Alan P. Boyle

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Education

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

Professional Experience

Exp. Sept. 2014	**Assistant Professor,** Department of Computational Medicine & Bioinformatics University of Michigan, Ann Arbor, MI
Jun 2010–present	**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

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

2013–2017 R00HG007356 Pathway to Independence Award (K99/R00) (PI: Boyle)
NIH/NHGRI Total Costs: $937,771
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.

Professional Service

2009–current	Ad hoc reviewer for the journals: *Nature Communications*, *Bioinformatics*, *BMC Bioinformatics*, *BioEssays*, *Gene*
2013–current	Member, International Society for Computational Biology (ISCB)
2012–current	Member, American Association for the Advancement of Science (AAAS)
2013–2014	Program Committee, Gene Regulation and Transcriptomics, ISMB/ECCB
2012–2014	DNA Day Essay Contest Detailed Review Judge for ASHG
2012	Distinguished contributor as a leading reviewer for the journal *Bioinformatics*
2008–2009	Duke Computational Biology & Bioinformatics student committee
2005–current	Member, Gamma Sigma Delta Agricultural Honor Society

Teaching and Mentorship

Teaching

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

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)

Industry Experience

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

Publications in process

* Indicates co-first authorship

Publications

* Indicates co-first authorship

[1] 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.

[2] 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, Kutyavin 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.

[3] **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, Weisdepp 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.

[4] 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.

[5] 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.

[6] *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.

[7] *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.

[8] **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.

[9] 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.

[10] The ENCODE Project Consortium. "An integrated encyclopedia of DNA elements in the human genome." ***Nature*** 2012, 489(7414):57–74. PMID: 22955616.

[11] *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.

[12] *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.

[13] *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.

[14] The ENCODE Project Consortium. "A user's guide to the encyclopedia of DNA elements (ENCODE)." ***PLoS Biology*** 2011, 9(4):e1001046. PMID: 21526222.

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[17] 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.

[18] Georgiev S, **Boyle AP**, Jayasurya K, Mukherjee S, Ohler U. "Evidence-ranked motif identification." ***Genome Biology*** 2010, 11(2):R19. PMID: 20156354.

[19] 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.

[20] 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.

[21] **Boyle AP**, Furey TS. "High-resolution mapping studies of chromatin and gene regulatory elements." ***Epigenomics*** 2009, 1(2):319–329. PMID: 20514362.

[22] **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.

[23] **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.

[24] **Boyle AP**, Boyle JA. "Global analysis of microbial translation initiation regions." In ***Journal of the Mississippi Academy of Sciences***, *Volume 48* 2003:138–150.

[25] **Boyle AP**, Boyle JA. "Visualization of aligned genomic open reading frame data." ***Biochemistry and Molecular Biology Education*** 2003, 31:64–68.

[26] 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

[27] 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).