

Alan P. Boyle

2017 Palmer Commons
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www.BoyleLab.org

Education

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| 2005–2009 | Doctor of Philosophy , Computational Biology and Bioinformatics Duke University, Durham, NC |
| 2001–2005 | Bachelor of Science , Biochemistry and Molecular Biology Bachelor of Science , Computer Science Mississippi State University, Starkville, MS |

Academic Appointments

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|--------------|--|
| 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

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| 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

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| 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 |
| 2017–2020 | U41 HG009293 | (Multi PI: Cherry, Boyle) |

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| | 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 | (PI: Boyle) |
| | NSF/BIO/DBI | Total Costs: \$979,984 |
| | 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. | |
| 2017–2018 | Eleanor and Larry Jackier U-M/Technion and Weizmann Collaborative Research Grant | (PI: Boyle, Mandel-Gutfreund) |
| | Michigan - Israel Partnership for Research & Education | Total Costs: \$50,000 |
| | 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. | |

Completed

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| 2015–2017 | FG-2015-65465 | (PI: Boyle) |
| | Alfred P. Sloan Foundation | Total Costs: \$50,000 |
| | Fellowship in Computational & Evolutionary Molecular Biology | |
| 2016–2020 | R01 HL130705 | (PI: Willer; Co-I with Effort) |
| | NIH/NHLBI | Total Costs: \$2,784,005 |
| | 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. | |

Professional Service

Service

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| 2017–current | DCM&B Preliminary Exam Abstract Review Committee (PARC) |
| 2017–current | DHG Faculty Recruitment and Promotions Committee |
| 2016–current | DCM&B Faculty Recruitment Committee |
| 2016–current | DCM&B Seminar Series Committee Chair |
| 2015–current | 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 |
| 2013–current | Member, International Society for Computational Biology (ISCB) |
| 2012–current | Member, American Association for the Advancement of Science (AAAS) |
| 2008–2009 | Duke Computational Biology & Bioinformatics student committee |
| 2005–current | Member, Gamma Sigma Delta Agricultural Honor Society |

Reviewing Activity

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| Since 2009 | <i>Ad hoc</i> reviewer for the journals: <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 Bioinformatics</i> , <i>Oncotarget</i> , <i>Scientific Reports</i> , <i>Atherosclerosis</i> , <i>BioEssays</i> , <i>Gene</i> |
| 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) |

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| 2015 | Reviewer for Michigan Institute for Clinical & Health Research (MICHR) 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 <i>Bioinformatics</i> |

Teaching and Mentorship

Teaching

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| 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 | Introduction to Bioinformatics & Computational Biology (BIOINF 527) [2 lectures + 3 labs / yr.] |
| 2015–current | Bioinformatics Journal Club (BIOINF 602/603) |
| 2015–current | 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

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|--------------|---|
| 2017–current | Melissa Englund (Ph.D. Student, Human Genetics, University of Michigan) <i>NIH Human Genetics Training Program (T32)</i> |
| 2017–current | Samuel Zhao (M.S. Student, Bioinformatics, University of Michigan) |
| 2016–current | Haley Amemiya (Ph.D. Student, Cellular and Molecular Biology, University of Michigan) <i>NIH Cellular & Molecular Biology Training Program (T32)</i> <i>Rackham Graduate Student Research Grant (pre-candidate)</i> |
| 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) <i>NIH Bioinformatics Training Program (T32)</i> <i>Rackham Merit Fellow</i> <i>Rackham Graduate Student Research Grant (pre-candidate)</i> |
| 2015–current | Ningxin Ouyang (Ph.D. Student, Bioinformatics, University of Michigan) |
| 2015–current | Torin 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

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|------|---|
| 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

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| 2016–2017 | Cody Morterud (Undergraduate, UROP Computer Science, University of Michigan) |
| 2016–2017 | Colten Williams (Undergraduate, UROP Computer Science, University of Michigan) |

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| 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

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|--------------|--|
| 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

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| 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 Personalized medicine / genomics startup |
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Publications

* Indicates co-first authorship Indicates co-senior authorship

underscore indicates mentored students

- [1] Nielsen, Jonas B and Fritsche, Lars and Zhou, Wei and Teslovich, Tanya M and Holmen, Oddgeir L and Gustafsson, Stefan and Elvestad, Maiken B and Schmidt, Ellen M and Beaumont, Robin Beaumont and Woldford, Brooke N and Lin, Maoxuan and Brummett, Chad M and Preuss, Michael H and Refsgaard, Lena and Bottinger, Erwin P and Graham, Sarah E and Surakka, Ida and Chu, Yunhan and Skogholt, Anne Heidi and Dalen, Hvard and **Boyle AP** and Oral, Hakan and Herron, Todd J and Kitman, Jacob and Jalife, Jos and Svendsen, Jesper H and Olesen, Morten S and Njølstad, Inger and Løchen, Maja-Lisa and Baras, Aris and Gottesman, Omri and Marcketta, Anthony and ODushlaine, Colm and Ritchie, Marylyn D and Wilsgaard, Tom and Looos, Ruth JF and Frayling, Timothy M and Boehnke, Michael and Ingelsson, Erik and Carey, David J and Dewey, Frederick E and Kang, Hyun M and Abecasis, Gonalo R and Hveem, Kristian and Willer, Cristen J. “Genome-wide association analysis of atrial fibrillation identifies two new risk loci and highlights biological pathways and regulatory elements involved in cardiac development.” *American Journal of Human Genetics* 2017. Accepted.
- [2] Diehl AG, **Boyle AP**. “Transcription factor co-binding patterns drive conserved regulatory outcomes.” *bioRxiv* 2017.
- [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, Bo and *Zhou, Wei and *Jiao, Jiao and Nielsen, Jonas B and Mathis, Michael R and Heydarpour, Mahyar and Lettre, Guillaume and Folkersen, Lasse and Prakash, Siddharth and Schurmann, Claudia and Fritsche, Lars and Farnum, Gregory A and Lin, Maoxuan and Othman, Mohammad and Hornsby, Whitney and Driscoll, Anisa

- and Levasseur, Alexandra and Thomas, Marc and Farhat, Linda and Dubé, Marie-Pierre and Isselbacher, Eric M and Franco-Cereceda, Anders and Guo, Dong-chuan and Bottinger, Erwin P and Deeb, G Michael and Booher, Anna and Kheterpal, Sachin and Chen, Y Eugene and Kang, Hyun Min and Kitzman, Jacob and Cordell, Heather J and Keavney, Bernard D and Goodship, Judith A and Ganesh, Santhi K and Abecasis, Gonçalo and Eagle, Kim A and **Boyle AP** and Loos, Ruth J F and Eriksson, Per and Tardif, Jean-Claude and Brummett, Chad M and Milewicz, Dianna M and Body, Simon C and Willer, Cristen J. “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, Kutayavin 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, Skoultschi 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, Frietze 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-Than 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.
- [24] McDaniell R, Lee B, Song L, Liu Z, **Boyle AP**, Erdos MR, Scott LJ, Morken MA, Kucera KS, Battenhouse A, Keefe D, Collins FS, Willard HF, Lieb JD, Furey TS, Crawford GE, Iyer VR, Birney E. "Heritable individual-specific and allele-specific chromatin signatures in humans." *Science* 2010, 328(5975):235–239. PMID: 20299549.
- [25] Georgiev S, **Boyle AP**, Jayasurya K, Mukherjee S, Ohler U. "Evidence-ranked motif identification." *Genome Biology* 2010, 11(2):R19. PMID: 20156354.
- [26] Babbitt CC, Fedrigo O, Pfefferle AD, **Boyle AP**, Horvath JE, Furey TS, Wray GA. "Both noncoding and protein-coding RNAs contribute to gene expression evolution in the primate brain." *Genome Biology and Evolution* 2010, 2:67–79. PMID: 20333225.
- [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. “Method and system for the use of biomarkers for regulatory dysfunction in disease.” 2013, (US Patent Application 20130116931).