

# Alan P. Boyle

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[www.BoyleLab.org](http://www.BoyleLab.org)

## Education

|           |  |
|-----------|--|
| 2005–2009 | <b>Doctor of Philosophy</b> , Computational Biology and Bioinformatics<br>Duke University, Durham, NC  |
| 2001–2005 | <b>Bachelor of Science</b> , <i>summa cum laude</i> , Biochemistry and Molecular Biology<br><b>Bachelor of Science</b> , <i>summa cum laude</i> , Computer Science<br>Mississippi State University, Starkville, MS |

## Academic Appointments

|              |   |
|--------------|---|
| 2020–present | <b>Associate Professor with tenure</b> , Department of Computational Medicine & Bioinformatics<br><b>Associate Professor</b> , Department of Human Genetics |
| 2021–present | <b>Affiliate</b> , Michigan Neuroscience Institute  |
| 2020–present | <b>Affiliate Member</b> , Rogel Cancer Center   |
| 2017–present | <b>Member</b> , Cellular and Molecular Biology Program  |
| 2016–present | <b>Member</b> , Center for RNA Biomedicine  |
| 2015–present | <b>Member</b> , Genome Science Training Program (GSTP)<br><b>Member</b> , Michigan Predoctoral Training Program in Genetics (GTP)                           |
| 2014–present | <b>Member</b> , Program in Biomedical Sciences<br><b>Member</b> , Bioinformatics Training Program   |
| 2015–2020    | <b>Assistant Professor</b> , Department of Human Genetics   |
| 2014–2020    | <b>Assistant Professor</b> , Department of Computational Medicine & Bioinformatics<br>University of Michigan, Ann Arbor, MI                                 |
| 2010–2014    | <b>Postdoctoral Scholar</b> , Genetics<br>Stanford University, Stanford, CA; Advisor: Dr. Michael Snyder  |
| Spring 2010  | <b>Postdoctoral Associate</b> , Computational Biology<br>Duke University, Durham, NC; Advisor: Dr. Terrence S. Furey  |

## Scholarships, Fellowships, and Honors

|             |  |
|-------------|--|
| 2023        | University of Michigan 'Making a Difference' Award from Office for Health Equity & Inclusion |
| 2022        | Valuing our Own Award, Michigan Medicine   |
| 2019        | Endowment for the Basic Sciences Teaching Award  |
| 2018        | First Place in CAGI5 Regulation Saturation Challenge   |
| 2017        | NSF CAREER Award   |
| 2016        | Institutional nominee for W.M. Keck Foundation Medical Science Research Program              |
| 2016        | Institutional nominee for Searle Scholar Award   |
| 2015–2017   | Alfred P. Sloan Foundation Fellowship in Computational & Evolutionary Molecular Biology      |
| 2013–2014   | NIH Pathway to Independence Award (K99/R00) [1K99HG007356-01]                                |
| 2012        | AAAS/Science Program for Excellence in Science   |
| 2005–2008   | NSF Graduate Research Fellowship   |
| 2005–2009   | James B. Duke Fellowship   |
| Summer 2004 | Mayo Clinic Summer Undergraduate Research Fellow   |
| 2003        | Barry M. Goldwater Memorial Scholarship  |
| Summer 2003 | The Institute for Genomic Research (TIGR) Summer Fellow                                      |
| 2001        | Robert C. Byrd Honors Scholarship  |
| 2001        | Mississippi State University Presidential Scholarship  |
| 2001        | National Merit Scholarship   |

## Grant Support

### Active

|           |  |                                     |
|-----------|--|-------------------------------------|
| 2017–2025 | U24 HG009293<br>NIH/NHGRI<br>RegulomeDB: A Resource for the Human Regulome<br>This project seeks to expand and support a RegulomeDB, a database for prioritizing and predicting functional variants in the human genome.   | (Multi-PI: Boyle, Cherry)           |
| 2020–2023 | R21 HG011493<br>NIH/NHGRI<br>New technologies for accurate capture and sequencing of repeat-associated regions<br>This project seeks to map mobile elements in a trio of cell lines and develop technologies for improving this mapping.   | (Multi-PI: Boyle, Mills)            |
| 2022–2025 | R21 CA2578964<br>NIH/NCI<br>High-throughput inverted reporter assay for characterization of silencers and enhancer blockers<br>This project seeks to develop tools for the study of negative regulatory elements in cancer development.  | (PI: Boyle)                         |
| 2021–2026 | U01 HG011952<br>NIH/NHGRI<br>Predicting the impact of genomic variation on cellular states<br>This project seeks to develop tools for interpretation of genomic variation on cellular state through modeling single cell data as part of the IGVF consortium.                                | (PI: Boyle)                         |
| 2022–2026 | R01 GM144484<br>NIH/NIGMS<br>Mobile element derived chromatin looping variability in human populations<br>This project seeks to study the impact of polymorphic LTR13 integrations on 3D chromatin conformation.   | (PI: Boyle)                         |
| 2023–2028 | UG3 NS132084<br>NIH/OD<br>Molecular and Computational Tools for Identifying Somatic Mosaicism in Human Tissues<br>As part of the SMaHT consortium this project seeks to develop long-read methods to study somatic mosaicism in normal human tissues.  | (Multi-PI: Mills, Boyle, McConnell) |
| 2022–2024 | Taubman Institute Innovation Projects<br>University of Michigan<br>Short Tandem repeats in precision health and human disease<br>The goal of this project is to develop any assay to measure STRs in human genomes and develop bioinformatic tools to predict STR expansions from genotypes. | (co-PI: Todd, Boyle, Mills)         |
| 2018–2024 | R01 HD093570<br>NIH/NICHHD<br>Genetic Diagnosis of Neurodevelopmental Disorders in India<br>This study will establish whole-exome sequencing to study mendelian genetic disorders at the All India Institute of Medical Sciences.  | (PI: Bielas; Co-I with Effort)      |
| 2020–2023 | W81XWH2010336<br>DoD/Army<br>Understanding & Enhancing the Regenerative Capacity of Skeletal Muscle to Trauma by Targeting Muscle-Nerve Synergy<br>This project seeks to study the single cell chromatin and RNA landscape in skeletal muscle repair.  | (PI: Aguilar; Co-I with Effort)     |
| 2021–2026 | F32 HL153799<br>NIH/NHLBI<br>Predisposition for Lung Injury in Sepsis Survival<br>The goal of this project is to understand the biological mechanisms predisposing to these complications in order to prevent and treat them.  | (PI: Denstaedt; Consultant)         |

|           |   |                                 |
|-----------|---|---------------------------------|
| 2021–2026 | R01 HD104680<br>NIH/NICHD<br>Sperm Chromatin: Implications on organismal development and fertility<br>This project seeks to explore protamine chromatin structure in mouse sperm.   | (PI: Hammoud; Co-I with Effort) |
| 2021–2026 | R01 NS122165<br>NIH/NINDS<br>Uncover the role of H3.3-G343R mutation in shaping the DNA damage response, anti-tumor immunity and mechanisms of resistance in glioma<br>This project seeks to study pediatric high-grade gliomas with H3.3-G343R, ATRX, and TP53 inactivating mutations to understand the impact of H3.3-G343R on the tumor immune microenvironment. | (PI: Castro; Co-I with Effort)  |
| 2022–2026 | R01 CA260677<br>NIH/NCI<br>The Biology of Mutant STAT6 in Follicular Lymphoma<br>This project seeks to study STAT6 gene regulation in the context of B cell lymphoma.   | (PI: Malek; Co-I with Effort)   |
| 2023–2028 | R01 NS099280<br>NIH/NCI<br>Hexanucleotide repeat translation in ALS and Frontotemporal Dementia<br>This project seeks to study RAN translation in ALS and FTD at a hexonucleotide expansion in C9orf72.   | (PI: Todd; Consultant)          |
| 2022–2024 | Michigan Alzheimer's Disease Center Developmental Project<br>University of Michigan<br>Explore the functional impact of transposable elements in Alzheimer's disease and related dementias<br>This project seeks to explore the connection between the somatic transposable elements in the human genome and Alzheimer's disease and related dementias.             | (PI: Zhou; Consultant)          |

**Completed**

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|-----------|---|----------------------------------|
| 2013–2017 | R00 HG007356 Pathway to Independence Award (K99/R00)<br>NIH/NHGRI<br>Global Discovery and Validation of Functional Regulatory Elements<br>This project seeks to extend current assays demonstrating function of genomic regions into an equivalent genome-wide assay.   | (PI: Boyle)                      |
| 2015–2017 | FG-2015-65465<br>Alfred P. Sloan Foundation<br>Fellowship in Computational & Evolutionary Molecular Biology   | (PI: Boyle)                      |
| 2016–2020 | R01 HL130705<br>NIH/NHLBI<br>Large-scale human genetics to understand molecular mechanisms of atrial fibrillation and related traits<br>This project seeks to provide new insights into atrial fibrillation mechanisms through whole-genome screening.  | (PI: Willer; Co-I with Effort)   |
| 2017–2018 | Eleanor and Larry Jackier U-M/Technion and Weizmann Collaborative Research Grant<br>Michigan - Israel Partnership for Research & Education<br>Identifying novel disease related mutations in the genomic environments around Transcription Factor binding sites<br>The goal of this project is to identify variants in the proximity of TF binding sites that have an indirect effect on their binding. | (co-PI: Boyle, Mandel-Gutfreund) |
| 2017–2024 | R35 HL135824<br>NIH/NHLBI<br>Using Genetics to Inform Mechanism of Cardiovascular Disease   | (PI: Willer; Co-I with Effort)   |

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|-----------|---|-----------------------------|
|           | The goal of this project is to uncover novel genetic discoveries and biological mechanisms underlying association with devastating cardiovascular diseases.   |                             |
| 2019      | NVIDIA GPU Grant<br>NVIDIA Corporation  | (PI: Boyle)                 |
| 2017–2022 | DBI-1651614<br>NSF/BIO/DBI<br>CAREER: Conservation of cohesin-containing cis regulatory modules in the human and mouse lineages<br>The goal of this project is the study of the turnover of cohesin binding sites in the human and mouse genomes.   | (PI: Boyle)                 |
| 2022–2022 | R21 HG011493 S1<br>NIH/NIA<br>New technologies for accurate capture and sequencing of repeat-associated regions (Supplement)<br>This project seeks to map mobile elements in a set of Alzheimer's samples.  | (Multi-PI: Boyle, Mills)    |
| 2019–2022 | Precision Health Investigators Award<br>University of Michigan<br>Short Tandem repeats in precision health and human disease<br>The goal of this project is to develop any assay to measure STRs in human genomes and develop bioinformatic tools to predict STR expansions from genotypes. | (co-PI: Todd, Boyle, Mills) |
| 2022      | NVIDIA GPU Grant<br>NVIDIA Corporation  | (PI: Boyle)                 |
| 2021–2022 | Cancer Center Discovery<br>University of Michigan<br>Direct capture of complete HPV integration sites using long-read sequencing<br>This project seeks to develop methods to capture of complete HPV integration events in the human genome.  | (PI: Boyle)                 |

## Professional Service

### Service

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|--------------|--|
| 2021–current | Impact of Genomic Variation on Function (IGVF) Consortium Steering Committee |
| 2022–current | University of Michigan Biomedical Research Council (BMRC) (Standing Member)  |
| 2020–2022    | DHG M.S. Admissions Committee  |
| 2018–current | DCM&B Diversity, Equity, & Inclusion Committee [Ally/Chair 2018–2020]        |
| 2018–current | Lab Safety Liaison for DCM&B   |
| 2017–current | DCM&B Preliminary Exam Abstract Review Committee (PARC) [Chair 2018–2022]    |
| 2019–2020    | DHG Ph.D. Admissions Committee   |
| 2017–2020    | DHG Faculty Recruitment and Promotions Committee                             |
| 2016–2020    | DCM&B Seminar Series Committee [Chair]                                       |
| 2018–2019    | Cellular and Molecular Biology Admissions Committee                          |
| 2017–2019    | EBS Faculty IT Committee   |
| 2016–2019    | DCM&B Faculty Recruitment Committee  |
| 2015–2018    | DCM&B Admissions Committee   |
| 2015–2017    | DHG Computational Support Committee  |
| 2015–2016    | DCM&B Retreat Planning Committee Chair (including 1st annual)                |
| 2014         | <i>Ad hoc</i> admissions reviewer, University of Michigan DCM&B              |
| 2008–2009    | Duke Computational Biology & Bioinformatics student committee                |

### Memberships

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|--------------|--|
| 2018–current | Member, American Society of Human Genetics (ASHG)                  |
| 2013–current | Member, International Society for Computational Biology (ISCB)     |
| 2012–current | Member, American Association for the Advancement of Science (AAAS) |
| 2005–current | Member, Gamma Sigma Delta Agricultural Honor Society               |

## Manuscript Reviewing Activity

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| Since 2009 | <i>Ad hoc</i> reviewer (>100 verified reviews) for the journals: <i>Science</i> , <i>Nature Biotechnology</i> , <i>Nature Genetics</i> , <i>Genome Research</i> , <i>Genome Biology</i> , <i>Nature Neuroscience</i> , <i>Nature Communications</i> , <i>Nature Protocols</i> , <i>Bioinformatics</i> , <i>Nucleic Acids Research</i> , <i>BMC Biology</i> , <i>BMC Bioinformatics</i> , <i>PLOS Computational Biology</i> , <i>Oncotarget</i> , <i>Scientific Reports</i> , <i>Atherosclerosis</i> , <i>BioEssays</i> , <i>Gene</i> |
| 2023       | Program Committee, Genome Sequence Analysis, ISMB/ECCB   |
| 2023       | Program Committee, Biomedical Informatics, ISMB/ECCB   |
| 2018, 2020 | Program Committee, Comparative and Functional Genomics, ISMB/ECCB  |
| 2018, 2019 | Program Committee, Studies of Phenotypes and Clinical Applications, ISMB/ECCB  |
| 2019       | Program Committee, General Computational Biology, ISMB/ECCB  |
| 2017       | Program Committee, Regulatory Genomics Special Interest Group Meeting (RegGenSIG), ISMB/ECCB   |
| 2015–2018  | Program Committee, Great Lakes Bioinformatics and Canadian Computational Biology Conference (GLBIO/CCBC)   |
| 2015–2016  | Program Committee, Algorithms for Computational Biology (ALCOB)  |
| 2013–2016  | Program Committee, Gene Regulation and Transcriptomics, ISMB/ECCB  |
| 2012–2015  | DNA Day Essay Contest Detailed Review Judge for ASHG   |
| 2012       | Distinguished contributor as a leading reviewer for the journal <i>Bioinformatics</i>  |

## Grant Reviewing Activity

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|-----------|--|
| 2023      | NSF Review Panel - Molecular and Cellular Biosciences (MCB) - Genetic Mechanisms (Ad Hoc)  |
| 2023      | NIH Study Section - Multi-Omics of Health and Disease – Data Analysis and Coordination Center  |
| 2023      | NIH Study Section GVE - Genetic Variation and Evolution Study Section (Ad Hoc)   |
| 2022      | NIH Study Section ZRG1 ISB-S (57) - Academic-Industrial Partnerships for Translation of Technologies for Diagnosis and Treatment                                   |
| 2022      | NASA Study Section E.11 Space Biology: Animal Studies - Omics Systems [21SBAS-OmisSys] (Ad Hoc)  |
| 2020      | NIH/NIMH Study Section ZMH1 ERB-C (08) - Fine-Mapping Genome-Wide Associated Loci to Identify Proximate Causal Mechanisms of Serious Mental Illness                |
| 2019      | NIH/NIMH Study Section ZMH1 ERB-C (01) - PsychENCODE: Non-Coding Functional Elements in the Human Brain and Their Role in the Development of Psychiatric Disorders |
| 2018–2019 | University of Michigan internal review for Searle Scholars Program   |
| 2015      | UK Medical Research Council (RCUK MRC) - Methodology Research Panel (Ad Hoc)   |
| 2015      | UK Biotechnology and Biological Sciences Research Council (RCUK BBSRC) (Ad Hoc)  |
| 2015      | Michigan Institute for Clinical & Health Research (MICHR) Postdoctoral Translational Scholars Program (Ad Hoc)   |

## Teaching and Mentorship

### Teaching (F = Fall Term, W = Winter Term, S = Summer Term)

|                                   |   |
|-----------------------------------|---|
| W19, W20, W21, W22, W23           | Bioinformatics Concepts and Algorithms (BIOINF 529) [Course Director]                           |
| F15, F16, F17, F18, F19, F20, F21 | Gene Structure and Regulation (HUMGEN 541) [3 lectures + 2 discussions / yr.]                   |
| F19, F22                          | Research Responsibility and Ethics (PIBS 503) [1 discussion / yr.]                              |
| F21, W22                          | Genetics Student Seminar (HUMGEN 821/822) [Mentor]  |
| F17, F18                          | Experimental Genetics Systems (HUMGEN 632) [Course Director]                                    |
| F15, W16, F16, W17, F17, W18, F18 | Bioinformatics Journal Club (BIOINF 602/603) [Course Director F18]                              |
| S17, S18                          | Introduction to Biocomputing Bootcamp (BIOSTAT/BIOINF/HUMGEN 606) [2 full days / yr.]           |
| F15, F16, F17                     | Introduction to Bioinformatics & Computational Biology (BIOINF 527) [2 lectures + 3 labs / yr.] |
| S15, S16, S17                     | Basic Biology for Graduate Students with Quantitative Training (BIOINF 523) [2 lectures / yr.]  |
| F03                               | Lab TA for Isotopes Tech I (MS. State, BCH 4414)  |

### Guest Lectures / Panels

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|-----------|---|
| 2018–2019 | Lecturer, REU Site: Mathematical and Theoretical Biology Institute (MTBI), Arizona State University (NSF1757968) [2 days] |
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| 2017 | Panel member, U. Michigan “New Faculty Orientation to Corporate & Foundation Relations” [ 70 attendees] |
| 2016 | Experimental Genetics Systems (HUMGEN 632) [1 discussion]   |
| 2014 | Panel member, BIOINF 527 “Challenges in Biology, Biomedicine, Data & Analysis”                          |
| 2010 | Co-taught Cold Spring Harbor Systems Biology Pre-meeting Workshop                                       |
| 2009 | Duke student panelist for “How to prepare for and get into graduate school”                             |
| 2008 | Taught Duke mini-course on Genome Browsers & Databases  |

## Mentorship

### Graduate Students

|              |   |
|--------------|---|
| 2023–current | Zongrui Dai (M.S. Student, Bioinformatics, University of Michigan)  |
| 2023–current | Xinyi Liu (M.S. Student, Bioinformatics, University of Michigan)  |
| 2022–current | Emily Pogson (Ph.D. Student, Genetics and Genomics, University of Michigan)   |
| 2022–current | Katarina Pavlovic (Ph.D. Student, Bioinformatics, University of Michigan)   |
| 2022–current | Rintsen Sherpa (Ph.D. Student, Bioinformatics, University of Michigan)  |
| 2021–current | Kinsey Van Deynze (Ph.D. Student, Bioinformatics, University of Michigan)<br><i>NIH Genome Science Training Program (T32)</i><br><i>Rackham Graduate Student Research Grant (pre-candidate)</i>   |
| 2020–current | Andrea Valenzuela (Ph.D. Student, Chemical Biology, University of Michigan)<br><i>NIH Cellular Biotechnology Training Program (T32)</i>   |
| 2020–current | Breanna McBean (Ph.D. Student, Genetics and Genomics, University of Michigan)<br><i>Joint M.S. in Bioinformatics, University of Michigan</i><br><i>NIH Genome Science Training Program (T32)</i><br><i>Rackham Graduate Student Research Grant (pre-candidate)</i><br><i>Rackham Graduate Student Research Grant (candidate)</i>  |
| 2019–2020    | Monica Holmes (M.S. Student, Bioinformatics, University of Michigan)  |
| 2020–current | Camille Mumm (Ph.D. Student, Genetics and Genomics, University of Michigan)<br><i>Joint M.S. in Bioinformatics, University of Michigan</i><br><i>NIH Genome Science Training Program (T32)</i><br><i>Rackham Graduate Student Research Grant (pre-candidate)</i>  |
| 2018–current | Bradley Crone (Ph.D. Student, Bioinformatics, University of Michigan)<br><i>Rackham Graduate Student Research Grant (candidate)</i>   |
| 2017–2023    | Melissa Englund (Ph.D. Student, Genetics and Genomics, University of Michigan)<br><i>NIH Human Genetics Training Program (T32)</i><br><i>Rackham Graduate Student Research Grant (candidate)</i>  |
| 2018–2023    | Nanxiang (Samuel) Zhao (Ph.D. Student, Bioinformatics, University of Michigan)  |
| 2017–2018    | Nanxiang (Samuel) Zhao (M.S. Student, Bioinformatics, University of Michigan)<br><i>Rackham Graduate Student Research Grant (pre-candidate)</i><br><i>Rackham Graduate Student Research Grant (candidate)</i>   |
| 2016–2018    | Haley Amemiya (Ph.D. Student, Cellular and Molecular Biology, University of Michigan)<br><i>Joint M.S. in Bioinformatics, University of Michigan</i><br><i>NIH Cellular &amp; Molecular Biology Training Program (T32)</i><br><i>NIH Cellular Biotechnology Training Program (T32) (Declined)</i><br><i>PIBS Excellence in Service Award</i><br><i>Rackham Graduate Student Research Grant (pre-candidate)</i><br><i>Rackham Graduate Student Research Grant (candidate)</i><br><i>Maas Professional Development Award</i><br><i>Rackham Graduate School Scholar-Activist Award</i> |
| 2016–2020    | Shriya Sethuraman (Ph.D. Student, Bioinformatics, University of Michigan)   |

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| 2016–2023 | Christopher Castro (Ph.D. Student, Bioinformatics, University of Michigan)<br><i>NIH Bioinformatics Training Program (T32)</i><br><i>Rackham Merit Fellow</i><br><i>Rackham Graduate Student Research Grant (pre-candidate)</i><br><i>Rackham Graduate Student Research Grant (candidate)</i><br><i>Global Research Engagement Opportunity Fellowship</i> |
| 2017–2022 | Ningxin Ouyang (Ph.D. Student, Bioinformatics, University of Michigan)  |
| 2015–2017 | Ningxin Ouyang (M.S. Student, Bioinformatics, University of Michigan)<br><i>Rackham Graduate Student Research Grant (candidate)</i>   |
| 2016–2021 | Shengcheng Dong (Ph.D. Student, Bioinformatics, University of Michigan)<br><i>Rackham Graduate Student Research Grant (candidate)</i>   |
| 2015–2021 | Torrin McDonald (Ph.D. Student, Genetics and Genomics, University of Michigan)<br><i>NIH Human Genetics Training Program (T32)</i><br><i>Rackham Graduate Student Research Grant (pre-candidate)</i><br><i>Rackham Graduate Student Research Grant (candidate)</i>  |
| 2015–2017 | Greg Farnum (Ph.D. Student, Cellular and Molecular Biology, University of Michigan)   |
| 2015–2020 | Sierra Nishizaki (Ph.D. Student, Genetics and Genomics, University of Michigan)<br><i>Joint M.S. in Bioinformatics, University of Michigan</i><br><i>NIH Genome Science Training Program (T32)</i><br><i>Rackham Merit Fellow</i><br><i>Rackham Summer Award</i><br><i>Rackham Graduate Student Research Grant (candidate)</i>                            |

### Additional Graduate Rotation Students

|      |   |
|------|---|
| 2022 | Brandt Bessell (Rotation Student, Bioinformatics, University of Michigan)                     |
| 2022 | Xiaomeng Du (Rotation Student, Bioinformatics, University of Michigan)                        |
| 2022 | Mahnoor Gondal (Rotation Student, Bioinformatics, University of Michigan)                     |
| 2022 | Xin Li (Rotation Student, Biological Chemistry, University of Michigan)                       |
| 2022 | Bohan Chen (Rotation Student, Cell and Developmental Biology, University of Michigan)         |
| 2021 | Amelia Lauth (Rotation Student, Cellular and Molecular Biology, University of Michigan)       |
| 2019 | Margarita Brovkina (Rotation Student, Cellular and Molecular Biology, University of Michigan) |
| 2018 | Steve Ho (Rotation Student, Human Genetics, University of Michigan)                           |
| 2018 | Matthew Pun (Rotation Student, Medical Science Training Program, University of Michigan)      |
| 2017 | Amanda Moccia (Rotation Student, Human Genetics, University of Michigan)                      |
| 2017 | Stephen Carney (Rotation Student, Human Genetics, University of Michigan)                     |
| 2016 | Tingyang Li (Rotation Student, Bioinformatics, University of Michigan)                        |

### Postdoctoral Fellows

|              |  |
|--------------|--|
| 2023–current | Melissa Englund (University of Michigan) |
| 2022–current | Torrin McDonald (University of Michigan) |
| 2021–2022    | Shengcheng Dong (University of Michigan) |

### Non-student Lab Volunteers

|           |   |
|-----------|---|
| 2019–2021 | Greg Farnum (University of Michigan)            |
| 2018–2019 | Monica Holmes (Postbac, University of Michigan) |

### Undergraduate and High School Students

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|--------------|--|
| 2022–current | Summer Ann (Undergraduate, Neuroscience, University of Michigan)   |
| 2022–current | Kobe Howcroft (Undergraduate, Computer Science, University of Michigan)  |
| 2021–current | Preston Parana (Undergraduate, UROP Molecular, Cellular, and Developmental Biology, University of Michigan)<br><i>UROP Blue Ribbon Award</i> |

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|-----------|---|
| 2021–2022 | Julia Tweadey (Undergraduate, LSA Honors Program, Life Science Informatics, University of Michigan)                                       |
| 2021      | Aryn Booker (Undergraduate, UROP Molecular, Cellular, and Developmental Biology, University of Michigan)<br><i>UROP Blue Ribbon Award</i> |
| 2020      | Marcela Alcaide Aligio (Undergraduate, SROP, Hunter College CUNY)   |
| 2019–2020 | David Wang (Undergraduate, UROP Computer Science, University of Michigan)   |
| 2019–2020 | Jack Lu (Undergraduate, UROP Computer Science, University of Michigan)  |
| 2019–2020 | Diana Davis (Undergraduate, Neuroscience and German, University of Michigan)  |
| 2019      | Sheila Rasouli (Undergraduate, Neuroscience, University of Toronto)   |
| 2019      | Vibhasri Davuluri (High School, Girls Who Code Summer Intern)   |
| 2016–2019 | Cody Morterud (Undergraduate, UROP Computer Science / Honors Capstone, University of Michigan)  |
| 2016–2017 | Colten Williams (Undergraduate, UROP Computer Science, University of Michigan)  |
| 2016–2017 | Courtney Asman (Undergraduate, Neuroscience, University of Michigan)  |
| 2014–2017 | Maxwell Spadafore (Undergraduate, LS&A Honors Informatics, University of Michigan)  |
| 2013–2014 | Natalie Ng (High School, Stanford Institutes of Medicine Summer Research)   |
| 2013–2014 | Dana Wyman (Undergraduate, Biology, Stanford University)  |
| 2013      | Justin Young (High School, Stanford Institutes of Medicine Summer Research)   |
| 2012      | Melanie Connick (Undergraduate, Biology, University of New Mexico)  |
| 2012      | Edward Dai (Undergraduate, Computer Science, Stanford University)   |

## Doctoral Thesis Committees

|              |   |
|--------------|---|
| 2022–current | Kaiwen Deng (Bioinformatics, University of Michigan, Committee Member)  |
| 2022–current | Emily Peirent (Neuroscience, University of Michigan, Committee Member)  |
| 2022–current | Franco Tavella (Biophysics, University of Michigan, Committee Member)   |
| 2021–current | Zijun Gao (Bioinformatics, University of Michigan, Committee Member)  |
| 2021–current | Wenjin Gu (Bioinformatics, University of Michigan, Committee Member)  |
| 2021–current | Kinsey Van Deynze (Bioinformatics, University of Michigan, Chair)   |
| 2021–current | Mashiat Rabbani (Human Genetics, University of Michigan, Committee Member)  |
| 2020–current | Andrea Valenzuela (Chemical Biology, University of Michigan, co-Chair)  |
| 2020–current | Breanna McBean (Human Genetics, University of Michigan, co-Chair)   |
| 2020–current | Camille Mumm (Human Genetics, University of Michigan, Chair)  |
| 2018–current | Rucheng Diao (Bioinformatics, University of Michigan, Committee Member)   |
| 2018–current | Bradley Crone (Bioinformatics, University of Michigan, Chair)   |
| 2018–2023    | Nanxiang (Samuel) Zhao (Bioinformatics, University of Michigan, Chair)<br><i>Decoding Regulatory Variants with Computational Methods in Non-coding Regions of the Human Genome</i>                                      |
| 2020–2023    | Ashley Melnick (Cellular and Molecular Biology, University of Michigan, Committee Member)<br><i>Cdc73 Protects Notch-Induced Leukemia Cells From DNA Damage and Mitochondrial Stress</i>                                |
| 2016–2023    | Christopher Castro (Bioinformatics, University of Michigan, Chair)<br><i>Investigating the Role of Noncoding De Novo Single-Nucleotide Variants in Autism Spectrum Disorder</i>   |
| 2017–2023    | Melissa Englund (Human Genetics, University of Michigan, Chair)<br><i>Identification and Characterization of Cis-Regulatory Elements in the Human Genome</i>  |
| 2018–2023    | Stephen Carney (Cancer Biology, University of Michigan, Committee Member)<br><i>Epigenetic reprogramming in mutant IDH1 glioma influences radioresistance and neural lineage differentiation</i>                        |
| 2019–2023    | Benjamin Yang (Biomedical Engineering, University of Michigan, Committee Member)<br><i>Towards Defining Principles of Cell Fate Plasticity</i>  |
| 2018–2022    | Marcus Sherman (Bioinformatics, University of Michigan, Committee Member)<br><i>Cultivation of enhanced bioinformatic-specific pedagogical manipulatives, interventions, and professional development</i>               |
| 2021–2022    | Kuan-Han Hank Wu (Bioinformatics, University of Michigan, Committee Member)<br><i>Integrating Electronic Health Records with Genetic Information to Advance Precision Medicine Approaches in Cardiovascular Disease</i> |
| 2017–2022    | Amanda Moccia (Human Genetics, University of Michigan, Committee Member)  |



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|-----------|---|
| 2017–2022 | <i>Investigation of Developmental Disorders: Genetic Discovery and Functional Validation</i><br>Ningxin Ouyang (Bioinformatics, University of Michigan, Chair)<br><i>Deciphering Transcriptional Regulatory Circuits: Transcription Factor Binding and Regulatory Variants Identification</i> |
| 2015–2021 | Torrin McDonald (Human Genetics, University of Michigan, Chair)<br><i>Leveraging New Technologies to Explore Regulatory and Structural Elements of the Human Genome</i>   |
| 2018–2021 | Heming Yao (Bioinformatics, University of Michigan, Committee Member)<br><i>Machine Learning and Image Processing for Clinical Outcome Prediction: Applications in Medical Data from Patients with Traumatic Brain Injury, Ulcerative Colitis, and Heart Failure</i>                          |
| 2016–2021 | Mohd Hafiz Bin Mohd Rothi (Molecular, Cellular, and Developmental Biology, University of Michigan, Committee Member)<br><i>Control of Chromatin by RNA-mediated Transcriptional Silencing</i>   |
| 2016–2021 | Shengcheng Dong (Bioinformatics, University of Michigan, Chair)<br><i>Computational Methods to Identify Regulatory Variants in the Non-coding Regions of the Human Genome</i>   |
| 2017–2021 | Steven Romanelli (Molecular & Integrative Physiology, University of Michigan, Committee Member)<br><i>Viral CRISPR/Cas9 Gene Transfer for Somatic Knockout in Brown Adipose Tissue</i>  |
| 2018–2021 | Negar Farzaneh (Bioinformatics, University of Michigan, Committee Member)<br><i>Automated Decision Support System for Traumatic Injuries</i>  |
| 2016–2020 | Shriya Sethuraman (Bioinformatics, University of Michigan, co-Chair)<br><i>Genome-wide Identification of Non-coding Transcription by RNA Polymerase V and Its Involvement in Transcriptional Gene Silencing</i>   |
| 2015–2020 | Sierra Nishizaki (Human Genetics, University of Michigan, Chair)<br><i>Decoding the Non-coding Genome: Novel Technologies for the Characterization of Non-coding Elements and Variation</i>   |
| 2017–2020 | Christopher Lee (Biostatistics, University of Michigan, Committee Member)<br><i>Improvements and Developments in Gene Regulation and Single-Cell Gene Expression Data Analysis</i>  |
| 2018–2019 | Christine Ziegler (Biological Chemistry, University of Michigan, Committee Member)  |
| 2015–2018 | Ari Allyn-Feuer (Bioinformatics, University of Michigan, Committee Member)<br><i>The Pharmacoepigenomics Informatics Pipeline and H-GREEN Hi-C Compiler: Discovering Pharmacogenomic Variants and Pathways with the Epigenome and Spatial Genome</i>  |
| 2015–2017 | Raymond Cavalcante (Bioinformatics, University of Michigan, Committee Member)<br><i>Beyond the Transcriptome: Facilitating Interpretation of Epigenomics and Metabolomics Data</i>  |
| 2015–2017 | Zhengting Zou (Bioinformatics, University of Michigan, Committee Member)<br><i>Model-based genomic studies of protein sequence evolution: convergence, epistasis, and amino acid acceptance rates</i>   |

### Preliminary Exam Committees

|      |   |
|------|---|
| 2023 | Elysia Chou (Bioinformatics, University of Michigan)                    |
| 2022 | Sean Moran (Bioinformatics, University of Michigan)                     |
| 2022 | Lu Lu (Bioinformatics, University of Michigan)                          |
| 2022 | Linghua Jiang (Bioinformatics, University of Michigan)                  |
| 2022 | Kaiwen Deng (Bioinformatics, University of Michigan)                    |
| 2022 | Yufeng Zhang (Bioinformatics, University of Michigan)                   |
| 2021 | Anthony Nguyen (Human Genetics, University of Michigan)                 |
| 2021 | Hanbyul Cho (Bioinformatics, University of Michigan)                    |
| 2021 | Charles Ryan (Cellular and Molecular Biology, University of Michigan)   |
| 2021 | Kuan-Han Wu (Bioinformatics, University of Michigan)                    |
| 2021 | Wenjin Gu (Bioinformatics, University of Michigan)                      |
| 2020 | Jie Cao (Bioinformatics, University of Michigan)                        |
| 2020 | Zijun Gao (Bioinformatics, University of Michigan)                      |
| 2020 | Ashley Melnick (Cellular and Molecular Biology, University of Michigan) |
| 2019 | Benjamin Yang (Biomedical Engineering, University of Michigan)          |

|      |   |
|------|---|
| 2019 | Maria Virgilio (Cellular and Molecular Biology, University of Michigan) |
| 2018 | Zhi Carrie Li (Bioinformatics, University of Michigan)                  |
| 2018 | Kevin Hu (Bioinformatics, University of Michigan)                       |
| 2018 | Siyu Liu (Bioinformatics, University of Michigan)                       |
| 2018 | Alexandra Weber (Bioinformatics, University of Michigan)                |
| 2018 | Mitch Fernandez (Bioinformatics, University of Michigan)                |
| 2017 | Tingyang Li (Bioinformatics, University of Michigan)                    |
| 2017 | Marcus Sherman (Bioinformatics, University of Michigan)                 |
| 2017 | Adrienne Shami (Human Genetics, University of Michigan)                 |
| 2017 | Trenton Frisbie (Human Genetics, University of Michigan)                |
| 2017 | Melissa Englund (Human Genetics, University of Michigan)                |
| 2017 | Peter Orchard (Bioinformatics, University of Michigan)                  |
| 2017 | Li Guan (Bioinformatics, University of Michigan)                        |
| 2016 | Shriya Sethuraman (Bioinformatics, University of Michigan)              |
| 2016 | Jed Carlson (Bioinformatics, University of Michigan)                    |

## Industry Experience

|           |  |
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| 2013–2014 | Consultant, Color Genomics<br>Personalized medicine / genomics startup |
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## Publications

\* Indicates co-first authorship † Indicates co-senior authorship  
underscore indicates lab members

- [1] McAfee JC, Lee S, Lee J, Bell JL, Krupa O, Davis J, Insigne K, Bond ML, Zhao N, **Boyle AP**, Phanstiel DH, Love MI, Stein JL, Ruzicka WB, Davila-Velderrain J, Kosuri S, Won H. “Systematic investigation of allelic regulatory activity of schizophrenia-associated common variants.” *medRxiv* 2023.
- [2] Yee C, Xiao Y, Chen H, Reddy A, Xu R, Medwig-Kinney T, Zhang W, **Boyle AP**, Xiang YK, Matus DQ, Shen K. “EGL-43 and FOS-1 directly activate synaptic genes and coordinate mRNA export with transcription.” *submitted* 2023.
- [3] Zhao N, Wang S, Huang Q, Dong S, **Boyle AP**. “Explain-seq: an end-to-end pipeline from training to interpretation of sequence-based deep learning models.” *bioRxiv* 2023.
- [4] Holmes MJ, Mahjour B, Castro CP, Farnum GA, Diehl AG, **Boyle AP**. “LRphase: an efficient method for assigning haplotype identity to long reads.” *bioRxiv* 2023.
- [5] Ouyang N, **Boyle AP**. “Quantitative assessment of association between noncoding variants and transcription factor binding.” *bioRxiv* 2022.
- [6] Rothi MH, Sethuraman S, Dolata J, **Boyle AP**, Wierzbicki AT. “DNA methylation directs nucleosome positioning in RNA-mediated transcriptional silencing.” *bioRxiv* 2020.
- [7] Castro CP, Diehl AG, **Boyle AP**. “Challenges in screening for de novo noncoding variants contributing to genetically complex phenotypes.” *Accepted, Human Genetics and Genomics Advances* 2022.
- [8] Moritz L, Schon SB, Rabbani M, Sheng Y, Pendlebury DF, Agrawal R, Sultan C, Jorgensen K, Zheng X, Diehl AG, Ragunathan K, Hu YC, Nandakumar J, Li JZ, **Boyle AP**, Orwig KE, Redding S, Hammoud SS. “Single residue substitution in protamine 1 disrupts sperm genome packaging and embryonic development in mice.” *Accepted, Nature Structural & Molecular Biology* 2023.
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- [11] Nishizaki SS, **Boyle AP**. “SEMplMe: A tool for integrating DNA methylation effects in transcription factor binding affinity predictions.” *BMC Bioinformatics* 2022, 23:317. PMID: 35927613.

- [12] Qin T, Lee C, Li S, Cavalcante RG, Orchard P, Yao H, Zhang H, Wang S, Patil S, **Boyle AP**, Sartor MA. “Comprehensive enhancer-target gene assignments improve gene set level interpretation of genome-wide regulatory data.” *Genome Biology* 2022, 23:105. PMID: 35473573.
- [13] Bao Y, Wadden J, Erb-Downward JR, Ranjan P, Zhou W, McDonald TL, Mills RE, **Boyle AP**, Dickson RP, Blaauw D, Welch JD. “SquiggleNet: real-time, direct classification of nanopore signals.” *Genome Biology* 2021, 22:298. PMID: 34706748.
- [14] Dong S, **Boyle AP**. “Prioritization of regulatory variants with tissue-specific function in the non-coding regions of human genome.” *Nucleic Acids Research* 2021, 50:e6–e6. PMID: 34648033.
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## Patents

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