

# Joshua T. Burdick

University of Pennsylvania  
Genomics and Computational Biology

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## Education

B.S. Computer Science, Swarthmore College, 1995. *also* B.A. Music.

Graduate studies, Computer Science, University of Maryland, College Park, 1995–1997.

M.S.E. Computer and Information Science, University of Pennsylvania, 2002.

Ph.D. Genomics and Computational Biology, University of Pennsylvania, *expected* 2014.

*Committee:* Russ Carstens, Shane Jensen, and Junhyong Kim.

## Employment

### *University of Maryland, College Park, Department of Computer Science*

Teaching Assistant, Introduction to Programming (C and Pascal), 1995–1996.

Teaching Assistant, Introduction to Programming Languages, Alex Dekhtyar, Summer 1996.

Teaching Assistant, Introduction to Algorithms, Dana Nau, Spring 1997.

### *The Franklin Institute, Philadelphia, PA*

Java programmer, April 1998 – March 1999. Assisted with Java and VRML development for a multi-user virtual training environment. Used Java RMI to implement a client-server message-passing protocol.

### *Children's Hospital of Philadelphia / University of Pennsylvania*

Research Assistant, laboratory of Vivian Cheung, 1999–2007. Maintained local copies of several genomic databases using Perl and SQL. Analyzed and visualized experiment results using SQL, Perl CGI, Java, C++, and R. Located locally-sequenced DNA in public databases using BLAT and BLAST.

## Research

### *Publications*

Burdick JT, Chen WM, Abecasis GR and Cheung VG (2006). In silico method for inferring genotypes in pedigrees. *Nat Genet* 38:1002-4.

Smirnov DA, Burdick JT, Morley M, Cheung VG (2004). Method for manufacturing whole-genome microarrays by rolling circle amplification. *Genes, Chromosomes & Cancer* 40:72-77.

Watts JA, Morley M, Burdick JT, Fiori JL, Ewens WJ, Spielman RS, Cheung VG (2001). Gene expression phenotype in heterozygous carriers of ataxia telangiectasia. *Amer. J. Hum. Genet.* 71: 791-800.

Morley M, Arcaro M, Burdick J, Yonescu R, Reid T, Kirsch IR, Cheung VG (2001). GenMapDB: a database of mapped human BAC clones. *Nucleic Acids Research* 29(1): 144-147.

### *Working Papers*

Gapped RNA-Seq alignment using Burrows-Wheeler indexes.

Finding triangles in 6-vertex graphs requires 21 NAND gates. Available online at

<http://www.cs.umd.edu/~gasarch/BLOGPAPERS/burdick1.pdf> (part 1) and

<http://www.cs.umd.edu/~gasarch/BLOGPAPERS/burdick2.pdf> (part 2).

### *Scientific Software*

Genotype inference: a C++ program for inferring genotypes in pedigrees (2006).

Last updated: May 26, 2010