

# 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
- 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**

*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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### **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

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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 programmable recombination of target and donor DNA. *Nature*, DOI: <https://doi.org/10.1038/s41586-024-07552-4>. \*Authors contributed equally
- 2) [Hiraizumi, M.](#), [Perry, N.](#), [Durrant, M.](#), [Soma, T.](#), [Nagahata, N.](#), [Okazaki, S.](#), [Athukoralage, J.](#), [Isayama, Y.](#), [Pai, J.](#), [Pawluk, 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>
- 3) [\\*Nguyen, E.](#), [\\*Poli, M.](#), [\\*Durrant, M.](#), [Thomas, A.](#), [Kang, B.](#), [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. *bioRxiv*, DOI: <https://doi.org/10.1101/2024.02.27.582234>. \*Authors contributed equally
- 4) [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)
- 5) [\\*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. *Nature Biotechnology*, DOI: <https://doi.org/10.1038/s41587-022-01494-w>, \*Authors contributed equally
- 6) [Smail, C.](#), [Ferraro, N.](#), [Hui, Q.](#), [Durrant, M.](#), [Aguirre, M.](#), [Tanigawa, Y.](#), [Keever-Keigher, M.](#), [Rao, A.](#), [Justesen, J.](#), [Li, X.](#), [Gloude-mans, M.](#), [Assimes, T.](#), [Koopergerg, C.](#), [Reiner, A.](#), [Huang, J.](#), [O'Donnell, 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) [Gloude-mans, 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>
- 8) [Balliu, B.](#), [Carcamo-Orive, I.](#), [Gloude-mans, 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>
- 9) [\\*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
- 10) [Durrant, M.](#), [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.](#), [Durrant, M.](#), [Knowles, D.](#), [Choudhry, H.](#), [Ashland, M.](#), [Bahmani, A.](#), [Enslin, 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) Durrant, M., 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., 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.
- 14) Durrant, M., Bhatt, A. (2019), Microbiome genome structure drives function. *Nature Microbiology*, News & Views. doi: 10.1038/s41564-019-0473-yx
- 15) Durrant, M., 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) Durrant, M., 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

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- 1) \*Durrant, M., \*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.
- 2) Durrant, M., (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).
- 3) \*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*. \*Presented jointly.
- 4) \*Durrant, M., \*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.
- 5) 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*.
- 6) Durrant M., 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*.
- 7) 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*.
- 8) 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*.

- 9) Durrant M., 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*.
- 10) Durrant M., 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

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

## Code Portfolio

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- 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

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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
- 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, workflow automation tools, anaconda, shiny web applications
- Speaks Slovak and Czech Languages
- Eagle Scout