

Serafim Batzoglou

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EDUCATION

Massachusetts Institute of Technology, Cambridge, Massachusetts.

- S.B. in Mathematics, S.B. in Computer Science, June 1996
- Masters of Engineering in Electrical Engineering and Computer Science, June 1996
- Ph.D. in Computer Science, June 2000.

Fellowships: Merck/MIT; Program in Mathematics and Molecular Biology.

ACADEMIC APPOINTMENTS

Research Scientist, Whitehead Institute/MIT Genome Center, April 2000-August 2001

Assistant Professor of Computer Science, Stanford University, September 2001 - May 2008.

Associate Professor of Computer Science, Stanford University, May 2008 - present.

SELECTED PUBLICATIONS (out of about 80 publications)

1. Salari R, Saleh SS, Kashef-Haghighi D, Khavari D, Newburger DE, West RB, Sidow A, Batzoglou S. Inference of tumor phylogenies with improved somatic mutation discovery. In Proceedings of RECOMB 2013, 249-263, 2013.
2. Rodriguez JM, Bercovici S, Elmore M, Batzoglou S. Ancestry inference in complex admixtures via variable-length Markov chain linkage models. In Proceedings of RECOMB 2012, 12-28, 2012.
3. Gerstein MB, Kundaje A, et al. Architecture of the human regulatory network derived from ENCODE data. *Nature* 489: 91-100, 2012.
4. Kyriazopoulou-Panagiotopoulou S, Kashef-Haghighi D, Aerni SJ, Sundquist A, Bercovici S, Batzoglou S. Reconstruction of genealogical relationships with application to Phase III of HapMap. *Bioinformatics*. 2011 Jul 1;27(13):i333-41.
5. Sundquist A, Fratkin E, Do CB, Batzoglou S. Effect of genetic divergence in identifying ancestral origin using HAPAA. *Genome Research* 18:676-682, 2008.
6. Sundquist A, Ronaghi M, Tang H, Pevzner P, Batzoglou S. Whole-genome sequencing and assembly with high-throughput short-read technologies. *PLOS One* 2(5): e484, 2007.
7. Flannick J, Novak A, Srinivasan BS, McAdams HH, Batzoglou S. Graemlin: general and robust alignment of multiple large interaction networks. *Genome Research*, 16:1169-1181, 2006.
8. Gross SS, Do CB, Sirota M, Batzoglou S. CONTACT: A discriminative, phylogeny-free approach to multiple informant de novo gene prediction. *Genome Biology* 8:R269, 2007.
9. Do CB, Woods DA, Batzoglou S. CONTRAfold: RNA Secondary Structure Prediction without Physics-Based Models. *Special Issue on the Proceedings of the ISMB2006, Bioinformatics* 22:e90-98, 2006. Best Paper Award, ISMB 2006.
10. Do CB, Mahabhashyam MS, Brudno M, Batzoglou S. ProbCons: probabilistic consistency-based multiple sequence alignment. *Genome Research* 15:330-340, 2005. Abstract in ISMB/ECCB 2004, Best Paper Award.
11. Davydov EV, Goode DL, Sirota M, Cooper GM, Sidow A, Batzoglou S. Identifying a high fraction of the human genome to be under selective constraint using GERP++. *PLoS Computational Biology* 6: e1001025, 2010.
12. Brudno M, Do C, Cooper GM, Kim MF, Davydov E, NISC Comparative Sequencing Program, Green ED, Sidow A, Batzoglou S. LAGAN and Multi-LAGAN: Efficient tools for large-scale multiple alignment of genomic DNA. *Genome Research* 13: 721-731, 2003.
13. Batzoglou S, Jaffe D, Stanley K, Butler J, Gnerre S, Mauceli E, Berger B, Mesirov JP, Lander ES. ARACHNE: A whole genome shotgun assembler. *Genome Research* 12:177-189, 2002.