

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

- 2014–present **Assistant Professor**, Department of Computational Medicine & Bioinformatics
Member, Program in Biomedical Sciences
Member, Bioinformatics Training Program
- 2015–present **Assistant Professor**, Department of Human Genetics
Member, Genome Science Training Program (GSTP)
Member, Michigan Predoctoral Training Program in Genetics (GTP)
- 2016–present **Member**, Center for RNA Biomedicine
- 2017–present **Member**, Cellular and Molecular Biology Program
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

- 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

- 2017–2020 U41 HG009293 (Multi PI: Cherry, Boyle; Genomic Research Project PI: Boyle)
NIH/NHGRI Total Costs: \$2,171,753
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.

2017–2022	DBI-1651614 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.	(PI: Boyle) Total Costs: \$979,984
2017–2018	Eleanor and Larry Jackier U-M/Technion and Weizmann Collaborative Research Grant Michigan - Israel Partnership for Research & Education Identifying novel disease related mutations in the genomic environments around Transcription 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.	(PI: Boyle, Mandel-Gutfreund) Total Costs: \$50,000
2017–2024	R35 HL135824 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.	(PI: Willer; Co-I with Effort) Total Costs: \$4,650,000

Completed

2013–2017	R00 HG007356 Pathway to Independence Award (K99/R00) 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.	(PI: Boyle) Total Costs: \$987,771
2015–2017	FG-2015-65465 Alfred P. Sloan Foundation Fellowship in Computational & Evolutionary Molecular Biology	(PI: Boyle) Total Costs: \$50,000
2016–2020	R01 HL130705 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.	(PI: Willer; Co-I with Effort) Total Costs: \$2,784,005

Professional Service

Service

2018–current	DCM&B Diversity, Equity, & Inclusion representative
2018–current	Lab Safety Liason for DCM&B
2017–current	DCM&B Preliminary Exam Abstract Review Committee (PARC) [Chair 2018–current]
2017–current	EBS Faculty IT Committee
2017–current	DHG Faculty Recruitment and Promotions Committee
2016–current	DCM&B Faculty Recruitment Committee
2016–current	DCM&B Seminar Series Committee [Chair 2016–current]
2015–current	DCM&B Admissions Committee
2015–2017	DHG Computational Support Committee
2015–2016	DCM&B Retreat Planing 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

2018–current	Member, American Society of Human Genetics (ASHG)
2013–current	Member, International Society for Computational Biology (ISCB)
2012–2014	Member, American Association for the Advancement of Science (AAAS)

2005–current | Member, Gamma Sigma Delta Agricultural Honor Society

Reviewing Activity

Since 2009 | *Ad hoc* reviewer for the journals: *Nature Genetics*, *Genome Research*, *Genome Biology*, *Nature Neuroscience*, *Nature Communications*, *Nature Protocols*, *Bioinformatics*, *Nucleic Acids Research*, *BMC Bioinformatics*, *Oncotarget*, *Scientific Reports*, *Atherosclerosis*, *BioEssays*, *Gene*

2015–current | Program Committee, Great Lakes Bioinformatics and Canadian Computational Biology Conference (GLBIO/CCBC)

2015–2016 | Program Committee, Algorithms for Computational Biology (ALCOB)

2015 | Reviewer for UK Medical Research Council (RCUK MRC)

2015 | Reviewer for UK Biotechnology and Biological Sciences Research Council (RCUK BBSRC)

2015 | Reviewer for Michigan Institute for Clinical & Health Research (MICHHR) Postdoctoral Translational Scholars Program

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*

Teaching and Mentorship

Teaching

2019–current | Bioinformatics Concepts and Algorithms (BIOINF 529) [Course Director]

2018–current | Lecturer, Mathematical and Theoretical Biology Institute, Arizona State University [2 lectures]

2017 | Panel member, U. Michigan “New Faculty Orientation to Corporate & Foundation Relations” [70 attendees]

2017 | Experimental Genetics Systems (HUMGEN 632) [Course Director]

2016 | Experimental Genetics Systems (HUMGEN 632) [1 discussion]

2015–current | Gene Structure and Regulation (HUMGEN 541) [3 lectures + 2 discussions / yr.]

2015–current | Bioinformatics Journal Club (BIOINF 602/603) [Course Director Fall 2018]

2015–2017 | Introduction to Bioinformatics & Computational Biology (BIOINF 527) [2 lectures + 3 labs / yr.]

2015–2017 | Basic Biology for Graduate Students with Quantitative Training (BIOINF 523) [2 lectures / yr.]

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

Fall 2003 | Lab TA for Isotopes Tech I (MS. State, BCH 4414)

Mentorship

Graduate Students

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

2017–current | Samuel Zhao (Ph.D. Student, Bioinformatics, University of Michigan)
Rackham Graduate Student Research Grant (pre-candidate)

2016–current | Haley Amemiya (Ph.D. Student, Cellular and Molecular Biology, University of Michigan)
NIH Cellular & Molecular Biology Training Program (T32)
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–current | Shriya Sethuraman (Ph.D. Student, Bioinformatics, University of Michigan)

2016–current | Shengcheng Dong (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)

2015–current | Ningxin Ouyang (Ph.D. Student, Bioinformatics, University of Michigan)

2015–current	Torrin McDonald (Ph.D. Student, Human Genetics, University of Michigan) <i>NIH Human Genetics Training Program (T32)</i> <i>Rackham Graduate Student Research Grant (pre-candidate)</i>
2015–2017	Greg Farnum (Ph.D. Student, Cellular and Molecular Biology, University of Michigan)
2015–current	Sierra Nishizaki (Ph.D. Student, Human Genetics, University of Michigan) <i>NIH Genome Science Training Program (T32)</i> <i>Rackham Merit Fellow</i> <i>Rackham Summer Award</i>

Additional Graduate Rotation Students

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)

Undergraduate and High School Students

2016–2018	Cody Morterud (Undergraduate, UROP Computer Science, 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

2018–current	Marcus Sherman (Bioinformatics, University of Michigan)
2018–current	Christopher Lee (Bioinformatics, University of Michigan)
2018–current	Negar Farzaneh (Bioinformatics, University of Michigan)
2018–current	Rucheng Diao (Bioinformatics, University of Michigan)
2017–current	Steven Romanelli (Molecular & Integrative Physiology, University of Michigan)
2017–current	Amanda Moccia (Human Genetics, University of Michigan)
2017–current	Christopher Lee (Biostatistics, University of Michigan)
2016–current	Mohd Hafiz Bin Mohd Rothi (Molecular, Cellular, and Developmental Biology, University of Michigan)
2015–current	Ari Allyn-Feuer (Bioinformatics, University of Michigan)
2015–2017	Raymond Cavalcante (Bioinformatics, University of Michigan)
2015–2017	Zhengting Zou (Bioinformatics, University of Michigan)

Preliminary Exam Committees

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] Diehl AG, **Boyle AP**. “Conserved and species-specific transcription factor co-binding patterns drive divergent gene regulation in human and mouse.” *Nucleic Acids Research* 2018, 46(4):1878–1894. PMID: 29361190.
- [2] Nielsen JB, Fritsche LG, Zhou W, Teslovich TM, Holmen OL, Gustafsson S, Gabrielsen ME, Schmidt EM, Beaumont R, Wolford BN, Lin M, Brummett CM, Preuss MH, Refsgaard L, Bottinger EP, Graham SE, Surakka I, Chu Y, Skogholt AH, Dalen H, **Boyle AP**, Oral H, Herron TJ, Kitzman J, Jalife J, Svendsen JH, Olesen MS, Njølstad I, Løchen ML, Baras A, Gottesman O, Marcketta A, O’Dushlaine C, Ritchie MD, Wilsgaard T, Loos RJJ, Frayling TM, Boehnke M, Ingelsson E, Carey DJ, Dewey FE, Kang HM, Abecasis GR, Hveem K, Willer CJ. “Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development.” *American Journal of Human Genetics* 2017, 102:103–115. PMID: 29290336.
- [3] Spadafore M, Najarian K, **Boyle AP**. “A proximity-based graph clustering method for the identification and application of transcription factor clusters.” *BMC Bioinformatics* 2017, 18:530. PMID: 29187152.
- [4] *Yang B, *Zhou W, *Jiao J, Nielsen JB, Mathis MR, Heydarpour M, Lettre G, Folkersen L, Prakash S, Schurmann C, Fritsche L, Farnum GA, Lin M, Othman M, Hornsby W, Driscoll A, Levasseur A, Thomas M, Farhat L, Dubé MP, Isselbacher EM, Franco-Cereceda A, Guo Dc, Bottinger EP, Deeb GM, Booher A, Kheterpal S, Chen YE, Kang HM, Kitzman J, Cordell HJ, Keavney BD, Goodship JA, Ganesh SK, Abecasis G, Eagle KA, **Boyle AP**, Loos RJJ, †Eriksson P, †Tardif JC, †Brummett CM, †Milewicz DM, †Body SC, †Willer CJ. “Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve.” *Nature Communications* 2017, 8:15481. PMID: 28541271.
- [5] Nishizaki SS, **Boyle AP**. “Mining the Unknown: Assigning Function to Noncoding Single Nucleotide Polymorphisms.” *Trends in Genetics* 2017, 33:34–45. PMID: 27939749.
- [6] Diehl AG, **Boyle AP**. “Deciphering ENCODE.” *Trends in Genetics* 2016, 32(4):238–249. PMID: 26962025.
- [7] Phanstiel DH, **Boyle AP**, Heidari N, Snyder MP. “Mango: A bias correcting ChIA-PET analysis pipeline.” *Bioinformatics* 2015. PMID: 26034063.
- [8] *Cheng Y, *Ma Z, Kim BH, Wu W, Cayting P, **Boyle AP**, Sundaram V, Xing X, Dogan N, Li J, Euskirchen G, Lin S, Lin Y, Visel A, Kawli T, Yang X, Patacsil D, Keller CA, Giardine B, Mouse ENCODE Consortium, Kundaje A, Wang T, Pennacchio LA, Weng Z, †Hardison RC, †Snyder MP. “Principles of regulatory information conservation between mouse and human.” *Nature* 2014, 515(7527):371–375. PMID: 25409826.
- [9] *Yue F, *Cheng Y, *Breschi A, *Vierstra J, *Wu W, *Ryba T, *Sandstrom R, *Ma Z, *Davis C, *Pope BD, *Shen Y, Pervouchine DD, Djebali S, Thurman RE, Kaul R, Rynes E, Kirilusha A, Marinov GK, Williams BA, Trout D, Amrhein H, Fisher-Aylor K, Antoshechkin I, DeSalvo G, See LH, Fastuca M, Drenkow J, Zaleski C, Dobin A, Prieto P, Lagarde J, Bussotti G, Tanzer A, Denas O, Li K, Bender MA, Zhang M, Byron R, Groudine MT, McCleary D, Pham L, Ye Z, Kuan S, Edsall L, Wu YC, Rasmussen MD, Bansal MS, Kellis M, Keller CA, Morrissey CS, Mishra T, Jain D, Dogan N, Harris RS, Cayting P, Kawli T, **Boyle AP**, Euskirchen G, Kundaje A, Lin S, Lin Y, Jansen C, Malladi VS, Cline MS, Erickson DT, Kirkup VM, Learned K, Sloan CA, Rosenbloom KR, Lacerda de Sousa B, Beal K, Pignatelli M, Flicek P, Lian J, Kahveci T, Lee D, Kent WJ, Ramalho Santos M, Herrero J, Notredame C, Johnson A, Vong S, Lee K, Bates D, Neri F, Diegel M, Canfield T, Sabo PJ, Wilken MS, Reh TA, Giste E, Shafer A, Kutayin T, Haugen E, Dunn D, Reynolds AP, Neph S, Humbert R, Hansen RS, De Bruijn M, Selleri L, Rudensky A, Josefowicz S, Samstein R, Eichler EE, Orkin SH, Levasseur D, Papayannopoulou T, Chang KH, Skoultchi A, Gosh S, Disteche C, Treuting P, Wang Y, Weiss MJ, Blobel GA, Cao X, Zhong S, Wang T, Good PJ, Lowdon RF, Adams LB, Zhou XQ, Pazin MJ, Feingold EA, Wold B, Taylor J, Mortazavi A, Weissman SM, Stamatoyannopoulos JA, Snyder MP, Guigo R, Gingeras TR, Gilbert DM, Hardison RC, Beer MA, Ren B, Mouse ENCODE Consortium. “A comparative encyclopedia of DNA elements in the mouse genome.” *Nature* 2014, 515(7527):355–364. PMID: 25409824.

- [10] *Boyle AP, *Araya CL, Brdlik C, Cayting P, Cheng C, Cheng Y, Gardner K, Hillier LW, Janette J, Jiang L, Kasper D, Kawli T, Kheradpour P, Kundaje A, Li JJ, Ma L, Niu W, Rehm EJ, Rozowsky J, Slattery M, Spokony R, Terrell R, Vafeados D, Wang D, Weissdepp P, Wu YC, Xie D, Yan KK, Feingold EA, Good PJ, Pazin MJ, Huang H, Bickel PJ, Brenner SE, Reinke V, Waterston RH, Gerstein M, †White KP, †Kellis M, †Snyder M. “Comparative analysis of regulatory information and circuits across distant species.” *Nature* 2014, 512(7515):453–456. PMID: 25164757.
- [11] Araya CL, Kawli T, Kundaje A, Jiang L, Wu B, Vafeados D, Terrell R, Weissdepp P, Gevirtzman L, Mace D, Niu W, Boyle AP, Xie D, Ma L, Murray JI, Reinke V, Waterston RH, Snyder M. “Regulatory analysis of the *C. elegans* genome with spatiotemporal resolution.” *Nature* 2014, 512(7515):400–405. PMID: 25164749.
- [12] Phanstiel DH, Boyle AP, Araya CL, Snyder MP. “Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures.” *Bioinformatics* 2014. PMID: 24903420.
- [13] *Xie D, *Boyle AP, *Wu L, Kawli T, Zhai J, Snyder M. “Dynamic trans-acting factor colocalization in human cells.” *Cell* 2013, 155(3):713–724. PMID: 24243024.
- [14] *Kasowski M, *Kyriazopoulou-Panagiotopoulou S, *Grubert F, *Zaugg JB, *Kundaje A, Liu Y, Boyle AP, Zhang QC, Zakharia F, Spacek DV, Li J, Xie D, Steinmetz LM, Hogenesch JB, Kellis M, Batzoglou S, Snyder M. “Extensive variation in chromatin states across humans.” *Science* 2013, 342(6159):750–752. PMID: 24136358.
- [15] Boyle AP, Hong EL, Hariharan M, Cheng Y, Schaub MA, Kasowski M, Karczewski KJ, Park J, Hitz BC, Weng S, Cherry JM, Snyder M. “Annotation of functional variation in personal genomes using RegulomeDB.” *Genome Research* 2012, 22(9):1790–1797. PMID: 22955989.
- [16] Schaub MA, Boyle AP, Kundaje A, †Batzoglou S, †Snyder M. “Linking disease associations with regulatory information in the human genome.” *Genome Research* 2012, 22(9):1748–1759. PMID: 22955986.
- [17] The ENCODE Project Consortium. “An integrated encyclopedia of DNA elements in the human genome.” *Nature* 2012, 489(7414):57–74. PMID: 22955616.
- [18] *Gerstein MB, *Kundaje A, *Hariharan M, *Landt SG, *Yan KK, *Cheng C, *Mu XJ, *Khurana E, *Rozowsky J, *Alexander R, *Min R, *Alves P, Abyzov A, Addleman N, Bhardwaj N, Boyle AP, Cayting P, Charos A, Chen DZ, Cheng Y, Clarke D, Eastman C, Euskirchen G, Fietze S, Fu Y, Gertz J, Grubert F, Harmanci A, Jain P, Kasowski M, Lacroute P, Leng J, Lian J, Monahan H, O’Geen H, Ouyang Z, Partridge EC, Patacsil D, Pauli F, Raha D, Ramirez L, Reddy TE, Reed B, Shi M, Slifer T, Wang J, Wu L, Yang X, Yip KY, Zilberman-Schapira G, Batzoglou S, Sidow A, Farnham PJ, Myers RM, Weissman SM, Snyder M. “Architecture of the human regulatory network derived from ENCODE data.” *Nature* 2012, 489(7414):91–100. PMID: 22955619.
- [19] *Chen R, *Mias GI, *Li-Pook-Tham J, *Jiang L, Lam HYK, Chen R, Miriami E, Karczewski KJ, Hariharan M, Dewey FE, Cheng Y, Clark MJ, Im H, Habegger L, Balasubramanian S, O’Huallachain M, Dudley JT, Hillenmeyer S, Haraksingh R, Sharon D, Euskirchen G, Lacroute P, Bettinger K, Boyle AP, Kasowski M, Grubert F, Seki S, Garcia M, Whirl-Carrillo M, Gallardo M, Blasco MA, Greenberg PL, Snyder P, Klein TE, Altman RB, Butte AJ, Ashley EA, Gerstein M, Nadeau KC, Tang H, Snyder M. “Personal omics profiling reveals dynamic molecular and medical phenotypes.” *Cell* 2012, 148(6):1293–1307. PMID: 22424236.
- [20] *Song L, *Zhang Z, *Grasfeder LL, *Boyle AP, *Giresi PG, *Lee B, *Sheffield NC, Graff S, Huss M, Keefe D, Liu Z, London D, McDaniell RM, Shibata Y, Showers KA, Simon JM, Vales T, Wang T, Winter D, Zhang Z, Clarke ND, †Birney E, †Iyer VR, †Crawford GE, †Lieb JD, †Furey TS. “Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity.” *Genome Research* 2011, 21(10):1757–1767. PMID: 21750106.
- [21] The ENCODE Project Consortium. “A user’s guide to the encyclopedia of DNA elements (ENCODE).” *PLoS Biology* 2011, 9(4):e1001046. PMID: 21526222.
- [22] Boyle AP, Song L, Lee B, London D, Keefe D, Birney E, Iyer VR, †Crawford GE, †Furey TS. “High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells.” *Genome Research* 2011, 21:456–464. PMID: 21106903.
- [23] *Stitzel ML, *Sethupathy P, Pearson DS, Chines PS, Song L, Erdos MR, Welch R, Parker SCJ, Boyle AP, Scott LJ, Margulies EH, Boehnke M, Furey TS, Crawford GE, Collins FS. “Global epigenomic analysis of primary human pancreatic islets provides insights into type 2 diabetes susceptibility loci.” *Cell Metabolism* 2010, 12(5):443–455. PMID: 21035756.

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- [25] Georgiev S, **Boyle AP**, Jayasurya K, Mukherjee S, Ohler U. “Evidence-ranked motif identification.” *Genome Biology* 2010, 11(2):R19. PMID: 20156354.
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- [27] Xu X, Tsumagari K, Sowden J, Tawil R, **Boyle AP**, Song L, Furey TS, Crawford GE, Ehrlich M. “DNaseI hypersensitivity at gene-poor, FSH dystrophy-linked 4q35.2.” *Nucleic Acids Research* 2009, 37(22):7381–7393. PMID: 19820107.
- [28] **Boyle AP**, Furey TS. “High-resolution mapping studies of chromatin and gene regulatory elements.” *Epigenomics* 2009, 1(2):319–329. PMID: 20514362.
- [29] **Boyle AP**, Guinney J, Crawford GE, Furey TS. “F-Seq: a feature density estimator for high-throughput sequence tags.” *Bioinformatics* 2008, 24(21):2537–2538. PMID: 18784119.
- [30] **Boyle AP**, Davis S, Shulha HP, Meltzer P, Margulies EH, Weng Z, †Furey TS, †Crawford GE. “High-resolution mapping and characterization of open chromatin across the genome.” *Cell* 2008, 132(2):311–322. PMID: 18243105.
- [31] **Boyle AP**, Boyle JA. “Global analysis of microbial translation initiation regions.” In *Journal of the Mississippi Academy of Sciences*, Volume 48 2003:138–150.
- [32] **Boyle AP**, Boyle JA. “Visualization of aligned genomic open reading frame data.” *Biochemistry and Molecular Biology Education* 2003, 31:64–68.
- [33] Wan X, Boyle JA, Bridges SM, **Boyle AP**. “Interactive clustering for exploration of genomic data.” In *Proceedings of the Artificial Neural Networks in Engineering Conference*, Volume 12, St. Louis, MO 2002:753–758.

Patents

- [34] Karczewski K, Snyder M, Butte AJ, Dudley JT, Hong E, Boyle A, Cherry MJ, Park J. “Method and system for the use of biomarkers for regulatory dysfunction in disease.” 2018, (United States patent US 9,946,835 B2).