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Research Interests	Statistical/computational genetics, machine learning, algorithms and optimization.	
Education	Ph.D. in Computer Science, Georgia State University Mentor: Alexander Zelikovsky	2014
	B.S. in Computer Science, Georgia State University	2007
Professional Experience	Post-doctoral Fellow Dept of Pathology and Laboratory Medicine Institute for Quantitative and Computational Biology (QCB) Geffen School of Medicine University of California, Los Angeles Mentor: Bogdan Pasaniuc <ul style="list-style-type: none">– Bayesian prioritization of susceptibility genes for prostate cancer risk– Genome-wide genetic correlation between complex traits using predicted expression– Partitioning heritability of prostate cancer at known risk loci	2014 – Present
	Intern Division of Viral Hepatitis Centers for Disease Control and Prevention Mentor: Yury Khudyakov <ul style="list-style-type: none">– Error correction of NGS data for heterogeneous virus populations	2012 – 2014
	Graduate Research Assistant & Lecturer Dept of Computer Science Georgia State University Mentor: Alexander Zelikovsky <ul style="list-style-type: none">– Reconstruction and quantification of virus haplotypes from NGS data	2011 – 2014
	Software Engineer Catalyst Technologies Atlanta, Georgia	2007 – 2010
Honors and Awards	NIH T32 Neurogenetics Training Grant UCLA QCB Research Fellowship GSU Second Century Initiative (2CI) Research Fellowship ISBRA 2013 NSF Travel Grant GSU Molecular Basis for Disease Research (MBD) Fellowship 17th Summer Institute in Statistical Genetics (SIG 2012) Tuition Scholarship ISBRA 2012 NSF Travel Grant	July 2018 – Present June 2016 – June 2018 Sept 2012 – August 2014 May 2013 Sept 2011 – Sept 2012 May 2012 May 2012

Articles

17. *Probabilistic fine-mapping of transcriptome-wide association studies.* Mancuso N, M Freund, Johnson R, Shi H, Kichaev G, Gusev A, Pasaniuc B. **Nature Genetics.** 2019 (in press).
16. *Transcriptome-wide association study identifies new prostate cancer susceptibility genes in the OncoArray data.* Mancuso N, Gayther S, Gusev A, Zheng W, Penney KL, the PRACTICAL consortium, CRUK, BPC, CAPS, PEGASUS, Kote-Jarai Z, Eeles R, Freedman M, Haiman C, Pasaniuc B. **Nature Communications.** 2018.
15. *Genome-wide meta-analysis of gene-environmental interaction for insulin-resistance phenotypes and breast cancer risk in postmenopausal women.* Jung, SY, Mancuso, N, Yu, H, Papp, J, Sobel, EM, Zhang, ZF. **Cancer Prevention Research.** 2018.
14. *Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights.* Gusev A, Mancuso N, Won H, Finucane HK, Reshef Y, Song L, Safi A, Oh E, Schizophrenia Working Group of the Psychiatric Genomics Consortium, McCarroll S, Neale B, Ophoff R, O'Donovan MC, Katsanis N, Geschwind DH, Crawford GE, Sullivan PF, Pasaniuc B* and Price AL*. **Nature Genetics.** 2018.
13. *Appetite, cachexia regulator, and placental gene GDF15 associated with nausea and vomiting of pregnancy and hyperemesis gravidarum.* Fejzo MS, Sazonova OV, Sathirapongsasuti JF, Hallgrímsson IB, Vacic V, MacGibbon KW, Schoenberg FP, Mancuso N, Slamon DJ, Mullin PM. **Nature Communications.** Volume 9, Issue 1, 2018.
12. *Targeted mutagenesis in a human-parasitic nematode.* Gang SS, Castelletto ML, Bryant AS, Yang E, Mancuso N, Lopez JB, Pellegrini M, Hallem EA. **PLoS Pathogens.** 13.10, 2017
11. *Local genetic correlation gives insights into the shared genetic architecture of complex traits.* Shi H, Mancuso N, Spendlove S, and Pasaniuc B. **The American Journal of Human Genetics.** Volume 101, Issue 5, p737-751, 2017.
10. *A multi-stage genome-wide association study of uterine fibroids in African Americans.* Hellwege JN, Jeff JM, Wise LA, Gallaghe CS, Wellons M, Hartmann KE, Jones SF, Torsten-son ES, Dickinson S, Ruiz-Narváez EA, Rohland N, Allen A, Reich D, Tandon A, Pasaniuc B, Mancuso N, Im HK, Hinds DA, Palmer JR, Rosenberg L, Denny JC, Roden DM, Stewart EA, Morton CC, Kenny EE, Edwards TL, Velez Edwards DR. **Human Genetics.** 2017 Aug 23.
09. *Enhanced methods to detect haplotypic effects on gene expression.* Brown R, Kichaev G, Mancuso N, Boockch J, Pasaniuc B. **Bioinformatics.** 2017.
08. *Integrating gene expression with summary association statistics to identify susceptibility genes for 30 complex traits.* Mancuso N, Shi H, Goddard P, Kichaev G, Gusev A*, Pasaniuc B*. **American Journal of Human Genetics.** Volume 100, Issue 3, p473–487, 2 March 2017. **Included in Best of AJHG 2016-2017.**
07. *The contribution of rare variation to prostate cancer heritability.* Mancuso N*, Rohland N*, Rand K, Tandon A, Allen A, Quinque D, Mallick S, Li H, Stram A, Sheng X, Kote-Jarai Z, Easton DF, Eeles RA, the PRACTICAL consortium, Le Marchand L, Lubwama A, Stram D, Watya S, Conti D, Henderson B, Pasaniuc B, Haiman C, Reich D. **Nature Genetics.** 2016, Volume 48.
06. *Accurate viral population assembly from ultra-deep sequencing data.* Mangul S, Wu NC, Mancuso N, Zelikovsky A, Sun R, Eskin E. **Bioinformatics.** 2014, Volume 30.
05. *Reconstruction of Viral Population Structure from Next-Generation Sequencing Data Using Multicommodity Flows.* Skums P*, Mancuso N*, Artyomenko A*, Tork B, Măndoiu I, Khudyakov Y, and Zelikovsky A. **BMC Bioinformatics.** 2013, 14(Suppl 9):S2.
04. *kGEM: An Expectation Maximization Error Correction Algorithm for Next Generation Sequencing of Amplicon-based Data.* Artyomenko A*, Mancuso N*, Skums P, Măndoiu I,

Zelikovsky A. **Conf Proc 9th International Symposium on Bioinformatics Research and Applications**. 2013.

03. *Inferring Viral Quasispecies Spectra from Shotgun and Amplicon 454 Pyrosequencing Reads*. Astrovskaya I*, Mancuso N*, Tork B, Mangul S, Artyomenko A, Skums P, Ganova-Raeva L, Măndoiu I, and Zelikovsky A. **Genome Analysis: Current Procedures and Applications**. 2013. (book chapter)
02. *Reconstructing Viral Quasispecies from NGS Amplicon Reads*. Mancuso N, Tork B, Skums P, Ganova-Raeva L, Măndoiu I, and Zelikovsky A, **In Silico Biology**. Volume 11, 5. 2012.
01. *EDR2: A Sink Failure Resilient Approach for WSNs*. Valero M, Xu M, Mancuso N, Song W, and Beyah R. **Conf Proc IEEE International Conference on Communications (ICC)**. 2012.
00. *Viral Quasispecies Reconstruction from Amplicon 454 Pyrosequencing Reads*. Mancuso N, Tork B, Măndoiu I, Zelikovsky A, Skums P. **Conf Proc IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)**. 2011.

Posters / Presentations

16. *Transcriptome-wide association study identifies new prostate cancer susceptibility genes in the OncoArray data*. Mancuso N, Zheng W, Penney K, The PRACTICAL Consortium, Kote-Jarai Z, Haiman C, Gayther S, Freedman M, Pasaniuc B. **American Association for Cancer Research**. 2017.
15. *Probabilistic assignment of causal genes at transcriptome-wide significant risk loci*. Mancuso N, Kichaev G, Shi H, Giambartolomei C, Gusev A, Pasaniuc B. **American Society for Human Genetics**. 2017.
14. *Enhanced methods to investigate the role of Trans-eQTL to complex traits*. Giambartolomei C, Mancuso N, Shi H, Strober B, Battle A, Pasaniuc B. **American Society for Human Genetics**. 2017.
13. *Quantifying the shared genetic components of complex traits and Mendelian phenotypes*. Kumar M, Arboleda B, Shi H, Mancuso N, Pasaniuc B. **American Society for Human Genetics**. 2017.
12. *Local genetic correlation gives insights into the shared genetic architecture of complex traits*. Shi H, Mancuso N, Spendlove S, Pasaniuc B. **American Society for Human Genetics**. 2017.
11. *Probabilistic assignment of causal gene expression in GWAS risk loci*. Mancuso N, Kichaev G, Shi H, Giambartolomei C, Gusev A, Pasaniuc B. **RECOMB-Genetics**. 2017.
10. *Transcriptome-wide association study of thirty complex traits reveals novel risk genes*. Kichaev G, Mancuso N, Shi H, Goddard P, Gusev A, Pasaniuc B. **American Society for Human Genetics**. 2016.
09. *Computational discovery of epigenetic mediators in Alzheimer's disease from imputed methyome-wide association statistics*. Park Y, Sarkar A, Mancuso N, Gusev A, Pasaniuc B, Kellis M. **Biology of Genomes**. 2016.
08. *Methods to Detect Haplotype to Phenotype Associations*. Brown R, Kichaev G, Mancuso N, Pasaniuc B. **RECOMB-Genetics**. 2016.
07. *Enhanced methods for gene expression imputation from genetic variation data*. Mancuso N, Shi H, Gusev A, and Pasaniuc B. **RECOMB-Genetics**. 2016.
06. *Enhanced methods for gene expression imputation from genetic variation data*. Mancuso N, Shi H, Gusev A, and Pasaniuc B. **American Society for Human Genetics**. 2015.

05. *Inferring HIV Quasispecies from Paired-End Reads*. Mangul S, Wu N, Mancuso N, Zelikovsky A, Sun R, Eskin E. **International Conference on Research in Computational Molecular Biology (RECOMB)**. 2013.
04. *Quasispecies Spectrum Reconstruction using Multi-commodity Flows*. Mancuso N, Tork B, Skums P, Măndoiu I, Zelikovsky A. **RECOMB Satellite Workshop on Massively Parallel Sequencing**. 2012.
03. *An Integer Programming Approach to Novel Transcript Reconstruction from Paired-End RNA-Seq Reads*. Mangul S, Caciula A, Mancuso N, Măndoiu I, Zelikovsky A. **International Conference on Research in Computational Molecular Biology**. 2012.
02. *Multi-Commodity Flow Methods for Quasispecies Spectrum Reconstruction Given Amplicon Reads*. Mancuso N, Tork B, Skums P, Măndoiu I, Zelikovsky A. **8th International Symposium on Bioinformatics Research and Applications (ISBRA)**. 2012.
01. *A Maximum Likelihood Method for Quasispecies Spectrum Assembly*. Mancuso N, Tork B, Skums P, Ganova-Raeva L, Măndoiu I, Zelikovsky A. **Proc. 2nd Workshop on Computational Advances for Next Generation Sequencing (CANGS)**. 2012.

Teaching Experience

R Workshop (QCB UCLA)

A 3-day workshop introducing attendees to the basics of data analysis with R. Topics include: reading/writing data, logical control flows, querying data frames, plotting, and basics of differential gene expression analysis with DE-Seq2.

CSc 2510 Theoretical Foundations for Computer Science (GSU, Fall 2013)

This course covers the basic theoretical foundations required to study various sub-disciplines in computer science. Topics include: propositional and predicate logic; induction and its application in proving correctness and termination of programs; recurrence relations, combinatorics, and graph theory with applications to analysis of algorithms; sets, relations, and functions and their applications in databases, functional programming, and automata.

CSc 7351 UNIX/C for Bioinformatics (GSU, Fall 2011, Spring 2012)

An introduction to a high-level programming language and basic data structures with a structured approach to problem solving, algorithmic analysis, and program development with applications in Bioinformatics.

CSc 3320 System-Level Programming (GSU, Fall 2011)

This course provides an introduction to programming at the level of the operating system. Topics include editors, system calls, programming tools, files, processes, interprocess communication, and shells.

CSc 2010 Intro to Computer Science (GSU, Summer 2010) This course provides an introduction to the discipline of computer science. Topics include algorithmic foundations, hardware concepts, virtual machine concepts, software systems, applications, and social issues.

Software

FIZI

- Python library and software to impute GWAS summary statistics using reference LD and functional information.
- <http://github.com/bogdanlab/fizi>

FOCUS

- R package to probabilistically fine-map gene-trait associations from transcriptome-wide association studies.
- <http://github.com/bogdanlab/FOCUS>

RHOGE

- R package to compute the genome-wide genetic correlation between two complex traits at the level of predicted expression using TWAS summary statistics.
- <http://github.com/bogdanlab/RHOGE>

VirA: Viral Population Assembler from Amplicon-based data

- Pipeline that combines alignment, error-correction (local reconstruction), and global reconstruction of a viral quasispecies given Amplicon-based reads.
- Reconstruction methods: Maximum-Bandwidth Paths or Multi-commodity Flows.
- <http://alan.cs.gsu.edu/vira>

kGEM: Error Correction of Amplicon-based data

- Clustering and EM-based method for correcting sequencing errors in Amplicon-based reads.
- <http://alan.cs.gsu.edu/KGEM.jar>

Approximation Algorithms Library for Graphs and Networks

- Implemented modern approximation algorithms for NP-Hard optimization problems in graphs and networks.
- Merged into popular open-source module NetworkX.
- <https://bitbucket.org/nmancuso/apxa/>
- <http://networkx.github.com/>

**Other
Contributions****Reviewer / Referee Service**

- Reviewer for Nature Communications, Genetics, PLOS Genetics, Human Genetics, Bioinformatics, BMC Bioinformatics, ISMB, and ACM-BCB.