2014) Investigation of a recent rise of dual amantadine-resistance mutations in the influenza A M2 sequence. Article presented at the *11th Annual Biotechnology and Bioinformatics Symposium*.

## Intellectual Property

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Durrant, M., Hsu, P., Fanton, A., Moon, C. (2022), Integration of large nucleic acids into genomes (WO2023177424A1). Patent application.

Durrant, M., Bhatt, A., Tycko, J., Hsu, P., Fanton, A., Bassik, M., Bintu, L. (2022), Serine recombinases (WO2023081762A2). Patent application.

## Code Portfolio

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- 1) *SystematicDiscoveryRecombinases2022* - Code to accompany Durrant, Fanton & Tycko et al. (2022). Includes a custom pipeline for identifying engineered recombinase plasmid insertions in the human genome.
- 2) *GenomeSearch* - A command line tool to quickly identify closely related genomes using a marker-gene based approach. <https://github.com/bhattlab/GenomeSearch>
- 3) *SmORFinder* - A command line tool to identify and annotate small proteins in genomes and metagenomes. <https://github.com/bhattlab/SmORFinder>
- 4) *MGEFinder* - A toolbox for identifying mobile genetic element (MGE) insertions from short-read sequencing data of bacterial isolates. <https://github.com/bhattlab/MGEfinder>
- 5) Github: <https://github.com/durrantmm>

## Awards and Distinctions

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- 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
- \$15,000 Miller New Venture Challenge Prize Winner - Cofounder of Winning Company Vykon Technologies

## Other Skills and Accomplishments

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- Proficient in Bash, Python, and R
- Extensive experience with cloud computing, SQL, snakemake workflows, anaconda, shiny web applications
- Fluent in Slovak Language
- Eagle Scout