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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

Education

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

Employment

University of Utah Human Genetics, Postdoctoral Research Assistant, 2015-present
University of Virginia Biochemistry and Molecular Genetics, Postdoctoral Fellow, 2014-2015
University of Virginia Computer Science Department, Graduate Research Assistant, 2010-2014
University of Virginia Computer Science Department, Graduate Teaching Assistant, 2009-2010
The Johns Hopkins Applied Physics Laboratory, Cyber Security Analyst, 2005-2009

Refereed Journal Articles

- 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

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

Awards and Honors

NIH Cancer Training Grant Postdoctoral Fellow, 2014

University of Virginia Graduate Teaching Assistant Award, 2010-2011

Department of Computer Science Graduate Teaching Assistant Award, 2011

Teaching Experience

LEAD Computer Science Institute, Instructor, 2011-2014

University of Virginia, Introduction to Information Technology, Instructor, 2012

University of Virginia, Introduction to Programming, Teaching Assistant, 2009, 2010

University of Virginia, Program and Data Representation, Teaching Assistant, 2009