2017 Palmer Commons
100 Washtenaw Ave.
Ann Arbor, MI 48109-2218
apboyle@umich.edu
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

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: Boyle, Cherry)
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 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 Total Costs: $4,650,000
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.

2018–2023 R01 HD093570 (PI: Bielas; Co-I with Effort)
NIH/NICHD Total Costs: $2,304,265
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.

Completed

2013–2017 R00 HG007356 Pathway to Independence Award (K99/R00) (PI: Boyle)
NIH/NHGRI Total Costs: $987,771
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.

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

2018–current DCM&B Diversity, Equity, & Inclusion Ally
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 *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)
2012–2014	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*
2018	Reviewer for Internal Michigan Searle grants
2015–curent	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 (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 *Bioinformatics*

Teaching and Mentorship

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

W19	Bioinformatics Concepts and Algorithms (BIOINF 529) [Course Director]
S17, S18	Introduction to Biocomputing Bootcamp (BIOSTAT/BIOINF/HUMGEN 606) [2 full days / yr.]
F17, F18	Experimental Genetics Systems (HUMGEN 632) [Course Director]
F15, F16, F17, F18	Gene Structure and Regulation (HUMGEN 541) [3 lectures + 2 discussions / yr.]
F15, W16, F16, W17, F17, W18, F18	Bioinformatics Journal Club (BIOINF 602/603) [Course Director F18]
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	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]
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

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)* *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–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)
NIH Human Genetics Training Program (T32)
Rackham Graduate Student Research Grant (pre-candidate)
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)
NIH Genome Science Training Program (T32)
Rackham Merit Fellow
Rackham Summer Award
Rackham Graduate Student Research Grant (candidate)

Additional Graduate Rotation Students

2019 Margarita Brovkina (Rotation Student, Cellular and Molecular Biology, University of Michigan)
2018 Steve Ho (Rotation Student, Human Genetics, University of Michigan)
2018 Bradley Crone (Rotation Student, Bioinformatics, 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)

Undergraduate and High School Students

2019–current Sarah Haidar (High School, Crestwood High School)
2018–current Monica Holmes (Postbac, University of Michigan)
2016–current 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

2018–current Christine Ziegler (Biological Chemistry, University of Michigan)
2018–current Heming Yao (Bioinformatics, University of Michigan)
2018–current Stephen Carney (Cancer Biology, University of Michigan)
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)

2015–2018 | 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

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] Varshney A, VanRenterghem H, Orchard P, †**Boyle AP**, †Stitzel ML, †Ucar D, †Parker SC. "Cell specificity of regulatory annotations and their genetic effects on gene expression." ***Accepted, Genetics*** 2018.

[2] 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.

[3] 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 RJF, 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.

[4] 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.

[5] *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 RJF, †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.

[6] Nishizaki SS, **Boyle AP**. "Mining the Unknown: Assigning Function to Noncoding Single Nucleotide Polymorphisms." ***Trends in Genetics*** 2017, 33:34–45. PMID: 27939749.

[7] Diehl AG, **Boyle AP**. "Deciphering ENCODE." ***Trends in Genetics*** 2016, 32(4):238–249. PMID: 26962025.

[8] Phanstiel DH, **Boyle AP**, Heidari N, Snyder MP. "Mango: A bias correcting ChIA-PET analysis pipeline." ***Bioinformatics*** 2015. PMID: 26034063.

[9] *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.

[10] *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.

[11] ***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.

[12] 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.

[13] 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.

[14] *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.

[15] *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.

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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.

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[21] *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.

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[27] 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.

[28] 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.

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

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

[34] 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

[35] 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).