Joshua T. Burdick, Ph.D.

CONTACT INFORMATION	*Mail:* 295 Hiscock St., Ann Arbor, MI 48103 *Voice:* 610-457-2120 *E-mail:* `josh.t.burdick@gmail.com`

RESEARCH INTERESTS

RNA transcription and modification, algorithms, Bayesian statistics, genomics.

EDUCATION

University of Pennsylvania, Philadelphia, Pennsylvania USA

Ph.D., Genomics and Computational Biology, December 2015

- Dissertation Topic: "Regulation of Gene Expression in the *C. elegans* embryo"
- Advisor: John Isaac Murray

University of Pennsylvania, Philadelphia, Pennsylvania USA

M.S.E., Computer and Information Science, 2002

Swarthmore College, Swarthmore, Pennsylvania USA

B.A., Computer Science, May, 1995
B.A., Music, May, 1995

RESEARCH EXPERIENCE

Research programmer   October 2020 - present
Vivian Cheung lab, University of Michigan, Ann Arbor, Michigan USA
Computed and combined features of high-throughput datasets across the genome. Plotted RNA nanopore sequence traces.

Research programmer   September 2016 - October 2020
Vivian Cheung lab, HHMI, University of Michigan, Ann Arbor, Michigan USA
Identified peaks and allele-specific expression in high-throughput sequencing data. Combined multiple data sets to better understand aspects of RNA biology including PolII pausing and abasic sites.

Postdoctoral researcher   January 2016 - May 2016
John Isaac Murray lab, University of Pennsylvania, Philadelphia, Pennsylvania USA
Optimized performance of an existing Java image processing application, and refactored it to read multiple image formats.

Graduate Student   September 2007 - December 2015
University of Pennsylvania, Philadelphia, Pennsylvania USA
Developed deconvolution methods using sampling and expectation propagation. Annotated groups of tissue-specific genes with motif enrichment. Coursework included statistics, cell biology, and genomics.

Research Programmer   September 2001 - September 2007
Children's Hospital of Philadelphia, Philadelphia, Pennsylvania USA
Developed and implemented statistical methods to relate genotype and expression data.

Graduate Student   September 1995 - September 1997
University of Maryland, College Park, Maryland USA
Included graduate coursework in neural networks, approximation algorithms, and lower

bounds in computational complexity. Teaching assistant for introductory Pascal, C, and functional programming classes.

PUBLICATIONS Liu Y, Rodriguez Y, Ross RL, Zhao R, Watts JA, Grunseich C, Bruzel A, Li D, **Burdick JT**, Prasad R, Crouch RJ, Limbach PA, Wilson SH, Cheung VG. RNA abasic sites in yeast and human cells. Proc Natl Acad Sci U S A. 2020 Aug 25;117(34):20689-20695.

Watts JA, **Burdick J**, Daigneault J, Zhu Z, Grunseich C, Bruzel A, Cheung VG. *cis* Elements that Mediate RNA Polymerase II Pausing Regulate Human Gene Expression. Am J Hum Genet. 2019 Oct 3;105(4):677-688.

Wang IX, Grunseich C, Fox J, **Burdick J**, Zhu Z, Ravazian N, Hafner M, Cheung VG. Human proteins that interact with RNA/DNA hybrids. Genome Research. 2018 Sep 1;28(9):1405-14.

Grunseich C, Wang IX, Watts JA, **Burdick JT**, Guber RD, Zhu Z, Bruzel A, Lanman T, Chen K, Schindler AB, Edwards N, Ray-Chaudhury A, Yao J, Lehky T, Piszczek G, Crain B, Fischbeck KH, Cheung VG. Senataxin Mutation Reveals How R-Loops Promote Transcription by Blocking DNA Methylation at Gene Promoters. Mol Cell. 2018 Feb 1;69(3):426-437.

Burdick JT, Walton T, Preston E, Zacharias AL, Raj A, Murray JI. Overlapping cell population expression profiling and regulatory inference in *C. elegans*. BMC Genomics. 2016;17:159.

Richards JL, Zacharias AL, Walton T, **Burdick JT**, Murray JI. A quantitative model of normal *Caenorhabditis elegans* embryogenesis and its disruption after stress. Dev Biol. 2013 Feb 1;374(1):12–23.

Burdick JT, Murray JI. Deconvolution of gene expression from cell populations across the *C. elegans* lineage. BMC Bioinformatics. 2013;14:204.

Burdick JT, Chen W-M, Abecasis GR, Cheung VG. *In silico* method for inferring genotypes in pedigrees. Nat Genet. 2006 Sep;38(9):1002–4.

Cheung VG, Spielman RS, Ewens KG, Weber TM, Morley M, **Burdick JT**. Mapping determinants of human gene expression by regional and genome-wide association. Nature. 2005 Oct 27;437(7063):1365–9.

Smirnov DA, **Burdick JT**, Morley M, Cheung VG. Method for manufacturing whole-genome microarrays by rolling circle amplification. Genes, Chromosomes and Cancer. 2004 May;40(1):72–7.

Watts JA, Morley M, **Burdick JT**, Fiori JL, Ewens WJ, Spielman RS, et al. Gene expression phenotype in heterozygous carriers of ataxia telangiectasia. Am J Hum Genet. 2002 Oct;71(4):791–800.

COMPUTER SKILLS
- Languages: Python, R, Java, C. Some Javascript, Haskell, Perl, and C++.
- Bioinformatics tools: Bioconductor, samtools, bedtools, igv, relevant Python packages (numpy, matplotlib, pandas, pybedtools, pysam, deepTools)
- Operating systems: Unix/Linux, familiarity with Mac OS X and Windows.
- Sample source code available at `https://github.com/joshtburdick`