Ryan M. Layer, Ph.D.
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Research Interests
Algorithms for human genome interpretation; Parallel and distributed architectures; Succinct data structures; Structural variation; Cancer genomics; Population genetics; Applications of genomics to clinical care

Funding
NIH, R01 Mining Thousands of Genomes to Classify Somatic and Pathogenic Variants 2022-27 (PI)
NIH, K99/R00 Pathway to Independent Award 2017-2023 (PI)
NIH, R01 Characterizing the Landscape and Origin of Hybrid Peptides in Beta Cells 2019-2023 (co-I)
Children's Hospital Colorado, Clinical Exome Analysis Pipeline 2020-2023 (PI)
Intel Corp, Improving Human Health by Making Genomic Data More Accessible 2020-2023 (PI)

Employment
University of Colorado, BioFrontiers Institute, Computer Science, Assistant Professor, 2018-
University of Utah Human Genetics, Postdoctoral Research Assistant, 2015-2018
University of Virginia, Biochemistry and Molecular Genetics, Postdoctoral Fellow, 2014-2015

Education
PhD, University of Virginia, Computer Science, Efficient Genomic Interval Intersection Algorithms, 2014
MCS, Texas A&M University, Computer Science, 2005
BS, Texas A&M University, Computer Science, 2003

Refereed Journal Articles

Null M, Dupuis J, Sheinidashtegol P, Layer RM, Gignoux CR, Hendricks AE. RAREsim: A simulation method for very rare genetic variants. *The American Journal of Human Genetics*. 2022 April 7. 109(680-691)

Aganezov S, Yan SM, Soto DC, Kirsche M, Zarate S, Avdeyev P, Taylor D, Shafin K, Shumate A, Xiao C, Wagner J, McDaniel J, Olson ND, Sauria MEG, Vollger MR, Rhie A, Meredith M, Martin S, Lee J, Koren S, Rosenfeld JA, Paten B, Layer RM, Chin C, Sedlazeck FJ, Hansen NF, Miller DE, Phillippy AM, Miga KH, McCoy RC, Dennis MY, Zook JM, Schatz MC. A complete reference genome improves analysis of human genetic variation. *Science*. 2022 April 1; 376(6588)

Chowdhury M, Pedersen BS, Sedlazeck F, Quinlan AR, Layer RM. Searching thousands of genomes to classify somatic and pathogenic structural variants. *Nature Methods*. 2022 May 26; 19:445-448

Belyeu JR, Chowdhury M, Brown J, Pedersen BS, Cormier MJ, Quinlan AR, Layer RM. Samplot: a platform for structural variant visual validation and automated filtering. *Genome Biology*. 2021 May 25; 22:161

Liu S, Gao G, Layer RM, Thorgaard GH, Wiens GD, Leeds TD, Martin KE, Palti Y. Identification of High-Confidence Structural Variants in Domesticated Rainbow Trout Using Whole-Genome Sequencing. *Frontiers in Genetics.* 2021 February 25; 12

Kanduri C, Sandve GK, Hovig E, De S, Ryan Matthew Layer. Genomic Colocalization and Enrichment Analyses. *Frontiers in Genetics*. 2021 January; 26

Bertolotti AC, Layer RM, Gundappa MK, Gallagher MD, Pehlivanoglu E, Nome T, Robledo D , Kent MP, Røsæg LL, Holen MM, Mulugeta TD , Ashton TJ, Hindar K, Sægrov H, Florø-Larsen B, Erkinaro J, Primmer CR, Bernatchez L, Martin SAM, Johnston IA, Sandve SR Lien S, Macqueen DJ. The structural variation landscape in 492 Atlantic salmon genomes. *Nature Communications*. 2020 October; 11:5176

Carleton JB, Ginley-Hidinger M, Berrett KC, Layer RM, Quinlan AR, Gertz J. Regulatory sharing between estrogen receptor α bound enhancers. *Nucleic Acids Research*. 2020 July; 48(12):6597-610

Abel HJ, Larson DE, Regier AA, Chiang C, Das I, Kanchi KL, Layer RM, Neale RM, Salerno WJ, Reeves C, Buyske S, Matise TC, Muzny DM, Zody MC, Lander ES, Dutcher SK, Stitziel NO, Hall IM. Mapping and characterization of structural variation in 17,795 human genomes. *Nature*. 2020 May 27; 583:83-89

Arumilli M, Layer RM, Hytönen MK, Lohi H. webGQT: A Shiny Server for Genotype Query Tools for Model-Based Variant Filtering. *Frontiers in Genetics*. 2020 March 3; 11:152

Larson DE, Abel HJ, Chiang C, Badve A, Das I, Eldred JM, Layer RM, Hall IM. svtools: population-scale analysis of structural variation. *Bioinformatics*. 2019 June 20; 35(22):4782-7

Havrilla JM, Pedersen BS, Layer RM, and Quinlan AR. A map of constrained coding regions in the human genome. *Nature Genetics.* 2018 December 10; 51:88-95.

Ostrander BEP, Butterfield RJ, Pedersen BS, Farrell AJ, Layer RM, Ward A, Miller C, DiSera T, Filloux FM, Candee MS, Newcomb T, Bonkowsky J, Marth GT, and Quinlan AR. Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy. *Nature Genomic Medicine*. 2018 August; 3(22).

Simovski B, Kanduri C, Gundersen S, Titov D, Domanska D, Bock C, Bossini-Castillo L, Chikina M, Favorov A, Layer RM, Mironov AA, Quinlan AR, Sheffield NC, Trynka G, and Sandve GK. Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. *Nucleic Acids Research*. 2018 June; 46(W1):W186-93.

Belyeu JR, Nicholas TJ, Pedersen BS, Sasani TA, Havrilla JM, Kravitz SN, Conway ME, Lohman BK, Quinlan AR, and Layer RM. SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. *GigaScience*. 2018 July; 7(7).

Layer RM, Pedersen BS, DiSera T, Marth GT, Gertz J, and Quinlan AR. GIGGLE: a search engine for large-scale integrated genome analysis. *Nature Methods*. 2018 January 8; 15:123-6.

Werling DM, Brand H, An JY, Stone MR, Glessner JT, Zhe L, Collins RL, Dong S, Layer RM, Markenscoff-Papadimitriou EC, Farrell A, Schwartz GB, Currall BB, Dea JD, Docherty AR, Duhn C, Erdman C, Gilson M, Handsaker RE, Kashin S, Klei L, Mandell JD, Nowakowski TJ, Liu Y, Pochareddy S, Smith L, Wang HZ, Waterman MJ, He X, Kriegstein AR, Rubenstein JL, Sestan N, McCarroll SA, Neale BM, Coon HC, Willsey AJ, Buxbaum JD, Daly MJ, State MW, Quinlan AR, Marth G, Roeder K, Devlin B, Talkowski ME, and Sanders SJ. An analytical framework for whole genome sequence data and its implications for autism spectrum disorder. *Nature Genetics*. 2018 May; 50:727–736.

Brady SW, McQuerry JA, Qiao Y, Piccolo SR, Shrestha G, Jenkins DF, Layer RM, Pedersen BS, Miller RH, Esch A, Selitsky SR, Parker JS, Anderson LA, Dalley BK, Factor RE, Reddy CB, Boltax JP, Li DY, Moos PJ, Gray JW, Heiser LM, Buys SS, Cohen AL, Johnson WE, Quinlan AR, Marth G, Werner TL,

and Bild AH. Combating subclonal evolution of resistant cancer phenotypes. *Nature communications.* 2017 November 1; 8:1231

Pedersen BS, Layer RM, and Quinlan AR. Vcfanno: fast, flexible annotation of genetic variants. *Genome Biology*. 2016 June 1; 17:118

Layer RM, Kindlon N, Karczewski JK, and Quinlan AR. Efficient genotype compression and analysis of large genetic-variation data sets. *Nature Methods.* 2015 November 9; 13:63-5.

Layer RM and Quinlan AR. A parallel algorithm for N-way interval set intersection. Chiang C, Layer RM, Faust GG, Lindberg MR, Rose DB, Garrison EP, Marth GT, Quinlan AR, and Hall IM. SpeedSeq: Ultra-fast personal genome analysis and interpretation. *Nature Methods*. 2015 August 10; 12:966-8

Mueller AC, Cichewicz MA, Dey BK, Layer R, Reon BJ, Gagan JR, and Dutta A. MUNC: A lncRNA that induces the expression of pro-myogenic genes in skeletal myogenesis. *Molecular and Cellular Biology*. 2014 November 17; MCB. 01079-14.

Layer RM, Chiang C, Quinlan AR, and Hall IM. LUMPY: A probabilistic framework for structural variant discovery. *Genome Biology*. 2014 June 26; 15:R84.

Sun D, Layer RM, Mueller AC, Cichewicz MA, Negishi M, Paschal BM, and Dutta A. Regulation of several androgen-induced genes through the repression of the miR-99a/let-7c/miR-125b-2 miRNA cluster in prostate cancer cells. *Oncogene*. 2013 March 18.
Malhotra A, Lindberg MR, Faust GG, Leibowitz ML, Clark RA, Layer RM, Quinlan AR, and Hall IM, Breakpoint profiling of 64 cancer genomes reveals numerous complex rearrangements spawned by homology-independent mechanisms, *Genome Res*. 2013 May; 23(5):762-76.

Gagan J, Dey BK, Layer RM, Yan Z, Dutta A, Notch3 and Mef2c Are Mutually Antagonistic via Mkp1 and miR-1/206 in Differentiating Myoblasts , *J. Biol. Chem*. 2012 November 23; 287(48):40360-70.

Layer RM, Skadron K, Robins, G Hall IM, Quinlan AR, Binary Interval Search (BITS): A Scalable Algorithm for Counting Interval Intersections, *Bioinformatics*. 2013 January 1; 29(1):1-7.

Shibata Y, Kumar P, Layer RM, Willcox S, Gagan JR, Griffith JD, Dutta A, Extrachromosomal MicroDNAs and Chromosomal Microdeletions in Normal Tissues, *Science*. 2012 April 6; 336(6077):82-6.

Gagan J, Dey BK, Layer RM, Yan A, Dutta A, MICRORNA-378 targets the myogenic repressor MyoR during myoblast differentiation, *J. Biol. Chem*. 2011 June 3; 286(22):19431-8.

Keaton MA, Taylor CM, Layer RM, Dutta A, Nuclear Scaffold Attachment Sites within ENCODE Regions Associate with Actively Transcribed Genes, *PLoS ONE*. 2011 March 14; 6(3):e17912.
Henry M, Layer RM, Zaret D, Coupled Petri Nets for Computer Network Risk Analysis, *International Journal of Critical Infrastructure Protection*. 2010 July; 3(3):67-75.

Conference Proceedings
Layer RM, Sherriff M, Tychonievich L, "Inform, Experience, Implement" - Teaching an Intensive High School Summer Course, *In Proceedings of the 2012 IEEE Frontiers in Education Conference*. IEEE Computer Society, Washington, DC, USA, 1-6.

Henry M, Layer RM, Zaret D, Evaluating the risk of cyber attacks on SCADA systems via Petri net analysis with application to hazardous liquid loading operations, *In Proceedings of the 2009 IEEE*

International Conference on Technologies for Homeland Security. IEEE Computer Society, Washington, DC, USA, 607-14.

Lectures

Leveraging Populations to Interpret Structural Variants. Genome Informatics. Wellcome Genome Campus, Hinxton UK. September 21-23, 2022.

Structural Variant Detection in Animal Populations. Agricultural Genome to Phenome Initiative invited Workshop. December 2, 2021.

Finding and Trusting Structural Variants. University of Colorado Cancer Center Symposium Series. September 8, 2020.
Rapid Structural Variant Visualization with SAMPLOT. 2019 Rocky Mountain Genomics HackCon. Boulder, CO, June 2019

Methods for Exploring Large-Scale Genetic Datasets. Division Research Seminar, Division of Biomedical Informatics and Personalized Medicine. Anschutz Medical Campus, Denver CO, November 2018

STIX: A scalable index for mining large whole-genome sequence cohorts for reliable structural variant population allele frequency estimates. Genome Informatics, Cold Spring Harbor Laboratory, NY, November 2017

STIX: A scalable index for mining large whole-genome sequence cohorts for reliable structural variant population allele frequency estimates. American Society of Human Genetics (ASHG), Orlando, FL, October 2017

GIGGLE: a scalable and fast search engine for large-scale multi-omics data integration. Genome Informatics, Wellcome Genome Campus, UK, September 2016

Exploring Genetic Variation and Genotypes Among Millions of Genomes. Festival of Genomics, San Francisco, CA, November 2015
Exploring Genetic Variation and Genotypes Among Millions of Genomes. The Biology of Genomes, Cold Spring Harbor Laboratory, NY, May 2015

Exploring Genetic Variation and Genotypes Among Millions of Genomes. American Society of Human Genetics (ASHG), San Diego, CA, October 2014

Scaling Genotype-based Genetic Variation Discovery to Millions of Genomes. Genome Informatics, Cambridge, UK, November 2014

SpeedSeq: A 24-hour, open-source variant calling pipeline for clinical genome interpretation. Advances in Genome Biology and Technology (AGBT), Marco Island, FL, February 2014

Book Chapters

Henry MH, Zaret DR, Carr JR, Gordon JD, Layer RM. Cyber-security of SCADA and Other Industrial Control Systems. *Cyber Risk in Industrial Control Systems*. 133-66. Springer International Publishing, 2016.

Technical Reports

Kreuter B, Layer RM, McDaniel M, Robins G, and Skadron K. *Accelerating Genomic Analyses with Parallel Sliding Windows*. University of Virginia, Department of Computer Science Technical Report # CS-2009-14, October 2010.

Patents

Layer RM and Quinlan AR. *System, Method, and Computer Readable Medium for Rapid DNA Identification*. US Patent 20,160,132,640, 2016