

Noah A. Zaitlen

Department of Bioinformatics
University of California, San Diego
Powell Focht Bioengineering Hall
Room 228, Mail Code 0419
9500 Gilman Drive
La Jolla, CA 92093-0419

Cell: (858) 531-9675
Office: (310) 206-4490
Fax: (310) 825-2273 Email: nzaitlen@ucsd.edu
Homepage: <http://bioinf.ucsd.edu/~nzaitlen>
Date of Birth: December 25, 1977
Citizenship: United States

Research Interests

Primary: Computational and statistical genetics with emphasis on methods development related to the discovery of genetic basis of complex human disease and understanding the structure of genetic variation in populations. *Secondary:* Computational immunology, genomics, machine learning.

Education

Ph.D., Bioinformatics and Systems Biology, **University of California, San Diego**, 2009.

Committee: Eleazar Eskin, Pavel Pevzner, Vineet Bafna, Nicholas Schork, and Daniel O'Connor.

M.S., Bioinformatics, **University of California, San Diego**, 2006.

B.A., Mathematics (with Honors), **University of California, Berkeley**, 2001.

B.A., Computer Science (with Honors), **University of California, Berkeley**, 2001.

B.A. Cognitive Science (with Honors), **University of California, Berkeley**, 2001.

Honors & Awards

Microsoft Research Fellowship: University of California, San Diego. September 2006.

Best Poster Award: Welcome Trust Conference on the Genomics of Common Diseases. July 2007.

Dean's Honor List: University of California, Berkeley. Spring 1998.

Work Experience

Graduate Student Researcher: Department of Bioinformatics.

University of California, San Diego. September 2003 - present.

Research Intern: Machine Learning and Applied Statistics Group.

Microsoft Research. June 2006 - December 2006.

Mathematical Finance Intern: Fixed Income Division.

Morgan Stanley. May 2004 - September 2004.

Bioinformatics Programmer: Bioinformatics Division.

Centre National de Genotypage. November 2001 - May 2003.

Research Assistant: Department of Electrical Engineering and Computer Science.

University of California, Berkeley. May 1999 - October 1999.

Teaching Experience

Teaching Assistant: Graduate Bioinformatics II: Sequence and Structure Analysis - Methods and Applications. University of California, San Diego. Shankar Subramanian & Pavel Pevzner, Spring 2007.

Teaching Assistant: Molecular Sequence Analysis. University of California, San Diego. Pavel Pevzner, Spring 2006.

Instructor: Introduction to Physics. San Quentin Prison Education Program. Winter 1998 - Spring 2000.

Instructor: Computers for Kids. San Leandro Housing Projects Computer Education Center. Fall 2000 - Spring 2001.

Publications

Refereed Journal Papers

1. Erin N. Smith, Ph.D., Cinnamon S Bloss, Judith A Badner, Thomas Barrett, Pamela L Belmonte, Wade Berrettini, William Byerley, William Coryell, David Craig, Howard J Edenberg, Tatiana M Foroud, Elliot Gershon, Tiffany A Greenwood, Maria Hipolito, Daniel L Koller, William B Lawson, Chunyu Liu, Falk W Lohoff, Melvin G McInnis, Francis J McMahon, Caroline Nievergelt, John Nurnberger, Evaristus A Nwulia, James B Potash, John Rice, Thomas G Schulze, William Scheftner, Corrie Panganiban, Noah Zaitlen, Peter P Zandi, Sebastian Zollner, Nicholas J Schork, and John R Kelsoe. "Genome-Wide Association Study of Bipolar Disorder in European American and African American Individuals." (**in submission**), 2009.
2. Noah A. Zaitlen, Buhm Han, and Eleazar Eskin. "Powerful and Accurate Imputation Aware Meta-Analysis." (**in preparation**), 2009.
3. Noah A. Zaitlen, Hyun Min Kang, and Eleazar Eskin. "Linkage effects and analysis of finite sample errors in the HapMap." **Human Heredity (in press)**, 2009.
4. Chiara Sabatti, Susan K Service, Anna-Liisa Hartikainen, Anneli Pouta, Samuli Ripatti, Jae Brodsky, Chris G Jones, Noah A Zaitlen, Teppo Varilo, Marika Kaakinen, Ulla Sovio, Aimo Ruokonen, Jaana Laitinen, Eveliina Jakkula, Lachlan Coin, Clive Hoggart, Andrew Collins, Hannu Turunen, Stacey Gabriel, Paul Elliot, Mark I McCarthy, Mark J Daly, Marjo-Riitta Javelin, Nelson B Freimer, & Leena Peltonen. "Genome-wide association analysis of metabolic traits in a birth cohort from a founder population." **Nature Genetics 41:35-46**, 2008.
5. Hyun Min Kang, Noah A. Zaitlen, Claire M. Wade, Andrew Kirby, David Heckerman, Mark J. Daly, and Eleazar Eskin. "Efficient Control of Population Structure in Model Organism Association Mapping." **Genetics. 178(3):1709-23**, 2008.
6. Buhm Han, Hyun Min Kang, Myeong Seong Seo, Noah A. Zaitlen, and Eleazar Eskin, "Efficient association study via power-optimized tag SNP selection." **Annals of Human Genetics 72:834-47**, 2008.
7. Noah Zaitlen, Manuel Reyes-Gomez, David Heckerman, Nebojsa Jojic. "Shift-Invariant Adaptive Double Threading: Learning MHC II Peptide Binding." **Journal of Computational Biology. 15(7): 927-942**, 2008.

8. Noah Zaitlen, Hyun Min Kang, Eleazar Eskin, Eran Halperin. “Leveraging the HapMap Correlation Structure in Association Studies.” **American Journal of Human Genetics**. **80(4):683-91**, 2007.
9. Noah Zaitlen, Hyun Min Kang, Michael Feolo, Stephen Sherry, Eran Halperin, Eleazar Eskin. “Inference and Analysis of Haplotypes from Combined Genotyping Studies Deposited in dbSNP.” **Genome Research**. **15(11):1594-600**, 2005.

Refereed Conference Papers

10. Hyun Min Kang, Noah Zaitlen, Buhm Han, Eleazar Eskin. “An adaptive and memory efficient algorithm for genotype imputation.” *In Proceedings of the Thirteenth Annual Conference on Research in Computational Biology (RECOMB-2009)*.
11. Noah Zaitlen, Arthur Choi, Buhm Han, Knot Pipatsrisawat, Adnan Darwiche, Eleazar Eskin. “Efficient Genome Wide Tagging by Reduction to SAT.” *In Proceedings of the 8th Workshop on Algorithms in Bioinformatics (WABI-2008)*. Universitt Karlsruhe, Germany: September 15-17, 2008.
12. Sean ORourke, Noah Zaitlen, Nebojsa Jojic, Eleazar Eskin. “Reconstructing the Phylogeny of Mobile Elements.” *In Proceedings of the Eleventh Annual Conference on Research in Computational Biology (RECOMB-2007)*. Oakland, CA: April 21st-25th, 2007.
13. Noah Zaitlen, Manuel Reyes-Gomez, David Heckerman, and Nebojsa Jojic. “Shift-Invariant Adaptive Double Threading: Learning MHC II - Peptide Binding.” *In Proceedings of the Eleventh Annual Conference on Research in Computational Biology (RECOMB-2007)*. Oakland, CA: April 21st-25th, 2007.
14. Sean ORourke, Noah Zaitlen, Nebojsa Jojic, Eleazar Eskin. “Reconstructing the Phylogeny of Mobile Elements.” *In Proceedings of the NIPS 2006 Workshop on New Problems and Methods in Computational Biology*. Whistler, CA: December 8th-9th, 2006.

Invited Talks and Conference Presentations

- “Powerful and Accurate Imputation Aware Meta-Analysis.” *GAIN III Analysis Workshop*. November 10-11, 2008.
- “Powerful Imputation Aware Meta-Analysis of Genome Wide Association Studies.” *Human Genome Variation Meeting*. October 17th, 2008.
- “Optimal Genome Wide Tagging by Reduction to SAT.” *University of the Basque Country, San Sebastian*. June 28th, 2008.
- “Shift-Invariant Adaptive Double Threading: Learning MHC II - Peptide Binding.” *University of California, Berkeley*. April 2007.
- “Shift-Invariant Adaptive Double Threading: Learning MHC II - Peptide Binding.” *University of California, Los Angeles*. March 2007.
- “Reconstructing the Phylogeny of Mobile Elements.” *University of California, Los Angeles*. March 2007.

Conference and Journal Reviewing

Journal Referee: *Bioinformatics*, 2009.

Journal Referee: *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2009.

Journal Referee: *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2008.

Conference Reviewer: *The Thirteenth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2009)*, 2009.

The Seventeenth Annual International Conference on Intelligent Systems for Molecular Biology (ISMB-2009), 2009.

Advances in Neural Information Processing Systems 21 (NIPS-2008), 2008.

The Twelfth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2008), 2008.

The Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology (ISMB-2007), 2007.

The Eleventh Annual International Conference on Research in Computational Molecular Biology (RECOMB-2007), 2007.

2006 LSS Computational Systems Bioinformatics Conference, (CSB-2006), 2006.

Software Developed and Released

WHAP: Weighted haplotype association testing leverages the HapMap data to improve the power of association studies.

SIADT MHCII: Shift invariant adaptive double threading based peptide binding predictor for MHC Class II proteins.

SATtag: Optimal SNP tag selection minimizes the number of SNPs required for a “complete” tag set using a SATisfiability approach.

dbSNP Haplotypes: The structure and phased data for the complete set of genotype data stored at dbSNP.

Athletics

Climbing, Surfing, Crossfit

References

Eleazar Eskin
Assistant Professor of Computer Science and
Human Genetics
University of California, Los Angeles
eeskin@cs.ucla.edu

Eran Halperin
Assistant Professor of Computer Science
Tel-Aviv University
heran@icsi.berkeley.edu

David Heckerman
Manager, eScience Research Group
Microsoft Research
heckerma@microsoft.com

Nicholas Schork
Professor and Director of Research
Scripps Genomic Medicine
nschork@scripps.edu

Vineet Bafna
Associate Professor of Computer Science
University of California, San Diego
vbafna@cs.ucsd.edu

Shankar Subramaniam
Professor and Chair of Bioengineering
University of California, San Diego
shankar@sdsc.edu

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