2017 Palmer Commons
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www.BoyleLab.org

Alan P. Boyle

Education

2005–2009 **Doctor of Philosophy,** Computational Biology and Bioinformatics
Duke University, Durham, NC

2001–2005 **Bachelor of Science,** *summa cum laude,* Biochemistry and Molecular Biology
Bachelor of Science, *summa cum laude,* Computer Science
Mississippi State University, Starkville, MS

Academic Appointments

2020–present **Associate Professor with tenure,** Department of Computational Medicine & Bioinformatics
Associate Professor, Department of Human Genetics
2021–present **Affiliate,** Michigan Neuroscience Institute
2020–present **Affiliate Member,** Rogel Cancer Center
2017–present **Member,** Cellular and Molecular Biology Program
2016–present **Member,** Center for RNA Biomedicine
2015–present **Member,** Genome Science Training Program (GSTP)
Member, Michigan Predoctoral Training Program in Genetics (GTP)
2014–present **Member,** Program in Biomedical Sciences
Member, Bioinformatics Training Program
2015–2020 **Assistant Professor,** Department of Human Genetics
2014–2020 **Assistant Professor,** Department of Computational Medicine & Bioinformatics
University of Michigan, Ann Arbor, MI

2010–2014 **Postdoctoral Scholar,** Genetics
Stanford University, Stanford, CA; Advisor: Dr. Michael Snyder

Spring 2010 **Postdoctoral Associate,** Computational Biology
Duke University, Durham, NC; Advisor: Dr. Terrence S. Furey

Scholarships, Fellowships, and Honors

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 (Multi-PI: Boyle, Cherry)
NIH/NHGRI
RegulomeDB: A Resource for the Human Regulome
This project seeks to expand and support a RegulomeDB, a database for prioritizing and predicting functional variants in the human genome.

2020–2022 R21 HG011493 (Multi-PI: Boyle, Mills)
NIH/NHGRI
New technologies for accurate capture and sequencing of repeat-associated regions
This project seeks to map mobile elements in a trio of cell lines and develop technologies for improving this mapping.

2022–2022 R21 HG011493 S1 (Multi-PI: Boyle, Mills)
NIH/NIA
New technologies for accurate capture and sequencing of repeat-associated regions (Supplement)
This project seeks to map mobile elements in a set of Alzheimer's samples.

2022–2025 R21 CA2578964 (PI: Boyle)
NIH/NCI
High-throughput inverted reporter assay for characterization of silencers and enhancer blockers
This project seeks to develop tools for the study of negative regulatory elements in cancer development.

2021–2026 U01 HG011952 (PI: Boyle)
NIH/NHGRI
Predicting the impact of genomic variation on cellular states
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.

2019–2024 Precision Health Investigators Award (co-PI: Todd, Boyle, Mills)
University of Michigan
Short Tandem repeats in precision health and human disease
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.

2021–2022 Cancer Center Discovery (PI: Boyle)
University of Michigan
Direct capture of complete HPV integration sites using long-read sequencing
This project seeks to develop methods to capture of complete HPV integration events in the human genome.

2022 NVIDIA GPU Grant (PI: Boyle)
NVIDIA Corporation

2018–2023 R01 HD093570 (PI: Bielas; Co-I with Effort)
NIH/NICHD
Genetic Diagnosis of Neurodevelopmental Disorders in India
This study will establish whole-exome sequencing to study mendelian genetic disorders at the All India Institute of Medical Sciences.

2020–2023 W81XWH2010336 (PI: Aguilar; Co-I with Effort)
DoD/Army
Understanding & Enhancing the Regenerative Capacity of Skeletal Muscle to Trauma by Targeting Muscle-Nerve Synergy
This project seeks to study the single cell chromatin and RNA landscape in skeletal muscle repair.

2021–2026 F32 HL153799 (PI: Denstaedt; Consultant)
NIH/NHLBI
Predisposition for Lung Injury in Sepsis Survival
The goal of this project is to understand the biological mechanisms predisposing to these complications in order to prevent and treat them.

2021–2026 | R01 HD104680 (PI: Hammoud; Co-I with Effort)
NIH/NICHD
Sperm Chromatin: Implications on organismal development and fertility
This project seeks to explore protamine chromatin structure in mouse sperm.

2021–2026 | R01 NS122165 (PI: Castro; Co-I with Effort)
NIH/NINDS
Uncover the role of H3.3-G343R mutation in shaping the DNA damage response, anti-tumor immunity and mechanisms of resistance in glioma
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.

2022–2024 | Michigan Alzheimer's Disease Center Developmental Project (PI: Zhou; Consultant)
University of Michigan
Explore the functional impact of transposable elements in Alzheimer's disease and related dementias
This project seeks to explore the connection between the somatic transposable elements in the human genome and Alzheimer's disease and related dementias.

Completed

2013–2017 | R00 HG007356 Pathway to Independence Award (K99/R00) (PI: Boyle)
NIH/NHGRI
Global Discovery and Validation of Functional Regulatory Elements
This project seeks to extend current assays demonstrating function of genomic regions into an equivalent genome-wide assay.

2015–2017 | FG-2015-65465 (PI: Boyle)
Alfred P. Sloan Foundation
Fellowship in Computational & Evolutionary Molecular Biology

2016–2020 | R01 HL130705 (PI: Willer; Co-I with Effort)
NIH/NHLBI
Large-scale human genetics to understand molecular mechanisms of atrial fibrillation and related traits
This project seeks to provide new insights into atrial fibrillation mechanisms through whole-genome screening.

2017–2018 | Eleanor and Larry Jackier U-M/Technion and Weizmann Collaborative Research Grant
(co-PI: Boyle, Mandel-Gutfreund)
Michigan - Israel Partnership for Research & Education
Identifying novel disease related mutations in the genomic environments around Trascription Factor binding sites
The goal of this project is to identify variants in the proximity of TF binding sites that have an indirect effect on their binding.

2017–2024 | R35 HL135824 (PI: Willer; Co-I with Effort)
NIH/NHLBI
Using Genetics to Inform Mechanism of Cardiovascular Disease
The goal of this project is to uncover novel genetic discoveries and biological mechanisms underlying association with devastating cardiovascular diseases.

2019 | NVIDIA GPU Grant (PI: Boyle)
NVIDIA Corporation

2017–2022 | DBI-1651614 (PI: Boyle)
NSF/BIO/DBI
CAREER: Conservation of cohesin-containing cis regulatory modules in the human and mouse lineages
The goal of this project is the study of the turnover of cohesin binding sites in the human and mouse genomes.

Professional Service

Service

2022–current	University of Michigan Biomedical Research Council (BMRC) (Standing Member)
2020–current	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 Planing Committee Chair (including 1st annual)
2014	*Ad hoc* admissions reviewer, University of Michigan DCM&B
2008–2009	Duke Computational Biology & Bioinformatics student committee

Memberships

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

Since 2009	*Ad hoc* reviewer (>100 verified reviews) for the journals: *Science*, *Nature Genetics*, *Genome Research*, *Genome Biology*, *Nature Neuroscience*, *Nature Communications*, *Nature Protocols*, *Bioinformatics*, *Nucleic Acids Research*, *BMC Biology*, *BMC Bioinformatics*, *PLOS Computational Biology*, *Oncotarget*, *Scientific Reports*, *Atherosclerosis*, *BioEssays*, *Gene*
2019–current	Editorial Board, PLoS ONE
2019–current	Review Editor, Bioinformatics and Computational Biology for Frontiers in Genetics
2019–current	Review Editor, Bioinformatics and Computational Biology for Frontiers in Plant Science
2019–current	Review Editor, Bioinformatics and Computational Biology for Frontiers in Bioengineering and Biotechnology
2019	Program Committee, Studies of Phenotypes and Clinical Applications, 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–current	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 *Bioinformatics*

Grant Reviewing Activity

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 | 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.]

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

2018–2019 | Lecturer, REU Site: Mathematical and Theoretical Biology Institute (MTBI), Arizona State University (NSF1757968) [2 days]

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

2021–current | Kinsey Van Deynze (Ph.D. Student, Bioinformatics, University of Michigan)
NIH Genome Science Training Program (T32)
Rackham Graduate Student Research Grant (pre-candidate)

2020–current | Andrea Valenzuela (Ph.D. Student, Chemical Biology, University of Michigan)
NIH Cellular Biotechnology Training Program (T32)

2020–current | Breanna McBean (Ph.D. Student, Human Genetics, University of Michigan)
Joint M.S. in Bioinformatics, University of Michigan
NIH Genome Science Training Program (T32)
Rackham Graduate Student Research Grant (pre-candidate)

2019–2020 | Monica Holmes (M.S. Student, Bioinformatics, University of Michigan)

2020–current | Camille Mumm (Ph.D. Student, Human Genetics, University of Michigan)
Joint M.S. in Bioinformatics, University of Michigan
NIH Genome Science Training Program (T32)
Rackham Graduate Student Research Grant (pre-candidate)

2018–current | Bradley Crone (Ph.D. Student, Bioinformatics, University of Michigan)
Rackham Graduate Student Research Grant (candidate)

2017–current | Melissa Englund (Ph.D. Student, Human Genetics, University of Michigan)
NIH Human Genetics Training Program (T32)
Rackham Graduate Student Research Grant (candidate)

2018–current | Samuel Zhao (Ph.D. Student, Bioinformatics, University of Michigan)

2017–2018 | Samuel Zhao (M.S. Student, Bioinformatics, University of Michigan)

Rackham Graduate Student Research Grant (pre-candidate)
Rackham Graduate Student Research Grant (candidate)

2016–2018 Haley Amemiya (Ph.D. Student, Cellular and Molecular Biology, University of Michigan)
Joint M.S. in Bioinformatics, University of Michigan
NIH Cellular & Molecular Biology Training Program (T32)
NIH Cellular Biotechnology Training Program (T32) (Declined)
PIBS Excellence in Service Award
Rackham Graduate Student Research Grant (pre-candidate)
Rackham Graduate Student Research Grant (candidate)
Maas Professional Development Award
Rackham Graduate School Scholar-Activist Award

2016–2020 Shriya Sethuraman (Ph.D. Student, Bioinformatics, University of Michigan)

2016–current Christopher Castro (Ph.D. Student, Bioinformatics, University of Michigan)
NIH Bioinformatics Training Program (T32)
Rackham Merit Fellow
Rackham Graduate Student Research Grant (pre-candidate)
Rackham Graduate Student Research Grant (candidate)
Global Research Engagement Opportunity Fellowship

2017–2022 Ningxin Ouyang (Ph.D. Student, Bioinformatics, University of Michigan)
2015–2017 Ningxin Ouyang (M.S. Student, Bioinformatics, University of Michigan)
Rackham Graduate Student Research Grant (candidate)

2016–2021 Shengcheng Dong (Ph.D. Student, Bioinformatics, University of Michigan)
Rackham Graduate Student Research Grant (candidate)

2015–2021 Torrin McDonald (Ph.D. Student, Human Genetics, University of Michigan)
NIH Human Genetics Training Program (T32)
Rackham Graduate Student Research Grant (pre-candidate)
Rackham Graduate Student Research Grant (candidate)

2015–2017 Greg Farnum (Ph.D. Student, Cellular and Molecular Biology, University of Michigan)

2015–2020 Sierra Nishizaki (Ph.D. Student, Human Genetics, University of Michigan)
Joint M.S. in Bioinformatics, University of Michigan
NIH Genome Science Training Program (T32)
Rackham Merit Fellow
Rackham Summer Award
Rackham Graduate Student Research Grant (candidate)

Additional Graduate Rotation Students

2022 Rintsen Sherpa (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 Progran, 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

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

2021–current Preston Parana (Undergraduate, UROP Molecular, Cellular, and Developmental Biology, University of Michigan)
UROP Blue Ribbon Award
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)
UROP Blue Ribbon Award
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 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 Ashley Melnick (Cellular and Molecular Biology, University of Michigan, Committee Member)
2020–current Camille Mumm (Human Genetics, University of Michigan, Chair)
2019–current Benjamin Yang (Biomedical Engineering, University of Michigan, Committee Member)
2018–current Christine Ziegler (Biological Chemistry, University of Michigan, Committee Member)
2018–current Stephen Carney (Cancer Biology, University of Michigan, Committee Member)
2018–current Marcus Sherman (Bioinformatics, University of Michigan, Committee Member)
2018–current Rucheng Diao (Bioinformatics, University of Michigan, Committee Member)
2018–current Samuel Zhao (Bioinformatics, University of Michigan, Chair)
2018–current Bradley Crone (Bioinformatics, University of Michigan, Chair)
2017–current Melissa Englund (Human Genetics, University of Michigan, Chair)
2016–current Christopher Castro (Bioinformatics, University of Michigan, Chair)
2021–2022 Kuan-Han Hank Wu (Bioinformatics, University of Michigan, Committee Member)
Integrating Electronic Health Records with Genetic Information to Advance Precision Medicine Approaches in Cardiovascular Disease
2017–2022 Amanda Moccia (Human Genetics, University of Michigan, Committee Member)
Investigation of Developmental Disorders: Genetic Discovery and Functional Validation
2017–2022 Ningxin Ouyang (Bioinformatics, University of Michigan, Chair)

Deciphering Transcriptional Regulatory Circuits: Transcription Factor Binding and Regulatory Variants Identification

2015–2021 Torrin McDonald (Human Genetics, University of Michigan, Chair)
Leveraging New Technologies to Explore Regulatory and Structural Elements of the Human Genome

2018–2021 Heming Yao (Bioinformatics, University of Michigan, Committee Member)
Machine Learning and Image Processing for Clinical Outcome Prediction: Applications in Medical Data from Patients with Traumatic Brain Injury, Ulcerative Colitis, and Heart Failure

2016–2021 Mohd Hafiz Bin Mohd Rothi (Molecular, Cellular, and Developmental Biology, University of Michigan, Committee Member)
Control of Chromatin by RNA-mediated Transcriptional Silencing

2016–2021 Shengcheng Dong (Bioinformatics, University of Michigan, Chair)
Computational Methods to Identify Regulatory Variants in the Non-coding Regions of the Human Genome

2017–2021 Steven Romanelli (Molecular & Integrative Physiology, University of Michigan, Committee Member)
Viral CRISPR/Cas9 Gene Transfer for Somatic Knockout in Brown Adipose Tissue

2018–2021 Negar Farzaneh (Bioinformatics, University of Michigan, Committee Member)
Automated Decision Support System for Traumatic Injuries

2016–2020 Shriya Sethuraman (Bioinformatics, University of Michigan, co-Chair)
Genome-wide Identification of Non-coding Transcription by RNA Polymerase V and Its Involvement in Transcriptional Gene Silencing

2015–2020 Sierra Nishizaki (Human Genetics, University of Michigan, Chair)
Decoding the Non-coding Genome: Novel Technologies for the Characterization of Non-coding Elements and Variation

2017–2020 Christopher Lee (Biostatistics, University of Michigan, Committee Member)
Improvements and Developments in Gene Regulation and Single-Cell Gene Expression Data Analysis

2015–2018 Ari Allyn-Feuer (Bioinformatics, University of Michigan, Committee Member)
The Pharmacoepigenomics Informatics Pipeline and H-GREEN Hi-C Compiler: Discovering Pharmacogenomic Variants and Pathways with the Epigenome and Spatial Genome

2015–2017 Raymond Cavalcante (Bioinformatics, University of Michigan, Committee Member)
Beyond the Transcriptome: Facilitating Interpretation of Epigenomics and Metabolomics Data

2015–2017 Zhengting Zou (Bioinformatics, University of Michigan, Committee Member)
Model-based genomic studies of protein sequence evolution: convergence, epistasis, and amino acid acceptance rates

Preliminary Exam Committees

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

2013–2014 Consultant, Color Genomics
Personalized medicine / genomics startup

Publications

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

[1] Mumm C, Drexel ML, McDonald TL, Diehl AG, Switzenberg JA, **Boyle AP**. "Onramp: rapid nanopore plasmid validation." ***bioRxiv*** 2022.

[2] 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." ***bioRxiv*** 2021.

[3] Rothi MH, Sethuraman S, Dolata J, **Boyle AP**, Wierzbicki AT. "DNA methylation directs nucleosome positioning in RNA-mediated transcriptional silencing." ***bioRxiv*** 2020.

[4] Nishizaki SS, **Boyle AP**. "SEMplMe: A tool for integrating DNA methylation effects in transcription factor binding affinity predictions." ***BMC Bioinformatics*** 2022, 23:317.

[5] 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.

[6] 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.

[7] 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.

[8] *McDonald TL, *Zhou W, Castro CP, Mumm C, Switzenberg JA, †Mills RE, †**Boyle AP**. "Cas9 targeted enrichment of mobile elements using nanopore sequencing." ***Nature Communications*** 2021, 12:3586. PMID: 34117247.

[9] *Nishizaki SS, *McDonald TL, Farnum GA, Holmes MJ, Drexel ML, Switzenberg JA, **Boyle AP**. "The inducible lac operator-repressor system is functional in zebrafish cells." ***Frontiers in Genetics*** 2021, 12. PMID: 34220959.

[10] Zhao N, **Boyle AP**. "F-Seq2: improving the feature density based peak caller with dynamic statistics." ***NAR Genomics and Bioinformatics*** 2021, 3. PMID: 33655209.

[11] *Tsuzuki M, *Sethuraman S, Coke AN, Rothi MH, **Boyle AP**, Wierzbicki AT. "Broad noncoding transcription suggests genome surveillance by RNA polymerase V." ***Proceedings of the National Academy of Sciences*** 2020, 117(48):30799–30804. PMID: 33199612.

[12] Diehl AG, **Boyle AP**. "MapGL: Inferring evolutionary gain and loss of short genomic sequence features by phylogenetic maximum parsimony." ***BMC Bioinformatics*** 2020, 21:416. PMID: 32962625.

[13] The ENCODE Project Consortium. “Perspectives on ENCODE.” ***Nature*** 2020, 583(7818):693–698. PMID: 32728248.

[14] The ENCODE Project Consortium. “Expanded encyclopaedias of DNA elements in the human and mouse genomes.” ***Nature*** 2020, 583(7818):699–710. PMID: 32728249.

[15] Ouyang N, **Boyle AP**. “TRACE: transcription factor footprinting using chromatin accessibility data and DNA sequence.” ***Genome Research*** 2020, 30:1040–1046. PMID: 32660981.

[16] Diehl AG, Ouyang N, **Boyle AP**. “Transposable elements contribute to cell and species-specific chromatin looping and gene regulation in mammalian genomes.” ***Nature Communications*** 2020, 11:1796. PMID: 32286261.

[17] Lee CT, Cavalcante RG, Lee C, Qin T, Patil S, Wang S, Tsai Z, **Boyle AP**, Sartor MA. “Poly-Enrich: count-based methods for gene set enrichment testing with genomic regions.” ***NAR Genomics and Bioinformatics*** 2020, 2. PMID: 32051932.

[18] Nishizaki SS, Ng N, Dong S, Porter RS, Morterud C, Williams C, Asman C, Switzenberg JA, **Boyle AP**. “Predicting the effects of SNPs on transcription factor binding affinity.” ***Bioinformatics*** 2019, 50:2434. PMID: 31373606.

[19] Diehl AG, **Boyle AP**. “CGIMP: Real-time exploration and covariate projection for self-organizing map datasets.” ***Journal of Open Source Software*** 2019, 4(39):1520.

[20] Amemiya HM, †Kundaje A, †**Boyle AP**. “The ENCODE Blacklist: Identification of Problematic Regions of the Genome.” ***Scientific Reports*** 2019, 9:9354. PMID: 31249361.

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